

International Meeting on Emerging Diseases and Surveillance

Vienna, Austria • February 15-18, 2013

Co-sponsored by

ProMED-mail, the Program for Monitoring Emerging Diseases EcoHealth Alliance European Centre for Disease Prevention and Control (ECDC) European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Food and Agriculture Organization of the United Nations (FAO) HealthMap Skoll Global Threats Fund (SGTF) World Organisation for Animal Health (OIE)



Organized by the International Society for Infectious Diseases

FINAL PROGRAM

16th International Congress on Infectious Diseases

CAPE TOWN • SOUTH AFRICA APRIL 2~5, 2014





Organized by the International Society for Infectious Diseases



In collaboration with the Federation of Infectious Diseases Societies of Southern Africa



International Meeting on Emerging Diseases and Surveillance

Co-sponsored by

ProMED-mail, the Program for Monitoring Emerging Diseases EcoHealth Alliance European Centre for Disease Prevention and Control (ECDC) European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Food and Agriculture Organization of the United Nations (FAO) HealthMap Skoll Global Threats Fund (SGTF)

World Organisation for Animal Health (OIE)



Organized by the International Society for Infectious Diseases

FINAL PROGRAM

International Meeting on Emerging Diseases and Surveillance 2013

Welcome	. I
Committees	. 2
General Information	.4
Floorplans Hilton Vienna	. 6
Program-at-a-Glance	.7
Scientific Program	. 8
Friday, February 15, 2013	. 8
Saturday, February 16, 2013	.9
Sunday, February 17, 2013.	12
Monday, February 18, 2013	15
Poster Presentations I • Saturday, February 16, 2013.	16
Poster Presentations II • Sunday, February 17, 2013	26
Abstracts	37
Friday, February 15, 2013	
Session 01: Science and Sensationalism. Emerging Infections and Emergency!	37
Session 02: Ecology, Biodiversity, Climate and Emerging Infectious Disease	37
Session 03: Emerging Infectious Diseases and the Haii	38
Saturday, February 16, 2013	
Session 04: Emerging Disease Prevention	40
Session 05: Oral Presentations: One Health in Action	41
Session 06: Emerging Fungal Diseases and Species Extinction	44
Session 07: Of Bats and Men: Nipah and Other Infections.	45
Session 08: Oral Presentations: 'Contagion': Contemporary Viral Pathogens	46
Session 09: Emerging Disease Mysteries	48
Session 10:Vectorborne Diseases in Humans and Animals	50
Sunday, February 17, 2013	
Session 11: Neglected Zoonotic Diseases	51
Session 12: Oral Presentations: Infection, Detection, and Protection: Adventures in Epidemiology	52
Session 13: Global Approach to the Control of Foot and Mouth Disease.	56
Session 14: Cutting Edge Diagnostics for the Detection of Novel and Neglected Diseases	56
Session 15: Updates from ProMED (Panel Discussion).	57
Session 16: Disease Surveillance	57
Session 17: Oral Presentations: Hot Topics	58
Monday, February 18, 2013	
Session 18: Economics of Emerging Infectious Diseases	62
Session 19: Diseases Without Borders	62
Session 20: Big Data, Industry and Disease Surveillance	54
Poster Presentations	65
Saturday, February 16, 2013	
Session 21: Poster Presentations 1	65
Antimicrobial Resistance	65
Bioterrorism and Biological Warfare	76
Climate Change and Ecological Factors in Disease Emergence	77
Diseases at the Interface of Humans, Wildlife and Other Animals.	30
Diseases of Animals	ЭI
Foodborne and Waterborne Diseases	Э6
Infections of Public Health Significance)3
Infections Related to Travel and Migration	21
Innovations in Diagnostic Tests for Emerging Diseases	24
New Pathogen Discovery	26
Sunday, February 17, 2013	
Session 22: Poster Presentations II	27
Influenza and Other Respiratory Infections	27
New Approaches to Outbreak Surveillance and Monitoring	36
New, Emerging and Neglected Zoonotic Diseases	48
Outbreak Modeling	60
Outbreak Response and Control	śГ
Public Communication of Outbreaks and Emerging Diseases	6 8
Sociopolitical Factors in Disease Emergence	6 8
Vaccines and Emergence of Vaccine Preventable Diseases	70
Vectorborne Diseases	74
Index of Authors and Co-Authors	۶I

ii

Welcome to the great city of Vienna and the fourth International Meeting on Emerging Diseases and Surveillance, IMED 2013. Now established as a fixture for those whose work deals with threats from infectious agents, IMED 2013 will once again bring leading scientists, clinicians and policy makers together to present new knowledge and breakthroughs and discuss how to discover, detect, understand, prevent and respond to outbreaks of emerging pathogens.

Since the last IMED, newly emerged diseases and outbreaks of familiar ones have continued to challenge us and keep us vigilant. While the influenza pandemic that began in 2009 has quieted, an early and severe flu season has occurred in the Northern hemisphere and eruptions of H5N1 highly pathogenic avian influenza in poultry, wild birds and humans continue to occur. A new strain of H3N2 has transmitted from pigs to humans and, at least occasionally, from person to person. A novel coronavirus has caused severe human disease in several countries and the newly discovered Schmallenberg virus, has emerged in livestock in Northern Europe. Diseases at the human-wildlife interface ranging from rabies to plague to Nipah virus continue to draw our attention. Growing resistance by pathogens to all types of therapeutic agents raises fundamental obstacles to our ability to respond to outbreaks and pandemics. The threat of intentional use of biological agents for nefarious purposes remains as real as ever.

Since its inception, IMED has been a summit that unifies our approach to pathogens in the broadest ecological context. Drawing together human and veterinary health specialists, IMED serves as a true One Health forum where those working in diverse specialties and diverse regions can meet, discuss, present and challenge one another with findings and new ideas. This year, over 700 abstracts were submitted, a record number: A selection of the best among these will be presented in two poster sessions and four oral sessions.

A meeting of this scope could not occur without the help of many, and I particularly want to thank our co-sponsors for making IMED possible: EcoHealth Alliance, the European Centers for Disease Control and Prevention (ECDC), the European Society of Clinical Microbiology and Infectious Diseases (ESCMID), HealthMap, the Skoll Global Threats Fund (SGTF) and the World Organisation for Animal Health (OIE). We also acknowledge the generous technical contribution of the Food and Agriculture Organization of the United Nations (FAO) and the support from the Vienna Convention Bureau, the Mayor of Vienna and Austrian Airlines.

While pathogens emerge and mutate, our methodology for detection, surveillance, prevention, control, and treatment also continue to evolve. New approaches to the uses of social media and data mining, novel laboratory methods, rapid point-of-care diagnostics, risk communication, political and societal responses to outbreaks have all seen innovation and change that will be explored at IMED 2013.

Thank you for your participation.

Sincerely,

ELCOME

Jamme C. Mindy

Larry MADOFF Chair, Scientific Program Committee Editor, ProMED-mail, International Society for Infectious Diseases Boston, USA



International Meeting on Emerging Diseases and Surveillance 2013

Scientific Program Committee

Larry Madoff, Boston, MA, USA – Chair Jacques Acar, Paris, France Yin Myo Aye, Bangkok, Thailand Daniel Beltrán-Alcrudo, Rome, Italy Timothy Brewer, Montreal, Canada John Brownstein, Boston, MA, USA Ilaria Capua, Padova, Italy Giuseppe Cornaglia, Verona, Italy Sidi Coulibaly, Ouagadougou, Burkina Faso Benson Estambale, Nairobi, Kenya David Fisman, Toronto, Canada Antoine Flahault, Paris, France Johann Giesecke, Stockholm, Sweden David Heymann, London, United Kingdom Jim Hughes, Atlanta, GA, USA Damien Joly, Nanaimo, BC, Canada William Karesh, New York, NY, USA Keith Klugman, Atlanta, GA, USA Daniel Lucey, Washington, DC, USA Nina Marano, Nairobi, Kenya Abla Mawadeku, Ottawa, Canada Kazuaki Miyagishima, Paris, France Norbert Nowotny, Vienna, Austria & Muscat, Oman Philip Polgreen, Iowa City, IA, USA Marjorie Pollack, New York, NY, USA Natalia Psenichnaya, Rostov-on-Don, Russia Arnon Shimshony, Jerusalem, Israel Mark Smolinski, San Francisco, CA, USA Eric Summers, Boston, MA., USA Jaime Torres, Caracas, Venezuela Jack Woodall, Rio de Janeiro, Brazil









ESCAID EUROPEAN SOCIETY DE CLINICAL MICROBIDILIGI AND INFECTIOUS DISEASES









Co-Sponsors

ProMED-mail, the Program for Monitoring Emerging Diseases EcoHealth Alliance European Centre for Disease Prevention and Control (ECDC) European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Food and Agriculture Organization of the United Nations (FAO)* HealthMap Skoll Global Threats Fund (SGTF) World Organisation for Animal Health (OIE)

* With a technical contribution from the Food and Agriculture Organization of the United Nations.



International Meeting on Emerging Diseases and Surveillance 2013

Cooperating Organizations

Austrian Agency for Health and Food Safety (AGES) Austrian Federal Ministry of Health Austrian Society for Infectious Diseases (ÖEGIT) Austrian Society of Hygiene, Microbiology and Preventive Medicine (ÖGHMP) Austrian Society of Tropical Medicine and Parasitology (ÖGTP) International Society for Infectious Diseases (ISID) International Society for Disease Surveillance (ISDS) University of Veterinary Medicine Vienna – (Vetmeduni Vienna)

Contributors

Austrian Airlines City of Vienna EcoHealth Alliance International Society for Infectious Diseases (ISID) Vienna Hilton Am Stadtpark Vienna Convention Bureau

Exhibitors

Amplex BioSystems European Centre for Disease Prevention and Control (ECDC) Food and Agriculture Organization of the United Nations (FAO) International Society of Travel Medicine (ISTM) World Organisation for Animal Health (OIE) R-Biopharm

We invite you to visit the Exibits in the Pre-Function Area on the Ground Level.



Organizer & Conference Office

International Society for Infectious Diseases 9 Babcock Street, Unit 3, Brookline, MA 02446, USA phone: (617) 277-0551 • fax: (617) 278-9113 email: info@isid.org web: http://www.isid.org • http://imed.isid.org

Exhibition Office

Media Plan Freyung 6 1010 Vienna, Austria Phone: (+43 1) 536 63 0 Fax: (+43 1) 535 60 16 Email: mp@media.co.at





Opening Hours of the Registration and Information Desk

Friday, February 15, 2013	11:00 – 19:00hrs
Saturday, February 16, 2013	08:00 - 18:00hrs
Sunday, February 17, 2013	08:00 - 18:00hrs
Monday, February 18, 2013	08:00 - 12:00hrs

Congress Venue

Hilton Vienna • Am Stadtpark • 1030 Vienna • Tel: +43 | 717 000 • http://www.hilton.com

Registration Fees

Participants: EUR 495.00 Students: EUR 275.00

Social Program

The Welcome Reception will be held on Friday, February 15 from 17:30 to 19:00hrs at the Hilton Hotel Vienna on the Gallery (Upper Level).

The Mayor's Reception will take place on Sunday, February 17 at 20:00hrs at the Vienna City Hall (entrance: Lichtenfelsgasse, 1010 Vienna). An invitation card is needed to gain access to this reception. The price is EUR 20,00 per person. Onsite registration is subject to availability.

For both functions business attire is appropriate.

Badges

Please wear your name badge at all times during the conference in order to gain access to the scientific program and all conference functions.

Internet Access

The Hilton provides free internet access in the main hotel lobby.WiFi access in the sleeping rooms and conference area is available for a special conference fee if you present your IMED name badge.Tickets can be purchased from the reception desk on the ground level (EUR 10 for 24 hours).

CME

The International Meeting on Emerging Diseases and Surveillance–IMED 2013 is accredited by the European Accreditation Council for Continuing Medical Education (EACCME) to provide the following CME activity for medical specialists. The EACCME is an institution of the European Union of Medical Specialists (UEMS), www.uems.net.

The International Meeting on Emerging Diseases and Surveillance–IMED 2013 is designated for a maximum of, or up to 17 hours of European external CME credits. Each medical specialist should claim only those hours of credit that he/she actually spent in the educational activity.

Through an agreement between the European Union of Medical Specialists and the American Medical Association, physicians may convert EACCME credits to an equivalent number of AMA PRA Category I Credits.[™] Information on the process to convert EACCME credit to AMA credit can be found at www.ama-assn.org/go/internationalcme.

Live educational activities, occurring outside of Canada, recognized by the UEMS-EACCME for ECMEC credits are deemed to be Accredited Group Learning Activities (Section I) as defined by the Maintenance of Certification Program of The Royal College of Physicians and Surgeons of Canada.

RACE (Veterinary CE)

The American Association of Veterinary State Boards RACE committee has reviewed and approved IMED 2013 as meeting the Standards adopted by the AAVSB, (maximum CME for one veterinarian: 16.5). This course meets the requirements for hours of continuing education in jurisdictions which recognize AAVSB RACE approval; however, participants should be aware that some boards have limitations on the number of hours accepted in certain categories and/or restrictions on certain methods of delivery.

All CME forms are included in the congress bag. Please complete and return forms to the ISID after the conference is over as indicated on the form.

Poster Presentations

Poster presentations will be held on Saturday, February 16 and Sunday, February 17 from 11.45 to 13.15hrs. During this period all presenters must be available for discussion at their posters.

Set-up for Poster Presentations I: Saturday, February 16 from 08:00 to 10:30hrs Removal: Saturday, February 16 from 16:30 to 18:00hrs

Set-up for Poster Presentations II:

Sunday, February 17 from 08:00 to 10:30hrs Removal: Sunday, February 17 from 16:30 to 18:00hrs

Poster Areas (Upper Level)

Saturday, February 16, 2013 / Poster Presentations I 11:45-13:15

Room Bruckner/Mahler/Brahms / Upper Level:

Abstract Number	Торіс
21.001 - 21.032	Antimicrobial resistance
21.033 - 21.034	Bioterrorism and biological warfare
21.035 - 21.045	Climate change and ecological factors in disease emergence
21.046 - 21.079	Diseases at the interface of humans, wildlife and other animals
21.080 - 21.095	Diseases of animals
21.096 - 21.114	Foodborne and waterborne diseases
21.115 – 21.127	Infections of public health significance

Klimt Ballroom I / Upper Level:

Abstract Number	Торіс
21.128 - 21.169	Infections of public health significance (continued)
21.170 - 21.180	Infections related to travel and migration
21.181 - 21.184	Innovations in diagnostic tests for emerging diseases
21.185 - 21.187	New pathogen discovery

Sunday, February 17, 2013 / Poster Presentations II 11:45-13:15

Room Bruckner/Mahler/Brahms / Upper Level:

Abstract Number Topic

22001 – 22.027	Influenza and	other respiratory infections	
22001 - 22.027	Influenza and	other respiratory infections	

- 22..028 22.060 New approaches to outbreak surveillance and monitoring
- 22..061 22.093 New, emerging, and neglected zoonotic diseases
- 22..094 22.097 Outbreak modeling
- 22..098 22.116 Outbreak response and control
- 22.117 22.118 Public communication of outbreaks and emerging diseases
- 22.119 22.125 Sociopolitical factors in disease emergence

Klimt Ballroom I / Upper Level:

Abstract Number Topic

- 22.126 22.138 Vaccines and emergence of vaccine preventable diseases
- 22.139 22.185 Vectorborne diseases



GROUND LEVEL



FIRST LEVEL

ProMED-mail Meeting (Mon.)



PROGRAM-AT-A-GLANCE

International Meeting on Emerging Diseases and Surveillance 2013

Time	Friday, February 15, 2013	Room
:00- 9:00	Registration and Information Desk	Foyer/Park Congress/Ground Level
4:00- 4:20	Welcome & Opening	Park Congress/Ground Level
4:20- 5:00	Session I: <i>Plenary Lecture:</i> Science and Sensationalism, Emerging Infections and Emergency!	Park Congress/Ground Level
15:00–16:30	Session 2: <i>Plenary Lecture</i> : Ecology, Biodiversity, Climate and Emerging Infectious Disease	Park Congress/Ground Level
16:30–17:15	Session 3: <i>Plenary Lecture</i> : Emerging Infectious Diseases and the Hajj	Park Congress/Ground Level
17:30-19:00	Welcome: Cocktail Reception	Gallery/Upper Level
Time	Saturday, February 16, 2013	Room
08:30–10:30	2 Break-out Sessions: Session 4: Emerging Disease Prevention Session 5: Oral Presentations: One Health in Action	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
10:30-11:00	Coffee Break	Ground Level and Upper Level
:00– :45	Session 6: <i>Plenary Lecture:</i> Emerging Fungal Diseases and Species Extinction	Park Congress/Ground Level
:45– 3:15	Poster Presentations I (Session 21)	Bruckner/Mahler/Brahms/Upper Level and Klimt Ballroom I/Upper Level
14:30-16:00	2 Break-out Sessions: Session 7: Of Bats and Men: Ninah and Other Infections	Park Congress/Ground Level
	Session 8: Oral Presentations: 'Contagion': Contemporary Viral Pathogens	Klimt Ballroom 2&3/Upper Level
6:00– 6:30	Coffee Break	Ground Level and Upper Level
16:30-18:00	2 Break-out Sessions:	
	Session 9: Emerging Disease Mysteries	Park Congress/Ground Level
	Session 10: Vectorborne Diseases in Humans and Animals	Klimt Ballroom 2&3/Upper Level
Time	Sunday, February 17, 2013	Room
08:30-10:30	2 Break-out Sessions:	Park Congress/Ground Lovel
	Session 12: Oral Presentations: Infection, Detection, and Protection: Adventures in Epidemiology	Klimt Ballroom 2&3/Upper Level
10:30-11:00	Coffee Break	Ground Level and Upper Level
:00– :45	Session 13: <i>Plenary Lecture:</i> Global Approach to the Control of Foot and Mouth Disease	Park Congress/Ground Level
:45– 3: 5	Poster Presentations II (Session 22)	Bruckner/Mahler/Brahms/Upper Level and Klimt Ballroom I/Upper Level
4:30– 6:00	2 Break-out Sessions: Session 14: Cutting Edge Diagnostics for the Detection of Novel and Neglected Diseases	Park Congress/Ground Level
	Session 15: Updates from ProMED (Panel Discussion)	Klimt Ballroom 2&3/Upper Level
16:00-16:30	Coffee Break	Ground Level and Upper Level
16:30-18:00	2 Break-out Sessions:	
	Session 16: Disease Surveillance	Park Congress/Ground Level
20.00 22.00	Session 17: Oral Presentations: Hot Topics	Nimt Bailroom 2&3/Opper Level
20.00-22.00		
	Monday, February 18, 2013	Room
08:30-10:30	2 break-out sessions: Session 18: Economics of Emerging Infectious Diseases	Park Congress/Ground Level
	Session 19: Diseases without Borders	Klimt Ballroom 2&3/Upper Level
10:30-11:00	Coffee Break	Ground Level and Upper Level
:00- :45	Session 20: Plenary Lecture: Big Data, Industry and	Park Congress/Ground Level
	Disease Surveillance	

International Meeting on Emerging Diseases and Surveillance 2013

Opening Session

Room: Park Congress Ground Level

14:00-14:20 Friday, February 15, 2013

Welcome by the President of the International Society for Infectious Diseases (ISID) **Keith Klugman** Atlanta, GA (USA)

Welcome to Vienna **Norbert Nowotny** Vienna (Austria)

Official Opening of the Conference Pamela Rendl-Wagner, Director General, Public Health, Austria Vienna (Austria)

Welcome to IMED 2013 Larry Madoff Boston, MA (USA)



Science and Sensationalism, Emerging Infections and Emergency!

14:20-15:00 Friday, February 15, 2013

01.001 Science and sensationalism, emerging infections and emergency! A. Schuchat Atlanta, GA (USA)

Session 02

Plenary Lectures

Ecology, Biodiversity, Climate and **Emerging Infectious Diseases**

Co-Chairs: William Karesh, USA Juan Lubroth, Italy

Room: Park Congress	15:00-16:30
Ground Level	Friday, February 15, 2013

02.001 Different views of looking at biodiversity and health W. Karesh

New York, NY (USA)

02.002 Concerns of the biodiversity community for integrating health **D.** Coates Montreal (Canada)

02.003 Climate change, biodiversity loss, desertification and human health - the WHO Perspective **D.** Campbell-Lendrum Geneva (Switzerland)

02.004 Wildlife trade and emerging diseases- Impacts on biodiversity and health K. Smith New York, NY (USA)

Co-sponsored by EcoHealth Alliance

Session 03

Plenary Lecture

Emerging Infectious Diseases and the Hajj

Chair: Marjorie Pollack, USA

Room: Park Congress	16:30-17:15
Ground Level	Friday, February 15, 2013

03.001 Emerging infectious diseases and the Hajj Z. Memish Riyadh (Saudi Arabia)

Welcome Cocktail Reception

Gallery	17:30-19:00
Upper Level	Friday, February 15, 2013







International Meeting on Emerging Diseases and Surveillance 2013

Session 04

Emerging Disease Prevention

Co-Chairs: Julio Pinto, Italy

Nina Marano, Kenya Room: Park Congress 8:30-10:30

Ground Level Satur	day, February 16, 2013

04.001 Introduction to FAO's role in emerging disease prevention J. Lubroth

Rome (Italy)

04.002 Strengthening laboratory networks and strategies to meet the challenges of emerging and transboundary animal diseases (TADs) threats F. Claes

Rome (Italy)

04.003 Innovation to fill the gaps in disease surveillance: Participatory surveillance, applied technologies for better understanding and reporting J. Pinto

Rome (Italy)

04.004 Dealing with the biocomplexity of emerging infectious diseases (EIDs): An ecosystem health approach D. Beltrán-Alcrudo

Rome (Italy)

With a technical contribution from the Food and Agriculture Organization of the United Nations.

Session 05

Oral Presentations

One Health in Action

Co-Chairs: Tim Brewer, USA

Natalia Pshenichnaya, Russian Federation

Room: Klimt Ballroom 2&3 8:30-10:30 Saturday, February 16, 2013 Upper Level

- **05.001** Evaluating long-term behavior change resulting from an intervention to prevent Nipah virus transmission from bats to humans in Bangladesh R. Sultana, U. K. Mondal, J. Abedin, M. J. Hossain, M. A.Y. Sharker, N. A. Rimi, E. Gurley, N. Nahar, S. P. Luby Dhaka (Bangladesh)
- 05.002 Characterizing high risk disease transmission interfaces in the global pursuit of emerging zoonotic diseases

C. K. Johnson¹, T. W. Smiley¹, T. Goldstein¹, W. Karesh², D. Joly³, P. Daszak², J. Mazet¹ ¹Davis, CA (USA), ²New York, NY (USA), ³Nanaimo, BC (Canada)

05.003 Rabies control in Bali: A "one health" approach E. Russell, **F. Abson** London (United Kingdom)

05.004 Monitoring of influenza virus in pigs and humans in Switzerland M. Engels¹, Y. Thomas², E. Fuchsini³, R. Born⁴, S. Bruhn⁴

¹Zurich (Switzerland), ²Geneva (Switzerland), ³Sempbach (Switzerland), ⁴Berne (Switzerland)

05.005 Coxiella burnetti seroprevalence and risk factors in dairy cattle farmers and farm residents in the Netherlands

J. Hautvast¹, N. Schotten¹, B. Schimmer², P. Schneeberger³, P. Vellema⁴, Y. van Duynhoven² ¹Nijmegen (Netherlands), ²Bilthoven (Netherlands), ³Den Bosch (Netherlands), ⁴Deventer (Netherlands)

- **05.006** High colonization rate of farmers, their relatives and employees at pig farms with emerging Clostridium difficile PCR ribotype 078 E. Keessen¹, M. Hensgens², M. Bos¹, W. Dohmen¹, J. Wagenaar³, D. Heederik¹, E. Kuijper², L. Lipman¹ ¹Utrecht (Netherlands), ²Leiden (Netherlands), ³Netherland (Netherlands)
- 05.007 West Nile Disease in Italy: Animal surveillance activities as an early warning system for the prevention and control of the infection in humans R. Bruno, **D. Di Sabatino**, A. Carvelli, F. De Massis, P. Calistri Teramo (Italy)
- 05.008 Sylvatic origin and geographic spread of St. Louis encephalitis virus A. Kopp¹, T. Gillespie², D. Hobelsberger³, A. Estrada⁴, I. Eckerle¹, M. Mueller¹, L. Podsiadlowski⁵, F. Leendertz³, C. Drosten¹, S. Junglen¹ ¹Bonn (Germany), ²Atlanta, GA (USA), ³Berlin (Germany), ⁴Mexico City (Mexico), ⁵Bonn (Germany)
- **05.009** Considerable relation with foot-and-mouth disease (FMD) infection in Japan, 2010; Traffic roads and pig farming area R. Ushijima Miyazaki (Japan)
- 05.010 West Nile Virus in Canada: 2002-2012 H. Zheng, A. S. Yasseen, P.A. Buck, F. Welsh, M. Raizenne Ottawa, ON (Canada)
- **05.011** Zoonotic diseases monitored by Brazil National IHR Focal Point from March 2006 to June 2012 M. É. Santos, S. Lopes Dias, E.T. Masuda, P. Pereira Vasconcelos de Oliveira, G. S. Dimech Brasilia (Brazil)



Coffee Break

Ground Level and Upper Level

10:30-11:00 Saturday, February 16, 2013

Session 06 Plenary Lecture

Emerging Fungal Threats to Animal, Plant and Ecosystem Health

Chair: John Brownstein, USA

Room: Park Congress	s :00– :45
Ground Level	Saturday, February 16, 2013

06.001 Emerging fungal threats to animal, plant and ecosystem health M. Fisher London (United Kingdom)

Poster Presentations I (Session 21)

11:45-13:15 Saturday, February 16, 2013 Bruckner/Mahler/Brahms - Upper Level and Klimt Ballroom I - Upper Level

Sessions 21.001–21.187 (see pages 65–126)

Session 07

Of Bats and Men: Nipah and **Other Infections**

Co-Chairs: Daniel Lucey, USA Damien Joly, Canada

Room: Park Congress	s 14:30–16:00
Ground Level	Saturday, February 16, 2013

- **07.001** Understanding the ecology of Nipah virus in frugivorous bats in Bangladesh J. H. Epstein New York, NY (USA)
- 07.002 From bats to human-to-human transmission of Nipah virus in Bangladesh H.S.Sazzad Dhaka (Bangladesh)
- 07.003 "One Health" Surveillance for Nipah virus in Thailand S. Wacharapluesadee Bangkok (Thailand)

Session 08

Oral Presentations

'Contagion': Contemporary Viral Pathogens

Co-Chairs: Sidi Coulibaly, Burkina Faso

Stuart Handysides, United Kingdom		
Room: Upper	Klimt Ballroom 2&3 Level Sature	14:30–16:00 day, February 16, 2013
08.001	Hepatitis E virus antiger An early diagnostic mar R. Ratho , M. Majumda Chandigarh (India)	n detection: ·ker r, M. P. Singh, Y. Chawla
08.002	Evolution of H3N2 influ the Philippines B. C. Torres ¹ , Y. C. F. Su ² , A. K. Cruz ¹ , D. C. Klinz Natividad ¹ ¹ Quezon City (Philippin (Singapore)	uenza viruses from M. S. H. Chua ² , H. Guo ² , t ing ¹ , G. J. D. Smith ² , F. F. nes), ² Singapore
08.003	Influence of the viral m different host species, o viruses in water S. Shigematsu, A. Dublin I. Leclercq, JC. Manugu Paris (France)	embrane, inherited from n survival of influenza A eau, L. I. O. Sawoo , erra
08.004	Investigation of deaths of pdm09 in Southern Bra R. Soletti ¹ , W. Oliveira R. Moreira ¹ , L. Garay ² , M C. N. Igansi ¹ , W. Araújo ¹ ¹ Brasília (Brazil), ² Porto	due by Influenza A(H1N1) izil, July-August, 2012 ', F. Costa', F. de Paula', 1. Bercini ² , E. M. Macario', Alegre(Brazil)
08.005	Enhancing the specificit detection of Monkeypo of Congo (DRC). L. U. Osadebe ¹ , A. Mo E. Pukuta ² , S. Karhemere I. Damon ¹ , J. J. Muyembe ¹ Atlanta, GA (USA), ² Kii	y of surveillance case x in Democratic Republic Collum ¹ , R. S. Lushima ² , ² , J. Kabamba ² , B. Nguete ² , ³² , M. Reynolds ¹ nshasa (Congo,

08.006 First autochthonous outbreak of dengue in the island of Madeira, October 2012: A challenge for the European Union Region P.Vasconcelos¹, H. Zeller², C. Abreu Santos¹, B. Sudre², J. Gomes Dias², J. Jansa², A. C. Silva³, A. Nunes³, A. Leça¹, K. Mansinho¹ ¹Lisbon (Portugal), ²Stockholm (Sweden), ³Funchal (Portugal)

Democratic Republic of)

IMED 2013

SATURDAY • FEBRUARY 16, 2013

SATURDAY • February 16, 2013

International Meeting on Emerging Diseases and Surveillance 2013

- 08.007 Dengue fever outbreak in North Eastern Kenya, 2011
 M. O. Obonyo, W. Arvelo, V. O. Ofula, A. Fidhow, B. Fields, R. Sang, E. Wurapa, K. Njenga, J. Montgomery Nairobi (Kenya)
- 08.008 Evaluation of innate immune response in acute and fulminant hepatitis E
 M. Majumdar, R. Ratho, Y. Chawla, M. P. Singh Chandigarh (India)

Coffee Break

Ground Level and Upper Level 16:00-16:30 Saturday, February 16, 2013

Session 09

Emerging Disease Mysteries

Co-Chairs: Joseph Wamala, Uganda Leo Liu, USA

Room: Park Congress	s 16:30–18:00
Ground Level	Saturday, February 16, 2013

09.001 Magnitude and distribution of Nodding Syndrome in Northern Uganda **J. F. Wamala**

J. F. Warnala

Kampala (Uganda)

09.002 Nodding Syndrome: An emerging epilepsy disorder of sub-Saharan Africa A.Winkler

Munich (Germany)

09.003 EV71 virus

P. Chua

Singapore (Singapore)

09.004 Ebola and Marburg viruses emergence at the human-animal interface **P. Formenty** Geneva (Switzerland)

Session 10

Vectorborne Diseases in Humans and Animals

Room: Klimt Ballroom 2&316:30–18:00Upper LevelSaturday, February 16, 2013

- 10.001 A novel orthobunyavirus in European livestock: the emergence of Schmallenberg virus
 M. Beer Greifswald-Insel Riems (Germany)
- 10.002 Emerging zoonotic vector-borne diseases in EuropeN. NowotnyMuscat (Oman)
- 10.003 Emerging insect vector-borne animal diseases in the eastern MediterraneanE. Klement

Rehovot (Israel)



Subscribe for free email updates about threats to human, animal, and food plant health around the world.

www.promedmail.org



Co-Chairs: Arnon Shimshony, Israel Norbert Nowotny, Oman



Session 11

Neglected Zoonotic Diseases

Co-Chairs: Matt Levison, USA Tam Garland, USA

Room: Park Congress	08:30-10:30
Ground Level	Sunday, February 17, 2013

11.001 The economic and health burden of neglected zoonotic diseases
 P.Torgerson Zurich (Switzerland)
 11.002 Rabies: the path to elimination

A. L. Willingham

- Geneva (Switzerland)
- 11.003 Echinococcosis: endemic and re-emergent P. Craig Salford (United Kingdom)
- 11.004 Implementing the roadmap to combat CysticercosisA. L. Willingham

Geneva (Switzerland)

Session 12 Oral Presentations

Infection, Detection, and Protection: Adventures in Epidemiology

Co-Chairs: Philip Polgreen, USA Tom Yuill, USA

Room: Klimt Ballroom	2&3	8:30-10:30
Upper Level	Sunday, Februa	ary 17, 2013

- 12.001 Evaluation of cholera and other diarrheal diseases surveillance system, Niger State, Nigeria, 2012
 A.T. Bashorun¹, A. Ahumibe¹, S. Olugbon¹, A. Taju¹, P. Nguku¹, K. Sabitu²
 ¹Abuja (Nigeria), ²Zaria (Nigeria)
- 12.002 Surveillance during Haji: Patterns and causes of mortality amongst Indonesian pilgrims
 M. Pane¹, S. Imari¹, N. Kandun¹, G. Samaan²
 ¹Jakarta (Indonesia), ²Canberra, ACT (Australia)
- 12.003 ECDC/EpiNorth epidemic intelligence activities during EURO 2012 in Poland and Ukraine
 A. M. Gherasim¹, I. Linina², G. Rimseliene³, L. Paine Hallström¹, J. Mantero¹, P. Penttinen⁴
 ¹Stockholm (Sweden), ²Brussels (Belgium), ³Oslo (Norway), ⁴Stockhokm (Sweden)
- 12.004 Improving capacity to investigate and respond to emerging infectious disease outbreaks in East and Central Africa

H. M. Amuguni¹,T. Odoch², R. Nauma² ¹North Grafton, MA (USA), ²Kampala (Uganda) 12.005 Characterizing zoonotic disease outbreaks in the United StatesH.Allen

McLean,VA (USA)

- 12.006 Estimating global mortality associated with the influenza A H1N1 pandemic in 2009: the WHO Global Pandemic Mortality Assessment (GLaMOR) project
 L. Simonsen¹, P. Spreeuwenberg², R. Lustig³, R. J.Talyor³, D. M. Fleming⁴, M. Kroneman², L. W. Kim³, M. D. Van Kerkhove ⁵, A. W. Mounts⁶, J.W. Paget²
 ¹Washington DC, DC (USA),
 ²Utrecht (Netherlands), ³Bethesda, DC (USA),
 ⁴Birmingham (United Kingdom), ⁵London (United Kingdom), ⁶Geneva (Switzerland)
- 12.007 Domestic birds as surveillance systems for monitoring West Nile virus lineage 2 enzootic circulation: three years of experience in Greece
 C. I. Dovas¹, S. C. Chaintoutis¹,
 A. Chaskopoulou¹, S. Gewehr¹,
 M. Papanastassopoulou¹, S. Mourelatos¹,
 S. Zientara², S. Lecollinet², K. Danis³,
 T. Panagiotopoulos³
 ¹Thessaloniki (Greece), ²Maisons-Alfort (France),
 ³Athens (Greece)
- 12.008 Weekly monitoring of human cases of West Nile fever: an efficient way to assess the evolution of the disease in Europe

L. Marrama Rakotoarivony, C. Bogaardt, E. Robinson, V. Estevez, J. Jansa, H. Zeller, D. Coulombier Stockholm (Sweden)

- 12.009 Determinants of active participation in internetbased surveillance systems
 D. Paolotti, P. Bajardi Turin (Italy)
- 12.010 An investigation of Salmonella enteritidis PTI cases linked to consumption of a pasteurized liquid egg white product in England and Wales, 2012
 O. Esan, C. Lane, T. Peters

London (United Kingdom)

12.011 Effects of climate change on the distribution of bluetongue and epizootichaemorrhagic disease vector in Southern Alberta (Canada) and Montana(USA)

A. Zuliani¹, A. Massolo¹, S. Marshall¹, T. J. Lysyk², G. Johnson³, S. Cork¹ ¹Calgary, AB (Canada), ²Lethbridge, AB (Canada), ³Bozeman, MT (USA)

Scientific Program

International Meeting on Emerging Diseases and Surveillance 2013

Coffee Break

Ground Level and Upper Level

10:30-11:00 Sunday, February 17, 2013

Session 13 Plenary Lecture

Global Approach to the Control of Foot and Mouth Disease

Chair: Jacques Acar, France

Room: Park Congress	:00- :45
Ground Level	Sunday, February 17, 2013

13.001 Global approach to the control of foot and mouth disease **B.Vallat** Paris (France)

Poster Presentations II (Session 22)

Sunday, February 17, 2013 11:45-13:15 Bruckner/Mahler/Brahms - Upper Level

and Klimt Ballroom - Upper Level

Sessions 22.001–22.185 (see pages 127–190)

Session 14

Cutting Edge Diagnostics for the Detection of Novel and Neglected Diseases

Co-Chairs: Giuseppe Cornaglia, Italy Keith Klugman, USA

Room: Park Congress 14:30-16:00 Ground Level Sunday, February 17, 2013

- 14.001 MALDI-TOF MS beyond bacterial and fungal identification J.Vila Barcelona (Spain)
- 14.002 Next generation sequencing in clinical microbiology diagnosis, what have we achieved so far? J.Van Eldere

Louvain (Belgium)

14.003 Detection of emerging antimicrobial threats in developing countries K. Klugman

Atlanta, GA (USA)

Co-sponsored by ESCMID

Session 15

Panel Discussion

Updates from ProMED

Co-Chairs: Stephen Morse, USA Eskild Petersen, Denmark

Room: Klimt Ballroom 2&3 14:30-16:00 Upper Level Sunday, February 17, 2013

> Introduction L. Madoff Boston, MA (USA)

15.001 Novel coronavirus in the Eastern Mediterranean M. Pollack New York, NY (USA)

15.002 Continuing global emergence of dengue S. Chotivichien¹, Q. Nguyen¹, J. Torres³ ¹Bangkok (Thailand), ²Hanoi (Vietnam). ³Caracas (Venezuela).

- **15.003** Fungal meningitis outbreak L. Lutwick New York, NY (USA)
- 15.004 Yellow fever in Darfur, Sudan J. Woodall¹, T. Yuill² ¹Rio de Janeiro (Brazil), ²Mapleton, UT (USA)

Coffee Break

Ground Level 16:00-16:30 and Upper Level Sunday, February 17, 2013

Session 16

Disease Surveillance

Co-Chairs: John Brownstein, USA Ann Marie Kimball, USA

A
3
E
64

Room: Park Congress 16:30-18:00 Ground Level Sunday, February 17, 2013

16.001 Integrating data mining and crowd-sourcing for disease surveillance J. Brownstein

Boston, MA (USA)

16.002 Participatory epidemiology:putting the public in public health surveillance M. Smolinski

San Francisco, CA (USA)

16.003 Towards synergy between surveillance systems for Epidemic Intelligence. L.Vaillant Saint Maurice (France)



Session 17

Oral Presentations

Hot Topics

Co-Chairs: Daniel Beltrán-Alcrudo, Italy Larry Lutwick, USA

Room: Klimt Ballroom	2&3	16:30-18:00
Upper Level	Sunday, Febru	ary 17,2013

- 17.001 Anthrax pleural effusions and drainage 1979–2011: A Russia-USA partnership study.
 D. Lucey¹, L. Grinberg², F. Abramova²
 ¹Washington, DC (USA), ²Yekaterinburg (Russian Federation)
- 17.002 Schmallenberg virus—Harmonized European data collection for an emerging disease
 A.Afonso¹, F. Berthe¹, K. Willgert², D. Verloo¹, J. Cortinas Abrahantes¹, A. Bau¹, J. Richardson¹
 ¹Parma (Italy), ²London (United Kingdom)

17.003 No evidence for zoonotic transmission of Schmallenberg virus in areas with veterinary activity

C. Reusken¹, C. van den Wijngaard¹, M. Beer²,
R. Bouwstra³, H. van den Kerkhof¹,
W. van der Poel³, J. Schmidt-Chanasit⁴,
P.Vellema⁵, I. Wouters⁶, M. Koopmans⁷
¹Bilthoven (Netherlands), ²Greifswald-Insel Riems (Germany), ³Lelystad (Netherlands), ⁴Hamburg (Germany), ⁵Deventer (Netherlands), ⁶Utrecht (Netherlands), ⁷Rotterdam (Netherlands)

17.004 The interaction of the spike glycoproteins of bat-borne SARS-like-CoVs with chiropteran cells during the entry process
 M. Hoffmann, N. Krüger Hanover (Germany)

17.005 Tick species and tick-borne viruses of Eastern cancelled and North Eastern parts of Kenya: Health risk implications among pastoral communities
J. Mutisya¹, J. Lutomiah¹, L. Musila¹, S. Khamadi¹, H. Koka¹, E. Chepkorir¹, A. Makio¹, J. Bast², E. Wurapa¹, R. Sang¹
¹Nairobi (Kenya), ²Kisumu (Kenya)

- 17.006 Spotted fever group *Rickettsia* species and *Anaplasma* phagocytophilum in lizards ticks, Algeria
 H. Soualah-Alila¹, Z. Bouslama²
 ¹Annaba, AL-AN (Algeria), ²Annaba (Algeria)
- 17.007 Sequelae of human *Cryptosporidiosis* in patients living in Östersund during a large waterborne outbreak
 J. Lindh¹, A. Wallensten¹, J. Bergstrom¹, M. Lilja², M. Widerstrom²
 ¹Solna (Sweden), ²Östersund (Sweden)

17.008 Evolution of gonococcal strain susceptibility to antibiotics in France: data from a national sentinel surveillance network, 2001–2012
G. La Ruche¹, P. Sednaoui², B. Bercot², E. Cambau², A. Goubard²
'Saint-Maurice (France), ²Paris (France)



Mayor's Reception

Sunday, February 17, 2013 20:00–22:00 Vienna City Hall (Entrance: Lichtenfelsgasse) - no transportation provided

International Meeting on Emerging Diseases and Surveillance 2013

Session 18

Economics of Emerging Infectious Diseases

Co-Chairs: Nilufar Rakhmanova, USA David Fisman, Canada

Room: Park Congress08:30-10:30Ground LevelMonday, February 18, 2013

- 18.001 Emerging infections and poverty: Lessons from the Americas
 L. Ivers Boston, MA (USA)
- **18.002** Vaccination choices and their impact on immunization programmes

P. Manfredi

- Pisa (Italy)
- **18.003** Externalities, transaction costs and infectious diseases

P. Polgreen lowa City, IA (USA)

- **18.004** Is it cost-effective? Best practices on evaluating
 - the bang-for-the-buck in communicable disease control **D. Fisman**

Toronto (Canada)

Session 19

Diseases Without Borders

Co-Chairs: Adriano Duse, South Africa Benson Estambale, Kenya

Room: Klimt Ballroom 2&308:30–10:30Upper LevelMonday, February 18, 2013

- 19.001 Hepatitis E outbreak at a refugee campJ.AhmedNairobi (Kenya)
- 19.002 Dynamics of the Uganda Ebola outbreakA. Duse Johannesburg (South Africa)
- 19.003 From surveillance to prevention: developing a risk assessment framework for "novel" emerging infectionsS. Morse

New York, NY, and Davis, CA (USA)

19.004 NDM-1 and the international spread of antibiotic resistanceM.Toleman

Cardiff, (United Kingdom)

Coffee Break

Ground Level	10:30-11:00
and Upper Level	Monday, February 18, 2013

Session 20

Plenary Lecture

Big Data, Industry and Disease Surveillance

Chair: Larry Madoff, USA

Room: Park Congress	:00- :45
Ground Level	Monday, February 18, 2013

20.001 Big data, industry and disease surveillance
 A. Signorini
 Iowa City, IA (USA)



International Meeting on Emerging Diseases and Surveillance 2013

Session 21

Poster Presentations I

Saturday, February 16, 2013 II:45–13:15 Bruckner/Mahler/Brahms • Upper Level

Antimicrobial Resistance

- 21.001 Ertapenem-resistance in Klebsiella pneumoniae isolates from Croatia
 B. Bedenic¹, M. Barisic¹, Z. Bosnjak¹, J.Vranes¹, V. Plecko¹, D.Varda-Brkic¹, S. Sardelic²
 ¹Zagreb (Croatia), ²Split (Croatia)
- 21.002 Importance of clonal properties in addition to antibiotic consumption in determining the differences between macrolide resistant and susceptible *Streptococcus pyogenes*C. Silva-Costa, A. Friães, M. Ramirez,
 J. Melo-Cristino, P. Portuguese Group for the Study of Streptococcal Infections Lisbon (Portugal)
- 21.003 Carbapenem resistance of *Pseudomonas* aeruginosa and *Acinetobacter baumannii* strains in the intensive care unit in Romania
 S. L. Pandrea, L. Matros, M. I. Ciontea Cluj (Romania),
- **21.004** Antibiotic resistance of *Pseudomonas aeruginosa* strains isolated from nosocomial infections in Romania

S. L. Pandrea, L. Matros, M. I. Ciontea Cluj (Romania)

21.005 Antimicrobial resistance of gram-negative bacilli causing infections in intensive care units in Makkah hospitals, Saudi Arabia

A.Asghar

Makkah (Saudi Arabia)

 21.006 Inhibitory effects of Lactobacillus plantarum and Lactobacillus rahmnosus on the growth of Pseudomonas aeruginosa
 S.Aminnezhad, K. Kermanshahi, R. Ranjbar, O.

> Baghery Tehran (Iran, Islamic Republic of)

21.007 Infection due to colistin-resistant *Enterobacteriacae*: A single tertiary centre experience in critically ill patients from Saudi Arabia

M.A. Garbati¹, A. Bin Abdulhak², A. I. AlGodair³, H. Sakkijha¹

¹Riyadh, Riyadh (Saudi Arabia), ²Kansas City, MO (USA)

21.008 Infection with *Escherichia coli* and antimicrobial susceptibility

I. Zurak

Zagreb (Croatia)

- 21.009 Are the neurological rehabilitation wards at higher risk for multi-drug resistant micro-organisms infections? A retrospective analysis from a rehabilitation center in Northern Italy focusing on clinical risk factors
 M. Riccò¹, D. Nicolotti², C. Signorelli¹, P. Camia¹, S. Cattani¹, V. Ciorba¹, F. Pezzetti¹, H. Cerrel Bazo²
 ¹Parma (Italy), ²Piacenza (Italy)
- 21.010 Successful management of nosocomial ventriculitis and meningitis caused by extensive drug resistant Acinetobacter baumannii, Austria M. Drescher, M. Hoenigl, G. Feierl, T. Valentin, K. Seeber, E. Leitner, G. Zarfel, W. Duettmann, R. Krause, A. J. Grisold Graz (Austria)
- 21.011 Antimicrobial resistance of human Salmonella serovar Typhimurium U302 strains in Slovakia: prevalence of R-type ASSuT
 L. Majtanova, V. Majtan Bratislava (Slovakia)
- 21.012 Inducuble clindamycin resistance in methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* of inpatient, outpatient and healthy carriers
 S. Uzunovi¹, A. Ibrahimagi¹, F. Kamberovi²,

S. OZUNOV, A. Drammagr, T. Kamberov,
M. Kunarac¹, M. I. A. Rijnders³, E. E. Stobberingh³
¹Zenica (Bosnia and Herzegovina), ²Ljubljana
(Slovenia), ³Mastricht (Netherlands)

- 21.013 Serotype and clindamycin-resistance of Streptococcus suis in diseased pigs and humans in upper northeast Thailand S.Angkititrakul¹, T. C. Nutravong² 'Khon Kaen (Thailand), ²Khon Kaen, (Thailand)
- 21.014 Escherichia coli B2 and D virulent phylotypes carry extended-spectrum and pAmpC betalactamases in healthy dogs with no antimicrobial pressure
 A. Belas, N. Couto, C. Pomba Lisbon (Portugal)
- 21.015 Antimicrobial resistance of Salmonella stanley isolated from pigs, dogs and humans in northeast of Thailand
 A. Polpakdee, S. Angkititrakul Khon Kaen (Thailand)
- 21.016 Analysis of the plasmid profile in Salmonella typhimurium strains isolated in the Republic of Uzbekistan
 L.Tuychiev, G. Abdukhalilova, A. Ibragimov, I. Akhmedov

Tashkent (Uzbekistan)

 21.017 Characterization of uropathogenic *E. coli* and detection their ESBL TEM and SHV genes
 S. N. EI-Sukhon Irbid (Jordan)

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

- 21.018 Copper alloys beneficial effects on ICU operation P. Efstathiou, E. Doe Kouskouni, S. Papanikolaou, K. Karageorgou, Z. Manolidou, M. Tseroni²
 E. Logothetis, I. Agrafa Athens (Greece),
- **21.019** Prevalence of drug-resistant tuberculosis in rural eastern China

Q. Zhao, Y. Hu, W. Wang, W. Jiang, T. Tao, B. Xu Shanghai (China)

- 21.020 Minced meat as a source for MRSA and ESBL-producing *E. coli*C. Petternel, J. Posch, D. Haas, H. Galler, G. Zarfel, V. Strenger, E. Marth, F. Reinthaler, G. Feierl
- Graz (Austria) 21.021 Prevalence of commensal ESBL-producing Escherichia coli strains isolated from piglets from
- *Escherichia coli* strains isolated from piglets from birth to nursery on three Portuguese industrial pig farms.

M. M. Centeno¹, N. Couto¹, A. Belas¹, T. Nunes¹, V. Almeida¹, L. Alban², C. Pomba¹ ¹Lisbon (Portugal), ²Kobenhavn (Denmark)

- 21.022 Relative activity over time of chlorhexidine and benzalkonium chloride against methicillin-resistant staphylococci isolates from horses
 N. Couto¹, A. Belas¹, P.Tilley¹, L.Telo da Gama¹, I. Couto¹, K. Kadlec², S. Schwarz², C. Pomba¹
 ¹Lisbon (Portugal), ²Neustadt-Mariensee (Germany)
- 21.023 Detection of bacteria resistant to critically important antimicrobials from lower urinary tract infections in cats and dogs from Portugal
 C. Pomba, D. Saial, M. M. Centeno, A. Belas, N. Couto
 Lisbon (Portugal)
- 21.024 Trends in the prevalence of methicillin resistance in staphylococci isolated from companion animals
 N. Couto, A. Belas, M. M. Centeno, C. Pomba Lisbon (Portugal)
- 21.025 Isolation and characterization of anti-Pythium insidiosum compounds from Pseudomonas stutzeri isolated from aquatic environment
 Y.Thongsri¹, C. Aromdee¹, S. Kanokmedhakul¹, C. Yenjai¹, A. Chaiprasert², P. Hamal³, C. Prariyachatigul¹
 ¹Thailand, Khon Kaen (Thailand), ²Khon Kaen (Thailand), ²Bangkok, Thailand (Thailand), ³Olomouc (Czech Republic)
- **21.026** Detection of extended-expectrum ß-lactamase (ESBL) producing *Enterobacteriaceae* in organic bovine milk

A. K. Siqueira¹, M. M. G. Ferraz¹, T. Salerno², G. H. B. Lara², F. J. P. Listoni², C. Lambertini¹, A.V. da Silva³, A. C. Paes², M. G. Ribeiro², D. D. S. Leite¹ ¹Campinas, SP (Brazil), ²São Paulo, SP (Brazil), ³Feira de Santana,(Brazil)

- 21.027 Antibiotic resistant urinary tract infections and Zataria multifolora Boiss: can it help us?
 Z. Sepehri¹, F. Javadian¹, E. Javadian², O. Aloosh³, M. Mohammadi¹, N. Keikhaee⁴, F. Rakhshani⁵
 ¹Zabol (Iran, Islamic Republic of), ²Zahedan (Iran, Islamic Republic of), ³Hamedan (Iran, Islamic Republic of), ⁵Tehran (Iran, Islamic Republic of)
- **21.028** Resistance phenotypes of *Staphylococcus aureus* strains isolated from intensive care unit in Romania

S. L. Pandrea¹, L. Matros², M. I. Ciontea¹ ¹Cluj-Napoca (Romania), ²Cluj (Romania)

21.029 Evaluation of in-vitro anti-mycobacterial activity of some Indian medicinal plants: Isolation of active constituents from *Urtica dioica* L. and *Cassia sophera* (Linn.) Roxb.
 S. H. Kelam

Jhansi (India)

21.030 Antibiotic resistance of uropathogens from

cancelled community-acquired urinary tract infections in Besat University Hospital in Tehran, Iran in 2011 **A.A. Saeedi**, M. Aminianfar, E. Soleimani, M. Darvishi, S. Faraji Tehran (Iran, Islamic Republic of)

21.031 Antimicrobial resistance surveillance of cancelled Acinetobacter baumannii isolated from Besat University Hospital in Tehran, Iran from 2009 to 2011

A.A. Saeedi, S. Faraji, F. Rahimi, M. Aminianfar, M. Khosravi, E. Soleimani, M. Darvishi Tehran (Iran, Islamic Republic of)

21.032 Occurrence of plasmid-mediated enrofloxacin and tetracycline resistance determinants, among *Escherichia coli* isolated from lambs in Greece
G. Filioussis¹, E. Petridou¹, A. Tzivara², S. Kritas¹
¹Thessaloniki (Greece), ²Karditsa Thessaly (Greece)

Bioterrorism and Biological Warfare

- 21.033 A guide to the diagnosis and management of CDC Category A bioterrorism agents ("Be Past")
 J.Varco, D. Lucey Washington, DC (USA)
- 21.034 Antimicrobial susceptibility and molecular characteristics of *Bacillus anthracis* strains isolated in Slovenia
 M. Ocepek¹, I. Zdovc¹, S. Duvnjak², U. Zajc¹, T. Pirš¹, M. Pate¹, M. Golob¹, S. Spicic², I. Racic², Z. Cvetnic²

¹Ljubljana (Slovenia), ²Zagreb (Croatia)

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

Climate Change and Ecological Factors in Disease Emergence 21.035 Occurrence of the Asian tiger mosquito Aedes (Stegomyia) albopictus (albopicta) in Austria B. Seidel¹, A. Rose², A. Indra³, P. Hufnagl³, F. Allerberger³ ¹Persenbeug (Austria), ²Regensburg (Germany), ³Vienna (Austria) 21.036 The influence of the environment on anthrax in Ukraine I. S. Kovalenko, O. B. Khaytovych Simferopol (Ukraine) **21.037** Biome specific hanta epidemiologies in Europe **H. Henttonen** Vantaa (Finland) 21.038 West Nile Virus—Is Asia at risk? G.Yap Singapore (Singapore) **21.039** Climate impact on the occurrence, distribution and activity of potential dipterans vectors in Eastern Slovakia A. Kočišová, E. Bocková, A. Sarvašová, M. Halán Kosice (Slovakia) **21.040** Vector populations in different climatic conditions in Romania and the emergence of human cases of infection with West Nile Virus (WNV) L. Baltesiu¹, M.T. Gomoiu², R. Mudura¹, G. M. Nicolescu¹, V. Purcarea-Ciulacu¹ ¹Bucharest (Romania), ²Constanta (Romania) 21.041 Climatic anomalies and reemergence of West Nile virus in the United States M.Wimberly¹, T.-W. Chuang², A. Lamsal¹ ¹Brookings, SD (USA), ²Taipei (Taiwan, R.O.C.) 21.042 Implementation of an early warning system to predict zoonotic cutaneous leishmaniasis epidemics in central Tunisia H. Bellali, J. Daaboub, I. Nouiri, A. Mrabet, M. K. Chahed Tunis (Tunisia) **21.043** The ENHanCE project: a large scale risk assessment of the most likely human and animal pathogens to be affected by climate change K. M. McIntyre¹, C. Setzkorn¹, P. J. Hepworth¹, S. Morand², M. Baylis¹ ¹Chester (United Kingdom), ²Montpellier (France) **21.044** Detection of morphological differences between Batrachochytrium dendrobatidis Brazilian strains C. Lambertini, D. D. S. Leite, A. K. Siqueira, L. F. Toledo Campinas, SP (Brazil) 21.045 Climate change modelling of West Nile Virus and avian malaria in Madagascar C. L. Risley¹, S. Goodman², M. Baylis¹ ¹Chester (United Kingdom), ²Chicago, IL (USA)

Diseases at the Interface of Humans, Wildlife and Other Animals

- 21.046 Mass spectrometric approaches for the identification of candidate serum biomarkers for Schistosomiasis mansoni infected mice
 M. I. H. I. Kardoush, B. Ward Montreal, Qc (Canada)
- 21.047 Improved collaboration at the animal-human interface a European initiative to facilitate early detection and joint rapid risk assessments of outbreaks of non-foodborne zoonoses
 A. Gervelmeyer¹, C. Gossner²
 ¹Parma (Italy), ²Stockholm (Sweden)
- **21.048** Human interactions with wildlife associated with monkeypox in Tshupa District, Democratic Republic of Congo

B. Monroe¹, M. Reynolds¹, D. Tack¹, C. Moses², J. Malakani³, D. Carroll¹ ¹Atlanta, GA (USA), ²Washington, DC (USA), ³Kinshasa XI (Congo, Democratic Republic of)

- 21.049 Epizootic situation and development tools for detection of Q-fever in Ukraine
 L. Marushchak, A. Golovko, O. Deriabin Kiev (Ukraine)
- 21.050 Hepatitis E in Belgium: an imported disease or a viral zoonosis?
 M.Wautier, V. Hutse, S. Van Gucht Brussels (Belgium)
- 21.051 Evaluation of risk factors for autochthonous Leptospirosis in Austria
 C. Wallner¹, H. Flick¹, F. Allerberger², T. Valentin¹, K. Seeber¹, I. Zollner-Schwetz¹, J. Wagner¹, W. Duettmann¹, R. Krause¹, M. Hoenigl¹
 ¹Graz (Austria), ²Vienna (Austria)
- 21.052 VNTR-based molecular epidemiological study of *Francisella tularensis* ssp. *holarctica* biovar II strains isolated from humans, European brown hares and red foxes in Austria from 1995 to 2010
 S. Revilla-Fernández¹, K. Reisp¹, E. Hofer², H. Plicka³, F. Schmoll²
 ¹Moedling (Austria), ²Mödling (Austria),

³Vienna (Austria), ²Modling (Austria)

- 21.053 Echinococcus multilocularis, etiological agent of alveolar echinococcosis, in Slovakia
 D.Antolova, M. Miterpakova, G. Hr ková Kosice (Slovakia)
- 21.054 Parasite circulation in the protected areas of the Tatra National Park, Slovakia
 Z. Hurnikova¹, M. Miterpakova¹, B. Chovancova² ¹Kosice (Slovakia), ²Tatranská Lomnica (Slovakia)
- **21.055** Contact with rodents in Khon Kaen Province, Thailand

K. Suwannarong¹, S. Woldehanna², Z. Rambeloson², R. Chapman³, S. Zimicki² ¹Bangkok (Thailand), ²Washington DC, (USA), ³Pathumwan (Thailand)

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

- 21.056 Orf virus infection in a hunter presumably transmitted by game in Western Austria M. Kitchen, N. Romani, A. Zobl, A. Windisch, W. Glawischnig, M. Schmuth, H. P. Huemer Innsbruck (Austria)
- **21.057** First description of *Bartonella bovis* in domestic ruminants in Israel

N. Rudoler Rehovot (Israel)

- 21.058 Analysing phylogenetic relationships of *Pneumocystis carinii f. Sp. suis* to other *Pneumocystis* species
 C.Weissenbacher-Lang, N. Nedorost, H. Weissenboeck
 Vienna (Austria)
- 21.059 Toxoplasma gondii detected in wild and captive European woodchuck (Marmota marmota)
 S. Richter, Z. Bagó, S. Revilla-Fernández, H. Weinberger, F. Schmoll Mödling (Austria)
- **21.060** Monitoring of avian influenza and Newcastle Disease among wild birds of different ecological groups in Azov and Black sea region of Ukraine in 2006–2011

D. Muzyka¹, B.T. Stegniy¹, M. Pantin-Jackwood², A. Stegniy¹

¹Kharkiv (Ukraine), ²Athens, GA (USA)

- 21.061 Risk factors for acquiring nephropatia epidemica in Sweden, 2011–2012: A case control study
 A. M. Gherasim¹, M. Hjertqvist², Å. Lundkvist³, S. Kühlmann-Berenzon³, J.Verner Carlsson³, A. Wallensten³
 ¹Stockholm (Sweden), ²SOLNA (Sweden), ³Solna (Sweden)
- 21.062 Case report: Outbreak of Salmonella Dublin in wildlife associated with infection in cattle
 W. Glawischnig', A. Wallner', C. Kornschober², K. Schoepf¹
 'Innsbruck (Austria), ²Graz (Austria)
- **21.063** Using wildlife surveillance to provide evidence of freedom from *Echinococcus multilocularis* in Northern Ireland.

E. Courcier¹, S. Fee², F. Malone², K. McBride¹, I. McKeown¹, D. Abernethy³, F. Menzies¹ ¹Belfast (United Kingdom), ²Omagh (United Kingdom), ³Pretoria (South Africa)

- 21.064 Zoonotic Poxviruses isolated from symptomatic cattle in Sirajganj District, Bangladesh E. Lederman¹, S. U. Khan², S. Luby³, H. Zhao⁴, Z. Braden⁴, K. Karem⁴, I. Damon⁴, M. Reynolds⁴, Y. Li⁴
 ¹San Diego, CA (USA), ²Dhaka (Bangladesh), ³Stanford, CA (USA), ⁴Atlanta, GA (USA)
- 21.065 Surveillance of West Nile Virus in birds in Los Angeles County—A successful and proactive program to anticipate human outbreaks
 G. Lamielle, K. Ehnert, E. Beeler, T. Scott Los Angeles, CA (USA)

- 21.066 Survey of infectious disease agents of zoonotic or epizootic significance in Austrian wildlife
 A. Steinrigl¹, Z. Bago¹, S. Revilla-Fernández¹, E. Hofer¹, M. Dünser², E. Wodak¹, A. Loitsch¹, J. Hofrichter³, A. Deutz⁴, F. Schmoll¹
 ¹Mödling (Austria), ²Linz (Austria), ³Graz (Austria), ⁴St. Lambrecht (Austria)
- 21.067 Ecology of hemorrhagic fever with the renal syndrome (HFRS) in the West Kazakhstan Oblast (WKO)
 T. Ayazbayev, F. Bidashko, A. Grazhdanov,
 M. Pak, V. Surov, L. Belonojkina, A. Andriushenko,
 A. Zakharov, B. Kdyrsikh, A. Kuspanov Uralsk (Kazakhstan)
- 21.068 Epidemiological and clinical manifestations of Crimean-Congo hemorrhagic fever (CCHF) in the Southern Kazakhstan Region (SKR)
 R. Egemberdiyeva, Z. Shapiyeva Almaty (Kazakhstan)
- 21.069 Building capacity in ecohealth in Asia: impact on research activities
 D. Hall¹, M. Lunney², Q. B. Le¹, J. Davidson³
 ¹Calgary, AB (Canada), ²Santiago (Chile), ³Charlottetown, PE (Canada)
 21.070 Animal bites and the prevention of rabies
- 21.070 Animal bites and the prevention of rabies in Albania
 E.Tomini¹, K. Mersini¹, J. Sulo¹, S. Tobli², S. Bino¹

¹Tirana (Albania), ²Kukes (Albania) **21.071** Evaluation of cross-reactivity of human influenza

antibodies against H1, H2 and H3 avian influenza virus subtypes

M. S. Pizzuto¹, I. Monne¹, S. Maniero¹, A. Burattin¹, M. S. Beato¹, V.Valastro¹, M. Mancin¹, E.Vicenzi², G. Cattoli¹, I. Capua¹ ¹Padua (Italy), ²Milan (Italy)

- 21.072 Detection and phylogeny of coronavirus in Costa Rica neotropical bats
 A. E. Moreira-Soto¹, L. M.Taylor¹, B. Rodriguez¹, E. Corrales-Aguilar¹, C. Jimenez²
 ¹San Jose (Costa Rica), ²Heredia (Costa Rica)
- 21.073 Genetic diversity of *Brucella* isolates in Georgia
 E. Zghenti, M. Zakalashvili, L. Malania, L. Sanodze,
 T. Akhvlediani, N. Kokaia, E. Mamisahsvili, N. Trapaidze
 Tbilisi (Georgia)
- 21.074 Human brucellosis in Georgia: prevalence and distribution of the infection
 N.Trapaidze, T. Akhvlediani, L. Sanodze, N. Garuchava, N. Kokaia, N. Chitadze, S. Saghinadze, L. Malania, M. Ramishvili Tbilisi (Georgia)
- 21.075 Evidence for transfer of West Nile Virus between African countries by migrating birds: comparing migratory connectedness with West Nile phylogenetic connectedness
 C. L. Risley, A. Rich, M. Baylis Chester (United Kingdom)

International Meeting on Emerging Diseases and Surveillance 2013

- 21.076 Avian influenza H5 subtype antibodies in apparently healthy local poultry in live bird markets in Jigawa State, Nigeria
 R. Miko¹, A. Assam², P.A. Abdu²
 ¹Dutse (Nigeria), ²Zaria (Nigeria)
- 21.077 Perils of pigs and PICCs: septic shock secondary to two plant pathogens in a pig farmer
 H.Yadav, D. Manning
 Rochester, MN (USA)
- 21.078 Two outbreaks of hemorrhagic fever with renal syndome in Albania
 P. Biberaj, M. Kota, N. Como, E. Koreta, E. Tomini, D. Kraja, A. Ndreu, S. Bino Tirana (Albania)
- 21.079 Pathogenic *Leptospira* in wild rodents in Cape Verde
 A. Martín-Alonso¹, P. Foronda¹, A. Fernandez-Alvarez¹, G. Bonnet¹, C. Feliu², B.Valladares¹
 ¹Santa Cruz de Tenerife (Spain), ²Barcelona (Spain)

Diseases of Animals

21.080 Brucella abortus in cattle and buffaloes in *cancelled* Bangladesh

M. S. Rahman

Mymensingh (Bangladesh)

21.081 Evolution of U.S. foot-and-mouth disease response strategy
 H.Allen, A. Taylor
 McLean, VA (USA)

21.082 Health problems on the pig farm and detection of antibodies against *Mycoplasma hyopneumoniae* (case study)

M. Prokeš, A. Ondrejková, R. Ondrejka, Ľ. Korytár, E. Slepecká, P. Čechvala, A. Récky Kosice (Slovakia)

- 21.083 Prion expression inhibition by antisenseoligodeoxynucleotides for Transmissible Spongiform Encephalopathy (TSE) treatment and prevention
 L. Ivanytska, A. Zaichenko, V.VIizIo
 Lviv (Ukraine)
- 21.084 Associations between intestinal lesions and detection of *Clostridium perfringens* type A or beta-2 toxin in neonatal piglets with diarrhoea H. Kongsted¹, B. Jonach², B. Kokotovic², J. P. Nielsen²

¹Kjellerup (Denmark), ²Copenhagen (Denmark)

21.085 Prevalence of *Toxoplasma gondii* in Greek swine industry

V. Papatsiros¹, **D. Stougiou**², S. Boutsini², L. Athanasiou¹, G. Christodoulopoulos¹, P.Tsampalis³, A. Bisias² ¹Karditsa (Greece), ²Athens (Greece), ³Larissa (Greece)

- 21.086 Serosurveillance of foot and mouth disease virus in Asian elephants in Thailand
 D. Ounpomma¹, W. Linchongsubongkoch², P. Charoenphan³, W. Pintawong³, T. Yano³
 ¹Meung, Khon Kaen (Thailand), ²Pakchong, Nakhonratchasima (Thailand), ³Meung, Surin (Thailand)
- 21.087 Chemical decontamination of live animals contaminated with African swine fever virus Y. Selyaninov¹, I. Egorova¹, V. Balishev¹,
 O.Tatarchuk²

¹Pokrov (Russian Federation), ²Moscow (Russian Federation)

- 21.088 Detection of AsHV-5 in a herd of 266 Lipizzaners throughout a period of two years
 J. O. Rushton, J. Kolodziejek, N. Nowotny Vienna, Vienna (Austria)
- 21.089 Occurrence of *Clostridium perfringens* type A and its toxins in neonatal piglets from four Danish pig farms.
 B. Jonach¹, B. Kokotovic¹, H. Kongsted², M. Boye¹, T. Kåre Jensen¹
 ¹Copenhagen (Denmark), ²Kjellerup (Denmark)
- 21.090 Seroepidemiology of Contagious Bovine Pleuropneumonia in Kaduna State, Nigeria
 A. Suleiman, M. Bello, L.T. Zaria, A. A. Dzikwi Zaria (Nigeria)
- 21.091 Efficiency of *B. anthracis* detection in soils having different physicochemical properties
 I. Egorova, Y. Selyaninov
 Pokrov (Russian Federation)
- 21.092 Sero-prevalence of foot and mouth disease in small ruminants of Pakistan
 U. Farooq, A. Ullah, A. Latif, K. Naeem, A. Bin Zahur, M. Hussain Islamabad, ICT (Pakistan)
- **21.093** Persistence of equine piroplasmosis in polo *cancelled* and pleasure horses in Nigeria

P.W. Mshelia Zaria (Nigeria)

- 21.094 Real-time PCR for diagnosis of contagious equine metritis (CEM)
 S.Artiushin¹, U. Balasuriya¹, M. Erdman²
 ¹Lexington, KY (USA), ²Ames, IA (USA)
- 21.095 Understanding the pig backyard sector for realistic prevention and control of African swine fever

D. Beltrán-Alcrudo Rome (Italy)

Foodborne and Waterborne Diseases

21.096 Study on effect of acetic acid spray on *Escherichia coli* load and meat PH at an export abattoir, Modjo, Ethiopia. **T. J. Beyene**, A. W. Wudie, G. Zewude, T. Ali Debre Zeit (Ethiopia)

International Meeting on Emerging Diseases and Surveillance 2013

21.097 Study of *Listeria monocytogenes* contamination in raw milk and some Moroccan traditional dairy derivatives (*Lben* and *Jben*)

B. El Marnissi, L. Bennani, A. El Ouali Ialami, R. Belkhou Fès (Morocco)

- 21.098 Rapid cessation of acute diarrhea in pediatric patients using a novel plant extract
 A. S. Dover¹, T. Noguera²
 ¹Aptos, CA (USA), ²Managua (Nicaragua)
- 21.099 Occurrence of *Echinostoma revolutum* metacercariae and other larval trematode infections in freshwater snails from Chiang Mai, Thailand
 K. Chantima¹, J.Y. Chai², C. Wongsawad¹
 ¹Chiang Mai (Thailand), ²Seoul (Korea, Republic of)
- 21.100 Characterization of Salmonella enterica subsp. enterica monophasic variant 4,[5],12:i:- human isolates in Slovakia
 V. Majtan, L. Majtanova, J. Majtan Bratislava (Slovakia)
- 21.101 Fresh fish as a potent vehicle for the transmission of Salmonellosis in Egypt
 A.A.Tayel¹, W. El-Tras², O. A. Abdel-Monem¹
 ¹El-Sadat City (Egypt), ²Kafrelsheikh (Egypt)
- **21.102** Evaluation of completeness of the mandatory notification system for salmonellosis and shigellosis, Greece, 2011.

K. Mellou, T. Sideroglou, A. Kallimani, M. Potamiti-Komi, E. Lillakou, T. Georgakopoulou, C. Hadjichristodoulou Athens (Greece)

- 21.103 Viral gastroenteritis outbreaks in school settings in a Greek village, January 2012
 K. Mellou¹, T. Sideroglou¹, M. Potamiti-Komi¹, E. Lillakou¹, P. Kokkinos², P. Ziros², A. Vantarakis², T. Georgakopoulou¹
 ¹Athens (Greece), ²Patras (Greece)
- 21.104 Early detection of severe complications with Escherichia coli OIII in a large outbreak in Japan
 T. Misaki, Y.Yahata, M. Nagira, Y.Tada, K. Taniguchi, K. Oishi, N. Okabe Tokyo (Japan)
- 21.105 Prevalence and risk association for *Trichinella* infection in domestic and free range pigs in Greece
 S. Boutsini¹, D. Stougiou¹, V. Papatsiros²,
 A. Panteli¹, M. Bisia²
 ¹Athens (Greece), ²Karditsa (Greece)
- 21.106 Sorbitol-fermenting VTEC O157 caused an outbreak via unpasteurized milk and farm visits, Finland 2012
 S. Salmenlinna¹, R. Rimhanen-Finne¹, H. Lundström², A. Jaakkonen¹, A. Pihlajasaari¹, A. Vainio¹, S. Toikkanen¹, O. Lyytikäinen¹,

A. Siitonen¹, S. Hallanvuo¹ ¹Helsinki (Finland), ²Turku (Finland) **21.107** Characterization of *Staphylococcus aureus* cancelled producing biofilm isolated from food and clinical samples

G. La Salandra, M. G. Basanisi, R. Pedale, A. Di Taranto, D. Chiocco Foggia (Italy)

- 21.108 The Italian survey on prevalence of *Listeria monocytogenes* in RTE meat products and cheeses
 V.A. Prencipe, S. Antoci, R. D'Aurelio,
 D. Neri, G. A. Santarelli, F. Cito, S. Iannetti,
 F. De Massis, P. Calistri
 Teramo (Italy)
- **21.109** Detection of monophasic Salmonella Typhimurium and its antimicrobial susceptibility throughout pigs' life cycle from three industrial pig herds in Portugal

M. M. Centeno¹, L. Fernandes¹, A. Belas¹, N. Couto¹, T. Nunes¹, V. Almeida¹, L. Alban², C. Pomba¹ ¹Lisbon (Portugal), ²Kobenhavn V (Denmark)

- 21.110 Kudoa septempunctata caused outbreak in humans with raw flounder ingestion
 Y.Yahata¹, T. Ohnishi², Y. Sugita-Konishie³, T. Toyokawa⁴, N. Nakamura⁵, K. Taniguchi¹, N. Okabe⁶
 ¹Tokyo (Japan), ²Setagaya (Japan), ³Setagaya-ku (Japan), ⁴Haebaru-cho (Japan), ⁵Cyuo-ku (Japan), ⁶Kawasaki (Japan)
- **21.111** High prevalence of antibodies against *Leptospira* in Austrian adults: a nationwide cross sectional survey

W. Poeppl¹, M. J. Orola¹, H. Herkner¹, A. Faas¹, G. Mooseder¹, M. Müller², F. Allerberger¹, H. Burgmann¹ ¹Vienna (Austria), ²Mödling (Austria)

- 21.112 Seasonality of diarrhea in children of Gilgit, northern Pakistan: nastier episodes and shift to older ages as summer unfolds
 Z. Rasmussen¹, B. McCormick¹, W. J. Alonso¹, N. Samji², J. Baker¹
 ¹Bethesda, MD (USA), ²Hamilton, ON (Canada)
- 21.113 Molecular characterization and epidemiological trend of Hepatitis A virus isolates in a tertiary care hospital in North India
 M. P. Singh¹, M. Majumdar¹, B. R. Thapa¹,
 D.K. Cuntal J. Khumpal, B. Budhathalii, B. Batha²

P. K. Gupta¹, J. Khurana¹, B. Budhathoki¹, R. Ratho² ¹Chandigarh (India), ²Chandigarh, Chandigarh (India)

21.114 Food safety requires public-private partnerships
T.Wilke ,V. Raab, O. Breuer, M. Hamer,
B. Petersen
Bonn (Germany)

International Meeting on Emerging Diseases and Surveillance 2013

Infections of Public Health Significance

- 21.115 Knowledge attitude and behavior of medical students towards safety in student laboratory K. Chaicom, B. Palaeng, P. Kungsang Khon Kaen (Thailand)
- 21.116 A 20-years retrospective cohort study of HIV/AIDS situation among hill tribe vulnerable population, Thailand
 T.Apidechkul Chiang Rai (Thailand)
- 21.117 Prevalence of human metapneumovirus infection in hospital wards comprising patients with severe motor and intellectual disabilities
 S. Matsuda¹, M. Noda²

Tohon (Japan), ²Tokyo (Japan)

- 21.118 The first report of *Mycobacterium riyadhense* lung infection with HIV and CMV co-infection
 M.A. Garbati, A. M. Hakawi Riyadh, (Saudi Arabia),
- 21.119 Prevalence of B6, B12 and folic acid deficiency in HIV positive patients
 B.Achappa, D. Madi Mangalore (India)
- 21.120 TB/HIV among hill tribe marginalized vulnerable population, Thailand
 T.Apidechkul
 Chiang Rai (Thailand)
- 21.121 Highly active antiretroviral therapy maintains the population of Langerhans cells in the tongue from Human Immunodeficiency Virus - I infected patients
 R. Gondak¹, F.V. Mariano¹, T. Mauad²,

C. P. Almeida¹, P.A. Vargas¹ ¹Piracicaba, (Brazil), ²São Paulo (Brazil)

- 21.122 Outbreak of tuberculosis among elderly in geriatric home
 B.Achappa, D. Madi, P. Adhikari, S. Raj, M. Tripathy
 Mangalore, Karnataka (India)
- 21.123 Prevalence of *Clostridium difficile* among cases of antibiotic associated diarrhea in hospitalized patients in an Egyptian hospital
 M. M. AbdelHaleim, N. Nawar, R. Elsherif, A. Farouk
 Cairo (Egypt)
- 21.124 Tuberculous meningitis at the Hospital Nacional Dos de Mayo, Lima, Peru: 2005–2010
 T. Metcalf¹, J. Soria², S. Montano³, E.Ticona², M. Kasper³, J. Zunt⁴
 ¹Bangkok (Thailand), ²Lima (Peru), ³Callao (Peru), ⁴Seattle, WA (USA)

21.125 The epidemiology and burden of Q fever in the UK 1999–2011

H. Kirkbride, A. Walsh, K. Halsby, D. Morgan London (United Kingdom)

- 21.126 Role of antiplatelet antibodies in the development of trombocytopenia in patients with chronic hepatitis C
 N. Pshenichnaya, G. Kuznetsova, E. Romanova Rostov-on-Don (Russian Federation)
- 21.127 The outcome of chronic hepatitis C (CHC) depends of degree of intensity and rate of progression of fibrosis in liver tissue
 E. Romanova, N. Pshenichnaya, G. Kuznetsova, M. Ladychuk, T. Belashova
 Rostov-on-Don (Russian Federation)

Poster Presentations I

Saturday, February 16, 2013 Klimt Ballroom I • Upper Level 11:45-13:15

Infections of Public Health Significance (continued)

21.128 The efficiency of *Helicobacter pylori* eradication therapy in prevention of thrombocytopenia in patients with HCV and *Helicobacter pylori* co-infection

N. Pshenichnaya, G. Kuznetsova, E. Romanova Rostov-on-Don (Russian Federation)

- 21.129 Epidemiological evaluation of spatio-temporal and genotypic clustering of *Mycobacterium tuberculosis* in Ontario, Canada
 A. Tuite¹, D. Fisman¹, D. Alexander², J. Guthrie², A. Marchand-Austin², K. Lam², J. Ma², M. Whelan², B. Lee², F. Jamieson²
 ¹Toronto, ON (Canada), ²Etobicoke, ON (Canada)
- 21.130 Has the epidemiology of bacterial meningitis changed in a limited-resource country (Kosovo)
 S. A. Namani, R. Koci, B. Koci, E. Qehaja, L. Ajazaj, M. Mehmeti
 Prishtine (Kosovo, Republic of)
- 21.131 Identification of bacterial community in biofilms formed in biliary stents retrieved from patients
 C.Vaishnavi, P. Kapoor, R. Kochhar Chandigarh (India)
- 21.132 Risks factors and level of awareness of bovine tuberculosis in Kaduna metropolis, Nigeria
 E. G. Haruna, C. A. Kudi, M. Bello, I. Ajogi Zaria (Nigeria)

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

21.133 Multidrug-resistant tuberculosis: A review of diagnosed cases over a 5 year-period in a Portuguese hospital

D. Póvoas, J. Machado, F. Maltez Lisbon, Not US/Canada (Portugal)

21.134 suPAR correlates with renal function and may predict bacteremia in SIRS patients: A cohort study
W. Krammer, J. Wagner, R. Raggam, E. Leitner, F. Prüller, A. J. Grisold, K. Seeber, W. Duettmann, R. Krause, M. Hoenigl

Graz (Austria)

- 21.135 Mycobacterial infection in cosmetic surgery: A case report and review of the literature
 L. Frye, S. Hasan, K. J. Leneweaver, P. Dilanchian, N. Bray, D. Droller
 Fort Lauderdale, FL (USA)
- **21.136** Prevalence of *S. hematobium* infection among school children living along the south-western shores of Lake Malawi

S.A. Kayuni¹, R. Peeling², P. Makaula³ ¹Blantyre (Malawi), ²London (United Kingdom), ³Mangochi (Malawi)

21.137 The duration of effects of antibiotic exposures on the risk of *Clostridium difficile* infection (CDI): a cohort study

K.A. Brown, N. Daneman, R. Moinedden, D. Fisman

Toronto, ON (Canada)

- 21.138 Tuberculosis—major killer of adult urban
- cancelled women: Demographic and Health Survey (DHS) from Pakistan

S.Awan

Karachi (Pakistan)

- 21.139 Healthcare-associated infections due to carbapenemase-producing *Enterobacteriaceae* in Hungary
 R. Szabó, K. Böröcz, A. Szönyi Budapest (Hungary)
- **21.140** The discovery of EMRSA-15 in environmental *staphylococci* isolates

H. Mkrtchyan, R. Cutler London (United Kingdom)

- 21.141 Risk factors associated with seropositivity against Lyme borreliosis: Results from a representative serosurvey of adults in Germany
 H.Wilking¹, V. Fingerle², C. Klier², M.Thamm¹, K. Stark¹
 ¹Berlin (Germany), ²Oberschleissheim (Germany)
- 21.142 Pulmonary involvement of Brucellosis in patients treated in Kosovo
 E. Qehaja Bucaj, S. A. Namani, L. Ajazaj Berisha, M. Mehmeti
 Prishtina (Kosovo, Republic of)

 21.143 Clostridium difficile infection in a private hospital of Mexico City. Incidence rate and epidemiological features during 2011 - 2012
 J. Reyes Mar, L. Rojo Gutierrez, P. Leal Moran,

J. Reyes Mar, L. Rojo Gutierrez, P. Leal Moran, L. Cabrera Ruiz, N. Perez Hernandez, C.Y. Ruiz Hernandez, G. Santillan Lopez, M. D. L. Robles Hernandez, E. Aleman Aguilar, L. E. Soto Mexico City, Mexico City (Mexico)

21.144 Human parasitic ova and cyst in local food drinks sold in open markets in Enugu municipality, South-East, Nigeria
C.A. Ekwunife¹, C. I. Okafor¹, D. N. Aribodor¹,

C.A. Ekwunite⁺, C. I. Okator⁺, D. N. Arit M. N. Ezeunala², C. N. Ukaga³ ¹Awka (Nigeria), ²Abuja (Nigeria), ³Owerri (Nigeria)

- 21.145 Seroprevalence of Lassa fever and infection control practice among health workers in an endemic suburban community in Nigeria
 E.A.Tobin¹, D.A. Asogun¹, G. Akpede¹, P. Okokhere¹, S. Gunther², C. Happi³
 ¹Irrua, Edo (Nigeria), ²Hamburg (Germany), ³Boston, MA (USA)
- 21.146 Status of TB indicators in Austria
 E. J. Simons, A. Indra, S. Pfeiffer, F. Allerberger, D. Schmid Vienna (Austria)
- 21.147 Increasing incidence of pertussis in Austria, 2005–2011
 S.-W. Jian, D. Schmid Vienna (Austria)
- 21.148 Assessment of awareness and practices of secondary school students on lassa fever in Nigeria
 D.A.Asogun¹, E. A. Tobin¹, N. Akpede¹,

G. Akpede¹, S. Gunther², S. Okogbenin¹ ¹Irrua, Edo (Nigeria), ²Hamburg (Germany)

- 21.149 Potential outbreak of rabies in bats in Los Angeles County, USA
 T. Scott, G. Lamielle, K. Ehnert, E. Beeler Los Angeles, CA (USA)
- 21.150 Performance of QuantiFERON TB Gold in the detection of latent tuberculosis infection among healthcare workers (HCWs) in Akwa Ibom State, Nigeria
 A. N. Umoh¹, A. E. Asuquo², L. N. Abia-Bassey², E. O. Ibeneme²
 ¹Uyo (Nigeria), ²Calabar (Nigeria)
- 21.151 Prevalence of methicillin-resistant Staphylococcus aureus (MRSA) in high-density livestock farming areas along the Dutch-German border:
 H.Aangenend¹, R. Köck², K. Velden van der¹, J. Hautvast¹, A. Friedrich³, A. Voss¹, J. W. Paget¹
 ¹Nijmegen (Netherlands), ²Munster (Germany), ³Groningen (Netherlands)

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

- 21.152 Lassa fever control: Assessment of food hygiene practice among market traders in Nigeria
 E.A.Tobin¹, D. A. Asogun¹, N. Akpede¹,
 E. Ogbaini¹, C. Happi², G. Akpede¹
 ¹Irrua, Edo (Nigeria), ²Boston, MA (USA)
- 21.153 Active tuberculosis in patients under therapy with TNF-α inhibitors
 L. Mejdoubi¹, T. Barisani-Asenbauer², R. Rumetshofer¹

¹Vienna (Austria), ²Wien, Austria (Austria)

- 21.154 Evaluation of acute flaccid paralysis suspected cases reported to the surveillance system in Akwa-Ibom State April 2006–April 2012.
 W. E. Nwachukwu¹, B. E. Bassey², J. G. Ebuk², P. Nguku³, M. N. Aghaji¹
 ¹Enugu (Nigeria), ²Uyo (Nigeria), ³Abuja (Nigeria)
- 21.155 Evaluation of Acute Flaccid Paralysis surveillance system- Zamfara State, Nigeria, 2011
 K. I. Getso¹, S. Gidado¹, P. Nguku¹, O. Biya¹, S. H. Idris², K. Sabitu²
 ¹Abuja (Nigeria), ²Zaria (Nigeria)
- 21.156 KAP, housing standards and risk factor analysis for seroprevalence to Lassa fever in a rural community of Edo state, Nigeria
 D.A.Asogun¹, G. Akpede¹, E. A. Tobin¹, S. Gunther², N. Akpede¹
 ¹Irrua, Edo (Nigeria), ²Hamburg (Germany)
- 21.157 A study of viral load and genotype association among HCV infected patients in a tertiary care hospital of Pakistan
 S.Aslam¹, T. Ijaz², B. Munir Ahmad¹,
 - S. Ali Raja¹, S. Ijaz¹
 - ¹Lahore (Pakistan), ²Lahore, punjab (Pakistan)
- 21.158 Immune-based therapy against *Clostridium difficile* infection

J.A. Steele, J. Sponseller, S. Tzipori, D. Schmidt North Grafton, MA (USA)

- 21.159 Cross-sectional survey on seroprevalence of hepatitis E virus in Austria: pilot study at the Austrian armed forces
 H. Lagler, W. Poeppl, H.-M. Winkler, H. Herkner, A. Faas, G. Mooseder, H. Burgmann Vienna (Austria)
- 21.160 Incidence of tuberculosis after initiation of antiretroviral therapy in Georgia; Risk factors of mortality among HIV-infected patients
 A.Abutidze¹, T.Tsertsvadze¹, R. Kempker², L. Sharvadze¹, N. Chkhartishvili¹, M. Magee², C. del Rio²

- 21.161 Trends in the clinical features and mortality in hospitalised Lassa fever patients in Nigeria
 P. Okokhere, D. Asogun², G. Akpede Irrua (Nigeria)
- 21.162 Detection and genetic characterization of a Brucella infection in Saudi patients
 T. Uzzaman, M. Elfakhei Riyadh (Saudi Arabia)
- 21.163 Serologic evaluation of Crimean-Congo hemorrhagic fever in human population of endemic and non endemic areas in Albania
 S. Bino¹, E.Tomini¹, M. Kota¹, S.Tobli², J. Sulo¹, A. Simaku¹, N. Como¹, A. Papa³
 ¹Tirana (Albania), ²Kukes (Albania), ³Thessaloniki (Greece)
- 21.164 Epizootic and laboratory diagnostic methods of anthrax within the scope of CBR GG-18 project
 M. Zakareishvili, M. Donduashvili, M. Kokhreidze, M. Nikolaishvili Tbilisi (Georgia)
- 21.165 Opportunistic infections in HIV/AIDS patients in Jayapura City Papua Province, Indonesia
 Y.Y. R. Mirino, A. Oktavian, A. M. Juliana Jayapura (Indonesia)
- 21.166 West Nile Virus is moving eastward in North Eastern Italy
 P. D'Agaro¹, V. De Angelis², D. Franchi³,
 T. Gallo², P. Martelli⁴, M. Palei¹, A. Perosa⁵,
 M. Ruscio⁶, D. Santon¹, M. Stecchina³
 ¹Trieste (Italy), ²Udine (Italy), ³Gorizia (Italy),
 ⁴Pordenone (Italy), ⁵Latisana (Italy),
 ⁶San Daniele (Italy)
- 21.167 Challenges in the management of patients with leprosy in Msambweni District, Kenya
 S. K. Kazi
 Nairobi (Kenya)
- 21.168 Disaster medical assistance team (DMAT) activity and infectious disease and control in 2011 Great East Japan earthquake
 Y. Kohayagawa, Y. Koido, H. Kondo Tokyo (Japan)
- 21.169 Wild polio virus outbreak in Kebbi State, Nigeria 2011
 B. S. Bako¹, P. Nguku¹, O. Biya¹, K. Sabitu², S. Gidado¹

¹Abuja (Nigeria), ²Zaria (Nigeria)

¹Tbilisi (Georgia), ²Atlanta, GA (USA)

International Meeting on Emerging Diseases and Surveillance 2013

Infections Related to Travel and Migration

21.170 Global migration and tuberculosis trends in non-endemic country

A. M. S.A. AL-Harbie Rumaithiya (Kuwait)

21.171 A case of imported dracunculiasis—South Omo, *cancelled* Southern Ethiopia, May 2011

G. E. Yembo

Addis Ababa (Ethiopia)

- 21.172 The use of diagnostic databases for arbovirus monitoring and surveillance; a feasibility study with a focus on dengue virus
 N. Cleton¹, C. Reusken¹, M. de Jong², J.-L. Murk³, A. van der Eijk³, M. Koopmans³
 ¹Bilthoven (Netherlands), ²Amsterdam (Netherlands), ³Rotterdam (Netherlands)
- 21.173 Dengue virus 4 infection with thrombocytopenia and acaclculous cholecystitis in a British traveller
 S. Mankad, B. Kapadiya Ahmedabad, (India)
- 21.174 Understanding causes of death amongst Indonesian Hajj pilgrims: Comparison of verbal autopsy and death certificate data
 M. Pane¹, S. Imari¹, K. Alwi¹, N. Kandun¹,
 G. Samaan²

¹Jakarta (Indonesia), ²Canberra, ACT (Australia)

- 21.175 Disseminated histoplasmosis in a domestic cat imported from the USA to Austria
 A. Klang, I. Loncaric, J. Spergser, S. Eigelsreiter, H. Weissenboeck
 Vienna (Austria)
- 21.176 Learning from a case of imported rabies to establish a rabies control zone
 W. Petsophonsakul¹, T. Sripanya¹, P. Khawplod², W. Kheuanrat¹, S. Phornwisedsirikun¹, M. Srijun¹, S. Jaisuda¹, M. Moonpo³, A. Noguchi⁴, S. Inoue⁴
 ¹Chiang Mai (Thailand), ²Bangkok (Thailand), ³Lampang (Thailand), ⁴Tokyo (Japan)
- 21.177 Profile of measles confirmed cases notified to National CIEVS from January to June 2011, Brazil
 S. Lopes Dias¹, E.T. Masuda¹, M. É. Santos¹, W.A. Oliveira¹, P. Pereira Vasconcelos de Oliveira², G. S. Dimech¹
 ¹Brasilia, DF (Brazil), ²Brasilia (Brazil)
- 21.178 Risk of latent tuberculosis infection (LTBI) among personnel after conducting humanitarian assistance aboard a United States military hospital ship N.Adams, E. Lederman, J. S. Parrish San Diego, CA (USA)
- 21.179 Intervention strategies for preventing pathogen spread via illegal tiger trade network
 N. G. Patel¹, A. Sonricker Hansen²,
 J. Brownstein², D. Joly³
 ¹Philadelphia, PA (USA), ²Boston, MA (USA),
 ³Nanaimo, BC (Canada)

Innovations in Diagnostic Tests for Emerging Diseases

- 21.181 Isolation of the emerging foodborn pathogen Arcobacter from human stool A.-M.Van den Abeele¹, K. Houf² ¹Ghent (Belgium), ²Merelbeke (Belgium)
- 21.182 Use of saliva and urine for early dengue diagnosisG.YapSingapore (Singapore)
- 21.183 Unbiased detection of infectious agents in respiratory syndromes of poultry using a metagenomic approach
 E. Liais¹, G. Croville¹, J. Mariette², C. Klopp², C. Donnadieu², J. Lluch², M. Ducatez¹, C. Camus-Bouclainville¹, J.-L. Guérin¹
 ¹Toulouse (France), ²Castanet-Tolosan (France)
- 21.184 SHERPA×MAP: An innovative multiplex microsphere assay platform for the surveillance and rapid serodiagnosis of emerging viral diseases J.Vanhomwegen, S. Paulous, J.-C. Manuguerra, P. Despres, L. I. O. Sawoo Paris (France)

New Pathogen Discovery

- 21.185 Molecular identification and susceptibility pattern of clinical *Nocardia* species: emergence of *Nocardia* crassostreae as an agent of invasive nocardiosis
 S. J.Taj-Aldeen¹, A. Deshmukh¹, S. Doiphode¹, A. Abdul Wahab¹, M. Al lankawi¹, A. AlMuzrkchi¹, C. H. Klaassen², J. Meis²
 ¹Doha (Qatar), ²Nijmegen (Netherlands)
- 21.186 Bronchoalveolar lavage lateral-flow device test for diagnosing invasive pulmonary aspergillosis
 M. Hoenigl¹, W. Duettmann¹, C. Koidl¹, B. Waitzl¹,

K. Seeber¹, J. Wagner¹, K. Troppan¹, R. Raggam¹, R. Krause¹, C. Thornton² ¹Graz (Austria), ²Exeter (United Kingdom)

21.187 Acute febrile illness outbreak investigation— Zone I, Afar, Ethiopia, 2011
A. B. Woyessa, A. Ahmed, N. Asamneh Addis Ababa (Ethiopia)

International Meeting on Emerging Diseases and Surveillance 2013

<u> </u>	$\sim \sim$
Seccion))
20221011	~~

Poster Presentations II

Sunday, February 17, 2013 11:45-13:15

```
Bruckner/Mahler/Brahms • Upper Level
```

Influenza and Other Respiratory Infections

22.001 2009 H1N1 influenza A in Mexico City, second season: Clinical, laboratory and roentgenological characteristics of patients complicated with pneumonia during January and February 2012 at a Mexican General Hospital J. Reyes Mar, R.Valdez Vazquez, P. Rodriguez

Zulueta, F. Velez Perez, J. A. Garcia Vera Mexico City (Mexico)

22.002 Etiological surveillance of influenza like illness in pediatric population at the University Teaching Hospital in Lusaka, Zambia

P. Simusika

Lusaka (Zambia)

22.003 Northern or southern hemisphere vaccine composition: comparison of circulating influenza isolates in Uganda to the WHO recommended vaccine composition, 2007 to 2012

J.T. Kayiwa, T. Byaruhanga, R. Chiiza, B. Namagambo, B. Bakamutumaho, J. J. Lutwama Entebbe (Uganda)

- 22.004 Analysis of respiratory infectious diseases on a university campus: Application of mathematical models to pandemic influenza and other diseases
 H. Kamano¹, T. Mori¹, C. Murakami¹, T. Kugoh², C. Izumi², K. Tomiie², A. Nozaki¹
 ¹Takamatsu (Japan), ²Miki (Japan)
- 22.005 Severe acute respiratory infections in Nigeria: analysis of surveillance data 2010–2012
 M. S. Balogun, A. Adedeji, I. Olorundare, P. Nguku Abuja, FCT (Nigeria)
- **22.006** Clinical characteristics and laboratory admission values for differentiation between H1N1 influenza and influenza like illnesses

M. Hoenigl, J. Prattes, M. Drescher, K. Tovilo, H. Kessler, K. Vander, K. Seeber, A. Avian, R. Krause, H. Flick Graz (Austria)

22.007 SRSF3 interacts with nucleoprotein of Influenza A virus: Implications on viral mRNA nuclear export?
V. RMT Balasubramaniam¹, B. A. Tejo², T. H. Wai¹, A. R. Omar², I. Othman¹, S. S. Hassan¹
¹Bandar Sunway (Malaysia), ²Serdang (Malaysia)

- 22.008 Clinical features of human H5N1 influenza survival cases in Indonesia
 E. Sariwati, V. Setiawaty, B. Sutrisna, S. Giriputro Jakarta (Indonesia)
- 22.009 Improving decisions in clinical medicine: serum antibody titres and specific symptom patterns may classify categories of pandemic H1N1 influenza infection during pregnancy
 G.Arteaga, A. Cerbulo-Vazquez, C. Lopez-Macias, G. Cruz-Cureño, I. Bosco-Garate, L. A. Arriaga-Pizano, A. Isibasi, J. Mancilla Mexico City (Mexico)
- 22.010 Enhancing respiratory infection surveillance on the US/Mexico border- Arizona BIDS program sentinel surveillance data
 C. Golenko¹, O. McCotter¹, L. M. Erhart², D. M. Wolk¹, F. Vanskike¹, L. Patel¹

¹Tucson, AZ (USA), ²Phoenix, AZ (USA)

- 22.011 Integration of syndromic surveillance for monitoring influenza epidemic among children in rural China, 2011–2012
 M.Yu¹, Q. Zhao¹, Y. Zhu¹, T.Tao¹, V. K. Diwan², L. Cheng³, L. Palm⁴, G. Zhao¹, B. Xu¹
 ¹Shanghai (China), ²Stockholm (Sweden), ³Wuhan (China), ⁴Gävle (Sweden)
- 22.012 Influenza surveillance in the Pacific island countries and territories during the 2009 pandemic
 J. L. Kool¹, B. I. Pavlin², J. Musto³, A. Dawainavesi¹
 ¹Suva (Fiji), ²Boroko, NCD (Papua New Guinea), ³North Sydney (Australia)
- 22.013 Influenza mortality in the United States, 2009: Burden and timing
 A. M. Nguyen¹, A. Noymer²
 ¹Escondido, CA (USA), ²Irvine, CA (USA)
- 22.014 Clinical features of infections caused by influenza virus in 2009-2012
 K. Herrmannova, M. Trojanek, O. Dzupova, Z. Blechova, D. Tomickova, M. Havlickova, H. Jirincova, J. Kyncl, V. Maresova Prague (Czech Republic)
- 22.015 Influenza sentinel surveillance-Addis Ababa, Ethiopia, 2008–2012
 A. B. Woyessa, W. Ayele, E. Zemelak, D. Jima Addis Ababa, Addis Ababa (Ethiopia)
- 22.016 Monitoring of influenza and respiratory syncytial virus activity in children under 5 years of age in Dibrugarh district of Assam, northeast India, 2009–2011

D. Biswas, K.Yadav, P. J. Baruah, B. Borkakoty, J. Mahanta Dibrugarh, Assam (India)

International Meeting on Emerging Diseases and Surveillance 2013

- 22.017 Antiviral susceptibility of influenza A viruses obtained in Kenya 2008–2011
 M.Wadegu, W. Bulimo, R. Achilla, J. Majanja, S. Mukunzi, F. Osuna, J. Wangui, B. Opot, E. Wurapa Nairobi (Kenya)
- 22.019 Full genome analysis of H1N1pdm2009 influenza viruses circulating in italian pig herds
 A. Boni¹, A. Moreno², L. Di Trani¹, G. Zaccaria¹, S. Faccini², L. Alborali², M. B. Boniotti², D. Lelli², P. Cordioli², G. Vaccari¹
 ¹Rome (Italy), ²Brescia (Italy)
- 22.020 Full-length genome sequencing of Influenza A on Ion Torrent PGM[™] Sequencer
 G. Zaccaria¹, A. Boni¹, E. Alm², A. M. Moreno Martin³, P. Cordioli³, L. Di Trani¹, G. Vaccari¹
 ¹Rome (Italy), ²Solna (Sweden), ³Brescia (Italy)
- 22.021 Enterovirus 68 in Cuban Children with Acute Respiratory Tract infections
 M. D. L. C. Muné, A. Piñon La Havana (Cuba)
- 22.022 Severe acute respiratory infection surveillance on the US/Mexico border, 2010–2011 influenza season data from Arizona and California P. Kriner¹, M. Fierro¹, O. McCotter², C. Golenko², J. Smith³, L. Fajardo³, M. Fonseca-Ford³, R. M. Philen⁴, S. H. Waterman³, A. Phippard³
 ¹El Centro, CA (USA), ²Tucson, AZ (USA), ³San Diego, CA (USA), ⁴Atlanta, GA (USA)
- 22.023 Clinical and epidemiological pcture of respiratory infections causing viruses among hospitalized children in a rural community in India
 B. Pandey¹, S. Broor¹, S. Rai¹, V. Gupta¹, R. Wigh¹,

B. Pandey^{*}, S. Broor^{*}, S. Ral^{*}, V. Gupta^{*}, R. Wign^{*}, A. Krishnan¹, W. Sullender², D. Erdman³, R. Lal³ ¹Delhi (India), ²Alabama, AB (USA), ³Atlanta, GA (USA)

- 22.024 Assessing the mortality link between respiratory infections and heart disease: a time-series approach
 A. M. Nguyen¹, C. Li², A. Noymer²
 ¹Escondido, CA (USA), ²Irvine, CA (USA)
- 22.025 Respiratory virus mortality in the Southwest of England during the winter of 2010/2011
 K. Sithamparanathan, J. Lagan, P. Muir, R. Brindle
 Bristol (United Kingdom)

- 22.026 Application of nanofluid technology to multiple detection of respiratory viruses in pediatric respiratory diseases during 2011–2012 winter season in Mexico City
 C.O.Orozco-Sanchez, V.A.Hernandez-Hernandez, Y. Moreno-Valencia, J.A.Vazquez-Perez Mexico City (Mexico)
- 22.027 European surveillance network for influenza in pigs 3 (ESNIP 3)—Expanding our knowledge of the epidemiology and evolution of swine influenza viruses
 G. Simon¹, S. Reid², L. E. Larsen³, P. Kellam⁴, L. Kaartinen⁵, K.Van Reeth⁶, I. Markowska-Daniel⁷, E. Foni⁸, Á. Dan⁹, W. Loeffen¹⁰
 ¹Ploufragan (France), ²Surrey (United Kingdom), ³Copenhagen V (Denmark), ⁴Cambridge (United Kingdom), ⁵Helsinki (Finland), ⁶Ghent (Belgium), ⁷Puławy (Poland), ⁸Brescia (Italy), ⁹Budapest (Hungary), ¹⁰Lelystad (Netherlands)

New Approaches to Outbreak Surveillance and Monitoring

22.028 Adaptive-based system development association for early awareness-based dengue area in the city of Padang, West Sumatra Province I. Irene

Padang, West Sumatra (Indonesia)

22.029 SAGES update: open-source electronic disease surveillance software for use in resource-limited settings

B. Feighner, T. Campbell, J. Coberly, R. Wojcik, **S. Patel**, S. Lewis Laurel, MD (USA)

22.030 Reporting to international health and veterinary organizations using national electronic integrated disease surveillance system
 T.Wahl¹, A. Burdakov¹, A. Oukharov¹,
 S. Schillinger²

¹Overland Park, KS (USA), ²Copenhagen (Denmark)

22.03 I Timeliness of syndromic surveillance system in the early warning of influenza epidemics in rural China

T.Tao¹, Q. Zhao¹, M.Yu¹, F.Yang², H.Yuan², L. Palm³, W.Yan⁴, W.Yan⁵, B. Xu¹ ¹Shanghai (China), ²Nanchang (China), ³Gävle (Sweden), ⁴Stockholm (Sweden), ⁵Wuhan (China)

22.032 Digital disease surveillance: the global safety net C.Wenham

Aberystwyth (United Kingdom)

22.033 Are informal digital surveillance systems currently capable of detection disease outbreaks in real-time?
A. Magid, A. Gesser-Edelsburg, M. S. Green Haifa (Israel)

SUNDAY • February 17, 2013

International Meeting on Emerging Diseases and Surveillance 2013

- 22.034 Are developed countries missing polio cases?
 B. J. Paterson¹, D. Durrheim²
 ¹Newcastle (Australia), ²Wallsend (Australia)
- 22.035 Using influenza-like illness (ILI) data for early warning of respiratory disease outbreaks in rural China
 L.Tian¹, L.Tan¹, L. Liu¹, J. Zhang¹, S. Wei¹, W.Yan¹, W.Yan², L. Cheng¹, Y. Ding³, S. Nie¹
 ¹Wuhan (China), ²Stockholm (Sweden), ³Heideberg (Germany)
- 22.036 Applicability of different data sources in syndromic surveillance system for detecting infectious disease outbreaks in China
 J. Zhang¹, L. Tan¹, L. Liu¹, L. Cheng¹, W.Yan¹, W.Yan², S. Wei¹, V. K. Diwan², H. Dong³, S. Nie¹
 ¹Wuhan (China), ²Stockholm (Sweden), ³Heidelberg (Germany)
- 22.037 Open source health intelligence (OSHINT) for biological event characterization
 J. Blake¹, C. Ordun², S. Aslam³, A. Gentilcore³,
 V. Grigoryan³, C. Reffett⁴, N. Rosidi³, M. Shelton⁴,
 J. Klenk⁴
 ¹Washington, DC (USA), ²Atlanta, GA (USA),
 ³Rockville, MD (USA), ⁴McLean, VA (USA)
- 22.038 Intravenous Immunoglobulin—a serological sentinel

C. Planitzer, J. Modrof, T. R. Kreil Vienna (Austria)

22.039 Establishing a web-based application for *cancelled* respiratory pathogen biosurveillance within a diverse global partner network

J.A. Cockrill¹, A.Y.Tsai¹, T. Campbell², M. J. Cooper¹ ¹Silver Spring, MD (USA), ²Laurel, MD (USA)

- 22.040 Implementation of modern approaches to surveillance and outbreak investigation in Kazakhstan: evaluation of the long-term success of an epidemiology training course, 2011
 Y. Bumburidi¹, A. Zholshorinov ², C. Pitenko¹
 ¹Almaty (Kazakhstan), ²Astana (Kazakhstan)
- 22.041 Geographic information systems in epidemiological monitoring of malaria in UzbekistanF. Saipov

Tashkent (Uzbekistan)

22.042 Development of systems to detect hospital outbreaks from automated laboratory surveillance

R. Freeman, S. Hopkins, N. Andrews, J. Freed, A. Holmes, A. Charlett, M. Catchpole London (United Kingdom)

- 22.043 Health care seeking initiation of symptomatic patients in an integrated syndromic surveillance system in Jiangxi Province, China
 Q. Zhao¹, T.Tao¹, X. Li², Z. Pu³, H. Cheng³, V. K. Diwan⁴, G. Zhao¹, B. Xu¹
 ¹Shanghai (China), ²Gävle/SE (Sweden), ³Nanchang (China), ⁴Stockholm (Sweden)
- 22.044 Automated learning of naive medical language to support syndromic surveillance via blog mining
 A. E.Tozzi, M. De Vincenzi, P. Velardi, F. Gesualdo, M. Gonfiantini, E. Pandolfi, E. Agricola Rome (Italy)
- 22.045 Timeliness of data reporting in a web-based syndromic surveillance system in rural China T.Tao¹, Q. Zhao¹, J. Yang², J. Zhou³, K. Engstrom⁴, Y. Zhu¹, H. Cheng⁵, B. Xu¹
 ¹Shanghai (China), ²Yongxiu, Jiangxi Province (China), ³Fengxin, Jiangxi Province (China), ⁴Gävle (Sweden), ⁵Nanchang (China)
- 22.046 Holistic assessment of country surveillance, early detection and response systems: towards a European approach
 G. Fraser¹, F. Hruba², T. Mollet¹, P. Penttinen¹, P. Rosin¹
 ¹Stockhokm (Sweden), ²Solna (Sweden),
- 22.047 Identifying unobserved heterogeneity of influenza-like illness trajectories within health care units
 X. Song¹, Q. Zhao¹, C. Zhou¹, H. Yuan², X. Lu³, V. K. Diwan³, B. Xu¹
 ¹Shanghai (China), ²Nanchang (China), ³Stockholm (Sweden)
- 22.048 Syndromic surveillance systems in Albania, from a humanitarian emergency to an integrated surveillance system
 5. Bino, A. Simaku, E.Tomini, A.Vasili, D. Ulqinaku Tirana (Albania)
- 22.049 Developing a common approach to monitor and evaluate completeness of public health surveillance in European Union Member States K. Mellou¹, I. Devaux², S. Mc Nabb³, G. Priotto⁴, L. Ferland³, J. Brazil⁵, J. Freed⁶, J. Kerlic⁷, S. van der Plas⁸, B. Ciancio²
 ¹Athens (Greece), ²Solna (Sweden), ³Atlanta, GA (USA), ⁴Lyons (France), ⁵Dublin (Ireland), ⁶London

(United Kingdom), ⁷Bratislava (Slovakia), ⁸Blthoven (Netherlands)

22.050 Developing national syndromic epidemic intelligence for early detection of health threats linked to a mass gathering event: the Olympic Games London 2012

A. Backx¹, L. Vaillant¹, J. Linge², V. Bousquet¹, C. Caserio-Schönemann¹, P. Barboza¹ ¹Saint Maurice (France), ²Ispra (Italy)

International Meeting on Emerging Diseases and Surveillance 2013

- 22.051 Use of different data sources for syndromic surveillance in Europe
 A. Ziemann¹, T. Krafft¹, M. Sala Soler², A. Fouillet², A. Hulth³, L. Müller⁴, S. Conti⁵, M. Kanieff⁵, C. Dupuy⁶, S. Medina²
 ¹Maastricht (Netherlands), ²Saint Maurice (France), ³Solna (Sweden), ⁴Copenhagen (Denmark), ⁵Rome (Italy), ⁶Lyons (France)
- 22.052 Open-intelligence analysis for disease and pest surveillance
 A. Lyon¹, G. Grossel²
 ¹College Park, MD (USA), ²Canberra, (Australia)
- 22.053 Epidemiology of sudden unexplained death in young persons, at an acute care hospital in Singapore
 R. Sridhar, I. Venkatachalam, H. C. Chan,
 G. K. Goh, P.A. Tambyah
 Singapore (Singapore)
- 22.054 INDICATOR: One Health surveillance using primary and secondary data
 I. Brooks, W. Edwards, S. Rao, M. Vaughan, B. A'cs, M. Felarca
 Urbana, IL (USA)
- 22.055 Epizootic monitoring of classical swine fever (CSF), Aujeszky's disease, Teschen Disease, Circovirus infection in wild boars population in Ukraine
 A. Golovko, S. Nychyk, M. Sytyuk Kiev (Ukraine)
- 22.056 Biosecurity evaluation of Poultry Production Cluster (PPCs) in Thailand
 W.Aengwanich Maha Sarakham (Thailand)
- 22.057 Exploring disease indicators: an interdisciplinary approach to surveillance, detection, and modeling of Chagas Disease in southwestern United States
 M. McConnell
 Albuquerque, NM (USA)
- 22.058 Sixty years of Indonesian Hajj demographic and health surveillance
 M. Pane¹, G. Samaan²
 ¹Jakarta (Indonesia), ²Canberra (Australia)
- 22.059 A mobile phone application for pertussis classification based on machine learning
 M.Adamczyk¹, D. Parker², J. Cremer¹, J. Picone³, A. Harati³, P. Polgreen¹
 ¹Iowa City, IA (USA), ²Oxford, MS (USA), ³Philadelphia, PA (USA)
- 22.060 Enhancement of existing infectious disease early warning system using a novel modeling approach in a resource poor setting: Pakistan
 K.Ahmed, M. Rahim, R. Kakar, G. Sabatinelli Islamabad (Pakistan)

New, Emerging and Neglected Zoonotic Diseases

- 22.061 Serological and cultural detection of *Brucella* infection in cameland its public health significance in selected districts of Afar region, Ethiopia
 S.W. Zeweld Mekelle (Ethiopia)
- 22.062 Vector transmission of human cutaneous anthrax during an animal outbreak
 A. Fasanella¹, R. Adone², M. Galella¹, L. Pace¹, A. Aceti¹, L. Serrecchia¹
 ¹Foggia (Italy), ²Rome (Italy)
- 22.063 Fatal case of Crimean–Congo haemorrhagic fever imported into the UK: Laboratory diagnostics, genomic sequencing and phylogenetic characterisation
 R. Hewson
 Salisbury (United Kingdom)
- 22.064 An interesting case of cutaneous melioidosisD. Madi, B. AchappaMangalore, Karnataka (India)
- 22.065 Toxocariasis: underdiagnosed in Europe due to broad range of presenting features?
 M. Hoenigl¹, K. Seeber¹, T.Valentin¹, I. Zollner-Schwetz¹, J. Wagner¹, W. Duettmann¹, N. Wutte¹, M. Palfner¹, H. Auer², R. Krause¹
 ¹Graz (Austria), ²Vienna (Austria)
- **22.066** First results from the Hanta Hunting study: "Hantavirus infection in leptospirosis suspected patients in the Netherlands."

M. Goeijenbier¹, C. Reusken², M. Goris³, A. Osterhaus¹, R. Hartskeerl³, J. Wagenaar¹, J. Reimerink², B. Martina¹, M. Koopmans¹, E. van Gorp¹ ¹Rotterdam (Netherlands), ²Bilthoven (Netherlands), ³Amsterdam (Netherlands)

22.067 The status and challenges for the control of rabies in Nepal

G. R. Pant Kathmandu (Nepal)

- 22.068 Clinical features of *Helicobacter cinaedi* bacteremia
 Y. Uwamino, K. Muranaka, H. Kitazono, N. Hosokawa
 Chiba (Japan)
- 22.069 Diagnosis of a suspected Rift Valley Fever outbreak using IgM captured ELISA in Sudan.
 T. M. A. A. Elhassan, A. M. Elhassan, M. B. Abdelrahman, M. E. A. Mansour, A. M. Elhussein, N. A. Ibrahim Khartoum (Sudan)

International Meeting on Emerging Diseases and Surveillance 2013

- 22.070 Farming system affects seroprevalence of hepatitis E virus in pigs
 S. Rutjes, M. Bouwknegt, J. van der Giessen, A. M. De Roda Husman, C. Reusken Bilthoven (Netherlands)
- 22.071 Seroprevalence of brucellosis among high-risk individuals in suburban Khartoum, Sudan
 N. Osman¹, A. A. A. I. Ismail¹, A. H. Elduma¹, E. S. Saeed¹, M. E. Hamid²
 ¹Khartoum (Sudan), ²Abha (Saudi Arabia)
- 22.072 Prevalence and presence of virulence associated gene profiles of *Streptococcus suis* in pigs and humans in upper northeast Thailand
 T. C. Nutravong, S. Angkititrakul, N. Panomai Khon Kaen, (Thailand)
- 22.073 Virulence determinants in clinical and non-clinical human and animal *Arcobacter butzleri* strains
 K. Houf, L. Douidah Merelbeke (Belgium)
- 22.074 Investigating the role of forages in acquired equine polyneuropathy
 H. K.Telama, A.-M.Virtala, R.-M.Tulamo Helsinki (Finland)
- **22.075** Sero-epidemiology of *Coxiella burnetii* in companion animals

S.Anastacio¹, K. Sidi-Boumedine², G. J. da Silva³ ¹Coimbra, Coimbra (Portugal), ²Sophia Antipolis (France), ³Coimbra (Portugal)

22.076 First report and molecular characterization of hepatitis E virus in renal transplant recipients in Brazil

A. M. Passos, T. P. Heringer, J. Medina-Pestana, M. L. G. Ferraz, **C. H. Granato** Sao Paulo, SP (Brazil)

- **22.077** Use of wild birds surveillance and GIS spatial analysis for determining predictive epidemiological patterns of future spatial dispersion of West Nile virus: the example of Greece
 - **G. Valiakos**¹, A. Giannakopoulos¹, K. Papaspyropoulos², P. Birtsas¹, A. Touloudi¹, L. Athanasiou¹, C. Chadjichristodoulou³, V. Spyrou³, L. Petrovska⁴, C. Billinis¹ ¹Karditsa (Greece), ²Thessaloniki (Greece), ³Larissa (Greece), ⁴New Haw, Addlestone (United Kingdom)
- 22.078 An Interesting Case Of Eosinophilic Meningitis
 D. Madi¹, B. Achappa¹, S. Pai²

¹Mangalore, Karnataka (India), ²Mangalore (India)

22.079 *Coxiella burnetii* in small ruminants: assessing the public health risk

T. Dewé¹, A. Nigsch², K. Stärk³ ¹London (United Kingdom), ²Bregenz (Austria), ³North Mymms (United Kingdom) 22.080 Study of *Giardia duodenalis* in rodents from the Canary Islands (Spain) and the possible role in the transmission of zoonotic genotypes
A. Fernandez-Alvarez¹, A. Martín-Alonso¹, N. Abreu-Acosta¹, C. Feliu², B.Valladares¹, P. Foronda¹
¹Santa Cruz de Tenerife (Spain),

²Barcelona (Spain)

- 22.081 Key determinants of vulnerability to Zoonotic Cutaneous Leishmaniasis in central Tunisia H. Bellali, A. Mrabet, S. Ennigrou, N. Ben Alaya, S. Dridi, N. Achour, M. K. Chahed Tunis (Tunisia)
- 22.082 Characterization of genetic diversity of *Brucella* isolates from South East Asia
 K. K.Tan, L.-Y. Chang, S. S. Nor'e, F. L. Jafar,
 S.AbuBakar
 Kuala Lumpur (Malaysia)

22.083 Risk factors associated with cutaneous leishmaniasis en Chontalpa, Tabasco, México G. Carrada, B. Cadena, V. Leal, B. Sanchez, A. Jimenez, I. Becker Villahermosa (Mexico)

22.084 Disseminated cutaneous leishmaniasis in Tabasco, México

G. Carrada

Villahermosa (Mexico)

22.085 Human rabies confirmed cases reported to Brazil National IHR Focal Point from March 2006 to June 2012

S. Lopes Dias¹, E.T. Masuda¹, M. É. Santos¹, W.A. Oliveira, P. Pereira Vasconcelos de Oliveira, G. S. Dimech Brasilia, (Brazil)

22.086 How does Rhodesian sleeping sickness affect rural households? Results from a qualitative study in Uganda
 K. L. Bardosh

Edinburgh (United Kingdom)

- 22.087 Austria's role in the Europe-wide outbreak of the emerging Salmonella Stanley strain since 2011
 E. Kanitz¹, S.-W. Jian¹, S. Maritschnik¹,
 E. J. Simons¹, C. Kornschober², F. Allerberger¹,
 D. Schmid¹
 ¹Vienna (Austria), ²Graz (Austria)
- 22.088 Changing patterns of Puumala hantavirus outbreaks in Baden-Württemberg 2007–2012
 C.Wagner-Wiening, I. Boone, G. Pfaff Stuttgart (Germany)
- 22.089 Seroprevalence of leptospirosis in veterinary students, Botota, Colombia
 I. Mendez, A. Rodriguez, D. Pachón, L. Cabrera
 Bogota (Colombia)

SUNDAY • FEBRUARY 17, 2013

International Meeting on Emerging Diseases and Surveillance 2013

22.090 Ecohealth assessment on poultry production cluster (PPC) in West Java Indonesia—Focus on biosecurity

E. Basuno, N. Ilham, E. Martindah, Y. Yusdja Bogor (Indonesia)

22.091 Detection of imported case of tick-borne encephalitis in the UK (ex Sweden) **R. Hewson**

 Salisbury (United Kingdom)
 22.092 Serologic evidence of Crimean-Congo hemorrhagic fever virus infection in Hungary V Németh M Oldall C Kemenesil

V. Németh¹, M. Oldal¹, G. Kemenesi¹, M. Gyuranecz², K. Kvell¹, N. Kalvatchev³, H. Zeller⁴, K. Bányai², **F. Jakab**⁵

¹Pécs (Hungary), ²Budapest (Hungary), ³Sofia (Bulgaria), ⁴Lyons (France), ⁵Pécs, Baranya (Hungary)

22.093 Human and canine dirofilariasis in Greece: an emerging second main focus
E.Vassalou, C.Vassalos, G. Spanakos,
A. Mpimpa, V. Kontos, N.Vakalis
Athens (Greece)

Outbreak Modeling

22.094 Modeling ST-246, vaccination, and the effect of contagiousness in a smallpox outbreak
E. Graeden
Takoma Park, MD (USA)

- 22.095 Modelling reporting chain delays and their impact on outbreak control: room for improvement
 A.A. Bonacic Marinovic, C. Swaan,
 J.Van Steenbergen, M. Kretzschmar Bilthoven (Netherlands)
- 22.096 The analysis of the factor to affect to outbreak of resistant type malaria: Application of Mathematical Epidemiology to the control of the drug-resistant type
 K. Shirakawa, M. Nishibuchi Kyoto (Japan)
- 22.097 The H index as a measure of disease impact— When and why it works
 K. M. McIntyre¹, I. Hawkes¹, S. Morand², M. Baylis¹
 ¹Chester (United Kingdom),
 ²Montpellier (France)

Outbreak Response and Control

22.098 Strategy to prevent *Clostridium difficile* infection outbreak in municipal hospital
H. Ishikawa¹, K. Kojima¹, T. Watanabe¹,
S. Maruyama², S. Matsuo²
¹Gifu (Japan), ²Aichi (Japan)

22.099 Foodborne outbreak in Ugljevik municipality, North-east Bosnia, August 2012
Z. Dakić, Z. Maksimović Bijeljina (Bosnia and Herzegovina)
22.100 Outbreak of salmonellosis in pastoral setting— Borena Zone, Ethiopia, 2012
G. Defi Addis Ababa (Ethiopia)

22.101 Knowledge, attitudes and occupational exposure to needle stick injury among health care workers in Tripoli Central Hospital
A. M. Elbahi, H. Zeglam Tripoli (Libya)

- 22.102 Meningococcal meningitis outbreak investigation cancelled Harenabuluk District, Southeastern Ethiopia, 2011
 G. E.Yembo, D. J. Wayessa Addis Ababa (Ethiopia)
- **22.103** Malaria outbreak investigation: Abobo Town, *cancelled* Southwest lowland of Ethiopia, 2011

G. E. Yembo, G. A. Estayew, D. J. Wayessa Addis Ababa (Ethiopia)

- 22.104 Outbreak of mumps at village jumma khan lund,
- cancelled Tando Allahyar, Sindh Pakistan 2011 **M. Nadeem Shah Syed**¹, D. R. Muhammad Safdar², D. Jawed Junejo¹ ¹Hyderabad, Sindh (Pakistan), ²Islamabad (Pakistan)
- **22.105** Investigation of post-flood dengue cases in *cancelled* Hyderabad city, Sindh, Pakistan 2010

M. Nadeem Shah Syed¹, D. R. Muhammad Safdar² ¹Hyderabad, Sindh (Pakistan), ²Islamabad (Pakistan)

22.106 Is hospital-based sentinel pneumonia surveillance system useful for pandemic preparedness and response? Lessons learned from the Indonesian surveillance system
 Y. Praptiningsih, A. Bratasena, M. Sitorus, M. Amalya, G. Samaan

Jakarta (Indonesia)

- 22.107 European Union "Yellow Pages" for Microbiology Laboratory Services to support outbreak response and control—A needs analysis A. J. Ozin-Hofsaess¹, J. I. M. Vaz¹, A. Pierson², F. Guedez², M. Struelens¹
 ¹Solna (Sweden), ²Lyons (France)
- 22.108 Visit delay and report delay of patients and health facilities in a syndromic surveillance system for infectious diseases in rural China
 C. Zhou¹, Q. Zhao¹, X. Li², B. Xu¹,
 X. Song¹, H. Yuan³
 ¹Shanghai (China), ²Gävle/SE (Sweden),
 ³Nanchang (China)

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

- Yellow Fever outbreak investigation and response, Darfur State, Sudan, September–November 2012
 M. Nogoudalla¹, D. Bashir², M. Nogoudalla¹
 ¹Khartoum (Sudan), ²Hershey, PA (USA)
- 22.110 Cholera outbreak in Akinyele local government area, Oyo State, Nigeria, August, 2012—effect of multi-sectoral intervention

A. O. Gbolahan¹, P. B. Adewuyi², O. Iyiola¹, V. Fapohunda³ ¹Ibadan (Nigeria), ²Abuja (Nigeria),

³Remo (Nigeria)

22.111 Case control investication of an outbreak of *cancelled* acute jaundice in a refugee population in

Dadaab, Kenya, 2012 **L. Chepkurui** Nairobi (Kenya)

- 22.112 Aedes albopictus as vector in Dengue Hemorhagic Fever (DHF) outbreak in Kaimana District, West Papua Province : an entomological investigation T. N. Kridaningsih, H. Krismawati, M. Rahardjo, E. Natalia, Y.Y. R. Mirino Jayapura (Indonesia)
- 22.113 A food handler-associated Norovirus outbreak following a wedding, Austria, 2012
 S. Maritschnik¹, E. J. Simons¹, I. Lederer², M. Höhne³, E. Kanitz¹, D. Schmid¹
 ¹Vienna (Austria), ²Graz (Austria), ³Berlin (Germany)
- 22.114 Characterisation of cholera outbreaks, preparedness and response in Niger State, Nigeria 2012:Transition to best practice
 A.T. Bashorun¹, A. Ahumibe¹, S. Olugbon¹, P. Nguku¹, K. Sabitu²
 ¹Abuja (Nigeria), ²Zaria (Nigeria)
- 22.115 Epidemiological analysis of a large restaurant-associated outbreak of hemolytic uremic syndrome and encephalopathy caused by *Escherichia coli* OIII in Japan
 Y.Yahata', T. Misaki', M. Nagira', Y.Tada', K.Taniguchi', K. Oishi', N. Okabe²
 'Tokyo (Japan), ²Kawasaki (Japan)
- 22.116 Epidemiological characterization of Chikungunya outbreak in Lahj Governorate, Southern Yemen, March–April 2012

A.A. Q. Thabet¹, S. M. A. M. Al-Eryani², N. AbdulAziz², M. Obadi², M. Saleh², A. AlKohlani², A. Al-Samei² ¹Dhamar (Yemen), ²Sanaa (Yemen)

Public Communication of Outbreaks and Emerging Diseases

- 22.117 Assessment of the compliance of poultry farmers and live poultry sellers to preventive measures against bird flu in Benin City, Nigeria
 A. M. M. Qasim¹, V.Y. Adam², M. O. Kazeem³
 ¹Vom (Nigeria), ²Benin City (Nigeria), ³Ilorin (Nigeria)
- 22.118 Knowledge of HIV/AIDS and attitude towards HIV patients among the educated youth of Pokhara valley: a Cross-sectional study from Western Nepal
 R. P.Adhikari, B. Sathian
 - Pokhara (Nepal)

Sociopolitical Factors in Disease Emergence

- 22.119 Refugees, reforms and drug resistance: Political transition and artemisinin resistant malaria in Myanmar
 I. M. P. Ghinai, T.T.W. HIa, T. Hesketh London (United Kingdom)
- 22.120 Influence sociopolitical factors to human leptospirosis in Crimea (Ukraine)
 O. L. Pavlenko, O. B. Khaytovych Simferopol (Ukraine)
- **22.121** Understanding risky behaviours among those
- *cancelled* slaughtering, selling and buying poultry in live bird markets in Indonesia **S. Naysmith**

London (United Kingdom)

- 22.122 The 1994 Outbreak of Pneumonic Plague in Surat, India: A Retrospective Analysis
 J.Varco Washington, DC (USA)
- 22.123 The use of compulsory powers to control the spread of HIV in New Zealand: The case of a man detained without trial for eleven years; a challenge for legislators, public health practitioners and community alike.
 A. R. G. Humphrey

Christchurch (New Zealand)

22.124 Disclosure of HIV status by HIV positive patients attending adult anti-retrovival therapy (ART) clinic at Gombe State Specialist Hospital, Gombe, Nigeria 2011

R. Dankoli¹, A. A. Aliyu², P. Nguku³, T. Dahiru², O. Ossai³ ¹Gombe (Nigeria), ²Zaria (Nigeria), ³Abuja

(Nigeria)

22.125 Quantification of factors influencing pig farmers' intention to apply On-Farm Biosecurity measures based on theory of planned behavior
 T.Wilke , B. Petersen Bonn (Germany)

32 IMED 2013
International Meeting on Emerging Diseases and Surveillance 2013

Poster Presentations II

Sunday, February 17, 2013 II:45–13:15 Klimt Ballroom I • Upper Level

Vaccines and Emergence of Vaccine Preventable Diseases

22.126 Epidemiological pattern of measles infection in children under five in Oyo State, Nigeria, 2007–2011

L.A. Okeke¹, P. B. Adewuyi¹, O. Ajumobi², S. Gidado¹, P. Nguku¹, O. Fawole², H. Akpan¹ ¹Abuja (Nigeria), ²Ibadan (Nigeria)

22.127 Production of tissue culture rabies vaccine for human in Nepal

G. R. Pant

Kathmandu (Nepal)

22.128 Evaluation of the immune response during experimental infection of vaccinated and unvaccinated pigs with Classical Swine Fever Virus (CSFV) using Fluorescent Activate Cell Scanning (FACS)
 G. Curina, M. Bazzucchi, G. M. De Mia, M. Mari,

L. Molinari, K. Forti, G. Rizzo, M. Cagiola, **G. Severi** Perugia (Italy)

- 22.129 Cytokines expression in vaccinated and unvaccinated pigs infected with Classical Swine Fever Virus strain ISS 60: preliminary results.
 M. Bazzucchi, G. Curina, G. M. De Mia, F. Feliziani, M. Giammarioli, A. De Giuseppe, G. Rizzo, K. Forti, M. Cagiola, G. Severi Perugia (Italy)
- **22.130** Outbreak investigation of measles among fully
- cancelled vaccinated children in Village Khair Muhammad (KM) Dasti, District Naushahro Feroze, Sindh, April 2012.

M. P. Jokhio

Naushahro Feroze. (Pakistan)

- 22.131 The ocular conjunctiva as a possible mucosal immunization route
 A. Inic-Kanada¹, M. Stojanovic², S. Belij¹,
 E. Marinkovic², I. Stojicevic², J. Montanaro¹,
 E. Stein¹, N. Bintner¹, **T. Barisani-Asenbauer¹**¹Vienna (Austria), ²Belgrade (Serbia)
- 22.132 Detection of rabies antibodies in dog sera
 A. Ondrejková, E. Slepecká, J. Süli, R. Ondrejka,
 L'. Korytár, M. Prokeš, P. Čechvala
 Kosice (Slovakia)
- 22.133 Sublingual immunization as an alternative route for vaccine delivery
 H. M. Amuguni, S. Lee, X. Sun, S. Tzipori North Grafton, MA (USA)

- 22.134 Implementation of rotavirus surveillance in Albania
 A. Simaku, M. Kota, I. Preza, A. Ahmeti, S. Bino Tirana (Albania)
- 22.135 Clinical and host genetic characteristics of the patients with BCG osteomyelitis
 T. Hoshina¹, H. Takada¹, Y. Mihara¹,
 K. Kusuhara², T. Hara¹
 ¹Fukuoka (Japan), ²Kitakyushu (Japan)
- 22.136 A mobile phone application for recording vaccine refusals
 D. Murphy, J. Cremer, P. Polgreen lowa City, IA (USA)
- 22.137 Immunogenicity and safety of a Vero cell culture-derived whole-virus H5N1 influenza vaccine in immunocompromised and chronically ill patients G.Aichinger¹, M. van der Velden¹, D. Portsmouth², W. Herr³, E. Distler³, E. M. Wagner³, M. Zeitlinger¹, R. Sauermann¹, C. Stephan⁴, N. Barrett²
 ¹Vienna (Austria), ²Orth/Donau (Austria), ³Mainz (Germany), ⁴Frankfurt am Main (Germany)
- 22.138 Evaluation of polio supplementary immunization activity (SIA) in Bungoma Kenya, 2012
 N. M. Muriu, Y. Ajack, S. Amwayi, Z. Gura, I. Njeru, D. Langat Nairobi (Kenya)

Vectorborne Diseases

22.139 Betraying the redox system for leishmania parasite

V. K. Dubey Guwahati (India)

22.140 Malaria outbreak investigation in a rain relief camp of internally displaced persons at village Bhimani, Kandiaro district Naushahro Feroze, Sind, Pakistan, August–September 2012
 A.A. Ghanghro

Naushahroferoze (Pakistan)22.141 Understanding the effects of the Chagas disease control program in Venezuela after 50 years

using eco-epidemiological modelling **E. Sulbaran Romero**¹, M. Lange¹, J. L. Concepcion², H.-H.Thulke¹ ¹Leipzig, Saxony (Germany), ²Merida (Venezuela)

- 22.142 Epidemiology of vector-borne zoonotic and livestock viral diseases in central Thailand, 2012: a pilot study
 N. Ketusing¹, P. Opaschaitat¹,
 C. Sirisukeepradit¹, P. Boonpornprasert¹,
 M.Tattiyapong¹, J. Wattanamethanont¹,
 - J. Ratthanophart¹, H. Shirafuji², T. Yanase²
 - ¹Bangkok (Thailand), ²Kagoshima (Japan)

International Meeting on Emerging Diseases and Surveillance 2013

- 22.143 Determination of the association of nTreg (natural regulatory T cells) and its produced cytokines IL-10,TGFB with Kala azar disease and detection of its variations with treatment
 M. Keshavarz, M. Rasouli, A. Alborzi Shiraz (Iran, Islamic Republic of)
- 22.144 Schmallenberg virus RNA detected in *Culicoides* biting midges in the Netherlands in 2011
 A. R.W. Elbers¹, R. Meiswinkel², E. van Weezep¹, M. Sloet van Oldruitenborgh-Oosterbaan³, B. Kooi¹
 ¹Lelystad (Netherlands), ²Rome (Italy), ³Utrecht (Netherlands)
- **22.145** Oxabicyclo derivatives as a new class of antileishmanial agents: target identification and understanding molecular mechanism of parasite death

P. Saudagar, V. K. Dubey Guwahati, Assam (India)

22.146 Schmallenberg Virus pathogenesis, tropism and interaction with the innate immune system of the host

M. Varela¹, E. Schnettler¹, M. Caporale², C. Murgia¹, G. Barry¹, A. Shaw¹, M. Beer³, W. Baumgärtner⁴, A. Kohl¹, M. Palmarini¹ ¹Glasgow (United Kingdom), ²Teramo (Italy), ³Greifswald-Insel Riems (Germany), ⁴Hanover (Germany)

- 22.147 Discovery of novel mosquito-dengue viral protein interactions: construction of whole adult Aedes aegypti cDNA library for use in yeast-two-hybrid system
 H.W.Tham¹, V. Balasubramaniam¹, H. Ahmad², I. Othman¹, S. S. Hassan¹
 ¹Kuala Lumpur (Malaysia),
 ²Pulau Pinang (Malaysia)
- 22.148 Detection of Usutu virus and a novel mosquitoborne virus in mosquitoes in north-western Italy
 F. Rizzo¹, M. Ballardini¹, S. Peletto¹, M. Calzolari², C. Boin¹, P. L. Acutis¹, C. Casalone¹, L. Chiavacci¹, M. Prearo¹, M. L. Mandola¹
 ¹Turin (Italy), ²Reggio Emilia (Italy)
- **22.149** The West Nile-induced encephalitis with respiratory distress mimicking Guillain-Barre syndrome

A. Ndreu, S. Bino, E. Ramosaco, E. Mingomataj Tirana (Albania) **22.150** Emergence control of mosquito vectors and surveillance of mosquito and water borne viruses in natural disaster areas

R. E. Morales Vargas¹, T. Okabayashi¹, N. Komalaminsra¹, R. Srisawat¹, N. Phumala-Morales¹, S. Lee², N. Orii³ ¹Bangkok (Thailand), ²Kyoto (Japan)

- 22.151 Development of a TaqMan assay for detection of arboviruses belonging to the genus Orthobunyavirus: Universal detection of Japanese strains of orthobunyaviruses and specific detection of Akabane, Aino and Peaton viruses H. Shirafuji¹, R. Yazaki², Y. Shuto³, T. Yanase¹, T. Kato¹, M. Yamakawa⁴
 ¹Kagoshima (Japan), ²Kusu (Japan), ³Oita (Japan), ⁴Tsukuba (Japan)
- 22.152 Organ distribution of Schmallenberg virus RNA in malformed calves

W.-I. Bock¹, F. Hühn¹, C. Schulze², A. Hlinak², S. Bilk² ¹Bad Langensalza (Germany), ²Frankfurtt/Oder (Germany)

22.153 Opisthorchiasis in the basin of the lower Don in Russia

N. Pshenichnaya, L. Ermakova, T.Tverdokhlebova, O. Dumbadze Rostov-on-Don (Russian Federation)

- 22.154 Recurrent echinococcosis in the Rostov region of Russia
 L. Ermakova, N. Pshenichnaya, Y. Kirtanasov, T.Tverdokhlebova
 Rostov-on-Don (Russian Federation)
- 22.155 Mosquito surveillance of West Nile and Usutu viruses in Emilia-Romagna region, Italy, 2008–2012
 M. Calzolari¹, P. Bonilauri¹, R. Bellini², M. Tamba³, P. Angelini³, M. Dottori¹
 ¹Reggio Emilia (Italy), ²Crevalcore (Italy), ³Bologna (Italy)
- 22.156 Seroprevalence of West Nile virus antibodies in poultry and risk factors associated with their occurrence at live bird markets in Kaduna, Nigeria
 W. S. Mshelia, J. Kabir, J. Umoh, B. D. J. George Zaria, Kaduna (Nigeria)
- 22.157 Detection and characterization of first outbreak of chikungunya, Papua New Guinea, 2012
 B. I. Pavlin¹, S. Jimmy², R. Dagina¹, P. Horwood³, B. Ropa¹
 ¹Port Moresby (Papua New Guinea), ²Vanimo (Papua New Guinea),

³Goroka (Papua New Guinea)



- 22.158 Dirofilariosis in Slovakia
 M. Miterpakova, A. Iglodyova Kosice (Slovakia)
- 22.159 Bioecological study of malaria vector Anopheles balabacensis in one of the buffer areas of Merapi Mountain
 N. I. Hariastuti¹, A. Tunissea², B. Yunianto³
 ¹Jakarta Pusat (Indonesia), ²Banjarnegara (Indonesia), ³Klaten (Indonesia)
- 22.160 Study of ticks infected with tick-borne encephalitis virus in the southern and southeastern regions of Kazakhstan
 P. Deryabin¹, T. Nurmakhanov¹, J. Hay², B. Atshabar¹, A. Vilkova¹
 ¹Almaty (Kazakhstan), ²Buffalo, NY (USA)
- 22.161 Serological and molecular detection of tick borne pathogens in horses from Central Italy
 M. Diaferia¹, F. Veronesi¹, F. Laus², E. Paggi²,
 M. Cerquetella², B. Tesei², D. Piergili Fioretti¹
 'Perugia, IT (Italy), ²Matelica, IT (Italy)
- 22.162 Culicoides—potential vectors of viral diseases in Eastern Slovakia
 A. Sarvašová¹, A. Kočišová¹, I. Sopoliga² ¹Kosice (Slovakia), ²Rozhanovce (Slovakia)
- 22.163 Borrelia in immature Ixodes ricinus feeding on lizards in Algeria
 H. Soualah-Alila¹, I. Bitam², Z. Bouslama¹,
 A. Beneldjouzi²
 ¹Annaba (Algeria), ²Algiers (Algeria)
- 22.164 Tick-borne encephalitis surveillance in the Czech Republic focused on the areas of the Czech/ Austrian border in the decade 2002–2011
 B. Kriz, M. Daniel, C. Benes Praha 10 (Czech Republic)
- 22.165 Cellular factors needed for the functions of the Rift Valley fever virus virulence factor NSs
 M. Kainulainen¹, M. Habjan², L. Busch¹, S. Lau¹, A. Pichlmair³, G. Superti-Furga³, F. Weber¹
 ¹Marburg (Germany), ²Freiburg (Germany), ³Vienna (Austria)
- 22.166 Outbreak of West Nile virus infection in humans and horses, Croatia, 2012
 T.Vilibic-Cavlek¹, L. Barbic¹, I. Pem-Novosel¹, I. Gjenero-Margan¹, E. Listes², N. Pandak³, L. Peric⁴, V. Stevanovic¹, G. Mlinaric-Galinovic¹, G. Savini⁵
 ¹Zagreb (Croatia), ²Split (Croatia), ³Slavonski Brod (Croatia), ⁴Osijek (Croatia), ⁵Teramo (Italy)
- 22.167 Rapid spread of Schmallenberg virus in Austrian domestic ruminants
 P. Schiefer, A. Steinrigl, E. Wodak, F. Schmoll Mödling (Austria)

22.168 Eccepidemiology of Anaplasma phagocytophylum in horses in France

A. Leblond¹, A. Chastagner², X. Bailly², S. Masseglia³, G. Vourc'h² ¹Marcy L'Etoile (France), ²Saint Genès Champanelle (France)

- 22.169 First description, molecular and phylogenetic analyses of Barkedji virus isolated from *Culex perexiguus* in Israel in 2011
 J. Kolodziejek ¹, K. Pachler¹, K. Sekulin¹, H. Lussy¹, H. Bin², N. Nowotny¹
 ¹Vienna (Austria), ²Tel Hashomer (Israel)
- 22.170 Mediterranean spotted fever a reemerging tickborn disease inBulgaria
 I. G. Baltadzhiev
 Plovdiv (Bulgaria)
- 22.171 Detection of SBV Antibodies in wild ruminants in Austria, 2012
 P. Schiefer¹, A. Steinrigl¹, E. Wodak¹, A. Deutz²,

F. Schmoll¹ ¹Mödling (Austria), ²St. Lambrecht (Austria)

22.172 Dengue virus seroprevalence survey in the inhabitants of the Croatian southern Adriatic coast
I. Pem-Novosel¹, I. Gjenero-Margan¹, T.Vilibic-Cavlek¹, M. Ljubic², S. Kurecic-Filipovic¹,

T. Nemeth-Blazic¹ ¹Zagreb (Croatia), ²Dubrovnik (Croatia)

22.173 Possible involvement of Schmallenberg virus in ruminant abortions and early embryonic death in cattle

A. Steinrigl¹, P. Schiefer¹, W. Peinhopf², S. Revilla-Fernández¹, F. Schmoll¹ ¹Mödling (Austria), ²Lebring (Austria)

- 22.174 Organ distribution of Schmallenberg virus RNA in malformed lambs
 S. Bilk¹, C. Schulze¹, F. Hühn², A. Hlinak¹, B. Hoffmann³, W.-I. Bock²
 ¹Frankfurt/Oder (Germany), ²Bad Langensalza (Germany), ³Greifswald-Insel Riems (Germany)
- 22.175 Pulmonary Sinvolvement of Crimean–Congo haemorrhagic fever
 L. Berisha-Ajazaj, S. Ahmeti, S. A. Namani, E. Qehaja-Bucaj, H. Ramadani, A. Vishaj Prishtina (Kosovo, Republic of)

International Meeting on Emerging Diseases and Surveillance 2013

- 22.176 First autochthonous Dengue virus infections in Madeira Island, Portugal in 2012
 L. Ze-Ze¹, F.Amaro¹, H. C. Osório¹, P. Parreira¹, T. Luz¹, G. Andrade², P. L. Fernandes², M.-J. Alves¹
 ¹Águas de Moura (Portugal), ²Funchal (Portugal)
- 22.177 2010–2011 Re-emergence of Chikungunya virus cancelled infection in National capital territory of India
 P. K. Singh, M. Mir, L. Dar, S. Broor Delhi (India)
- 22.178 Clinical and epidemiological aspects of Lyme borreliosis from Mures County, Romania
 B.Tilea, I.Tilea
 Tirgu Mures, Mures (Romania)
- 22.179 Genetic characterization of Chikungunya virus causing outbreaks in the Philippines
 A. K. Sy¹, I. A. Medado¹, M. Saito²
 ¹Muntinlupa (Philippines), ²Sendai (Japan)
- 22.180 Estimation of some biologic values with regards to prognostic outcome of patients suffering from Crimean-Congo Haemorrhagic Fever
 T. Kalo, P. Biberaj, A. Pilaca, S. Kurti, K. Shkurti, E. Puca, D. Kraja Tirana (Albania)
- 22.181 BTV serotype 14 detection in Catalonia (Spain) in imported cattle from the Baltic Area
 R. Rosell¹, M. Domingo¹, J. Pujols¹, I. Selga²,
 A. Sanz², I. Mercader², E. San Miguel³, A. Rochas³,
 M. Aguero³
 ¹Bellaterra (Cerdanyola del Valles) (Spain),
 ²Barcelona (Spain), ³Algete, Madrid (Spain)

- 22.182 Partial genetic characterisation of orthobunyavirus Sedlec, Europe
 T. Bakonyi¹, Z. Hubalek², I. Rudolf², R. L. Bercic³, N. Nowotny¹
 ¹Vienna (Austria), ²Brno (Czech Republic), ³Budapest (Hungary)
- 22.183 A systematic approach to revealing the phylogeography of Rift Valley Fever Virus
 C.A. Hercik
 Washington, DC (USA)

22.184 Dengue infection outbreak among travelers

cancelled at Koh Lanta, Krabi province, Thailand January–May 2012
K. Suwanna¹, **R. Buathong**², H. Kanjanasombut², P. Kleaw-orm¹, P. Klabpadung³, W. Manee³, P. Huayleuk³
¹Nakhon Si Thammarat (Thailand), ²Nonthaburi (Thailand), ³Krabi (Thailand)

22.185 New data on distribution and abundance of Aedes aegypty in Santiago Island (Cape Verde) H. Spence da Costa Lima¹, M. C. Pou Barreto², R. Melero Alcibar³, A. Fernandez-Alvarez², I. Monteiro de Pina Araujo¹, R. Molina³, B.Valladares²
¹Praia (Cape Verde), ²San Cristóbal de La Laguna (Spain), ³Madrid (Spain)

36 IMED 2013



Friday, February 15, 2013

, , , , , , , , , , , , , , , , , , ,	
Session 01:	Science and Sensationalism, Emerging Infections and Emergency!
Session 02:	Ecology, Biodiversity, Climate and Emerging Infectious Disease
Session 03:	Emerging Infectious Diseases and the Hajj
Saturday, Febr	uary 16, 2013
Session 04:	Emerging Disease Prevention
Session 05:	Oral Presentations: One Health in Action
Session 06:	Emerging Fungal Diseases and Species Extinction
Session 07:	Of Bats and Men: Nipah and Other Infections
Session 08:	Oral Presentations: 'Contagion': Contemporary Viral Pathogens
Session 09:	Emerging Disease Mysteries
Session 10:	Vectorborne Diseases in Humans and Animals50
Sunday, Febru	ary 17, 2013
Session 11:	Neglected Zoonotic Diseases
Session 12:	Oral Presentations: Infection, Detection, and Protection:
	Adventures in Epidemiology
Session 13:	Global Approach to the Control of Foot and Mouth Disease
Session 14:	Cutting Edge Diagnostics for the Detection of Novel and Neglected Diseases \dots 56
Session 15:	Updates from ProMED (Panel Discussion)57
Session 16:	Disease Surveillance
Session 17:	Oral Presentations: Hot Topics
Monday, Febru	iary 18, 2013
Session 18:	Economics of Emerging Infectious Diseases
Session 19:	Diseases Without Borders
Session 20:	Big Data, Industry and Disease Surveillance64
Saturday, Febr	uary 16, 2013
Session 21:	Poster Presentations I
	Antimicrobial Resistance
	Bioterrorism and Biological Warfare
	Climate Change and Ecological Factors in Disease Emergence77
	Diseases at the Interface of Humans, Wildlife and Other Animals
	Diseases of Animals
	Foodborne and Waterborne Diseases
	Infections of Public Health Significance
	Infections Related to Travel and Migration
	Innovations in Diagnostic Tests for Emerging Diseases
	New Pathogen Discovery
Sunday, Febru	ary 17, 2013
Session 22:	Poster Presentations II
	Influenza and Other Respiratory Infections
	New Approaches to Outbreak Surveillance and Monitoring
	New, Emerging and Neglected Zoonotic Diseases
	Outbreak Modeling
	Outbreak Response and Control
	Public Communication of Outbreaks and Emerging Diseases
	Sociopolitical Factors in Disease Emergence
	Vaccines and Emergence of Vaccine Preventable Diseases
	Vectorborne Diseases

International Meeting on Emerging Diseases and Surveillance 2013

SESSION 01 (Plenary)

Science and Sensationalism, Emerging Infections and Emergency!

Friday, February 15, 2013 Room: Park Congress • Ground Level 14:20–15:00

01.001 Science and Sensationalism, Emerging Infections and Emergency!

A. Schuchat

Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA

Emerging infections garner substantial public interest when their impact has consequences that are easily visible or understood, but an effective strategy for addressing emerging diseases includes early detection, prompt response, successful control and ultimately prevention of future consequences. The better the strategy, the smaller the problem will be. The emergence of the novel SARS coronavirus 10 years ago resulted in unprecedented economic and social effects, in addition to the direct illness and death associated with severe respiratory disease outbreaks that occurred in multiple countries. Subsequent adoption of the International Health Regulations offered the potential to mitigate delays in recognition and response to possible health events of international concern. While public health and scientific advances improve our ability to detect, control, and prevent emerging infections, a 24/7 sensationhungry media and competition for resources with "emergencies" in other sectors have introduced challenges to assuring that emerging diseases garner the serious, persistent focus they require. It is critical that we navigate today's communication challenges in ways that sustain the credibility of scientific and public health institutions but make an effective case for the need for attention to emerging disease threats.

SESSION 02 (Plenary) Ecology, Biodiversity, Climate and Emerging Infectious Diseases

Friday, February 15, 2013 Room: Park Congress • Ground Level 15:00–16:30

Co-sponsored by EcoHealth Alliance

02.001

2.001 Different views of looking at biodiversity and health

W. Karesh

EcoHealth Alliance, New York, NY, USA

The role of wildlife and environmental factors in zoonotic disease emergence specifically and health more broadly have been well documented, but engagement of experts and authorities in these sectors in One Health efforts is lagging. How do we strengthen participation from sectors outside of public health and veterinary services to create more effective and sustainable programs? Who are these people, agencies, and organizations and what are their interests and mandates? How do we find ways to achieve mutual benefits even if we do not share missions? This paper discusses current strengths and limitations of existing structures and offers guidance on identifying and engaging the wildlife and environment sectors (both public and private) in One Health to build collaboration, broaden impact, and improve and strengthen systems.

02.002 Concerns of the biodiversity community for integrating health

D. Coates

SCBD, Montreal, Canada

Biodiversity and health have inextricable links, with biodiversity offering critical health-supporting ecosystem services, and public health arguments increasingly acknowledged as an opportunity for the conservation and sustainable use of biodiversity. Emerging infectious disease presents an example of a direct link to biodiversity and ecosystem interactions with human health. Anthropogenic practices such as land use change, expansion of agriculture, and trade of wild animals and livestock, present opportunities for zoonotic disease spread as well as direct detrimental effects to biodiversity. Thus, human health should not be viewed in isolation of our environment. The Ecosystem Approach or One Health perspectives present allows us a broader understanding of health and biodiversity links to support both public health and sustainability use of biodiversity, including species conservation, social sustainability, and provision of other ecosystem services. Engagement of the biodiversity community in emerging disease research, prevention and control can offer important synergies.

02.003

2.003 Climate change, biodiversity loss, desertification and human health— The WHO Perspective

D. Campbell-Lendrum

WHO, Geneva, Switzerland

With increasing environmental pressures arising from climate change, biodiversity loss, desertification and other pressures, the role and effects of the environment on health are increasingly relevant for the health community. Modern day human practices are rapidly exacerbating environmental change and are also heightening our risks of both noncommunicable and emerging diseases. For example, trade and climate-related shifting species and corresponding habitat ranges are facilitating spread of disease in previously unaffected populations, and extreme weather events and changing weather patterns are threatening health-supporting resources, including water and food security. Low-income populations, which currently face high health and livelihood burdens from infectious diseases, are especially impacted by negative health effects from climate and other environmental changes.

International Meeting on Emerging Diseases and Surveillance 2013

All of these environmental pressures interact with rapid changes in social determinants of health, including economic and population growth, human movement, urbanization, technological advance, ageing and inequity. Traditional approachs to infectious disease control, with focus on early detection and treatment, are concurrenty being quickly advanced through technological advances, particularly in information technology for detection, data analysis and communication. At the same time they are being undermined by weaknesses in basic public health functions, and in management of the upstream environmental determinants of health.

In order to effectively address our current and prospective health challenges, the global health community must better consider the connections between climate change, environmental and social determinants and health.



U2.004 Wildlife trade and emerging diseases— Impacts on biodiversity and health

K. Smith EcoHealth Alliance, New York, NY, USA

The majority of recent emerging infectious diseases have originated from wildlife reservoirs. The global wildlife trade is one major source for emergence, driven through the enhanced human-animal contact and pathogen pollution opportunities it presents, as seen through the emergence of SARS and international movement of monkeypox. Although both the legal and illegal wildlife trade are widespread, little proactive risk assessment has been conducted to inform health policy and disease control responses. Given the immensity and relatively undescribed geographical pathways of the global wildlife trade, most responses to control health and biodiversity impacts have been reactive. Many developed countries fuel the demand for wildlife and wildlife products, and demand is increasing. The health and biodiversity communities have an important opportunity to work together to better monitor, anticipate and mitigate the negative effects of the wildlife trade.

SESSION 03 (Plenary) Emerging Infectious Diseases and the Hajj

Friday, February 15, 2013 Room: Park Congress • Ground Level 16:30–17:15

03.001 Emerging Infectious Diseases and the Hajj Z. Memish

Ministry of Health, Riyadh, Saudi Arabia

The annual Muslim pilgrimage, the Hajj, is the largest religious annual mass gathering in the world. The possible occurrence and global implications of spread of communicable diseases during this mass gathering is a fearful event. For disease surveillance during MGs, efforts to harmonize local preparedness and response efforts with increased global awareness of infectious diseases are often constrained by the complexities of integration of real-time intelligence from global surveillance systems with information about global travel between sites of reported infectious disease outbreaks and the sites of MGs. Despite the adoption of WHO's revised 2005 International Health Regulations, difficulties in reporting processes and multilateral coordination presents ongoing challenges. The Health authority of the Kingdom of Saudi Arabia in coordination with international health authorities continuously reviews the global situation of communicable diseases and updates its health requirements for pilgrims coming from over 185 countries worldwide. In 2012 outbreaks of Ebola hemorrhagic fever in Uganda & DRC and Cholera in Sierra Leone and the emergence of rapidly progressive acute respiratory infection in adults associated with a novel coronavirus have from KSA, Qatar and Jordan has challenged the robustness of the IHR in KSA. Updating Hajj recommendations requires careful update and continuous review of global infectious diseases outbreaks. The current Hajj requirements and guidelines for the prevention and control of possible communicable diseases among pilgrims call for mandatory vaccinations for certain diseases. These mandatory vaccinations are: yellow fever, meningococcal vaccines, and poliomyelitis vaccine. Influenza vaccine is strongly recommended to all pilgrims. Local and international stakeholders must collectively promote and foster a culture of cooperation, while ensuring that sufficient time and financial resources are available to plan and implement effective, innovative public health measures. Furthermore, the early and continued engagement of planners, health officials in the host city and country, and international public health organizations will be essential to ensure that new knowledge can be effectively converted into real benefits for both local and global public health security. For cities and countries hosting MGs, opportunities to strengthen risk assessment and risk mitigation capabilities through the novel integration of multidisciplinary scientific methods and multiagency public health practices would form the basis not only for a lasting domestic public health legacy, but also a repository of new knowledge that would benefit the hosts of future MGs worldwide



SESSION 04 (Invited Presentation)

Emerging Disease Prevention

Saturday, February 16, 2013 Room: Park Congress • Ground Level 08:30–10:30

With a technical contribution from the Food and Agriculture Organization of the United Nations.

04.001 Introduction

J. Lubroth FAO, Rome, Italy

Increased global food demand is driven by population, urbanization and economic growth, particularly in developing and in transition countries. This trend is expected to continue and will require a 70 percent increase need in total food demand by 2050, when the world's population is estimated to surpass 9 billion. Dietary patterns are changing towards more animal products-terrestrial and aquatic. While recognizing that the livestock sector is the largest user of land resources (grazing, pastures, cereal production, water), the answer does not lie in simply producing more. More efficiently in production is required if ecosystem services and natural resources are to be persevered. Animal diseasesendemic, chronic, transboundary, exotic, zoonotic, emerging or entrenched-erode efficiency by as much as 33%, should an animal or flock survive. Illnesses will do not allow animals mount a proper immune response or to reach their genetic potential or reproductive maturity. Furthermore, animal diseases can cripple trade opportunities and cause human suffering through direct health consequences (zoonoses and food-borne) or loss to people's livelihoods. This FAO session looks at some of the dynamics between animal production and health, drivers to disease emergency, maintenance and spread, and new approaches to tackle such uncertainties.

04.002

4.002 Strengthening laboratory networks and strategies to meet the challenges of emerging and transboundary animal diseases (TADs) threats

F. Claes¹, V. Martin¹, G. Dauphin¹

¹Emergency Prevention System (EMPRES), Animal Health Service, Food and Agriculture Organization of the United Nations, Rome, Italy

The Food and Agriculture Organization of the United Nations' (FAO's) mission is to contribute to economic growth, food security and safety, and animal health through timely early warning and disease intelligence based on the sharing of reliable, consistent and transparent information. National animal health laboratories responsible for disease detection and surveillance are central to this mission. Building technical capacity, competency, leadership and a critical mass of regionally networked epidemiology, surveillance and laboratory specialists is a strategic imperative for the efficient and effective coordination of risk management for transboundary animal diseases and zoonoses, including HPAI.

FAO's support to veterinary laboratories and laboratory networks has contributed to major achievements such as eradication of rinderpest and earlier diagnosis for the control of other animal diseases, including zoonoses and emerging diseases. FAO has supported the establishment of several regional laboratory networks (RLNs) and provides ongoing coordination and support. The sustainability of such networks is dramatically improved through recognition and support for national governments and linkages to regional economic organizations or other governance bodies. Under these regional frameworks, each network agrees on strategic approaches for strengthening diagnostic and investigation capacities, mapping regional gaps and resources through laboratory assessments, sharing information and biologic material, and improving linkages between human and animal health. At international level, FAO together with OIE has created OFFLU, the network of expertise on animal influenza. OFFLU's objective is to reduce the negative impacts of animal influenza viruses by promoting effective collaboration between animal health experts and with the human health sector.

Apart from these international and regional networks, FAO is also involved at country level to improve the linkage of laboratories and epidemiologists in both animal and public health sectors, to conduct national cross-sectoral risk assessments for avian influenza at the human-animal interface (4-way linking framework).

Finally, networking alone is not sufficient to overcome the challenges that emerging animal diseases pose. To develop control strategies for TADs access to genetic and epidemiological data is key, and linking and access of these data is instrumental for the control of TADs. Therefore, FAO developed specific tools to link epidemiological and genetic information (the EMPRES-I Genetic Module) and a strongly advocates for free access of genetic information of pathogens.

04.003 Innovation to fill the gaps in disease surveillance: Participatory surveillance, applied technologies for better understanding and reporting

J. Pinto FAO, Rome, Italy

Traditional surveillance tools for collecting disease information have made significant contributions to reporting of animal disease events and support the analysis of information on disease drivers and patterns of transmission and spread. However, there are ongoing challenges such as underreporting and the emergence and spread of new pathogens and sensitivity of surveillance systems that impedes capturing good quality information about new pathogens or old pathogen emergence, spread and persistence. Lack of timely reporting and overlapping indicates that data related to animal disease outbreaks is collected, processed at national, regional and global levels with significant delays and lack of appropriate analysis. The development and the growing use of new technologies and new mechanisms for data collection or reporting could help to improve surveillance, early warning and respond effectively to diseases threats.

FAO is supporting the design and adoption of new technologies for monitoring endemic diseases and detect emerging threats. In Bangladesh, syndromic surveillance is conducted for poultry diseases and to detect particularly Highly Pathogenic Avian Influenza (HPAI) surveillance as part of an USAID funded FAO project using Short Message Service (SMS).

Other examples, include the use participatory disease surveillance (PDS) schemes programs in Indonesia and Egypt to detect H5N1 HPAI; the use FAO introduced the Digital Pen Technology (DPT) into southern Africa as an innovative way of collecting and sending animal disease surveillance data from remote areas in the field to the Central Epidemiology Units for analysis and decision making and the introduction of rapid reporting systems using smart phones technologies [EMPRES-i Event Mobile Application (EMA)].

The use of new technologies can speed up disease detection, reporting and effective response and must be based on the priorities and objectives of disease control programs ensuring that cases of animal disease are timely communicated from farmers, local veterinarians to central veterinary services and to regional and global information systems. Often livestock farmers, communities and local veterinary services represent critical points in this disease communication chain. Cost-effectiveness of surveillance systems and social acceptance of stakeholders to new technologies need to be assessed regularly to compare and justify the introduction of those new technologies for animal disease surveillance and prompt reporting.

04.004 Dealing with the biocomplexity of emerging infectious diseases (EIDs): An ecosystem health approach

D. Beltrán-Alcrudo FAO, Rome, Italy

Today's epidemics of infectious diseases increasingly emerge and spread at the interface of human, domestic animal and wildlife populations. Such disease emergence is triggered by multiple, interrelated factors: changing human and animal demographics, climate change, globalization, increased mobility and trade, urbanization, land degradation, drug resistance and intensive production. Most of these factors are largely related to the booming demand for animal-source protein, which has driven dramatic changes in animal production and increases in trade. The resulting changes to host environments have led to adjustments in pathogen dynamics, such as expanding geographic range, jumping host species and shifts in virulence.

ABSTRACTS

Current approaches to animal disease prevention and control are based on disease transmission disruption, i.e. to eliminate the pathogens from populations through stamping out, vaccination, quarantine and other sanitary measures. While they have proven effective in the control of some diseases, these methods have been less successful in other instances as shown by the current persistence of H5N1 HPAI despite significant national and international efforts. These traditional approaches apply veterinary and medicine tools in isolation of other relevant disciplines such as economics, sociology, anthropology, communication, ecology and land management, thus not confronting the root causes (drivers) of disease emergence at the human-animal-environment interface. To address the global challenge of EIDs, an Ecosystem Health approach is needed, which takes into account the biocomplexity of emerging pathogens and investigates the interaction of these elements in a holistic fashion, rather than isolating one key element. Researchers and policy-makers must focus on the identification of the specific drivers of disease emergence and outbreaks, ensuring that the role of ecosystems, wildlife, and human factors are not neglected. This approach is especially important with EIDs, for which wildlife species are often the source. This multidisciplinary approach will minimize the impact of epidemics, and encourage more holistic approaches for solving health-related problems.

The international community is increasingly converging on crosssectoral, multidisciplinary and collaborative approaches of addressing threats and reducing risks of EIDs at the animal-human-ecosystem interface.

SESSION 05 (Oral Presentations) One Health in Action

Saturday, February 16, 2013 Room: Klimt Ballroom 2–3 • Upper Level 08:30-10:30

05.001 Evaluating long-term behavior change resulting from an intervention to prevent Nipah virus transmission from bats to humans in Bangladesh

R. Sultana, U. K. Mondal, J. Abedin, M. J. Hossain, M. A. Y. Sharker, N. A. Rimi, E. Gurley, N. Nahar, S. P. Luby icddr,b, Dhaka, Bangladesh

Background: In Bangladesh, Pteropus fruit bats, the natural reservoir of Nipah virus (NiV), drink fresh date palm sap made accessible by humans harvesting the sap during winter nights. Multiple outbreaks of NiV infection of humans in Bangladesh have been associated with ingestion of raw date palm sap. Applying a bamboo skirt around the shaved part of date palm tree can prevent bats from contaminating sap, and therefore, prevent NiV outbreaks in humans.

Objectives: The aim of this study was to assess the long-term uptake of a bamboo skirt intervention to reduce human exposure to batcontaminated sap

Methods and Materials: In December 2009 and January 2010, we promoted bamboo skirts in 15 villages in one district in central Bangladesh. We used community meetings to disseminate messages on NiV transmission, and how to make and use skirts to ensure a safe source of raw sap. We subsequently selected a random sample of 77 sap harvesters and 77 tree owners for follow-up. We compared the proportion of sap harvesters and tree owners that used skirts and abstained from consuming raw sap prior to intervention and 1 month and 1 year after the intervention.

Results: Prior to intervention, 3% of sap-harvesters and 1% of treeowners reported using skirts and 3% of sap-harvesters and 3% of treeowners did not drink raw date palm sap. One month after intervention, 30% of sap-harvesters and 10% of tree-owners reported using skirts and 24% of sap-harvesters and 36% of tree-owners reported not drinking raw date palm sap. One year after intervention, 9% of sap-harvesters and 4% of tree-owners reported using skirts and 21% of sap-harvesters and 37% of tree-owners reported not drinking raw date palm sap.

Conclusion: The intervention increased the use of skirts, but uptake was low and decreased over time. Although we did not discourage drinking raw date palm sap as part of the intervention, raw sap consumption decreased and was better sustained over time than skirt use, perhaps because people found it easier to abstain than to use skirts. Future intervention efforts should focus on achieving higher uptake and should consider formally including messages to discourage drinking raw date palm sap.

05.002

Characterizing high risk disease transmission interfaces in the global pursuit of emerging zoonotic diseases

C. K. Johnson¹, T. W. Smiley¹, T. Goldstein¹, W. Karesh², D. Joly³, P. Daszak², J. Mazet¹

¹University of California-Davis, Davis, CA, USA, ²EcoHealth Alliance, New York, NY, USA, ³Wildlife Conservation Society, Nanaimo, BC, Canada

Background: Effective prevention and control of infectious diseases without available vaccines calls for an appreciation of the biological, ecological, and social processes promoting disease transmission in the 21st century. Recent emerging infectious disease events involving wildlife have prompted large scale surveillance for novel zoonotic pathogens in areas where high density human populations coincide with wildlife biodiversity. Investigation of disease transmission interfaces common to zoonotic viruses will identify high risk settings and ecological niches that can be targeted for surveillance and disease control efforts.

Objectives: Characterize high risk interfaces involved in transmission of zoonotic viruses among wildlife, domestic animals and humans.

Methods and Materials: A systematic review of over 2,000 papers in the scientific literature was used to evaluate human activities, social settings, and animal hosts implicated at the point of disease spillover for zoonotic viruses transmitted between 2000 and 2010. Data were summarized for each virus and common interfaces enabling crossspecies disease transmission were identified.

Results: Among 88 viruses with data on zoonotic disease transmission to humans during the past decade, wild animal hosts were implicated in pathogen spillover for 93% of viruses and domestic animal hosts were implicated for 28% of viruses. Rodents, non-human primates, bats, and birds were common wildlife hosts for zoonotic viruses. Direct or indirect contact between wildlife and people was reported in the transmission of 49 viruses while insect vectors were required for transmission of 30 viruses between wildlife and humans. High risk interfaces enabling direct transmission of viruses from wildlife to humans involved hunted animals, animals held at sanctuaries, and animals in research laboratories. Direct and indirect contact with animals around human dwellings and in agricultural settings was the transmission interface shared by most viruses.

Conclusion: This systematic review is the first to compare disease transmission interfaces implicated recently in cross-species transmission of zoonotic viruses. These interfaces represent specific ecological niches with high human-animal contact and increased opportunities for disease transmission and these settings are being targeted for zoonotic pathogen discovery efforts in USAID's Emerging Pandemic Threats PREDICT Program as part of a risk-based surveillance strategy to identify wildlife viruses with potential to cause disease in humans.



05.003 Rabies control in Bali: A "one health" approach E. Russell, F. Abson

World Society for the Protection of Animals (WSPA), London, United Kinadom

Background: Rabies causes an estimated 55,000 human deaths annually, many of which are in children. This fatal zoonotic disease is endemic throughout most of Asia and Africa, where the majority of all human rabies deaths occur from exposure to canine rabies. The gravity of the human health burden, as well as an ignorance of the best methods to control the disease, and hence protect human health, can, and often does, result in extreme animal suffering (e.g. dog culling). In 2005, the WHO stated that "there is no evidence that removal of dogs alone has ever had a significant impact on dog population densities or the spread of rabies". However, dog culling is still often adopted as the initial method of rabies control: in 2008, in response to an outbreak on Bali, Indonesia, over 100,000 dogs were culled. Our hypothesis is that culling doesn't control rabies and that mass dog vaccination, alongside effective collaboration between public health and animal sectors (so a "one health" approach) is the most effective method.

Objectives: To demonstrate through a best practice model how a "one health" approach can control rabies.

Methods and Materials: A humane mass dog vaccination pilot on Bali with surveillance, monitoring and evaluation. For 6 months, from October 2010, local partners, with WSPA's support, vaccinated 210,000 dogs (70% of the island's dog population).

Results: There were near to 100 human rabies cases at the start of the pilot. However, within only 6 months, dog rabies cases fell by 76% and human rabies deaths by 35%. Following this success, the Balinese government, supported by the FAO, committed to further rounds of vaccinations and latest data suggests that, year on year, dog and human rabies cases are rapidly declining. Official figures pending, it is predicted that there will be close to zero human cases in 2013.

Conclusion: We know that mass dog vaccination is feasible and cost effective in a wide range of settings. Rabies can be eliminated and to ensure sustainability, on-going coordinated "one health" dog vaccination programmes will be needed.

05.004 Monitoring of influenza virus in pigs and humans in Switzerland

M. Engels¹, Y. Thomas², E. Fuchsini³, R. Born⁴, S. Bruhn⁵ ¹Institute of Virology, Zurich, Switzerland, ²National Influenza Center, Central Laboratory of Virology, Geneva, Switzerland, ³Swine health service, Sempbach, Switzerland, 4Swiss Federal Office of Public Health, Berne, Switzerland, ⁵Federal Veterinary Office, Berne, Switzerland

Background: Infuenza virus infection is a zoonosis. Pigs are susceptible to swine but also to human and avian influenza viruses. Double infections may allow reassortments leading to the development of new virus variants. Swine influenza virus (SIV) was involved in the development of the pandemic A(H1N1)pdm09 strain in 2009. Thus, monitoring of influenza virus in pigs and humans was strengthened in Switzerland.

Objectives: The monitoring aims to identify SIV subtypes circulating in the Swiss swine population, to detect SIV transmissions between pigs and humans living on pig farms and to determine new variants as early as possible.

Methods and Materials: Pig farmers voluntarily reported pigs with flu-like symptomes to the swine health service. Nasal swabs from three sick pigs per farm were collected. Pig farmers or family members having had concurrently flu-like symptoms were encouraged to take themselves nasal swabs. SIV were identified by real-time RT-PCR and/or virus isolation. Positive samples were subtyped using specific RT-PCRs. Viral genomic fragments from all positive human isolates and their corresponding swine isolates were sequenced by the Sanger method.

Results: From October 2009 to December 2011, 677 farms with pigs having flu-like symptomes were registered, mainly during winter and in regions with high pig density. 173 farms (25%) were sampled and 104

(60%) were tested positive for SIV, with a clear seasonal difference in the positivity rate (69% in winter and 40% in summer season). In Swiss pigs A(H1N1)pdm2009 was first detected in January 2011. All other isolates were A(H1N1). Four of 24 human samples were SIV positive. The genomic sequences confirmed a SIV A(H1N1) origin which corresponded to the swine SIV isolates of the same farm.

Conclusion: Our monitoring allowed us to detect SIV transmission from pigs to humans. We assume that A(H1N1)pdm09 has been transmitted from humans to pigs. Infections occurred the whole year but more frequently during winter. So far only SIV A(H1N1) seems to circulate in the Swiss pig population and there is no evidence for incursions of new subtypes or new strains or for further person-toperson spread of SIV.

05.005 Coxiella burnetti seroprevalence and risk factors in dairy cattle farmers and farm residents in the Netherlands

J. Hautvast¹, N. Schotten¹, B. Schimmer², P. Schneeberger³, P. Vellema⁴, Y. van Duynhoven²

¹Radboud University Nijmegen Medical Centre, Nijmegen, Netherlands, ²National Institute for Public Health and The Environment, Bilthoven, Netherlands, ³Jeroen Bosch Hospital, Den Bosch, Netherlands, ⁴Animal Health Service, Deventer, Netherlands

Background: From 2007 till 2010 a large outbreak of Q-fever occurred in the Netherlands, involving more than 4500 notified community cases. Infected dairy goat farms were the main source for these cases. Contact with ruminants is a known risk factor in Q fever outbreaks. However, there are no recent data on Q fever (Coxiella burnetti) seroprevalence or risk factors in high-risk occupational groups in the Netherlands such as farmers.

Objectives: To study the seroprevalence and risk factors of Q fever in dairy cattle farm residents in the Netherlands.

Methods and Materials: Dairy cattle farms with at least 50 cows aged two years or older were included. Up to maximum three farm residents each filled out an individual questionnaire and provided a blood sample. Blood was tested for Coxiella burnetii antibodies (IgG and IgM, phase I and II) using an immunofluorescence assay. In addition, one farm-based questionnaire was filled out by the farmer. Risk factors for seropositivity were identified by univariate, multivariate and multilevel analyses.

Results: In total, 311 farms participated and 755 residents provided a blood sample. The overall seroprevalence among cattle farm residents was 72.1% (95% CI: 68.8-75.3); farmers showed the highest seroprevalence (87.2%), while children under 18 years had the lowest seroprevalence (44.2%). Thirteen participants (1.7%) reported a diagnosis of clinical Q fever during 2008-2010 or were IgM phase II positive. Risk factors for seropositivity were working full time on the farm, contact with pigs, indirect contact with rats or mice, a higher number of cows on the farm, contact with cows at other farms, having beef cattle on the farm, a farm situated in the southern region and birds present in the stable. Protective factors were full compliance using gloves during birth care, contact with poultry and use of automatic milking.

Conclusion: The seroprevalence of Q fever among dairy cattle farmers and their family members was clearly higher than found in the community, even during the outbreak period. To prevent future infections with C. burnetii it is important that persons work hygienic and that birds and vermin are avoided from the stables. Vaccination of cows might be a future additional control measure.

05.006 High colonization rate of farmers, their relatives and employees at pig farms with emerging Clostridium difficile PCR ribotype 078

E. Keessen¹, M. Hensgens², M. Bos³, W. Dohmen⁴, J. Wagenaar⁵, D. Heederik⁴, E. Kuijper², L. Lipman⁶

¹IRAS- faculty of Veterinary Medicin- Utrecht University, Utrecht, Netherlands, ²LUMC, Leiden, Netherlands, ³Faculty of Veterinary medicine, Utrecht University, Utrecht, Netherlands, ⁴Faculty Veterinary Medicine, Utrecht University, Utrecht, Netherlands, ⁵Utrecht University, Netherland, Netherlands, ⁶IRAS VPH, Faculty of Veterinary Medicine, University Utrecht, the Netherlands, Utrecht, Netherlands

Background: Clostridium difficile Type 078 is emerging in humans and animals and is currently the third most frequently found type at the National Reference Laboratory in The Netherlands. The finding of identical Clostridium difficile PCR ribotype 078 isolates in piglets with diarrhea and in humans with Clostridium difficile infection (CDI) led to the suggestion that interspecies transmission could occur.

ABSTRACTS

Objectives: The aim of this study was to investigate intestinal colonization with C. difficile of pig farmers, employees, their relatives, and their pigs.

Methods and Materials: Farmers and employees (55), partners (31), and children (41) living on 32 pig farms participated in the study. Participants submitted a stool sample, and veterinarians collected pooled fecal samples of 10 different wards at each farm. Fecal samples were cultured using enrichment strategies. Suspected colonies for C. difficile were further identified and characterized by PCR ribotyping. Multiple-locus-variable-number-tandem-repeat analysis (MLVA) was used to investigate the genetic similarity of selected human and porcine isolates

Results: C. difficile was isolated from fecal samples of pigs at 31 of the 32 farms. Type 078 was the predominant ribotype at 30 of the farms positive for C. difficile, at 1 farm only type 045 was present. In total 14 (25%) of the farmers and employees were positive, 4 (13%) of the partners and none of the children. The Odd's ratio for colonization and daily contact with pigs versus no contact with pigs was >2. All positive farmers, employees and partners worked on positive farms and corresponding ribotypes were found in the pigs and the humans. This was type 078 in the humans and pigs on 13 farms and type 045 on 1 farm. Application of MLVA on C.difficile type 045 and 078 isolates from 3 different farms, revealed genetical related complexes encompassing human and pig isolates.

Conclusion: The intestinal carriage rate in the population of people with direct contact with pigs positive tested for C. difficile, is 25%. The finding of identical isolates from humans and pigs from the same farms with MLVA, indicates that transmission, either via direct contact or the environment, likely occurs. Prospective studies are needed to determine the risk for development of CDI in this population.

05.007 West Nile Disease in Italy: Animal surveillance activities as an early warning system for the prevention and control of the infection in humans

R. Bruno, D. Di Sabatino, A. Carvelli, F. De Massis, P. Calistri Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G.Caporale", Teramo, Italy

Background: West Nile Disease (WND) is a vector borne zoonosis caused by a virus of the family Flaviviridae, genre Flavivirus (WNV). During the last decades the number of reported cases of WND infection in horses and humans notified in the Mediterranean Basin increased significantly. In Italy the first outbreak of WND occurred in Tuscany in 1998.

Objectives: This paper describes the results of multi-species surveillance national plan as an early warning system for WNV circulation to implement preventive measures for human health.

Methods and Materials: Since 2001, a multi-species surveillance plan including birds, chicken, horses, mosquitoes and humans has been put in place to early detect the virus re-introduction and to monitor the possible spread of the infection. Organs and blood samples were collected for serological and virological survey. Risk areas and risk period were defined for this purpose; target activities were performed to investigate the ability of WNV to become endemic in some areas.

Results: WNV epidemics re-emerged in Italyfrom 2008 to 2012. Outbreaks in man or in animals occurred in different periods in different Italian regions. In Venetoregion (northern Italy) WNV was detected every year in man or animals. Clinical cases were generally observed from July to October. The case-fatality rate in horses was equal to 23.9% (95% CI: 17.6-31.6%), and to 16.3% in humans (95% CI: 8.2-30.1%). Clinical signs were also reported in one little owl (Athena noctua) and one common buzard (Buteo buteo). High levels of RT-PCR positivity were observed in synanthropic birds magpies (Pica pica), carrion crows (Corvus corone cornix) and rock pigeons (Columba livia). Moreover, 46 mosquito pools tested RT-PCR positive, and few serological positivity were detected in poultry. Both Lineage 1 and 2 circulated through the country.

Conclusion: The multi-species surveillance plan carried out confirmed the ability of the virus to spread to new areas and affect different host populations. Veterinary surveillance activities performed were useful both as an early warning system and for monitoring the evolution of the epidemiological situation, in the framework of implementing measures for the timely prevention and control of WND infection in humans.

05.008 Sylvatic origin and geographic spread of St. Louis encephalitis virus

A. Kopp¹, T. Gillespie², D. Hobelsberger³, A. Estrada⁴, I. Eckerle¹, M. Mueller¹, L. Podsiadlowski⁵, F. Leendertz³, C. Drosten¹, S. Junglen¹

¹Institute of Virology, 53127 Bonn, Germany, ²Department of Environmental Studies and Program in Population Biology, Atlanta, GA, USA, ³Robert Koch Institute, Berlin, Germany, ⁴Universidad Nacional Autónoma de México, Mexico, Mexico, ⁵University of Bonn, Bonn, Germany

Background: St. Louis encephalitis virus (SLEV) is the major representative of the Japanese encephalitis serocomplex of flaviviruses in the Americas. In its known cosmopolitan form, the virus is transmitted between Culex mosquitoes and birds in North- and South America. However, its geographic and ecological origins remain obscure.

Objectives: As for other arboviral flaviviruses, there must exist (or have existed) ancestral strains in sylvatic amplification cycles.

Methods and Materials: In an attempt to seek flaviviruses in sylvatic amplification cycles in Central America, we investigated 3.491 mosquitoes in and around the Palenque National Park, Mexico.

Results: Here we identified the first representatives of sylvatic SLEV. The tentatively named SLEV-Palenque strains were distinct from all presently known SLEV strains showing 94.2-95.7% amino acid identity within the predicted polyprotein and forming a phylogenetic sister clade to all known SLEV strains. Comparing growth of SLEV-Palenque to the epidemic MSI-7 strain revealed no differences in insect cells but a lower or no infectivity of SLEV-Palenque in Vero cells and cells derived from birds (Passer domesticus and Dumetella carolinensis), bats (Carollia perspicillata and Tadarida brasiliensis) and from cotton rats (Sigmodon hispidus), respectively. Phylogeographic reconstruction was done on E gene sequences using a Bayesian relaxed random walk approach to reconstruct continuous trait changes along a simultaneously inferred coalescent phylogeny. The two geographic co-ordinates, latitude and longitude, were reconstructed as separate traits. Results indicated that the common ancestor of all cosmopolitan (endemic and epidemic) strains existed until ca. 330 years before present in an area between southern Mexico and Panama. Expansion of the cosmopolitan lineage occurred in two waves, the first marking the emergence of viruses near the area of origin, the second entailing almost parallel appearances of a Southern hemisphere clade in the Amazonas delta and a Northern hemisphere clade in the lower Mississippi region.

Conclusion: In summary we were able to link the emergence of a major epidemic arbovirus with anthropogenic ecosystems invasion during colonial times. In particular, the phylogeographic investigation of sylvatic relatives to other arboviruses might enhance our understanding of the timing and localization of virus emergence in general.

05.009 **Considerable relation with Foot-and-Mouth** Disease (FMD) infection in Japan, 2010; traffic roads and pig farming area

R. Ushijima

University of Miyazaki, Miyazaki, Japan

Background: Foot-and-Mouth Disease (FMD) outbreak occurred in Japan, and in total 292 cases was found between April and July in 2010. Although stamping-out and movement restrictions were implemented since the first case was confirmed, it had to be taken an alternative measure of emergency vaccination. Epidemiological studies help to understand how the disease dispersed and what were contributed to spread the disease. Also it might be useful to improve the current control measures and find alternatives for the emergency responses.

43 **IMED 2013**

Objectives: To investigate whether if the densely area of pig farming and traffic roads could play a role to spread FMD in Japan in 2010.

ABSTRACTS

Methods and Materials: Generalized linear model was used to analyse the occurrence of infection by administrative area, which is closely related to the difference of pig farming, and road density among infected farms with showed clinical signs from 2^{nd} to 5^{th} week (n=215) and non-infected farms that were located around the infected farms (n=387) in the most affected area.

Results: Compared with the most affected administrative area called "Kawaminami", other five surround area had significantly lower infections (OR: 0.02 to 0.13, p<0.01). Kawaminami had a high density of pig farming with more than 75 % (90/116 farms) of pig farms in the study area was located, and 78% of them were infected at the end. Road density (road length, m/km²) had a relation to the location of infected farms (OR: 1.00043, p<0.01). Larger farms were more sensitive against the infection (p<0.01). Geographically the road density and farm density were correlated in the study area (r=0.34, p<0.01).

Conclusion: It is well known that FMD infected pigs produce more virus as amplifiers compared with infected ruminants. Infection in pig farms or densely pig farming area might contribute to spread the disease. Enough infrastructures of traffic roads seem to associate with the accessibility to farms. Even though the implementation of movement restrictions, related and unrelated vehicles passing through those roads might carry the virus easily to another susceptible area.

05.010 West Nile virus in Canada: 2002–2012

H. Zheng, A. S. Yasseen, P. A. Buck, F. Welsh, M. Raizenne Ottawa, ON, Canada

Background: West Nile virus (WNv) is an arbovirus in the family *Flaviviridae*. The disease is transmitted to humans by mosquitoes that have become infected by feeding on the blood of birds carrying the virus. WNv was first detected in the Western hemisphere in 1999 when an outbreak occurred in the New York City area. The first human cases of WNv in Canada were reported in 2002.

Objectives: The purpose of this report is to briefly summarize WNv human case data collected between 2002-2012, including geographic distribution, seasonality and demographic characteristics.

Methods and Materials: The Canadian WNv National Surveillance Program is a collaborative effort between multi-jurisdictional and multidisciplinary partners across three levels of government, Universities, and not-for-profit organizations. During the WNv season, human data are reported weekly by provinces/territories to the Public Health Agency of Canada. This information is incorporated into a National WNv Weekly Surveillance Report.

Results: For the period 2002-2012, 5339 human cases of WNv infection were reported from 10 of 13 provinces and territories in Canada, with most cases occurring in the central and prairie regions. The majority of the WNv cases occurred from July to September. The annual incidence varied considerably 0.1 cases/million to 7 cases/ million persons. Overall, the average incidence has increased with increasing age, ranging from 0.42 cases/million persons aged < 10 years, to 6.02 cases/million persons aged \geq 70 years. The incidence was higher among males versus females over 70 years (8.52 versus 4.23 cases/million persons, respectively). The case-fatality ratio and the relative incidence of reported cases of WNv neurological syndrome increased significantly with age. Of the 5339 cases, 973 (18%) were hospitalized due to their WNv infection.

Conclusion: WNv has become endemic in Canada. The incidence, and temporal and spatial distribution of the disease varies considerably from year-to-year and is difficult to predict. The economic impact of hospitalizations associated with WNv disease remains unknown. Age is a risk factor for severe health complications from infection with WNv. Public education campaigns need to be targeted both spatially and temporally, with a focus on getting the prevention message out to individuals in higher risk groups.

05.011 Zoonotic diseases monitored by Brazil National IHR Focal Point from March 2006 to June 2012

M. É. Santos¹, S. Lopes Dias¹, E. T. Masuda¹, P. Pereira Vasconcelos de Oliveira², G. S. Dimech³

¹Brazilian Ministry of Health, Brasilia, DF, Brazil, ²Ministry of Health, Brasilia, Brazil, ³Ministry of Health Brazil, Brasilia, DF, Brazil

Background: Zoonoses are diseases of public health concern because they represent 75% of emerging infectious diseases in the world and can affect the production and international trade in animal products. The Center of Strategic Information and Response for Health Surveillance (CIEVS) of the Secretariat of Health Surveillance, Brazil's Ministry of Health (SVS/MS), represents Brazil National IHR Focal Point and it is responsible for the detection and the risk assessment of public health events of national and international concern according to International Health Regulations (IHR, 2005).

Objectives: To describe the zoonoses of public health concern monitored by CIEVS from March/2006 to June/2012.

Methods and Materials: Descriptive analysis of events, between epidemiological weeks 14/2006 and 26/2012 from the database of Events Monitoring System.

Results: CIEVS monitored 917 public health events of national concern, of which 11% were zoonoses. The greater year of zoonoses reporting was 2006. The median opportunity of notification was 8 days, 22% reported up to 24 hours. The technical areas of the SVS/MS were responsible for reporting 66%, and the CIEVS of State Departments of Health submitted 17%. The primary way of notification was e-mail 93%. The North, Southeast and Midwest of Brazil concentrate most of the events. The median opportunity of events closing was 15 days. The mode of transmission by water/feed corresponds to 13%, vector transmission 12% and respiratory 8%. The most prevalent zoonosis was Human Rabies 42% and Creutzfeldt-Jacob Disease (CJD) 12%. All reported zoonoses were assessed as Risk to National Public Health, according to IHR 2005, considering the lethality, endemicity, outbreak or clustering of cases and the pattern epidemiological changes. With regard to CJD, the risk classification was based on initial suspicion of new variant of the disease; however, there have been no confirmation of the diagnosis.

Conclusion: The control of zoonoses requires an intersectoral and coordinated approach between government and health surveillance technical areas to enhance the capabilities for detection and monitoring of zoonoses of public health concern, thus enabling appropriate control measures. The zoonotic infectious disease surveillance in Brazil contributes with the control of emergence and reemergence diseases as it develops capacities for risk assessment, evaluation and response.

SESSION 06 (Plenary)

Emerging Fungal Diseases and Species Extinction

Saturday, February 16, 2013

Room: Park Congress • Ground Level 11:00–11:45

06.001

Emerging fungal threats to animal, plant and ecosystem health

M. Fisher

London, United Kingdom

The last two decades have witnessed an increasing number of virulent emerging pathogenic fungi in human and natural populations, with fungi causing with the first ever documented species extinction events attributed to the emergence of infection in nature. I show that fungal life-history characteristics, namely high virulence, environmental persistence, host-generality, genome diversity and recombination,

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

predispose this kingdom to emergence as terminal pathogens in natural populations. Anthropogenic activity is a key factor in forcing spatial and temporal increases in fungal infection rates by increasing long-distance dispersal, creating novel selection arenas, and by modifying natural environments to the detriment of host immunity. I demonstrate these concepts using global spatial genetic data from a variety of fungal systems including non-pathogenic and pathogenic species of ascomycete *Penicillium*, basidiomycete species of *Cryptococcus* and amphibian-infecting chytrids. I argue that ongoing 'fungal pollution' will increasingly cause the attrition of biodiversity, human health and nutrition unless steps are taken to tighten global biosecurity for this class of emerging pathogens.

SESSION 07 (Invited Presentation)

Of Bats and Men: Nipah and Other Infections

Saturday, February 16, 2013

Room: Park Congress • Ground Level 14:30–16:00

07.001 Understanding the ecology of Nipah virus in frugivorous bats in Bangladesh

J. H. Epstein EcoHealth Alliance, New York, NY, USA

Nipah virus (NiV) is an emerging zoonosis that has caused nearannual outbreaks of encephalitis in Bangladesh since 2001, with >75% mortality. Human infections are seasonal (Dec-Apr) and almost exclusively detected within a western region of the country termed the "Nipah Belt." Pteropus bat species are a reservoir for henipaviruses in other parts of their range, though little is understood about NiV in bats in Bangladesh. We are studying NiV dynamics in batsto determine how they relate to human infection patterns. Here we provide preliminary epidemiological data for bat species in Bangladesh. We collected blood, urine, and saliva from three bat species: Rousettus leschenaulti (n=140), Cynopterus spp (n=75), and Pteropus giganteus (n=2600) between 2006 and 2012. We sampled 800 Pteropus giganteus at 4 locations within and 4 outside the "Nipah Belt," and fitted 16 bats with satellite transmitters to trace movements. We sampled 1800 P. giganteus from a single population within the Nipah Belt quarterly for five years. Samples were screened for antibodies using indirect ELISA and Luminex assays; and for NiV RNA usinf RT-PCR. Bat NiV sequence data were compared to published human NiV sequences. Neither antibodies nor RNA were detected in species other than P. giganteus. In P. giganteus, antibodies were found with varying prevalence (20%-56%) depending on location. To date, we have detected Nipah virus RNA during and beyond the Nipah season, though in <1% of bats tested. We found little NiV sequence diversity in a single bat population over time compared to diversity seen among human sequences from different districts in Bangladesh during a similar period. Telemetry primarily showed short-range, year-round movement patterns with few long-distance movements. Our study provides evidence that P. giganteus is a natural reservoir for NiV in Bangladesh. Roost fidelity and limited migratory movement may limit intermingling among disparate populations, which supports our early findings of low NiV strain diversity over time in a single population. Strain diversity in humans suggests that there may be regional strain diversity in bats. Human activities within the Nipah Belt that increase contact with bat excreta may be particularly important for explaining observed human infection patterns.

07.002

7.002 From bats to human-to-human transmission of Nipah Virus in Bangladesh

H. S. Sazzad icddr,b, Dhaka, Bangladesh

From 2001–2012, 215 cases of human Nipah virus (NiV) infection were identified in 14 outbreaks in Bangladesh; 160 persons (75%) died.

Amultidisciplinary investigation team from the Institute of Epidemiology Disease Control and Research and icddr,b, including epidemiologists, anthropologists and veterinarians, explored pathways of transmission of NiV from its reservoir, the fruit bat, to humans.

In half of these outbreaks the risk factor associated with NiV infection was consumption of raw date palm sap, collected by shaving the upper stem of date palm trees during December to April, winter season in Bangladesh. Images from infrared cameras identified Pteropus bats frequently visiting the date palm trees and licking the sap at night. During 2011-2012, in two outbreaks, cases drank traditional liquor made of fermented date palm sap. NiV has also been isolated from human respiratory secretions, saliva and urine. Half of the human NiV cases in Bangladesh have developed NiV infection following contact with a NiV infected person. These secondary cases have been among family members, relatives and friends who came in close physical contact with the NiV cases when providing close personal care as per social norms in Bangladesh. In 2010, one case's only exposure was preparing a corpse for burial by removing oral secretions and anogenital excreta with a cloth and bare hands. In Dinajpur in 2011, the only known exposure for one case was hugging a NiV infected corpse of a case. In 2010, when NiV cases were admitted in the hospital, NiV infection was identified in a physician who came in close contact with unidentified meningoencephalitis cases while physically examining them without any personal protective equipment (PPE) and hand-washing. In 2011, another NiV case was a cleaner of a hospital where NiV outbreak and sporadic cases were admitted. She cleaned the medical waste of NiV cases without PPE.

Avoiding raw date palm sap consumption, promoting hand washing by family care givers following patient care giving, and ensuring family and health care providers avoid contamination from bodily secretions of febrile case with altered mental status by using PPE could prevent further outbreaks and NiV transmission.

07.003 "One Health" Surveillance for Nipah virus in Thailand

S. Wacharapluesadee¹, P. Duengkae², P. Maneeorn³, S. Suradhat⁴, R. Tantilertcharoen⁴, M. V. Callahan⁵, P. Rollin⁶, H. Wilde¹,

T. Hemachudha¹

¹Chulalongkorn University, Bangkok, Thailand, ²Kasetsart University, Bangkok, Thailand, ³Ministry of Natural Resources and Environment, Bangkok, Thailand, ⁴Chulalongkorn University, Bangkok, Thailand, ⁵Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA, ⁶Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Thailand borders Malaysia where Nipah virus (NiV) outbreaks were documented in 1998. There are an estimated 20 million bats in Thailand belonging to 138 species including several that are both migratory and which are confirmed reservoirs of NiV. Thailand also has over 9.7 million pigs, which come in contact with fruit-eating bat species in commercial and backyard fruit orchards. To date there has been no reports of pig or human cases of NiV infection in Thailand.

Objective: This study seeks to demonstrate that a "One Health" approach to disease surveillance can help investigators gain insight into epidemiologic factors influencing disease transmission and thus help public health authorities to implement effective control of zoonotic diseases originating from wildlife.

Methods: The risk of NiV exposure was assessed by longitudinal surveillance of villagers and domestic pigs in Wat Luang sub-district, Chonburi province where NiV is endemic in fruit-eating bats, (*Pteropus lylei*). Villagers living among NiV-positive bat colonies were evaluated for high-risk behaviors, for recent cases of encephalitis and underwent serology screening for NiV exposure. This study was done in parallel with studies of NiV transmission within local bat colonies. Bats were

International Meeting on Emerging Diseases and Surveillance 2013

trapped monthly at two commercial pig farms. Blood, saliva and urine was collected from each bat for further investigation. Pig's blood samples from these two farms were collected and tested for NiV IgG antibody.

Results: This study found no positive NiV serologies and no cases of encephalitis for the preceding annum among the 418 villagers who were evaluated. The study did identify an increase in seasonal fluctuations and differences in NiV transmission, and the number of bat visit to pig farms in May. There was no evidence of NiV infection in pigs in this study. The community-based network for monitoring disease outbreak was successfully established.

Conclusion: Inter-sectoral cooperation among wildlife-animalhuman sectors assists in recognition and response to emergence of NiV outbreak in Thailand. This study successfully demonstrates the viability of the transboundary "One Health" approach. Establishment of alert system and promotion of awareness at the level of rural villages is a second key success for this "One Health" initiative.

SESSION 08 (Oral Presentations)

'Contagion': Contemporary Viral Pathogens

Saturday, February 16, 2013 Room: Klimt Ballroom 2–3 • Upper Level 14:30–16:00

08.001 Hepatitis E Virus Antigen Detection: An Early Diagnostic Marker

R. Ratho¹, M. Majumdar², M. P. Singh², Y. Chawla² ¹Postgraduate Institute of Medical Education and Research, Chandigarh, Chandigarh, India, ²Postgraduate Institute of Medical Education and Research, Chandigarh, India

Background: Hepatitis E virus (HEV) is an important cause of epidemic and sporadic hepatitis in developing countries. Most of the epidemics are reported and diagnosed based on serology alone. Molecular characterization of the circulating strains is important for epidemiological purposes.

Objectives: The aim of our study was to find the usefulness of Hepatitis E virus antigen (HEVAg) detection in an outbreak setting and to carry out phylogenetic analysis of the strains responsible for the outbreaks.

Methods and Materials: Seventy one serum samples from acute viral hepatitis patients and 61 from the apparently health controls (HC) of the affected region were collected during various outbreaks from North India. Samples were tested for markers of viral hepatitis E; anti-HEV IgM, IgG and HEVAg. Nested reverse transcriptase PCR was carried out for HEV RNA detection and phylogenetic analysis.

Results: Out of 71 samples, 65 (91.5%), 39 (55%), 35 (49.2%) were positive for anti-HEV IgM, HEVAg and HEV-RNA respectively. A concordance of 77.5% was observed between HEVAg detection and HEV-RNA positivity. PCR and HEVAg detection gave highest positivity (100%) within first 3 days of illness. By day 4 to 7 the positivity of PCR declined to 57.5%, whereas antigen and IgM detection were 78.7% and 93.9% respectively. Fourteen HC (22.9%) were positive for both anti- HEV IgM and IgG. On further evaluation eleven (78.5%) showed the presence of high avidity anti-HEV IgG (90-100%), while in 3 avidity ranged between 40-50%. Molecular characterization showed strains responsible for the outbreaks in North India belonged to Genotype I, Subtype 1a

Conclusion: HEV antigen was found to be an early diagnostic marker of acute infection up to 4th day of illness. HEV antigen could detect 4 extra cases in early phase (1-3 Days), which were missed by the conventional serology (anti-HEV IgM). After day 7 anti-HEV IgM was the main indicator of acute infection. HEV antigen based ELISA has the prospect for wider usage in endemic, resource poor countries as it requires same instruments as for anti-HEV IgM detection. We document subclinical infections in healthy controls of endemic region, which needs further investigation to understand the epidemiology of Hepatitis E.

B. C. Torres¹, Y. C. F. Su², M. S. H. Chua², H. Guo², A. K. Cruz¹,

D. C. Klinzing¹, G. J. D. Smith², F. F. Natividad¹

¹St. Luke's Medical Center, Quezon City, Philippines, ²Duke-National University of Singapore, Singapore

Background: Influenza is a major respiratory infection of humans, with annual epidemics occurring in temperate regions, and more variable seasonal patterns observed in the tropics. The Philippines has a large population of approximately 12.5 million overseas workers in over 30 countries. However, few studies have investigated the evolution of influenza virus in the Philippines, particularly with regard to the global migration of influenza in the human population. Since August 2011we have been conducting clinical surveillance for influenza virus in patients presenting at St Luke's Medical Center, Quezon City, Philippines, with symptoms of acute respiratory infection.

Objectives: The objective of this study is to describe the evolutionary dynamics of influenza viruses in the Philippines within a global context.

Methods and Materials: Nasal swabs collected at St Luke's Medical Center from August 2011 to March 2012, were tested for the influenza virus M gene by PCR. Positives were passaged in MDCK-SIAT1 cells for virus isolation. Viruses were tested by RT-PCR for influenza A and B, with flu A positives subtyped for seasonal H3N2 and pandemic H1N1. H3N2 viruses were selected for full genome sequencing and phylogenetically analyzed along with data available in public databases.

Results: We isolated a total of 44 influenza viruses from the 100 PCR positive samples –42 influenza A (H3N2) and two influenza B. No pandemic H1N1 viruses were detected during the surveillance period. Genetic analysis indicated that all newly generated H3N2 sequences from the Philippines were closely related and formed a clade with viruses sampled globally. The Philippine sequences are distributed throughout this clade, suggesting that multiple independent introductions of H3N2 viruses occurred but with no clear pattern of introduction from any particular location observed. The majority of introductions did not result in sustained transmission within the Philippines but local clusters were detected in December 2011 and January 2012.

Conclusion: Surveillance of influenza virus coupled with complete genome sequencing can provide significant insights into virus transmission and evolution both regionally and globally. Surveillance and sequencing will continue, with estimation of divergence times and population dynamics of H3N2 viruses estimated to understand the global transmission of influenza.

08.003

US Influence of the viral membrane, inherited from different host species, on survival of influenza A viruses in water

S. Shigematsu, A. Dublineau, **L. I. O. Sawoo**, I. Leclercq, J.-C. Manuguerra Institut Pasteur, Paris, France

Background: Influenza A viruses (IAV) are major pathogens for animals and humans. These segmented single-stranded negative RNA viruses are composed of an envelope taken from the host in which two glycoproteins: the hemagglutinin (HA) and the neuraminidase (NA) are anchored. The viral structure is directly linked to its genetic make-up except for the glycosylation moieties and the composition of the lipid bilayer, which depend on the host cell. Besides, being in direct contact with the environment (such as air or water), they should play an important role in virus survival and thus for viral transmission from contaminated waters in the case of wild aquatic birds or from contaminated surfaces/ air in the case of humans. Here, we investigated whether the origin species of the host cell has an influence on IAV survival. We therefore determined the persistence in water at 35°C of A(H5N1) and A(H1N1) viruses either grown on mammalian cells or avian cells.

Objectives: Establish a link between IAV survival and the nature of the viral lipid bilayer

Methods and Materials: Persistence of IAVs amplified on mammalian or avian cells was evaluated in water at 35°C. Viral infectivity was assessed over time by microtiter endpoint titration and viral genome was quantified using qRT-PCR.

International Meeting on Emerging Diseases and Surveillance 2013

Results: Results showed that both A (H1N1) and A (H5N1) viruses remained infectious for periods of time as long as 15 days at 35°C, while viral RNA level remained unchanged. Moreover, RT-PCR targeting the whole M segment showed that a significant part of viral RNA was not degraded and remained intact in viral particles. We also found that within the same subtype, viruses grown on mammalian cells were significantly more stable in water at 35°C than their counterparts grown on avian cells, even though these viruses shared the same genetic background.

Conclusion: This difference in virus stability outside the host is probably connected to the nature of the lipid bilayer taken during the budding step or to the carbohydrate side chains of the viral surface glycoproteins. Moreover, the long lasting survival time at 35°C might have a critical role in the ecology of influenza viruses, especially for avian viruses.

08.004 Investigation of deaths due by Influenza A(H1N1)pdm09 in Southern Brazil, July-August. 2012

R. Soletti¹, W. Oliveira², F. Costa¹, F. de Paula¹, R. Moreira¹, L. Garay³, M. Bercini³, E. M. Macario⁴, C. N. Igansi⁵, W. Araújo⁶ ¹Secretariat of Surveillance in Health, Ministry of Health, Brasília, Brazil, Brasília, Distrito Federal, Brazil, ²Secretariat of Surveillance in Health, Ministry of Health, Brasília, Brasília, Distrito Federal, Brazil, ³Secretaria Estadual de Saúde do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil, ⁴Ministry of Health-Brazil, Brasilia, Brazil, ⁵Ministry of Health of Brazil, Brasilia, DF, Brazil, ⁶University of Brasília, Ceilândia-DF, Brasília, Brazil

Background: Between May and July 2012, an increase of cases and deaths of Influenza A(H1N1)pdm09 in Rio Grande do Sul State, Southern Region of Brazil, occurred and an investigation was performed.

Objectives: Describe the epidemiological profile of Deaths by Influenza A(H1N1)pdm09, identify risk factors for deaths and recommend measures for prevention.

Methods and Materials: A descriptive study was conducted. A case was defined as a fatality due to Influenza A (H1N1) pdm09 confirmed by real-time reverse transcription PCR-positive or clinical-epidemiological criteria in Rio Grande do Sul State, from May 25th to July 31st, 2012. A questionnaire including questions on demographic characterization, risk factors, comorbidities, vaccination history, visits to health services and hospitalization information was used to collect data from hospitals, primary care units and households; Risk factors and comorbidities were defined according to the Ministry of Health and Food and Nutrition Surveillance System protocols for nutritional assessment.

Results: We investigated 53 deaths in 43 cities. The median age was 45 (range=3 months-85 years) and 33 (62%) were female. By warning symptoms and risk factors for severity, 44 (83%) had fever, cough and dyspnea; 32 (60%) presented some risk factor and 26 (49%) comorbidity, being the most common were lung diseases and obesity with 13 (50%). Regarding treatment, 32 (60%) sought care within the first 48 hours of symptom onset, but only 2 (6%) received timely treatment. The beginning of treatment with oseltamivir occurred with a median of 6 days (range=2-22) after symptom onset. Most cases (90.6%) weren't vaccinated in 2012, but 28 (58.3%) were among the group eligible for vaccination.

Conclusion: Most cases resulting in death were associated with a more severe presentation of the disease, showed conditions of vulnerability or were not vaccinated. Medical attention was sought timely in most cases, but diagnostic and treatment were untimely, which may have contributed to the worsening of the clinical features and death. We recommend to train health professionals to achieve early diagnostic and treatment, focusing on patients with risk factors for complications, as well as to intensify actions that ensure an increase of vaccination rates in that same group.

08.005 Enhancing the specificity of surveillance case detection of Monkeypox in Democratic Republic of Congo (DRC).

L. U. Osadebe¹, A. McCollum¹, R. S. Lushima², E. Pukuta³,

S. Karhemere³, J. Kabamba⁴, B. Nguete⁵, I. Damon¹,

J. J. Muyembe³, M. Reynolds¹

¹US Centers for Disease Control and Prevention, Atlanta, GA, USA, ²Ministry of Health, Kinshasa, Congo, Democratic Republic of, ³Institut National de Recherche Bio-médicale(INRB), Kinshasa, Congo, Democratic Republic of, ⁴Kinshasa Centers for Disease Control and Prevention, Kinshasa, Congo, Democratic Republic of, ⁵Kinshasa School of Public Health, Kinshasa, Congo, Democratic Republic of

Background: Monkeypox is endemic in Democratic republic of Congo (DRC) with an annual incidence of 5.53/10,000 and case-fatality of 10-15%. Clinically, monkeypox is often confused with varicella, signaling the need for a more specific monkeypox case definition. To better estimate true disease burden, a collaborative effort was established in 2010 to enhance monkeypox surveillance in Tshuapa District of DRC.

Objectives: This study examines the sensitivity and specificity of the national and the enhanced monkeypox surveillance case definitions.

Methods and Materials: There were 368 suspect cases investigated from Tshuapa in 2010-2012. Case reports were matched with 520 samples tested at the national laboratory. Clinical characteristics were assessed to determine if suspect cases conformed to either or both surveillance case definitions. The sensitivity, specificity and predictive values of both case definitions were determined using laboratory results as confirmation.

Results: Of the 329 suspect cases assessed, 86 (26.1%) met the national case definition; 7 (8.1%) were confirmed. Conversely, 210 (63.8%) suspect cases met the enhanced case definition and 43 (20.5%) were confirmed. Sensitivity and specificity of the national case definition were 11.1% and 70%, respectively, while the enhanced had a sensitivity of 68.3% and specificity of 37.2%. Among the individual elements of the enhanced case definition (characteristic rash plus febrile prodrome or lesions on palms and soles, or lymphadenopathy) only rash plus lymphadenopathy had a positive predictive value (PPV) greater than 23%.

Conclusion: The enhanced case definition captured six times (43 vs 7) more true cases thereby meeting the objective to improve the efficiency of case detection. This study also suggests that each component of the enhanced definition contributed to its overall sensitivity. However, the specificity of the enhanced definition was suboptimal, indicating the need for a more precise case definition.

$\fbox{08.006}$ First autochthonous outbreak of dengue in the island of Madeira, October 2012: A challenge for the European Union Region

P. Vasconcelos¹, H. Zeller², C. Abreu Santos¹, B. Sudre², J. Gomes Dias², J. Jansa³, A. C. Silva⁴, A. Nunes⁵, A. Leça¹, K. Mansinho⁶ ¹Directorate-General of Health, Lisbon, Portugal, ²ECDC, Stockholm, Sweden, ³European Centre for Disease Pervention and Control, Stockholm, Sweden, ⁴Instituto de Administração de Saúde-RAM-Madeira, Funchal, Portugal, ⁵Instituto de Adminsitração em Saúde-RAM-Madeira, Funchal, Portugal, 6Centro Hospitalar de Lisboa Ocidental-Egas Moniz, Lisbon, Portugal

Background: On 3 October Portugal reported two confirmed cases of dengue (DENV-1) in citizens on the island of Madeira. Since then, Portugal and the rest of the EU have been facing the first recently documented autochthonous outbreak of dengue in Europe. The mosquito Aedes aegypti has been first detected on the island of Madeira in 2005; since then several measures has been taken to control the breeding sites of mosquitoes as well as implementing vector surveillance, training of professionals and health communication about mosquito population. Since October, national and European support has been provided to the regional authorities on monitoring and controlling the outbreak.

47 **IMED 2013**



Objectives: To present this outbreak at IMED is an opportunity to address into a comprehensive discussion among international experts the challenges such outbreak brings to Public Health professionals within EU.

Methods and Materials: The presentation will describe the outbreak from its detection and detail the measures put inplace to monitor, assess and control the outbreak in its clinical, blood safety, entomological, epidemiologic and public health points of view. Available data and guidance through the documents produced to implement prevention and control measures for the outbreak, will be included.

Results: From 3 October till 2 December 2012, 1993 cases of dengue fever have been reported on the island of Madeira. Cases present with mild symptoms, mainly fever, myalgia, headaches, arthralgia, retroorbital pain and exanthema, affecting mainly women (69%). A total of 118 patients have been hospitalized (average of 4-5 days of hospitalization). No deaths have been reported. Upon 2 December 2012, a total of 42 imported cases have been reported in several European countries.

Conclusion: Depending on the evolution of the outbreak, results will be discussed within the frame of main conclusions to be set and thus especially regarding the potential suitable environmental conditions for transmission during the winter period. After the Chikungunya outbreak in Italy in 2007, this dengue emergence highlights the key importance of surveillance, vector control measures. Vector borne disease outbreak preparedness, needs to be prioritized for the European Public Health community.

08.007 Dengue fever outbreak in North Eastern Kenya, 2011

M. O. Obonyo¹, W. Arvelo², V. O. Ofula³, A. Fidhow¹, B. Fields², R. Sang⁴, E. Wurapa⁵, K. Njenga⁶, J. Montgomery²

¹Ministry of Public Health and Sanitation, Nairobi, Kenya, ²US Centers for Disease Control and Prevention, Nairobi, Kenya, ³Kenya Medical research Institute, Nairobi, Kenya, ⁴Kenya Medical Research Institute, Nairobi, Kenya, ⁵US ARMY MEDICAL RESEARCH INSTITUTE-KENYA, Nairobi, Kenya, ⁶Centers for Disease Control and Prevention in Kenya, Nairobi, Kenya

Background: Dengue fever (DF), a mosquito-borne viral infection, accounts for >50 million infections and >22,000 deaths annually. Little is known about its transmission in Kenya. An outbreak of the disease was confirmed in Somalia in June 2011.

Objectives: In September, we conducted an investigation to confirm and characterize a suspected outbreak in an adjacent area of northern Kenya.

Methods and Materials: We reviewed a line list of suspect patients reported by the affected district surveillance office. A suspected DF case was defined as fever >38°C accompanied with headache, arthralgia, myalgia or hemorrhages in a person presenting to a health facility from August 1–October 2, 2011. We identified newly presenting cases from October 2–October 10, from whom we collected blood for DF virus testing using real time polymerase chain reaction, and obtained clinical information using a standardized form.

Results: We analyzed data on 1,332 suspect patients. Median age was 18 years (range: thand October 1, 2011. There were five deaths (4/1,000 persons). We identified additional 33 new suspect patients, of which 30 (91%) were positive for DF virus serotype 3. Among these, 20 (67%) required hospitalization due to severe outcome of dengue infection. Median hospitalization was two days (range: 1–4). Twenty-six (86%) patients reported aches and pain, 16 (53%) vomiting, and four (13%) gingival bleeding. Seven patients (23%) were also malaria positive. Twenty-four (80%) received antipyretics, 23 (77%) anti-malarials, 15 (50%) re-hydration fluids and 14 (47%) antimicrobials.

Conclusion: This was the second confirmed DF outbreak in Kenya, and highlighted the need for improved surveillance to better define disease burden. We recommended education of medical personnel on proper clinical management for minimizing severe outcome of DF infection and community education on personal protection practices like wearing protective clothing and use of insect repellants which decreases individual risk of infection. Local efforts to reduce breeding areas for mosquitoes and further vector assessment are required for specific

vector control. Clinicians in these regions should consider DF in their differential diagnosis for individuals presenting with acute febrile illness.

08.008 Evaluation of Innate Immune response in Acute and Fulminant Hepatitis E

M. Majumdar¹, R. Ratho², Y. Chawla¹, M. P. Singh¹ ¹Postgraduate Institute of Medical Education and Research, Chandigarh, India, ²Postgraduate Institute of Medical Education and Research, Chandigarh, Chandigarh, India

Background: WHO every year reports 20 million hepatitis E virus (HEV) infections, over three million people present with self limiting acute viral hepatitis (AVH) and 70, 000 hepatitis E-related fulminant hepatic failure (FHF) cases. Humoral immune response as evident by the presence of anti-HEV IgM, is well studied and used as the conventional method for diagnosis of clinically suspected HEV. In contrast, limited data is available on the cell mediated immune (CMI) responses and cytokine profile during HEV infection.

Objectives: The present study was carried out to evaluate the role of CMI and cytokine profile of acute (AVH) and fulminant (FHF) cases of HEV.

Methods and Materials: HEV infection was diagnosed by a positive anti-HEV IgM and /or positive HEV RNA.PBMCs were separated from 33 AVH-HEV, 15 FHF-HEV patients, and 20 apparently healthy-controls (HC). 2x10⁵ PBMCs were cultured in RPMI-1640 and stimulated with recombinant HEV-ORF2-peptide. After 3 days of incubation the cytokine levels were checked for Th1 (IFN γ , TNF α and IL12), Th2 (IL4, IL10) and TGF β in the culture-supernatant using multiplexed cytokine bead-array. Lymphocyte proliferation-index (PI) was estimated using non-radioactive, Colorimetric-MTT assay.

Results: The PBMCs of the patient group showed blast cell formation on stimulation with HEV-ORF-2 peptide in comparison to control group. The PI of AVH, ALF and healthy controls was found to be 3.040 ± 0.667 , 2.188 ± 0.722 and 1.215 ± 0.077 respectively. Significant antigenic reactivity was observed in AVH Vs HC (p<0.0001), ALF Vs HC (p 0.0006) and AVH Vs ALF (p=0.008). The PBMC's of AVH patients showed more proliferation as compared to ALF. Higher amount of IFN- γ was detected in the culture-supernatant of AVH Vs ALF (292.3 \pm 88 pg/ml Vs 3.235 \pm 0.8 pg/ml; p<0.0001). IFN- γ : IL-4 ratio in the AVH was 89.76 and in ALF was 0.589.

Conclusion: A lower level of INF- γ production and low lymphocyte proliferation index contributes to a marked Th2-bias in FHF patients. On the other hand patients capable of expressing high levels of IFN- γ and mount a robust CMI response are able to limit the disease and recover uneventfully. This study demonstrates the vital role played by cell mediated immune response in determining the disease severity of HEV infection.

SESSION 09 (Invited Presentation)

Emerging Disease Mysteries

Saturday, February 16, 2013

Room: Park Congress • Ground Level 16:30–18:00

09.001

9.001 Magnitude and distribution of Nodding Syndrome in Northern Uganda

J. F. Wamala¹, C. L. Okot², M. Malimbo¹, L. Lukwago³, R. Musoke³, E. M. Namukose¹, V. Tugumizemu¹, I. Makumbi³, M. Nanyunja², R. G. Downing ⁴

¹Uganda Ministry of Health, Kampala, Uganda, ²World Health Organization Country Office for Uganda, Kampala, Uganda, ³Ministry of Health, Kampala, Uganda, ⁴Centres for Disease Control and Prevention Uganda, Entebbe, Uganda

Nodding syndrome is an epileptic encephalopathy that is characterized by head nodding, cognitive impairment and physical decline in

affected children. The investigations show an escalating number of cases though the actual disease magnitude is not known. We therefore implemented a registration of all the NS and Epilepsy cases to establish their magnitude as a requisite for better planning to extend holistic care to the victims and their families.

ABSTRACTS

To determine the magnitude of NS as the basis for planning and establishing a comprehensive national surveillance system for the disease.

With support from WHO, CDC, AFENET & Partners, the MoH implemented a NS and Epilepsy case registration census in the three districts of Kitgum, Pader and Lamwo. The protocol was cleared by the Uganda National Council of Science and Technology. Two village health teams were identified and trained on the community case definitions for NS and Epilepsy. Registration was thereafter implemented using simplified registration forms.

A total of 3,541 NS cases were registered with the majority being residents of Pader (1,978 cases) followed by Kitgum (1,084 cases) and Lamwo (479 cases). A total of 161 NS deaths were registered with the majority occurring in Pader (107 deaths) followed by Kitgum (37 deaths) and Lamwo (17 deaths).

A total of 7,034 Epilepsy cases were registered with the majority being residents of Pader (3,178 cases) followed by Kitgum (2,651 cases) and Lamwo (1,205 cases). A total of 517 Epilepsy deaths were registered with the majority occurring in Pader (217 deaths), followed by Kitgum (216 deaths) and Lamwo (84 deaths).

The initial NS cases were reported starting 1997 with a progressive rise in cases till 2012. Nearly all the NS cases (91.7%) were 3–18 years of age with the geographical intensity of NS increasing with reducing distance from fast flowing rivers where endemic transmission on onchocerciasis has been reported.

We used very sensitive community case definitions and therefore these findings represent the worst case scenario for the magnitude of NS & Epilepsy. All the registered cases will be verified by trained healthcare workers get more accurate estimates.

09.002 Nodding syndrome: An emerging epilepsy disorder of sub-Saharan Africa

A. Winkler

Technical University of Munich, Munich, Germany

Background: Nodding syndrome, a newly recognized epilepsy disorder of sub-Saharan Africa, has been identified in three locations: northern Uganda, South Sudan and southern Tanzania.

Objective: We describe nodding syndrome and our knowledge of potentially involved pathophysiologic mechanisms across the three sites. **Method:** We reviewed all the literature currently available and included

our own unpublished observations. Results: There are both similarities and dissimilarities across the three

sites. The age of onset (5-15 years of age) is similar as are the clinical characteristics of the nodding episodes themselves. Detailed prevalence data are unavailable to date, but it is assumed that some thousands of children suffer from the illness and hundreds have been reported to have succumbed to it so far. A longitudinal study from Tanzania shows that the majority of children with nodding syndrome ultimately develop grandmal seizures. Response to antiepileptic medication has been anecdotally observed, but efficacy has not been assessed in any controlled studies. Cognitive impairment is present in children with nodding syndrome, but gross neurological abnormalities seem to be absent at least in the early stages of the illness. In northern Uganda and South Sudan children have been reported to be stunted in growth with delayed sexual development and some children demonstrate signs of malnutrition. Results of MRI investigations have been inconclusive and electroencephalography of affected children of northern Uganda has demonstrated that the nodding episodes themselves represent atonic seizures; results from southern Tanzania indicate the presence of atypical absence seizures. Cases of nodding syndrome seem to cluster in areas with high prevalence rates of onchocerciasis, although a causal association between nodding syndrome and infection with the parasite Onchocerca volvulus has not been demonstrated.

Conclusions: Nodding syndrome represents a new epilepsy disorder in the wider context of a progressive encephalopathy in at least three different sites of sub-Saharan Africa. Despite extensive investigations the cause remains unknown, but there are puzzling results as to an association with the parasite *Onchocerca volvulus*. Further studies to determine the prevalence, epidemiology, possible causal factors, and management and treatment options are needed in all affected areas.



P. Chua

Temasek Lifesciences Laboratory, Singapore, Singapore

Enterovirus 71 (EV71) belongs to the human Enterovirus A species of the *Enterovirus* genus within *Picornaviridae* family. The virion consists of a non-enveloped capsid of approximately 28 nm in diameter surrounding a core of a single-stranded, positive-polarity RNA of slightly more than 7.4 kb in size. The single open reading frame of the genome encodes a polyprotein of 2194 amino acids and is flanked by non-translated regions at the 5' and 3' ends, with a variable length of poly-A tract located at the 3' terminus. The polyprotein is subdivided into three regions; P1, P2, and P3. P1 encodes four structural proteins whereby P2 and P3 encode seven non-structural proteins. The functions of the 11 individual viral proteins are thought to be identical to that of other enteroviruses.

Enterovirus 71 causes both asymptomatic and symptomatic infections in humans. Symptomatic infections are seen mainly in young children and range from non-specific febrile illnesses, exanthemata and classical dermatological manifestation of hand foot and mouth disease (HFMD) to neurological diseases with or without other visceral involvement.

Since its discovery in 1969, EV71 has been recognised as a periodic cause of epidemics of HFMD associated with severe neurological complications in a small proportion of cases. Thus, its epidemiology so far is based chiefly on outbreak situations which are closely tied to outbreaks of HFMD. Past outbreaks due to EV71 appear to fall into two patterns; "small-scale" outbreaks with few CNS-complicated cases and "large-scale" outbreaks associated with frequent and severe CNS-complicated cases with high mortality rate.

The first large-scale outbreak of HFMD due to EV71 in the Asia-Pacific region occurred in Malaysia in 1997 and since then, EV71 epidemic appears to recur at a periodicity of approximately every three years. The controversy of aetiology in the 1997 outbreak, public health perspective with respect to HFMD and EV71 surveillance in Malaysia will be shared briefly together with the current status of development of EV71 vaccines in the region.

09.004

09.004 Ebola and Marburg viruses emergence at the human-animal interface

P. Formenty

World Health Organization, Geneva, Switzerland

Outbreaks of Ebola and Marburg occur sporadically in Central Africa. The case-fatality ratio varies generally within a range of 20–90%.

In Africa, infection has been documented through the handling of infected chimpanzees, gorillas, fruit bats, monkeys, forest antelope and porcupines found dead or ill in the rainforest. For Marburg human infection resulted from prolonged exposure to mines or caves inhabited by Rousettus bats colonies.

Recent studies have shown that *Rousettus aegyptiacus* bats should be considered natural hosts for Marburgvirus. In Africa, fruit bats, particularly species of the genera *Hypsignathus monstrosus, Epomops franqueti* and *Myonycteris torquata*, are considered possible natural hosts for Ebola virus.

Reston ebolavirus (REBOV) infection discovery in pigs in Philippines in 2008 prompted an intensive collaborative effort of animal health and public health authorities to assess the risk of REBOV in animal and humans. Possible routes of infection from pigs to humans include: transmission when handling infected pigs in farms, during slaughtering activities and preparation of meat, food chain, xenotransplantation, vaccine, cosmetics, etc.

Subsequent experimental infection demonstrated that pigs replicated Zaire ebolavirus (ZEBOV) to high titers mainly in the respiratory tract, and thus identified an unexpected site of virus amplification and shedding linked to possible virus transmission. Additional experiments showed ZEBOV transmission from pigs to cynomolgus macaques without direct contact.

International Meeting on Emerging Diseases and Surveillance 2013

Recent studies have reported serological evidence of Ebolavirus infection in Orangutans in Indonesia; in several bats species in China and in Rousettus bats in Bangladesh. In addition a new filovirus -provisionally named Lloviu virus- was identified in insectivorous bats in caves in Spain.

With more evidence of filovirus infection in wildlife from Africa to Asia, the geographic distribution of Ebola and Marburg virus should be consider to overlap with the range of Fruit bats of the Pteropodidae family.

Given results of recent experimental inoculations with pigs, they should be considered as a potential amplifier host during Ebola or Marburg outbreaks.

New mode of infection and transmission are possible for Filovirus at the human-Animal interface (e.g. Henipaviruses) and need to be studied during next outbreaks. This will impact prevention and control measures during Ebola and Marburg outbreaks.

SESSION 10 (Invited Presentation)

Vectorborne Diseases in Humans and Animals

Saturday, February 16, 2013 Room: Klimt Ballroom 2–3 • Upper Level 16:30-18:00

10.001 A novel orthobunyavirus in European livestock: The emergence of Schmallenberg virus

M. Beer¹, D. Hoeper¹, K. Wernike¹, H. Schirrmeier¹, M. Holsteg², F. Conrahts¹, T. Mettenleiter¹, B. Hoffmann¹ ¹Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany,

²Chamber of Agriculture for North Rhine-Westphalia, Bonn, Germany In summer 2011, Dutch and German veterinarians reported signs of

an infectious disease in cattle which was associated with primarily diarrhea in the Netherlands and with milk drop and fever in Germany. Samples were sent for testing for bluetongue virus which was excluded as well as other known viral infectious diseases of cattle. A pool of plasma samples from diseased dairy cattle from a farm near the city of Schmallenberg was analyzed by next generation sequencing resulting in sequence fragments with a high homology to viruses of the genus Orthobunyavirus. The novel virus was designated as 'Schmallenberg Virus' (SBV), the first member of the Simbu serogroup detected in Europe. Obviously, the introduction occurred in a region which also experienced the first bluetongue virus serotype 8 cases in Central Europe in 2006, and the virus spread very quickly over a wide geographical area. SBV-infection resulted in the birth of characteristically malformed domestic ruminants reflecting acute infections in summer and fall 2011. Until December 2012, more than 5500 SBV-cases have been reported in Europe, and the virus had spread to many countries in Europe. Phylogeny and cross neutralisation demonstrated the closest relationship of SBV with viruses of the Sathuperi species like the Australian Douglas virus. PCR tests with pooled midges caught in fall 2011 were able to detect SBV-RNA in biting midges such as Culicoides obsoletus, C. dewulfi and others indicating vector-transmission similar to other Simbu serogroup viruses. First animal experiments with cattle and sheep resulted in a uniform but short viremic period of about 3 to 5 days. However, viral RNA could be detected in some animals more than 28 days post inoculation in the mesenteric lymphnodes. A zoonotic potential of SBV could be excluded by serological studies performed by Dutch and German authorities on humans exposed to SBV. Possible ways of introduction, epidemiological data as well as results of the first pathogenesis studies will be presented, and the potential of metagenomics for pathogen discovery will be discussed.

merging zoonotic vector-borne diseases in Europe

N. Nowotny¹, T. Bakonyi², J. Kolodziejek², K. Sekulin²,

H. Lussy², K. Pachler², H. Weissenböck³

¹Sultan Qaboos University, College of Medicine and Health Sciences, Muscat, Oman, ²University of Veterinary Medicine Vienna, Institute of Virology, Vienna, Austria, ³University of Veterinary Medicine Vienna, Vienna, Austria

In my presentation I will focus on West Nile virus lineages 1 and 2, which emerged recently in Europe, and dispersed quickly in several central, southern and eastern European countries, resulting in significant veterinary and public health challenges. In particular I will talk on European aspects of West Nile virus epidemiology, molecular phylogeny and host susceptibility. In short I will also cover Usutu virus, another mosquito-borne flavivirus, closely related to West Nile virus.

I will also provide an update on tick-borne encephalitis virus, a significant human pathogen in Europe, which extended recently its range of distribution to the north and to higher altitudes.

As two examples for rodent-borne zoonotic diseases in Europe I will discuss hantavirus infections including shrew-borne hantaviruses, and cases of cowpox, which were transmitted to humans by cats and, more recently, by pet rats.

10.003 Emerging insect vector-borne animal diseases in the eastern Mediterranean E. Klement

Hebrew University, Jerusalem, Israel, Rehovot, Israel

Infection by insect vector borne animal viruses cause major burden to livestock and might result in significant economical losses. The ability of such viruses to invade new locations depends on the frequency of their introduction and the existence of adequate environmental conditions that support their vector population in the invaded location. Such conditions exists in major parts of the Eastern Mediterranean (EM), which includes Cyprus, Syria, Lebanon, Israel, Jordan and the Palestinian authority. Extensive livestock trade with countries in both Africa and Asia, movement of livestock and synoptic conditions that link the region with the adjacent continents are important causes for re-introduction of vector borne viruses into the EM. The existence of Mediterranean climate in large parts of the EM, which is characterized by relatively high humidity and high temperature, strongly supports vector multiplication, biting and virus transmission.

The aim of this lecture is to describe the insect vector borne viruses which emerged or re-emerged in the EM during the last decade and to characterize the factors influencing their dynamics.

The diverse climate of Israel, which is located in the center of the EM encourages constant re-introduction of vector borne viruses. The high proportion of livestock held under intensive farming in Israel is under constant observation. Furthermore, the veterinary services in Israel are highly transparent and therefore any incursion of a disease is immediately notified to the OIE. The insect vector borne viruses diagnosed in Israel during the last decade will be described, assuming that Israel represents the plethora of viruses which circulate in the EM.

In the last decades Israel suffered outbreaks caused by many vector borne viruses such as epizootic hemorrhagic disease virus, Akabane virus, bovine ephemeral fever virus, lumpy skin disease virus, equine encephalosis virus, West Nile virus and Turkey meningoencephalitis virus. These may be a result of primary introduction into Israel or secondary to other EM infected countries.

As represented by Israel, the frequency of incursion of new vector borne animal viruses to the EM is very high. Their early detection may enable better preparedness in case of possible invasion to adjacent regions like Europe.



SESSION II (Invited Presentation)

Neglected Zoonotic Diseases

Sunday, February 17, 2013 Room: Park Congress • Ground Level 08:30–10:30

11.001 The economic and health burden of neglected zoonotic diseases

P. Torgerson

University of Zurich, Zurich, Switzerland

A neglected zoonotic disease (NZD) is a zoonosis that is commonly associated with poverty and causes a considerable burden of ill health in humans and may also have a substantial financial burden on livestock. Despite this they often attract little funding for control of intervention. They disproportionately affect the livelihoods of large numbers of poor livestock keepers or those living in periurban slums in lower income countries. However upper income countries are not exempt from the impact of some of these diseases. There is a growing concern with the emergence and re-emergence of several zoonoses including echinococcosis, brucellosis, leptospirosis, leishmaniasis, toxoplasmosis and food-borne trematodes. Others such as rabies and zoonotic schistosmiasis remain major problems whose true societal impact is often underestimated. There is a clear need for data available on the burden of NZDs to inform policy with regard to interventions to control or eliminate NZDs. Benefits to intervention policies include not only improved human health but increased animal productivity. The costs of such interventions will drive the cost effectiveness of intervention strategies. Current data will be presented that demonstrates that that collectively, NZDs probably have a similar human disease burden, in terms of Disability Adjusted Life Years, to any one of the big three human infectious diseases: malaria, tuberculosis or HIV. In addition there are substantial animal health costs. Despite the fact that much of this high socio-economic burden is preventable these disease remain of low priority.

11.002 Rabies: The path to elimination

A. L. Willingham

World Health Organization, Geneva, Switzerland

Although rabies cannot be eradicated in view of the multitude of primary animal host species (especially bats) maintaining rabies viruses and other lyssaviruses in nature, evidence has accumulated through research particularly during the past 10 years, showing that canine rabies which is responsible for most of the human rabies deaths occurring in the world, can be cost-effectively controlled and eliminated through control of the disease at source. Eliminating canine rabies would save many tens of thousands human lives and reduce enormously throughout the world the need to provide post-exposure prophylaxis following contacts with rabies suspected animals. Canine rabies has been successfully eliminated in affluent countries and some low income countries such as Chile, South Korea and Malaysia in the past. Ongoing dog rabies control programmes in Latin America, Africa, and Asia are giving promising results indicating that in today's context the elimination of rabies in dogs remains an achievable goal. Various regional initiatives for prevention of human dog transmitted rabies through dog rabies elimination have been launched involving countries of Latin America and South, South east and East Asia. Deadlines for achieving the goal of human and dog rabies elimination have been set by 2015 for Latin America and 2020 for Asia. This latter date is also suggested for rabies elimination in Middle East, Central Asia and North Africa. Although pilot projects are ongoing in sub-Saharan Africa prolonged efforts will be required on that part of the continent and elimination may only be achieved by 2030. A global strategy to eliminate canine rabies by 2030 is being developed to provide a timeframe for implementation, a framework for resource mobilization and technical solutions for conducting reliable diagnoses and effective surveillance, providing easy access to modern rabies biologicals for proper post-exposure prophylaxis, carrying out thorough dog immunization campaigns achieving a 70% coverage combined with humane dog population management and coordinating disease control efforts across national and regional borders.

11.003 Echinococcosis: Endemic and re-emergent P. Craig

Salford, United Kingdom

In 2006 WHO listed 8 neglected zoonotic diseases (NZDs), which included echinococcosis and it was also included in the NTD road-map to 2020. Recent global disease burden estimates indicate up to 3 million cases of human cystic echinococcosis (CE), but also > 300,000 cases of alveolar echinococcosis (AE), and increased cases of the rare neotropical polycystic echinococcosis (PE). Echinococcosis is also reported to be re-emergent and spreading in several areas. A return to traditional husbandry for poor rural sheep keepers appears to have increased the risk of synanthropic transmission of Echinococcus granulosus and human CE in Kazakhstan and Kyrgyzstan. Increased peri-urban transmission of CE in Arab communities in North Africa, Israel, Peru and eastern Tibet, may be due to increased ownership of guard dogs and the occurrence of significant stray/community dog populations. Breakdown or relaxation of dog focussed interventions or control measures may also provide a driver for increased transmission and potential CE re-emergence, for example in semi-nomads of NW Kenya and western Mongolia, and sheep farmers in Wales and Cyprus. Wilderness encroachment may also lead to increased contact with sylvatic hosts with risk of cestode zoonoses, for example, indigeneous Indians in Amazonas use dogs to hunt large rodents for `bush-meat` with increased risk of dogs acquiring infection with E.vogeli and risk of human PE disease. Deforestation and agricultural expansion in western China (Gansu, Ningxia) may increase risk of human AE disease by increasing suitable small mammal host/ reservoir habitats and transmission potential of E. multilocularis; and this may also occur as a result of increased livestock grazing pressure in Tibetan pastoral communities in western Sichuan. By contrast, increasing populations of the red fox in Europe, in part as a result of rabies control, reduction in hunting and adaption to peri-urban/urban ecosystems, appears to have facilitated spread of E.multilocularis with concern about potential establishment and/or emergence of human AE in previously parasite-free and low-endemic areas. Surveillance systems in livestock, dogs, wildlife and human populations are important to understand transmission, to consider interventions and to evaluate control measures.

11.004 Implementing the roadmap to combat Cysticercosis

A. L. Willingham

World Health Organization, Geneva, Switzerland

Cysticercosis caused by the zoonotic pork tapeworm, *Taenia solium*, has emerged as a serious public health and agricultural problem in Latin America, Sub-Saharan Africa and South and Southeast Asia and was added by WHO to the list of major neglected tropical diseases in 2010. Neurocysticercosis (NCC) is considered to be the most frequent preventable cause of epilepsy in developing countries. The proportion of NCC cases among people with epilepsy in endemic countries is estimated to be 29.0% while the global NCC burden has been estimated to be over 2 million DALYs per annum. The increasing frequency of NCC in the USA, Canada, Europe and the Middle East, may relate to the



growing immigrant population who may come with tapeworm infections and so expose others, including those who do not consume pork, to infection. NCC has been found to impose a heavy financial burden to those suffering from the disease and their families and has especially serious impact on pig-producing communities being responsible for poor pork quality and reduced value or condemnation of pig carcasses, thereby reducing household income and making an important source of protein unsafe to consume. Although cysticercosis is theoretically amenable to control and even elimination, information about burden and transmission, practical and affordable diagnostic tools, and validation of simple intervention packages need to become available to enable this. A single approach to T. solium control is insufficient, thus for sustainable prevention, control and eventual elimination a combination of approaches is needed including: (1) improvements in chemotherapy for humans and pigs, (2) vaccination of pigs, (3) better pig management and pork production, (4) improved sanitation, and (5) education. Medium and long term needs for combating the disease include validating a strategy for control and elimination of T. solium cysticercosis by 2015 and then using the validated strategy for scaling up interventions in selected endemic countries by 2020. WHO and its partners are committed to facilitating attainment of these milestones through improvement of control tools and formulation of best practice guidelines for interrupting transmission of cysticercosis, which can then be tested in pilot projects in selected endemic sites.

ABSTRACTS

SESSION 12 (Oral Presentations) Infection, Detection, & Protection: Adventures in Epidemiology

Sunday, February 17, 2013 Room: Klimt Ballroom 2–3 • Upper Level 08:30–10:30

12.001 Evaluation of cholera and other diarrheal diseases surveillance system, Niger State, Nigeria, 2012

A. T. Bashorun¹, A. Ahumibe¹, S. Olugbon¹, A. Taju¹, P. Nguku², K. Sabitu³

¹Nigeria Field Epidemiology and Laboratory Training Program, Abuja, Nigeria, ²Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ³Ahmadu Bello University, Zaria, Nigeria

Background: Cholera outbreaks are frequent in Nigeria. In 2010 and 2011, 41,936 cases (case fatality rate [CFR]-4.1%) and 23,366 cases (CFR-3.2%) were reported. In 2011, Niger state had 2472 cholera cases (CFR-2%) and 45,111 other diarrhea diseases cases.

Objectives: To determine and assess the objectives, performance and attributes of cholera and other diarrheal disease surveillance system in Niger state.

Methods and Materials: We conducted evaluation in July, 2012. We adapted CDC guideline on surveillance system evaluation (2001). We conducted key informant/in-depth interviews with stakeholders. We examined cholera action plans for preparedness and response, conducted laboratory assessment, extracted and analyzed cholera surveillance data from 2007–2012 for frequencies/proportions using Microsoft Excel. Thematic analysis was done for qualitative data. We shared findings with stakeholders in state and Federal levels.

Results: Surveillance system was setup for early detection and monitoring towards evidence-based decision. Case definition used is any patient aged 5 years or more who develops acute watery diarrhea, with or without vomiting and is highly sensitive. It is a passive

surveillance system and active during outbreaks. It has formal and informal sources of information. Government funds system. It is simple and integrated into Integrated Disease and Surveillance Response (IDSR) system. Case definition is simple but laboratory confirmation makes surveillance complex. It takes 24-48hours between onset, confirmation and response.

Previous line list reviewed showed undefined/poorly labeled outcomes. Of 2472 cases in 2011 1320 (49%) were found in line list. 2011 monthly data completeness was75%. So far in 2012, 5 (0.02%) of all diarrhea cases were cholera. System captures age as the only socio-demographics.

Of 11 suspected cholera cases tested during 2011 epidemic, 7 confirmed as cholera (PPV-63%). Of 3 rumours of cholera outbreaks (2011–July 2012), one (PPV-33%) was true. Acceptability of system is high. Reporting timeliness -68.7%.

Laboratory has capacity for V.cholerae isolation but no Cary Blair transport medium and cholera test kits.

Conclusion: Evaluation revealed that surveillance system is meeting its objectives by early detection and response to cholera. System is simple, stable, flexible, sensitive, poor data quality, low PPV, fair laboratory capacity and moderate timeliness. We recommended internet-based reporting for timeliness and data quality and provision of laboratory consumables.

12.002 Surveillance during Hajj: Patterns and causes of mortality amongst Indonesian pilgrims

M. Pane¹, S. Imari¹, N. Kandun¹, **G. Samaan²** ¹Ministry of Health, Jakarta, Indonesia, ²Australian National University, Canberra, ACT, Australia

Background: Over 200,000 Indonesians undertake Hajj pilgrimage each year, constituting 10% of international pilgrims. Hajj is physically demanding and the mass gathering provides opportunity for disease transmission as well as exacerbation of chronic health conditions. Mortality rates amongst Indonesian pilgrims ranged between 200 and 380 per 100,000 pilgrims in recent years. Reasons for the high mortality rates have not been fully explored.

Objectives: This study assessed the patterns and causes of death for Indonesian pilgrims based on Hajj mortality surveillance in 2008.

Methods and Materials: Pre-departure, pilgrims undertake a medical test to confirm fitness-for-travel and to receive meningitis vaccine. During Hajj, one doctor and two nurses accompany each flight group and conduct health surveillance. For deaths, the Indonesian public health team based in Saudi Arabia maintains a database of demographic and cause of death data. Mortality data were analyzed descriptively to assess rates, timelines and cause of death.

Results: In 2008, 206,831 Indonesian undertook Hajj of which 28% of pilgrims were classified as high risk due to underlying health conditions or if they were >60 years. There were 446 deaths, with an overall mortality rate of 216 per 100,000 pilgrims. Mortality rates increased significantly with age (p<0.01). Most deaths occurred in Mecca (n=305, 68%), followed by Medinah (n=106, 24%) and Jeddah (n=35, 8%). Weekly mortality rates exceeded the expected crude motality rate in week 6 when most pilgrims were in Mecca, and remained high till the end of Hajj four weeks later. Deaths peaked earlier amongst those traveling to Mecca (X² for trend=9.23, p=0.002). Most deaths were due attributed to cardiovascular (n=292, 66%) and respiratory (n=126, 28%) diseases.

Conclusion: Surveillance during Hajj is critical for health policy development. Travel to Medinah prior to Mecca may provide more time for pilgrims to acclimatize to Saudi Arabia and Hajj conditions. Coupled with other strategies to reduce health risks in Mecca, this travel route may be more suited to high-risk pilgrims. Patterns of causes of death were aligned with findings from other countries, providing opportunity to learn lessons from their interventions to decrease pilgrim mortality rates.



12.003 ECDC/EpiNorth epidemic intelligence activities during EURO 2012 in Poland and Ukraine

A. M. Gherasim¹, I. Linina², G. Rimseliene³, L. Paine Hallström⁴, J. Mantero⁴, P. Penttinen⁵

ABSTRACTS

¹EPIET Fellow-European Centre for Disease Prevention and Control, Stockholm, Sweden, ²Scientific Institute of Public Health (WIV-ISP), Brussels, Belgium, ³Norwegian Institute of Public Health, Oslo, Norway, ⁴European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden, ⁵European Centre for Communicabled Disease prevention and Control, Stockhokm, Sweden

Background: Approximately two million people visited Poland and Ukraine during UEFA European football championship (EURO 2012) held between 8 June and 1 July 2012.

Objectives: From 1 June until 8 July, the European Centre for Disease Prevention and Control (ECDC), in collaboration with EpiNorth and hosting countries public health authorities, implemented tailored epidemic intelligence (EI) activities in order to detect and assess potential health threats in this mass-gathering (MG) setting, including event-based surveillance (EBS) of web-information.

Methods and Materials: Based on previous experiences, we customized several web-based EBS systems (MedISys, HealthMap, PULS and GPHIN) for automatic and semi-automatic selection of official and unofficial public health information relevant for EURO 2012; additional manual daily screening results were provided by EpiNorth considering authorities websites of participating and bordering countries. All the information screened was filtered for public health relevance using pre-defined criteria. Relevant events identified were shared with hosting countries, WHO and EpiNorth network for validation or further assessment and included in 24 ECDC daily bulletins shared with our partners.

Results: We identified 114 potential public health events, 76 (67%) related to hosting countries (58/76 in Ukraine); 30 events (26%) occurred in participating countries and 8 (7%) in other bordering countries. Of the 76 hosting country events, we evaluated and validated 39 public health threats with possible implication for these countries and 11 events as public health threats to visitors/participants. None of them represented at the end a major public health threat for EURO 2012.

Conclusion: Our continuous monitoring and assessment of the increased flow of media information, as well as other public health information channels did not lead to identification of any major public health threat and no event has occurred during the games. However the implemented EI activities provided real-time information on potential ongoing public health threats and measures in place during the MG. Considering the feedback of our public health partners during this and previous MG experiences we suggest using multiple EBS websystems as a complement to standard surveillance in order to monitor and assess the public health risk for infectious diseases during such events in real time.



12.004 Improving capacity to investigate and respond to emerging infectious disease outbreaks in **East and Central Africa**

H. M. Amuguni¹, T. Odoch², R. Nauma³ ¹Tufts University, North Grafton, MA, USA, ²Makerere University, Kampala, Uganda, 3RESPOND/USAID, Kampala, Uganda

Background: Infectious diseases of grave concern to human health are emerging from wildlife and livestock populations in regions of the world where boundaries between human, wildlife and livestock populations are undergoing rapid change. This occurs with greater frequency in tropical regions, areas with limited resources for disease prevention and control. Using a One Health approach, the USAID RESPOND project strengthens field training, educational programs and supports governments and universities to improve capacity to investigate and respond to emerging infectious diseases. The RESPOND project in collaboration with the African Field Epidemiology Network (AFENET) and Makerere University College of Veterinary Medicine (COVAB) is now in the second year of successfully implementing a One Health focused masters degree in veterinary public health with a field epidemiology component in Uganda.

Objectives: The goal is to create a regional East and Central Africa One Health training program that produces field based multi-disciplinary graduates trained in outbreak investigation and response with cohorts from Uganda, Rwanda, Kenya, Tanzania, Ethiopia and Democratic Republic of Congo. These teams would support their governments to investigate, respond to and counter existing and future emerging infectious disease threats.

Methods and Materials: The 24 month program has a multifaceted hands-on field based curriculum covering One Health approaches to emerging and re-emerging infectious disease surveillance, applied epidemiology, outbreak investigation, response and assessment.

Results: There are currently five fellows in the program who spend 75% of their time in the field. Mentorship for the fellows is provided by Makerere, Tufts and Minnesota universities, AFENET, and RESPOND. They participated in the Ebola, Brucellosis and Typhoid outbreaks in 2011; developed Rabies and FMD surveillance strategies; and analyzed animal health surveillance data. They are currently attached to 5 districts sites to pilot an infectious disease surveillance system. The next cohort includes students from six African countries and starts in January 2013.

Conclusion: The AFENET fellows are a great resource to Uganda's Ministries of Agriculture, Health and Environment in combating emerging and re-emerging infectious diseases, surveillance and outbreak investigation and response using the One Health approach. Continued support and implementation of similar programs will improve response to outbreaks in the region.

12.005 Characterizing zoonotic disease outbreaks in the United States

H. Allen LMI, McLean, VA, USA

Background: There is a documented disconnect in zoonotic disease surveillance and reporting, as well as a clear need for improved collaboration between veterinary and human medicine. Given the growing threat zoonotic diseases pose to public health, it is important to better understand zoonotic disease detection practice in the United States.

Objectives: This research characterizes who detects U.S. zoonotic disease outbreaks and how fast the outbreaks are detected from 1998-2008

Methods and Materials: A database of of zoonotic disease outbreaks was created from ProMed-Mail and Morbidity and Mortality Weekly Reports. Characteristics including who detected the outbreak, how fast the outbreak was detected, species affected, and species of origin was collected. Univariate statistics were calculated, including mean and median times to detection. Chi-square tests were used for bivariate analyses (p<.05); Kruskall-Wallis tests and Dunn's method were used to analyze how fast outbreaks were detected and the relationship between detection speed and other factors.

Results: One hundred one outbreaks were identified. Sixty one percent were caused by potential bioterrorism agents. Eighty percent of the outbreaks occurred in humans and one or more additional species. Outbreaks are most commonly detected by diagnostic laboratories (49 percent); median number of days to reporting is 13 (range 0-492). Laboratories and clinicians detect outbreaks more guickly than a state agency; there was no difference in time to detection based on whether it was identified by the animal health or human health entity. The mode of transmission, species of origin (of outbreak), and primary symptom of the disease agent did not affect time to detection.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: This research supplements prior work by reviewing only outbreaks of zoonotic diseases. While zoonotic disease outbreak detection is often complex because of the disconnect between animal health and human health sectors, the time to outbreak detection is not clearly affected by the species affected by the outbreak. State agencies detect outbreaks more slowly than other entities such as clinicians and laboratories, suggesting that it is important to have astute clinicians and electronic laboratory reporting to quickly detect a disease, aggregate results, and identify a zoonotic disease outbreak in humans or animals.

12.006 Estimating global mortality associated with the influenza A H1N1 pandemic in 2009: The WHO Global Pandemic Mortality Assessment (GLaMOR) project

L. Simonsen¹, **P. Spreeuwenberg**², R. Lustig³, R. J. Talyor³, D. M. Fleming⁴, M. Kroneman², L. W. Kim³, M. D. Van Kerkhove⁵, A. W. Mounts⁶, J. W. Paget²

¹George Washington University, Washington DC, DC, USA, ²NIVEL, Utrecht, Netherlands, ³Sage Analytica, Bethesda, DC, USA, ⁴Royal College of General Practitioners, Birmingham, United Kingdom, ⁵Imperial College, London, United Kingdom, ⁶World Health Organization, Geneva, Switzerland

Background: The global mortality burden of the 2009 influenza A H1N1 pandemic has been subject to considerable uncertainty. By the time WHO declared the pandemic to be over in August 2010, it had received reports of 18,500 laboratory-confirmed deaths, a figure that underestimated the true burden of disease and did not provide an accurate assessment of the geographical impact of the pandemic.

Objectives: The WHO Global Pandemic Mortality Burden (GLaMOR) project aims to generate a robust yet conservative estimate of the 2009 mortality burden associated with the influenza A H1N1 pandemic. Regional and global burden estimates have been generated and stratified by age (<65 and +65) and cause of death.

Methods and Materials: We used a novel two Stage modelling approach to produce the global estimate. In Stage 1, we collected adequate mortality (weekly data that is cause- and age-specific and includes a minimum of five years) and weekly virological data from 21 countries around the world: 4 countries in the Americas, 9 in Europe, 7 in the Western Pacific (including China) and one in Africa (South Africa). We then applied Multiple Regression Modelling to estimate the pandemic mortality burden by age group and cause of death. In Stage 2, we projected the estimates to other world countries using four distinct statistical approaches, with our final estimates being based on a Multiple Imputation method.

Results: We attribute 144,000 to 189,000 respiratory deaths (preliminary estimate) to pandemic influenza A H1N1 worldwide through December 31, 2009, with 61% of deaths were among people <65 years. Mortality varied substantially by region, with far higher rates in the Americas (North, Central and South) than other regions, especially the Europe region. Attempts to model all-cause and cardio-respiratory mortality failed to produce significant burden estimates except in a handful of countries with a substantial burden.

Conclusion: The overall global mortality impact of pandemic influenza A H1N1 in 2009 was modest and not unlike seasonal influenza; however, the young mean age of casualties and the marked geographical heterogeneity in severity makes the 2009 pandemic stand out as a significant global health event.

12.007 Domestic birds as surveillance systems for monitoring West Nile virus lineage 2 enzootic circulation: Three years of experience in Greece

C. I. Dovas¹, S. C. Chaintoutis¹, A. Chaskopoulou², S. Gewehr³, M. Papanastassopoulou¹, S. Mourelatos³, S. Zientara⁴, S. Lecollinet⁴, K. Danis⁵, T. Panagiotopoulos⁵

¹Aristotle University of Thessaloniki, Thessaloniki, Greece, ²United States Department of Agriculture-Agricultural Research Service (USDA-ARS), Thessaloniki, Greece, ³Ecodevelopment, Thessaloniki,

Greece, ⁴European Reference Laboratory for equine diseases, Maisons-Alfort, France, ⁵Hellenic Center for Disease Control and Prevention (HCDCP), Athens, Greece

Background: In Greece, West Nile virus (WNV) 2010-2012 epidemics have resulted in 382 human neuroinvasive cases (WNND). Horses were also affected. Studies in the USA and Europe have addressed surveillance methodologies for WNV lineage 1, but little is known in the context of WNV lineage 2 circulation.

Objectives: Three surveillance systems (domestic pigeons, freerange chickens, captive chickens) are continually evaluated from 2010 in Greece, for their efficacy in providing data on WNV enzootic circulation.

Methods and Materials: At the end of the 2010 and 2011 epidemics, pigeons 2–8 months old were tested by ELISA to determine WNV seropositivity rates in flocks from different regions. Young free-range chickens were also tested after the 2011 and 2012 epidemics. Seropositivity rates were correlated with the incidence of WNND cases by municipality and prefecture. Furthermore, at the beginning of the 2011 and 2012 epidemics, blood was tested from young pigeons and free-range chickens in Central Macedonia for early warning purposes. Finally, during the 2011 and 2012 epidemics, blood was sampled weekly from sentinel chickens in cages, placed around the city of Thessaloniki. These samples were examined by ELISA, and retrospectively for the presence of WNV using RT-PCR. Mosquitoes were collected in parallel and only one out of 150 pools tested in 2011 was found positive for WNV.

Results: Results indicated that all systems provided valuable data regarding local enzootic circulation of WNV and detected the virus before the onset of human cases, successfully predicting risk for local human transmission. Health authorities were informed timely for the implementation of preparedness plans to protect public health. The captive chicken system was more expensive, but provided weekly monitoring of WNV and enabled fast isolation and molecular characterisation of the circulating virus before the human epidemic onset.

Conclusion: Domestic pigeon and free-range chicken surveillance is convenient and cost-effective for early warning and identification of reservoir areas with early arbovirus transmission. Such low-cost systems could be easily implemented in large areas as risk indicators for WNV transmission via blood transfusions. Repetitive sampling in captive chickens is more informative regarding the determination of the epidemic development and the isolation and molecular identification of the circulating virus strain.

12.008 Weekly monitoring of human cases of West Nile fever: An efficient way to assess the evolution of the disease in Europe

L. Marrama Rakotoarivony, C. Bogaardt, E. Robinson, V. Estevez, J. Jansa, H. Zeller, D. Coulombier

European Centre for Disease Pervention and Control, Stockholm, Sweden

Background: Since 2010, epidemiological and virological findings in the European Union (EU) countries indicate a geographical expansion of West Nile (WN) virus circulation, involving viruses from lineages 1 and 2.

Objectives: In this context, the European Centre for Disease Prevention and Control has developed a tool to monitor spatial distribution of human cases in Europe, on a weekly basis.

ABSTRACTS

Methods and Materials: The scope of the WN mapping tool includes 65 countries (EU and neighboring countries). Event-based surveillance web-systems, international networks and official national websources are used to collect information on WN cases reported by these countries. Data are validated with the National Authorities and cases are classified according to the EU case definition. Finally, a geographic information system (GIS) is used to geo-reference and display the spatial distribution of cases at the sub-national level. Uupdated outputs (maps, tables and synthesis) are published every week on ECDC website during the transmission season (June to November).

Results: The WN mapping tool is in place since June 2011. Twentysix and 24 weekly maps have been published during the transmission seasons 2011 and 2012, respectively. In 2011, 327 cases, including 124 cases from EU countries, have been reported by 10 EU and non-EU countries. In 2012, 907 cases (237 from EU) have been reported by 15 EU and non-EU countries. The increase in the number of cases and in the number of countries reporting cases was associated with a rise in the number of affected areas by country.

Conclusion: The WN mapping tool has been designed to support the decision making process of stakeholders involved in blood donation management. However its outputs have already been linked to by a variety of national public health agencies, travel medicine networks and public health forums on their internet sites. Indeed, this tool also supports public health decision makers in their response to the risk posed by WN in the Europe. Moreover, this tool contributes to harmonize and enhance the surveillance of WN cases in and around the EU. Finally, data collected contribute to improve the analysis of favourable conditions for WN transmission and hence improve preparedness and response to WN outbreaks in Europe.

12.009 Determinants of active participation in internet-based surveillance systems

D. Paolotti¹, P. Bajardi²

¹ISI Foundation, Turin, Turin, Italy, ²ISI Foundation, Turin, Italy

Background: Internet-based platforms for infectious disease surveillance have advantages over traditional approaches as they can potentially recruit and monitor a wider range of subjects in a relatively inexpensive fashion.

Objectives: Loss to active participation is generally a problem in cohort studies, and it has been rarely investigated for large-scale cross-country internet-based cohort studies.

Methods and Materials: We studied the determinants of active participation of individuals in the www.influenzanet.eu project to monitor influenza-like-illness in the general population of seven European countries. The web-based system requires volunteers to fill in a background survey once, and then weekly questionnaires about symptoms. The background questionnaire collects socio-demographic information on the participants, as well as information on household composition, influenza risk status, vaccine history etc. The symptoms questionnaire, for which a reminder is sent every week over email, asks about respiratory symptoms, access to care, absenteeism and utilization of medications. If no symptoms are presented, then it can be completed in one click. For the purposes of this study active participants are defined as those that, during the 2011-12 influenza season, completed at least two weekly surveys within 60 days following their first symptoms questionnaire.

Data from background questionnaires are used as explanatory variables to predict the likelihood of participation through odds ratios. Furthermore, a multivariable logistic regression is used to evaluate the impact of the recruitment by different means of information on the retention behavior.

Results: Being a smoker and a lower educational status are significantly associated with a lower participation at follow-up. Younger volunteers are more prone to be lost at follow-up. A lower propensity to participate has been observed among individuals who got aware of the study through online advertising than through traditional off-line media.

Conclusion: It is possible to motivate participants sufficiently that they actively take part in a weekly survey over a period of several months. Similarly to traditional epidemiological studies, smoking behavior, educational level and age are determinants of participation to follows-up. An internet-based enrollment campaign for internet-based epidemiological studies seems to be less effective than the off-line advertising in enrolling volunteers that are more likely to participate at follow-up questionnaires.

12.010 An investigation of Salmonella Enteritidis PT1 cases linked to consumption of a pasteurised liquid egg white product in England and Wales, 2012

O. Esan, C. Lane, T. Peters

Health Protection Agency, London, United Kingdom

Background: On September 12, 2012 the European Commission's Rapid Alert System for Food and Feed issued an alert regarding Salmonella enterica subspecies enterica serovar Enteritidis (S. Enteritidis) isolated from a "ready to drink" liquid egg white product following a case linked to consumption of the product in Austria. The isolate was further typed as phage type 1 (PT1) and resistant to Nalixidic acid and Nitrofurantoin. A recall of the product was subsequently issued by the internet retailer. The product originated in France and was distributed with a six months shelf life from the United Kingdom to other European countries.

Objectives: To ascertain the morbidity associated with the consumption of the product

Methods and Materials: S. Enteritidis cases reported by the Gastrointestinal Bacteria Reference Unit (GBRU) are routinely resistance and phage typed. After 20th August 2012 all S. Enteritidis PT1 were also analysed using Multilocus variable-number Tandem Repeat Analysis (MLVA). Environmental health questionnaires (EHQ) were used to identify travel history. Microbiological testing was also carried out on the product.

A standardised postal questionnaire (PQ) was designed and sent to a subset of S. Enteritidis PT1 cases with a self-addressed return envelope. The questionnaire included questions on illness, travel history, consumption of eggs and purchase history including after-sales information. In addition, product information was requested from the Foods Standards Agency.

Results: Between August 20-October 10, 2012 a total of 84 cases of S. Enteritidis PT1 were reported by GBRU. Over half of the cases were resistant to Nalixidic acid with reduced susceptibility to Ciprofloxacin (61%, 54/84). Over one third reported travel (39%, 33/84) with most visiting Spain (33%, 11/33). Of the indigenous cases, eight cases consumed the product (6 EHQ, 2 PQ) of whom two were hospitalised and three were adult male bodybuilders.

Over half (53%, 39/74) of the cases responded and most were ill for five days (range 4-35).

MLVA pattern was consistent in both product and linked cases.

Conclusion: Our investigation identified cases linked to consumption of the product and travel associated cases. Due to the long-shelf-life of the product, its recall likely prevented more S. Enteritidis PT1 infections from occurring.

International Meeting on Emerging Diseases and Surveillance 2013

12.011 Effects of climate change on the distribution of bluetongue and epizootichaemorrhagic disease vector in Southern Alberta (Canada) and Montana(USA)

A. Zuliani¹, A. Massolo², S. Marshall³, T. J. Lysyk⁴, G. Johnson⁵, S. Cork²

¹University of Calgary-Faculty of Veterinary Medicine, Calgary, AB, Canada, ²University of Calgary, Faculty of Veterinary Medicine, Calgary, AB, Canada, ³University of Calgary, Calgary, AB, Canada, ⁴Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, ⁵Montana State University, College of Agriculture, Bozeman, MT, USA

Background: Climate change is likely to have an impact on the distribution of arthropod vectors, such as *Culicoides sonorensis*. In North America a change in the distribution of arthropod vectors could be expected to take place at their northern limit. *C. sonorensis* is the primary competent vector for Bluetongue (BT) and Epizootic Hemorrhagic Disease (EHD) viruses in western North America. BT and EHD are endemic in the United States and have occurred sporadically in Western Canada.

Objectives: The aim of this study is to determine the effects of different climate change scenarios on the distribution of *C. sonorensis* in Southern Alberta (Canada) and Montana (USA) in order to better target surveillance efforts towards potential emerging *Culicoides*-transmitted diseases in this area.

Methods and Materials: A maximum entropy distribution model was developed using fifty *C. sonorensis* presence records and four variables (Elevation, Land Cover, Precipitation and Vapour Pressure Deficit). The model obtained was then used to derive the distribution of the arthropod under different climate change scenarios. We selected three Representative Concentration Pathways (RCP 2.6, RCP 4.5, and RCP 8.5) to build scenarios using the Fourth Generation Canadian Coupled General Circulation Model. Climate change data for each variable were extracted for two time points, 2030s and 2050s and projections of future *C. sonorensis* distribution were developed.

Results: Two major trends are observable in *C. sonorensis* distribution under the climate change scenarios selected. Among the 2030s scenarios 13.3 % (RCP 2.6), 18.7% (RCP 4.5) and 19.7% (RCP 8.5) of the whole study area indicated a northward/westward increased probability of *C. sonorensis* occurrence. The same trend is observable for the 2050s scenarios with an additional increase ranging from 3.9% (RCP 2.6), 18.4% (RCP 4.5) and 16.3% (RCP 8.5). In contrast a reduction of *C. sonorensis* probability of occurrence was indicated in central Montana and the southernmost areas of Alberta for 2.6 and 8.5 RCP scenarios in the 2030s and 2050s. No retraction is forecasted by the RCP 4.5 scenario.

Conclusion: Our models illustrated potential changes in the distribution of *C. sonorensis* and can provide useful projections to inform the development of future vector surveillance programs and for the region.

SESSION 13 (Plenary) Global Approach to the Control of Foot and Mouth Disease

Sunday, February 17, 2013 Room: Park Congress • Ground Level 11:00–11:45

13.001 Global approach to the control of foot and mouth disease

B. Vallat

OIE, Paris, France

FMD is among the most devastating disease with severe impacts on animal productions and trade. The disease control strategies must be based on scientific evidences and the OIE international standards and recommendations to Member Countries provide clear guidance for the preparation of effective methods, strategies and policies. area majority of that texts are published in the "Terrestrial Code" and in the "Terrestrial Manual" and they represent real foundations to prepare prevention and control strategies.

Among several key elements, effective national Veterinary Services are key players and recognized as public goods. Also crucial are effective surveillance in domestic and wild animals, early detection and warning and emergency response to any disease outbreak. Transparent world animal health information and warning system are needed, as described and implemented by the OIE (WAHIS and WAHID systems), supplemented by a number of information and dataanalysis platforms such as GLEWs developed in partnership with other agencies (e.g. OIE, FAO, WHO).

While the commitment of national governments is a prerequisite, action at regional and international levels is also critical as evidenced by the successful eradication of rinderpest worldwide (e.g. regional networks of diagnostic laboratories and epidemiological surveillance teams, vaccine quality control) without forgetting permanent support to research.

The first OIE FAO International Conference on FMD control (Asuncion, Paraguay, 2009) recommended that a Global FMD Control Strategy be prepared and that a second International Conference be organized. The Global Strategy was finalized in 2012 and it was presented and adopted at the Second Global Conference on FMD Control (Bangkok, June 2012).

The aim of the global strategy is to maintain the status of already FMD-free 65 countries or zones and to progressively control and eradicate the disease in infected countries and zones. The strategy is tailored according to the national and regional situations and it follows a progressive-control approach based on risk assessments corresponding to stages of advancement along a Progressive Control Pathway (PCP). It is combined with the use of the OIE Performance of Veterinary Services (PVS) Pathway tools. The strategy will also seek economies of scale by simultaneously acting to control other priority transboundary diseases, where appropriate.

SESSION 14 (Invited Presentation) Cutting Edge Diagnostics for the Detection of Novel and Neglected Diseases

Sunday, February 17, 2013 Room: Park Congress • Ground Level 14:30–16:00

Co-sponsored by ESCMID

International Meeting on Emerging Diseases and Surveillance 2013

14.001 MALDI-TOF MS beyond bacterial and fungal identification

J. Vila Barcelona, Spain

Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) is a rapid technique used for bacterial identification performed by the analysis of the protein spectrum of the microorganism. However, applications other than bacterial and fungal identification can be implemented for MALDI-TOF MS. The first and most useful so far has been its use as a typing method. The use of MALDI-TOF MS to identify locally dominant bacterial clones would prompt the rapid identification of outbreaks and cross-transmission events and allow the implementation of containment measures. Recently, a genetic algorithm to identify *S. aureus* isolates belonging to the USA300 family based on only three discriminating mass peaks has been developed and other studies have also evaluated the potential of MALDI-TOF MS to differentiate MRSA lineages and even identify an outbreak-causing MRSA strain based on the presence of PVL.

We have evaluated the ability of MALDI-TOF MS to differentiate among distinct dominant MRSA lineages (clonal complexes, CC). Eight different sequence type (ST) groups: ST 146, ST125, ST 228 of CC5, ST 22 of CC22, ST 398 of CC398, and ST8, ST 247, ST1819 of CC8 were used. A reference MS database library originated from 36 S. aureus isolates, belonging to these four different CC, was developed. Reproducible spectrum differences were observed allowing the identification of specific mass peaks whose presence/absence could be associated with each clonal complex, thus providing a robust classification of the isolates. These results highlight the potential of MALDI-TOF MS as a rapid and accurate approach to evaluate the local epidemiology of MRSA. MALDI-TOF Ms has also being used to detect the presence of beta-lactamases such as extended-spectrum betalactamases (ESBLs) and carbapenemases, by analyzing the hydrolysis of a third generation-cephalosporin or a carbapenem, respectively. In this sense MALDI-TOF can contribute to the identification of these mechanisms of resistance and to a better selection of antibiotic treatment.

14.002

.002 Next generation sequencing in clinical microbiology diagnosis, what have we achieved so far?

J. Van Eldere Louvain, Belgium

Clinical microbiology includes the rapid identification and susceptibility testing of pathogens to direct management of infections at an individual patient level and the monitoring of pathogens at a public health level. Identification and prediction of antimicrobial resistance in clinical materials by molecular methods is now routinely used in many diagnostic laboratories but remains limited to specific questions and has evolved less rapidly than predicted. Next-generation sequencing technologies are now able to sequence multitudes of bacterial genomes and deliver and interpret the resultant sequence information in near "real-time". As a result, whole-genome sequencing of bacteria is emerging as a costeffective and convenient approach for addressing many microbiological questions. Next-generation sequencing has already begun to transform microbiology, in particular in the fields of fundamental microbiology and public health microbiology. The use of microbial sequence data for "real-time" patient management is not yet realized. However, given the current rate of technological evolution, it can be predicted that next-generation sequencing will soon be sufficiently fast, accurate and cheap to be used in routine patient-management clinical microbiology.

14.003 Detection of emerging antimicrobial threats in developing countries

K. Klugman

Rollins School of Public Health and School of Medicine, Emory University, Atlanta, GA, USA

The rapid financial emergence of the two most populated countries on earth, India and China, has created an emergency of emerging antimicrobial resistance. Access of millions of people to antibiotics has reduced important indicators of mortality, such as deaths in infants in those countries, but has been accompanied by a surge of antimicrobial resistance. The spread of resistance determinants selected by this massive increase in antimicrobial exposure, has been fuelled by a lack of infection control in hospitals and lack of sanitation in the community which allows hospital pathogens to spread widely. Capacity in developing countries to detect emerging antimicrobial threats is almost nil outside of a handful of internationally supported research units. The development of laboratory capacity by a number of donor Foundations and donor countries has recently increased capacity for detection of these threats in many developing countries, but a network of reference labs in developing countries, able to detect resistant pathogens, as well as an ability to track their epidemiology and spread, is a major need in the fight against emerging microbial threats.

SESSION 15 (Invited Presentation) Panel Discussion: Updates from ProMED

Sunday, February 17, 2013 Room: Klimt Ballroom 2–3 • Upper Level 14:30–16:00

15.001–15.004 Updates from ProMED-mail

L. Madoff, M.P. Pollack, S. Chotivichien, Q. Nguyen, J. Torres, J. Woodall, T. Yuill

The Program for Monitoring Emerging Diseases from the International Society for Infectious Diseases began in 1994. It serves to provide early warnings of outbreaks of emerging infectious diseases and provide a forum for discussion of these outbreaks. It relies on informal sources of data from a variety of sources including media reports (many retrieved by automated websearching in collaboration with HealthMap. org), official sources and reports from more than 65,000 readerparticipants. This session will describe ProMED's background and provide an overview of its operation and its regional networks. ProMED editors and moderators will describe some recent developments that have appeared in ProMED posts: The recent detection of a novel coronavirus in the Middle East, the ongoing resurgence of dengue (focusing on Southeast Asia and Latin America), the ongoing outbreak of fungal meningitis in the US due to a contaminated corticosteroid preparation, and the recent epidemic of Yellow Fever occurring in the Darfur region of Sudan. The session will provide ample time for questions and discussion.

SESSION 16 (Invited Presentation)

Disease Surveillance

Sunday, February 17, 2013 Room: Park Congress • Ground Level 16:30–18:00



16.001 Integrating data mining and crowdsourcing for disease surveillance

J. Brownstein Childrens Hospital, Boston, MA, USA

Over the past fifteen years, Internet technology has significantly changed the landscape of public health surveillance and epidemic intelligence gathering. Disease and outbreak data is disseminated not only through formal online announcements by government agencies, but also through informal channels such as social networking sites, blogs, chat rooms, Web searches, local news media and crowdsourcing platforms. These data streams have been credited with decreasing the time between an outbreak and formal recognition of an outbreak, allowing for an expedited response to the public health threat. Collectively, these online sources create an image of global public health that is fundamentally different from the one produced by traditional public health surveillance infrastructure. The talk will discuss the current capabilities and future directions in the use of the non-traditional data sources for the purposes of public health surveillance and rapid detection of emerging infectious diseases.

16.002 Participatory epidemiology: Putting the public in public health surveillance

M. Smolinski Skoll Global Threats Fund, San Francisco, CA, USA

Epidemiology is not just for public health specialists anymore. Understanding disease trends can now come from a variety of data sources ranging from SMS messages, blog posts, Internet searches, and news sources to conversations on social networks. The digital data that makes up our daily activities are a prime target for early detection of disease threats. Changes in the International Health Regulations have spurred innovations in surveillance and case detection using informal sources of data. The Global Public Health Intelligence Network (GPHIN), the Program for Monitoring Emerging Infections (ProMED), HealthMap, and Google Flu Trends are just a few examples of how the field of participatory epidemiology has evolved. More recently, selfreporting systems like Flu Near You have opened a new category of participatory epidemiology that puts the public directly into public health surveillance. If effective, Flu Near You will help us better understand how influenza spreads across the United States and, importantly, engage the public directly in combatting this yearly plague. But Flu Near You as a proof of concept is equally important. If people are willing to report symptoms on a regular basis, we can expand beyond flu to other diseases. Moreover, we can move beyond the United States to the developing world, where the challenges are significantly more complex. Participatory surveillance could become a crucial cornerstone of public health, helping us not only get a better handle on known diseases, but also catch novel diseases when they emerge anywhere on the planet. It may not be long before detecting and responding to local outbreaks within a short enough time will dramatically reduce the threat of pandemics. This presentation will lay out a vision for the future of participatory epidemiology.

16.003 Towards synergy between surveillance systems for Epidemic Intelligence.

L. Vaillant

Institut de Veille Sanitaire, Saint Maurice, France

Event-based (EB) surveillance has become an essential component for early detection of worldwide public health threats that remains a challenge for health security. EB surveillance relies mainly on informal and unstructured data available from multiple sources and complements the indicator-based surveillance. The pertinence of using informal information for early detection purpose has already been demonstrated. In practice, public health stakeholders usually implement epidemic intelligence (EI) systems to strengthen early detection functions. EI is nourished by EB surveillance and consolidated by indicator-based surveillance, integrating both formal and informal data. Its process is declined in early detection, selection, verification, assessment and communication of information in relation with health events. To help public health community experts in their task of early detection, systems able to mine unstructured data from Internet-based media have been developed. They retrieve and classify information into medical categories. By covering different scopes, languages, or geographical areas and providing different functionalities, the systems complement each other to provide broader data and improve the sensitivity. Public health experts can therefore use predefined criteria to select events that could impact public health. Information is verified and communicated through different way according their confidentiality and their significance. Hence EI is now widely used by national and trans-national public health organisations by providing a conceptual framework, which completes public health surveillance systems to cover vaster fields and to meet new challenges. EI can be adapted to specific goals: detection of global crises, strengthening of national surveillance (focused on specific diseases or implemented for specific events e.g. mass gathering events). A unique collaborative experience of systems has been initiated through a trusted network of experts in health threat surveillance of the Global Health Security Initiative (GHSI). The Early Alerting and Reporting (EAR) project developed an improved EI knowledge and a systematic and rational approach to biological threat detection and assessment. The escalating amount of available information and increasing expectations of stakeholders are the forthcoming EI challenges. Hence, combined Internet-based systems are playing a key role in detecting signals timely whereas human expertise remains fundamental to analyse and implement response.

SESSION 17 (Oral Presentations)

Hot Topics

Sunday, February 17, 2013 Room: Klimt Ballroom 2–3 • Upper Level 16:30–18:00

17.001 Anthrax pleural effusions and drainage 1979–2011: A Russia-USA partnership study.

D. Lucey¹, L. Grinberg², F. Abramova³

¹Georgetown University Medical Center, Washington, DC, USA, ²Ural State Academy, and Hospital 40, Yekaterinburg, Russian Federation, ³Ural State Academy, Hospital 40 Emeritus, Yekaterinburg, Russian Federation

Background: Inhalational anthrax is a highly fatal disease. We hypothesize that inhalation anthrax often causes pleural effusions that contribute to the high mortality rate, and thus new guidelines for therapy must emphasize pleural drainage.

Objectives: To test our hypothesis by analyzing data, unpublished and published, on pleural effusions due to inhalational anthrax in Russia and the USA 1979-2011.

Methods and Materials: Russian and English literature on inhalational anthrax 1979-2011 was reviewed and translated. The three authors met in Russia in 2011 with a clinician who performed pleural drainage in the 1979 Sverdlovsk outbreak. *Unpublished* data on effusion volumes were reviewed for 41 *individual* autopsy cases.

Results: Hemorrhagic pleuritis was found at autopsy in all 41 confirmed cases from the 1979 outbreak. Data documenting large volume (> one liter) pleural effusions were found for 24 cases, and > 2 liters in 15 cases. Most effusions were bilateral. Such large volumes contributed to some patients' respiratory compromise (Grinberg et al. Mod Path 2001;14: 482-95). In 1979 pleural effusions were drained by thoracocentesis, then several antibiotics were instilled into the pleural space. No records have been found of who received drainage,

IMED 2013

however and thus impact on survival cannot be measured. This is the first report of pleural drainage during the 1979 outbreak, and more data may appear.

ABSTRACTS

All 11 US patients in the 2001 outbreak, and the single cases in 2006 and 2011, had pleural effusions. 3 of 5 patients who died in 2001 had no pleural drainage and at autopsy had > 2000ml, 2000ml, and 750 ml of fluid. All 6 survivors had drainage, and 5/6 repeated or sustained drainage due to reaccumulation. The two surviving US cases in 2006 and 2011 had relatively high anthrax toxin levels documented in their pleural fluid, and had drainage.

Conclusion: Pleural effusions, often large, are typical with inhalational anthrax. In addition to the presence of an empyema, reasons to drain these pleural effusions are that such large volumes contribute to respiratory compromise and are a source of anthrax toxin in this toxinmediated rapidly-fatal disease. Available data support including pleural drainage as standard-of-care therapy in updated clinical guidelines.



17.002 Schmallenberg virus—Harmonised European data collection for a emerging disease

A. Afonso¹, F. Berthe¹, K. Willgert², D. Verloo³, J. Cortinas Abrahantes³, A. Bau³, J. Richardson³

¹European Food Safety Authority, Parma, Italy, ²Royal Veterinary College, London, United Kingdom, ³European Food Safey Authority, Parma. Italv

Background: An emerging disease was reported by Germany and the Netherlands in late 2011. In the subsequent months, other EU member states notified the disease. The causal agent was a virus not previously identified, Schmallenberg virus (SBV). The infection is associated with congenital malformations in lambs, calves and goat kids when it occurs at a vulnerable stage of gestation. The European Food Safety Authority (EFSA) was requested to provide an assessment of the possible risks for animal and public health of the disease caused by SBV.

Objectives: This paper describes the EU data collection coordinated by EFSA. It discusses the advantages of harmonized data collection between EU Member States (MS) but also the difficulties in estimating the impact of transboundary emerging animal diseases.

Methods and Materials: EFSA used its scientific network in MS and expertise in affected countries to produce a preliminary analysis of the SBV situation. Together with the MS, guidelines for data collection were prepared, containing case definitions for both adult and newborn cases as well as reporting guidelines for both a minimum and an extended dataset. The data were collected using an automated, web-based platform. Mathematical modelling was used to predict the spread of the disease and future impact.

Results: The data collected in the MS were used to characterize the spread of the disease in the EU. Maps with the total number of confirmed cases at a regional level and date of first occurrence were produced. The assessment of the impact of SBV on animal health was estimated as the proportion of affected herds/flocks.



Figure 1. Regions with at least one SBV confirmed herd.



Figure 2. Proportion of SBV confirmed sheep herds.

Conclusion: Collaboration between organizations is essential for the success of data collection exercises on transboundary diseases. The transparency and networking efforts made at a European level for SBV show that it is possible to rapidly obtain good quality information on an emerging disease.

The assessment of impact was restricted to estimating the morbidity and mortality. No other measures of impact, such as a decrease in production, were considered. The surveillance effort was restricted to case detection and assessment of the within herd impact was, therefore, not possible.



No evidence for zoonotic transmission of Schmallenberg virus in areas with veterinary activity

C. Reusken¹, C. van den Wijngaard¹, M. Beer², R. Bouwstra³, H. van den Kerkhof¹, W. van der Poel³, J. Schmidt-Chanasit⁴, P. Vellema⁵, I. Wouters⁶, M. Koopmans⁷

¹National Institute for Public Health and the Environment, Bilthoven, Netherlands, ²Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany, ³CVI, Lelystad, Netherlands, ⁴Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany, ⁵Animal Health Service, Deventer, Netherlands, ⁶Institute for risk assessment sciences, Utrecht, Netherlands, ⁷Erasmus Medical Centre, Rotterdam, Netherlands

Background: The emergence of Schmallenberg virus (SBV), a novel orthobunyavirus, as a cause for malformations in ruminants in Europe triggered a joint veterinary and public health response to address the potential human health consequences. Using a risk profiling algorithm, we concluded that the potential for human infection is low but could not be excluded

Objectives: To ascertain the public health risk of the emergence of SBV in ruminants in the Netherlands and most likely other European countries were SBV has emerged.

Methods and Materials: 1) Self-reported cases of febrile illness within 2 weeks of direct exposure to affected animals or their birth products were monitored. 2) A serological survey was conducted to determine the presence of SBV antibodies in serum from persons living and working on farms where SBV had been highly suspected on the basis of pathological findings consistent with typical SBVinduced malformations in calves or lambs, most confirmed by PCR and or /serology. The target cohort consisted of adult (≥ 18 years of age) farmers, farm residents, farm aids and veterinarians. Serum samples were donated and a questionnaire was filled in. The presence of SBVspecific antibodies was determined by virus neutralization (VNT).

Results: 1) None of four suspected case-persons showed evidence of an SBV infection. 2) The serological study comprised of 301 participants. Of these 234 worked or lived on affected farms; 67 were veterinarians. 229 participants specifically reported direct exposure to malformed new-borns and/or birth products. A total of 150 participants reported insect bites on SBV-infected farms, exposing them potentially to SBV during the vector season. None of the 301 individuals showed serologic evidence of SBV infection in the VNT.

Conclusion: In this study we found no evidence for human SBV infection, despite the high infection rates in ruminants of the same localities (up to 100% within herd seroprevalence) and the high level of reported insect bites during work on SBV-infected farms. The lack of evidence for zoonotic transmission from either syndromic illness monitoring or serological testing of presumably highly exposed individuals suggests that the public health risk of SBV given the current situation is absent/ extremely low.

17.004 The interaction of the spike glycoproteins of bat-borne SARS-like-CoVs with chiropteran cells during the entry process

M. Hoffmann, N. Krüger

University of Veterinary Medicine Hannover, Foundation, Hanover, Germany

Background: In 2002/03 the so far unknown *severe acute respiratory syndrome*-related coronavirus (SARS-CoV) emerged from China and caused a pandemic spread. Investigations revealed that SARS-CoV uses the angiotensin converting enzyme 2 (ACE2) as a receptor and horseshoe bats have been identified to act as a natural reservoir.

The worldwide detection of SARS-like coronavirus (SL-CoV) RNA and the presence of SARS-CoV reactive antibodies in african bats raise the questions if another zoonotic infection event can occur and under which conditions such a virus can succesfully cross the species barrier? The (so far) inability to isolate a bat-derived SL-CoV urges the need of alternative methods.

Objectives: Our work focusses on the interaction of SARS-CoV and bat-derived SL-CoVs with mammalian cell lines. Our primary target are chiropteran cell lines and we are particularly interested in the entry process and the interplay between the spike glycoprotein (S) and its cellular receptor.

Methods and Materials: In a binding assay, chiropteran cell lines are incubated with soluble SARS-CoV-S or SL-CoV-S to elucidate the presence of a proper receptor molecule. Further, we established a cell-based fusion approach, in which SARS-CoV-S or SL-CoV-S are co-expressed with either human (h) or chiropteran ACE2 and the functional activity of the CoV-S is indicated by the appearance of syncytia after trypsin treatment. Finally, we employ a pseudotype infection system, based on a replication-deficient vesicular stomatitis virus (VSV) to analyze if SL-CoV-S can mediate pseudotype entry into chiropteran or other mammalian cell lines.

Results: Soluble SL-CoV-S can bind to hACE2 expressing cells. However, the absence of syncytia in the cell-based fusion assay and the inability of SL-CoV-S pseudotyped VSV to infect those cells lead to the assumption that this restriction lies on a post binding step.

Conclusion: The binding of soluble SL-CoV-S to hACE2 shows the general potential of such a virus to gain access to the human population and cause a zoonotic event, although further adaptations seem to be necessary, which is highlighted by the results of the cell-based fusion assay and the pseudotype approach.

17.005 Tick species and tick-borne viruses of Eastern and North Eastern parts of Kenya: Health risk implications among pastoral communities

J. Mutisya¹, J. Lutomiah², L. Musila¹, S. Khamadi², H. Koka¹, E. Chepkorir³, A. Makio¹, J. Bast⁴, E. Wurapa¹, R. Sang² ¹USAMRU-K, Nairobi, Kenya, ²KEMRI, Nairobi, Kenya, ³ICIPE, Nairobi, Kenya, ⁴USAMRU-K, Kisumu, Kenya

Background: Arboviruses are transmitted by arthropods such as ticks and mosquitoes, and cause clinical syndromes in humans, ranging from febrile illnesses to life-threatening hemorrhagic fever. These include Crimean Congo hemorrhagic fever which is of great public health importance. The prevalence of tick-borne viruses among ticks in Kenya is poorly understood.

Objectives: The aim of this study was to determine the distribution of tick species and tick-borne viruses circulating in selected pastoral communities in Kenya.

Methods and Materials: From 2007–2012, ticks were sampled from the arid Garissa and Isiolo regions of North Eastern and Eastern province respectively. These regions are generally occupied by pastoral communities. Ticks were physically detached from livestock and identified into species by morphological means. The ticks were then pooled by species and sex and analysed in cell culture for virus presence and Virus infection was confirmed by rt-PCR.

Results: Over 34,377 ticks, 60% from Garissa and 40% from Isiolo, were collected and identified into 10 species. Overall predominant species was *Rhipicephallus pulchellus* 57% (11,711), 80% (11,139) from Garissa and Isiolo respectively. In both sites cattle was the most infested host in terms of numbers and species of ticks and was the preferred host for *R. pulchellus*. 5,760 pools, Garissa 3,366 and Isiolo 2,394, were analyzed and 42 viruses isolated from different tick species. The virus isolates comprised of 22 Dugbe (44.7%), 14 Kupe (29.8%) and 10 Dhori (21.3%). 3 Dugbe from Garissa; 1 each from *Hyalomma truncatum* and from *Amblyomma hebraeum* all from cattle while 1 from *Boophilus annulatus* from camel. All Dugbe from Isiolo came from *R. pulchellus* from Sheep (5), Cattle (1), and Camel (1). 9 Dhori isolates, 2 from Garissa and 7 from Isiolo were from *R. pulchellus* from sheep (4), cattle (1), Goat (1), camel (1). All the 14 Kupe isolates were from Isiolo tick collections from cattle (8), sheep (4), camel (1) and goat (1).

Conclusion: These results indicate that tick-borne arboviruses are circulating in Garissa and Isiolo. However their significance to human health is unknown since no human targeted surveillance has been conducted to establish exposure to these viruses.

17.006

OUO Spotted fever group Rickettsia species and Anaplasma phagocytophilum in lizards ticks, Algeria

H. Soualah-Alila¹, Z. Bouslama²

¹Mouhamed Chérif Messadia University-Souk-Ahras-Algeria, Laboratory of Ecology Terrestrial and Aquatic Systems, Department of Biology, Annaba University, Annaba, AL-AN, Algeria, ²University of Badji Mokhat, Laboratory of Ecosystem Aquatic and Terrestrial, Annaba, Algeria

Background: Our results raise the possibility that these agents transmitted to the human by the tick where the reservoir can be our biological model.

Objectives: To show the role of lizards in the transmission of diseases.

Methods and Materials: Study Area: The study was conducted in Elkala National Park (North East of Algeria) humid bioclimatic zone (72%-78, 9%). Tick and Lizard Collection: This survey was conducted from April 2008 to April 2009. Lizards were hand captured in the site or using a special pitfall in the complex zone. Ticks were removed from each lizard using forceps and stored in 70% ethanol for later identification to species and life stage using taxonomic keys (IPTM, version1.0 "AFPMB" and confirmed by Pasteur Institute of Tunis). DNA Extraction: DNA was extracted from ticks composed of males and unfed females, using the QIAmp DNA Mini Kit (QIAGEN GmbH, Hilden, Germany).

ABSTRACTS

Results: 184 lizards were captured belonging to tree species: 125 Psammodromus algirus, 07 lacerta pater, 52 Podarcis hv, were checked for attached ticks. In total 422 nymph and larval ticks were removed and further identifi ed as I. recinus. Moreover, 10 tails and 52 skin biopsy specimens were taken from the captured lizards. DNA isolation was further analyses for the presence of Rickettsia, Anaplasma. 37% ticks carried Rickettsia, 4% Anaplasma and 3% unknown pathogens. None of the tested tails were positive only one of the 52 skin biopsy specimen was positive. The vast majority of pathogens detected were R. helvetica (15%), 12% R.monacensis, the rest are unknown Rickettsia (Rickettsia sp). 4% were A. phagocytophilum and 3% unknown pathogens.

Conclusion: Our results show clearly the potential for lizards to play an important role in the ecology of rickettsia as dilution host. I. ricinus ticks are known to be the main vectors and reservoirs of the spotted fever group rickettsiae (SFG) worldwide. Our findings indicate that SFG rickettsiae transmitted by ticks could penetrate biotopes, especially when transmission cycle depends on environmental conditions. it is prudent for clinicians in North east of Algeria to be alert to possible appearances of infections caused by these pathogens. However, the apparent contributions of various other hosts to pathogen transmission highlight the need for a community approach to understanding vectorborne zoonoses.



17.007 Sequelae of human Cryptosporidiosis in patients living in Östersund during a large waterborne outbreak

J. Lindh¹, A. Wallensten¹, J. Bergstrom¹, M. Lilja², M. Widerstrom² ¹Swedish institute for communicable disease control, Solna, Sweden, ²Jämtland County Medical Office, Östersund, Sweden

Background: During 2010 а waterborne outbreak of Cryptosporidium hominis occurred in the city of Östersund, Sweden. Approximately 27000 humans were affected and demonstrated three or more diarrheas daily and/or watery diarrhea. To our knowledge no studies have been performed following up the long term health effects from a large Cryptosporidium outbreak. **Objectives:** To look for segelae in humans infected with C. hominis

Methods and Materials: Six months prior to this study, an outbreak questionnaire was sent to a representative part of the population in Östersund. The following case definition was used: a person living in Östersund during the outbreak period that had had three or more diarrheas daily and/or watery diarrhea. In this study, a follow-up questionnaire was sent to same group that received the outbreak questionnaire. Questionnaires were developed for adults and children and included questions about a variety of symptoms, e.g. joint pain, pain in the eyes, fatigue, abdominal pain, diarrhea and headache. Binary logistic regression was used to detect differences between the two groups and fuzzy cluster analysis to detect patterns in the different variables of symptoms.

Results: Answered questionnaires were received from 308 case patients and 479 non-case subjects. The case patients significantly reported to have more symptoms than the non-case subjects. Among the highest could loss of weight (odds ratio [OR], 3.07), loss of appetite (OR, 3.06), three or more diarrheas daily (OR, 3.04, watery diarrhea (OR, 2.9), abdominal pain (OR, 2.9), headache (OR, 2.22) and pain in the eyes (OR 2.05) be seen. The variables were further analyzed for patterns and three groups were identified. These were named stomach/intestine (OR, 2.27), fatigue/headache (OR 2.18) and joint pain (OR 1.87).

Conclusion: Infection with C. hominis increases the risk of getting sequelea 6 months after primary infection.

17.008 Evolution of gonococcal strain susceptibility to antibiotics in France: Data from a national sentinel surveillance network, 2001-2012

G. La Ruche¹, P. Sednaoui², B. Bercot³, E. Cambau³, A. Goubard² ¹Institut de veille sanitaire. Saint-Maurice. France. ²Institut Alfred Fournier, Paris, France, 3Saint-Louis/Lariboisière/Fernand Widal hospitals, Paris, France

Background: An increase in cases of gonorrhea is observed since the late 1990s in France as in other European countries. The recent emergence of resistance to extended-spectrum cephalosporins (ESCs) raises an important public health problem.

Objectives: This study aims to assess the emergence of antibiotic resistance in France.

Methods and Materials: A network of volunteer laboratories allows following the trends in gonorrhea. Gonococcal strains isolated are sent to the National Reference Laboratory (NRL) to study susceptibility to several antibiotics by E-test. Until 2011, approximately 200 public and private labs located throughout France participated in the network. Due to the increasing number of strains, the number of labs involved in sending strains has been halved in 2012.

Results: The number of strains with antibiotic susceptibility results increased tenfold between 2001 and 2011, from 150 to 1,524. With a number of participating labs divided by two, 915 strains were isolated in 2012 (until November). The strains were isolated from men in 88% of cases.

In 2012, 27% of strains were susceptible to penicillin (minimum inhibitory concentration [MIC] ≤0.064mg/L) (versus 37% in 2001) and 16% were sensitive to tetracycline (MIC ≤0.5mg/L) (40% in 2001).

The proportion of strains with a high level of resistance to ciprofloxacin (MIC ≥1mg/L) has significantly increased since 2004 and has remained high (6% in 2001, 38% in 2012).

No resistance to spectinomycin (MIC >64mg/L) was detected during this period.

In 2010 for the first time, two strains out of 1,400 had a decreased susceptibility to ceftriaxone (MIC >0.125mg/L), but none in 2011 and 2012. The proportion of strains with reduced susceptibility to cefixime (MIC >0.064mg/L) increased (1.5% in 2008, 5.8% in 2009 and 2010, 7.2% in 2011, 11.2% in 2012) whereas that of resistant strains (MIC >0.125mg/L) increased in 2012 (0.1% in 2008, 0.6% in 2009 and 2010, 0.7% in 2011, 3.3% in 2012).

Conclusion: The decreased susceptibility of gonococcal strains to oral ESC tends to increase, and justifies to reinforce surveillance. Our data support the recommendations of the French Drug Agency recommending the use of ceftriaxone with an adequate dose (500 mg IM in a single dose) as first-line treatment for uncomplicated urogenital gonorrhea.

SESSION 18 (Invited Presentation)

Economics of Emerging Infectious Diseases

Monday, February 18, 2013 Room: Park Congress • Ground Level 08:30-10:30

ABSTRACTS

18.001 Emerging infections and poverty: Lessons from the Americas

L. Ivers

Boston, MA, USA

Almost half of the world lives in poverty, including half of the world's children. Slow progress is being made on the first Millennium Development Goal to eradicate extreme poverty and hunger but the global economic crisis threatens this progress. As infectious diseases emerge and re-emerge, it is critical to consider the interaction of these diseases with poverty. Living in poverty may make individuals susceptible to disease and conversely, illness may precipitate or perpetuate a cycle of poverty for individuals and their families. Reduced access to healthcare, poor infrastructure, food insecurity, lack of adequate water and sanitation and the inequitable status of women are all potential contributing factors in these interactions.

In order to better plan and execute strategies for the control of emerging infectious disease, we should better understand if, how and when poverty relates to susceptibility to and outcomes from infections, how poverty may contribute to and/or amplify the emergence and reemergence of pathogens and how poverty may constrain effective responses to outbreaks of infectious disease.

These effects and potential effects of poverty are not unique to low or middle-income countries as the epidemiology of infections like toxocariasis, cysticercosis and Chagas disease in the United States demonstrates-these infections are concentrated in areas of extreme poverty in the USA such as the Mississippi Delta, the Mexican border and Appalachia. The return of cholera to the Americas in 1991 and the introduction of Vibrio cholerae to Haiti in 2010, resulting in a major ongoing epidemic of cholera on the Island of Hispaniola, offer an opportunity to learn and to apply lessons learned to improve prevention and control strategies of the future.

18.002 Vaccination choices and their impact on immunization programmes

P. Manfredi¹. A. d'Onofrio²

¹University of Pisa, Pisa, Italy, ²European Institute of Oncology, Milan, Italy

The very recent years have seen the outbreak of the new discipline of Behavioural Epidemiology (BE) of infectious diseases. The focus of BE is on the complex interplay between individuals' behavioral choices and the transmission dynamics and control of infectious diseases. A major area of Behavioural Epidemiology has investigated the interplay between vaccination choices and the control of vaccine preventable infections under voluntary immunization regimes. I combine recent results on infection models with agents' vaccination choices and historical trends in childhood infections morbidity to suggest that technological progress in public health and the high degree of herd immunity allowed by decades of sustained vaccination are potentially becoming killers of vaccination programmes in industrialised countries. I then propose a framework for the interplay between inter-human and public information on vaccines. This shows conditions which make elimination feasible, suggesting that maintaining some degree of public intervention is the only way to mitigate the pessimistic conclusions drawn for voluntary vaccination systems.

18.003 Externalities, transaction costs and infectious diseases

P. Polgreen¹, L. A. Polgreen²

¹University of Iowa, Iowa, USA, ²University of Iowa, Iowa City, IA, USA

In the field of infectious diseases, many activities (prescribing antibiotics, vaccinating specific populations, and practicing hand hygiene) are associated with externalities, both positive and negative. Externalities occur when the "price" of an activity does not reflect the full costs or benefits of the activity. For example, the vaccination of healthcare workers directly prevents healthcare workers from becoming ill. But vaccination also results in a positive externality: it decreases the likelihood of healthcare workers passing a vaccine-preventable disease on to patients under their care. On the other hand, antibiotic use is associated with negative externalities: some of the costs of antibiotic use are borne, not by the patient, but by society, in terms of increasing the probability of future drug resistance. In this talk we will discuss why it is important to consider externalities when focusing on the detection, treatment, and prevention of infectious diseases.



Is it cost-effective? Best practices on evaluating the bang-for-the-buck in communicable disease control

D. Fisman

University of Toronto, Toronto, Canada

The control of communicable diseases continues to challenge public health experts and epidemiologists. Novel disease control technologies, including emerging vaccines, are increasingly evaluated with respect not only to their effectiveness, but to their cost-effectiveness. In this lecture, I discuss basic concepts in costeffectiveness analysis, and also distinctive aspects of evaluating the cost-effectiveness of communicable disease control interventions. In particular, communicable disease control programs are characterized by indirect effects (including herd immunity) which may impact even program non-participants. Evaluation of the economic attractiveness of vaccines and other communicable disease control interventions needs to take such phenomena into account, using models that can capture changes in risk over time. Best practices in health economic evaluation of such control programs will be discussed, with reference to the recent report of the ISPOR-SMDM Modeling Good Research Practices Task Force (Med Decis Making. 2012 Sep-Oct;32(5):712-21).

SESSION 19 (Invited Presentation) Diseases Without Borders

Monday, February 18, 2013 Room: Klimt Ballroom 2–3 • Upper Level 08:30-10:30

19.001 Hepatitis E outbreak at a refugee camp J Ahmed

ABSTRACTS

US Centers for Disease Control and Prevention, Nairobi, Kenya

Background: Hepatitis E virus (HEV) is a common cause of viral hepatitis in developing countries. Although outbreaks have previously been documented among forcibly displaced persons, there have been no documented cases in Somali refugees for more than a decade. On 15 August 2012, the Centers for Disease Control and Prevention (CDC) was notified of an outbreak of acute jaundice syndrome (AJS) in the Dadaab refugee camps, Kenya. We present the findings from this outbreak.

Method: The United Nations High Commissioner for Refugees (UNHCR) and its partners enhanced AJS surveillance in the camp. Health care workers were trained on case identification. AJS was defined as acute onset of scleral icterus AND not due to another underlying condition. A standard surveillance form for AJS was developed and used to collect data from identified cases. Serum was obtained from consenting cases and tested by nested conventional polymerase chain reaction (PCR) for HEV and real time PCR for yellow fever virus at the Kenya Medical Research Institute/CDC laboratories in Nairobi, Kenya.

Results: Between 2 July-30 November 2012, 339 AJS cases, 184 (54.3%) female, were reported from the camps. Overall median age was 23.5 years (range 1 month-91 years). The median age among females and males was 24 years and 20 years, respectively. Of the 339 cases, the distribution among the smaller camps that make up Dadaab were Ifo II 232 (68.4%), Kambioos 57 (16.8%), Ifo 26 (7.7%), Dagahaley 12 (3.5%), Hagadera 10 (3.0%). There were 2 (1.2%) reported cases from two nearby Kenyan villages. Among the 134 women of reproductive age (15-49 years), 72 (53.7%) reported being pregnant with a median gestational age of 17.4 weeks (range 8.7-35.3). There were 10 deaths (case fatality ratio [CFR] 2.9%) including 9 postpartum deaths (pregnancy CFR 12.5%) reported. Of the 92 specimens tested, 47 (51.1%) were positive for HEV and none for yellow fever.

Conclusion: HEV remains a major public health threat in refugee camps especially to pregnant women. Due to the difficulty of implementing traditional sanitation interventions, innovative new measures should be considered. As vaccines become available, vaccination should be prioritized in this population.

19.002

Dynamics of the Uganda Ebola outbreak A. Duse

School of Pathology of the NHLS & University of the Witwatersrand, Gauteng, South Africa

Filoviral infection clusters have been occurring with increasing frequency in Uganda where during 2011-2012 this country has experienced four filoviral haemorrhagic fever outbreaks. Three of these were caused by Ebola virus and one by Marburg virus. The last of these, the Luwero Ebola South Sudan outbreak, was officially declared by the Ugandan Ministry of Health on 14 November 2012 and involved seven cases (one probable and six confirmed) including four deaths. This presentation will outline the key epidemiological features of recent filoviral outbreaks in Uganda. The impact of social and cultural factors on outbreak infection prevention and control activities will be discussed. Challenges and controversies related to VHF outbreak responses, infection prevention control decisions and social mobilization will be contextualized and highlighted."

19.003

From surveillance to prevention: Developing a risk assessment framework for "novel" emerging infections

S. Morse¹, J. Mazet², M. Woolhouse³, C. Parrish⁴, D. Carroll⁵, W. I. Lipkin⁶, W. Karesh⁷, C. Zambrana-Torrelio⁷, P. Daszak⁷ ¹Columbia University and University of California Davis, New York, NY, and Davis, CA, USA, ²UC Davis, Davis, CA, USA, ³University of Edinburgh, Edinburgh, United Kingdom, ⁴Cornell University, Ithaca, NY, USA, ⁵USAID, Washington, DC, USA, ⁶Columbia University Mailman School of Public Health, New York, NY, USA, 7EcoHealth Alliance, New York, NY, USA

Most emerging infectious diseases are zoonotic, and result from drivers that facilitate interspecies contact and transfer of infections. The emergence of such "novel" infectious diseases continues to increase. Despite their effects on global public health and a growing understanding of the process by which they emerge, no emerging infection has been predicted before infecting humans. Consequently, global surveillance for early warning of emerging infections has long been the primary recommendation of all expert groups.

The objective was to assess current progress towards predictive risk assessment criteria for zoonotic emerging infections.

Methods and Materials: Subject Matter Expert elicitation and review of literature.

In recent years, initiatives such as ProMED have demonstrated the feasibility of global early warning surveillance. Recent developments, including the revised International Health Regulations, have expanded on implementing this vision. The USAID PREDICT project was initiated in 2009 to identify potential emerging zoonotic pathogens in wildlife hosts at interfaces between humans and other animals, and to build laboratory and surveillance capacity in developing countries and globally. New technologies in diagnostics, modeling, and communications enable greater timeliness, coverage, and accuracy in early warning surveillance, even allowing identification of hitherto unknown microbes in other species. However, using this information effectively for prediction and prevention before human infection occurs requires a risk assessment framework, which does not presently exist. For example, there are no general models for predicting transmissibility and virulence from molecular data, and surveillance capacity is often limited to specific diseases and species. Despite these limitations, there are many of the elements of a risk assessment framework, including examination of historical patterns, phylogentic comparisons with known emerging pathogens, an expanding database of genomic comparisons, and new research strategies to further identify commonalities among pathogens. Developing operational criteria for risk assessment, and fully integrating human behavior into the framework, are still nascent aspects, but progressing.

Developing predictive capacity for emerging infections, especially the majority that originate in wildlife, will require a sustainable unified surveillance and risk assessment framework (a "One Health" approach), and developing capacity in the countries where capacity is least developed. This is feasible but will require sustained transdisciplinary research and especially sustained political commitment.



19.004 NDM-1 and the international spread of antibiotic resistance

M. Toleman

Cardiff Institute of Infection & Immunity, Cardiff, CF14 4XN, United Kingdom

The New Dehli Metallo-β-lactamase (NDM-1) has a short history yet has rapidly become a celebrity among antibiotic resistance genes. The first description of this gene was in Klebsiella pneumoniae and E. coli in 2009 and just four years later well over 250 publications have centred on it. It has been found worldwide in over 50 different countries typically with direct links to hospitalisation or travel in South Asia and in an exceptionally wide range of pathogens and commensals. The NDM-1 gene was initially constructed in Acinetobacter probably within the last 10-15 years by the fusion of two different resistance genes and is exceptionally mobile being able to transfer between bacterial species with ease. NDM-1 has a large active site groove that accomodates the hydrolysis of all β-lactam antibiotics with the sole exception of aztreonam, there are as yet no clinically available inhibitors. In addition, it is usually accompanied by many other genes including powerful 16sRNA methylases that give pan aminoglycoside resistance. Typically enteric bacteria carrying NDM-1 carry about 6 plasmids with 20-30 resistance genes and operons that also give copper, silver and mercury resistance leaving few if any therapy options. NDM-1 was initially found in infections associated with medical tourism to India and Pakistan which led to a political backlash in India and persecution of the Indian scientists involved in the study. The rapid emergence of NDM-1 in India is closely associated with poor sanitation and polluted drinking water. In New Delhi, a study of the environment found NDM-1 present in bacteria in 30% of all environmental waters sampled which included seepage water sewer outlets and puddles in the street. Recent studies on gut carriage of NDM-1 in Pakistan show gut carriage in the community between 14% and 40%. Similarly a recent study in Bangladesh records 60% presence of NDM-1 in all environmental samples. Together these results suggest that as many as 0.5 billion people in South Asia may already carry NDM-1 as normal flora. NDM-1 also has many characteristics in common with CTX-M-15 and is likely to go on to mirror its worldwide dissemination and prevalence.

SESSION 20 (Plenary)

Big Data, Industry and Disease Surveillance

Monday, February 18, 2013 Room: Park Congress • Ground Level 11:00–11:45

20.001 Big Data, Industry and Disease Surveillance A. Signorini

lowa City, USA

What a great world we live in. Computers are faster than ever and data is available in every corner. Millions of posts, pictures, likes and location data are produced every second and uploaded on the Internet by users around the world.

We all produce data even without knowing it. Credit card transactions, phone calls, webpage views, and even the simple use of wifi connections tell a lot about who we are, where we are and what we are interested in. Very soon we will produce more data that we know what to do with.

No wonder "Big Data" is a hot term these days. But what is "Big Data", really? How can we use it? And where can we find some, possibly for free?

I have been tinkering with these problems since I wasindexing the web for Ask.com, and I analyzed tons of posts and likes while building technology for OneRiot. I am fascinated byproblems that involve lots of data, hidden patterns and artificial intelligence.

In this talk I will speak about termite mounds and hack into your wifi. I will show how to create travel models using FourSquare data and explain why Google gives you Maps for free. You will walk away with a few ideas on where to find data and how to use it in future research.

International Meeting on Emerging Diseases and Surveillance 2013

SESSION 21

Poster Presentations I

Saturday, February 16, 2013 Room: Klimt Ballroom 1 • Upper Level 11:45–14:30

21.001 Ertapenem-resistance in *Klebsiella pneumoniae* isolates from Croatia

B. Bedenic¹, M. Barisic², Z. Bosnjak³, J. Vranes⁴, V. Plecko³, D. Varda-Brkic⁵, S. Sardelic⁶

¹School of Medicine, University of Zagreb, Clinical Hospital Center Zagreb, Zagreb, Croatia, ²Faculty for natural sciences, Zagreb, Croatia, ³University hospital center Zagreb, Zagreb, Croatia, ⁴School of Medicine, University of Zagreb, Zagreb, Croatia, ⁵University Hospital Center Zagreb, Zagreb, Croatia, ⁶University hospital Split, Split, Croatia

Background: β -lactamase mediated resistance to carbapenems has been reported in Enterobacteriaceae, mostly due to the expression of class A β -lactamases (KPC), class B MBLs (IMP, VIM or NDM) or OXA-48 β -lactamase. Furtermore, carbapenem resistance can be mediated by hyperproduction of ESBLs. Twenty strains of *K. pneumoniae* resistant to ertapenem, but susceptible or intermediate susceptible to meropenem and imipenem were collected in different geographic regions of Croatia.

Objectives: The aim of the study was to characterize the ertapenem resistance.

Methods and Materials: In total 20 ertapenem non-susceptible strains of Enterobacteriaceae were collected during 2010-2012 from five hospital centers in different geographic regions in Croatia. The antimicrobial susceptibility was determined by broth microdilution according to CLSI. Double-disk-synergy test (DDST) was performed to detect ESBLs and modified Hodge test (MHT) was used to screen for production of carbapenemases. Additionally, the isolates were phenotypically screened for KPC and MBL production by performing combined tests with 3-aminophenylboronic acid and with EDTA. The transferability of meropenem resistance was determined by conjugation. The presence of genes encoding broad and extendedspectrum β -lactamases (bla_{50SHV} , bla_{TEM} , bla_{CTX-M} , and bla_{PER-1}), plasmid-mediated AmpC β -lactamases, group A carbapenemases (*bla*_{KPC}), MBLs (*bla*_{VIM}, *bla*_{IMP}, and *bla*_{NDM}), and oxacillinases (*bla*_{OXA-48}), was determined by PCR. Genotyping of the strains was performed by PFGF

Results: The isolates were uniformly resistant to amoxycillin alone and combined with clavulanate, piperacillin, cefazoline, ceforoxime, ceftazidime, cefotaxime, ceftraxone, ertapenem, piperacillin/ tazobactam and gentamicin but uniformly susceptible to colistin. Ertapenem MIC was significantly reduced by clavulanate (more than eighfold). DDST was positive indicating production of ESBLs. Modified Hodge test was negative indicating the lack of carbapenemase. Combined disk tests with phenylboronic acid and EDTA were negative showing the absence of group A and group B carbapenemases respectively. Ertapenem resistance was not transferred to recipient strain. All strains yielded amplicons with primers specific for CTX-M, TEM and SHV β -lactamases. Multiplex PCR revelaled the presence of CTX-M group 1. The strains showed distinct PFGE patterns.

Conclusion: The ertapenem-resistance was due to hyperproduction of an ESBL (as proven by reduction of ertapenem MIC by clavulanate). The fact that the strains were not clonally related points out that there is no common source of isolates.



Importance of clonal properties in addition to antibiotic consumption in determining the differences between macrolide resistant and susceptible *Streptococcus pyogenes*

C. Silva-Costa, A. Friães, M. Ramirez, **J. Melo-Cristino**, P. Portuguese Group for the Study of Streptococcal Infections Faculdade de Medicina, Universidade de Lisboa, Lisbon, Portugal

Background: A steady decline in macrolide resistance among *Streptococcus pyogenes* (Group A streptococci–GAS) in Portugal was reported in 1999–2006. This was accompanied by alterations in the prevalence of macrolide resistance phenotypes and in the clonal composition of the population.

Objectives: In order to test if changes in the macrolide resistant population reflected the same changing patterns of the overall population, we characterized both macrolide susceptible and resistant GAS associated with a diagnosis of tonsillo-pharyngitis recovered in the period 2000–2005 in Portugal.

Methods and Materials: We characterized the isolates by Pulsed field gel electrophoresis profiling (PFGE), *emm* typing, T typing and multilocus sequence typing (MLST). The relationships between sequence types (STs) was determined using PHYLOViZ.

Results: PFGE was the best predictor of *emm* type and the only typing method that could discriminate clones associated with macrolide resistance and susceptibility within each *emm* type. Six PFGE clusters were significantly associated to macrolide susceptibility: T3-emm3-ST406, T4-emm4-ST39, T1-emm1-ST28, T6-emm6-ST382, B3264-emm69-ST101/ST408 and T2-emm2-ST55. Four PFGE clusters were associated with macrolide resistance: T4-emm4-ST39, T28-emm28-ST52, T12-emm22-ST46 and T1-emm1-ST28. We found no evidence for frequent ongoing horizontal transfer of macrolide resistance determinants. The diversity of the macrolide resistant population was lower than that of susceptible isolates.

Conclusion: The differences found between the two populations suggest that the macrolide resistant population of GAS has its own dynamics, independent of the behavior of the susceptible population.

21.003 Carbapenem resistance of *Pseudomonas aeruginosa* and *Acinetobacter baumannii* strains in the intensive care unit in Romania

S. L. Pandrea¹, L. Matros², M. I. Ciontea³

¹University of Medicine and Pharmacy, Cluj- Napoca, Romania, ²University of Medicine and Pharmacy, Cluj, Romania, ³Regional Institute of Gastroenterology and Hepatology, Cluj- Napoca, Romania

Background: One of the most difficult problems in hospitals is the appearance of an increased number of *Pseudomonas aeruginosa* and *Acinetobacter baumannii* antibiotic resistant strains. Multidrug resistance in clinical *P. aeruginosa* and *A. baumannii* isolates is worrying, mainly in severe infections in wich few options remain available. Carbapenemase-producing *P. aeruginosa* and *A. baumannii* have increased substantially.

Objectives: The objective of this study was to evaluate carbapenemresistant *P. aeruginosa* and *A. baumannii* isolated from intensive care unit (ICU) during the year 2010 in Regional Institute of Gastroenterology and Hepatology Cluj- Napoca, Romania.

Methods and Materials: During January-December 2010 we monitorized 447 bacterial strains isolated from ICU patients of the Cluj-Napoca Regional Institute of Gastroenterology and Hepatology. Of these, 89 strains were *P. aeruginosa* and 45 *A. baumannii*, with the exclusion of duplicates. Strains were collected from nosocomial infections, in a national surveillance program. Identification and sensitivity testing were performed using the automatic Vitek 2 Compact analyser with the corresponding GN and AST cards, according with CLSI 2010. Etest for the screeening of MBL (metalobeta-lactamases) producers was used for *P. aeruginosa*.

International Meeting on Emerging Diseases and Surveillance 2013

Results: The majority of strains originated from bronchial aspirates: 62.92% for *P.aeruginosa* and 57.77% for *A. baumannii*.

P.aeruginosa showed resistance for almost all antibiotics: ticarcillin/ clavulanic acid 80%, piperacillin/tazobactam 77.7%, ceftazidime and cefepime 84.4%, aztreonam 24.5%, imipenem and meropenem 77.7%, amikacin 80%, netilmicin and gentamicin 82.2%. Resistance to ciprofloxacin and levofloxacin was 80%. 6.6% was resistant to colistin. Etest detected phenotypically MBL producer *P.aeruginosa* for 53.62% from 69 strains.

Resistance of *A. baumannii* was: ticarcillin, piperacillin and ticarcillin/ clavulanic acid 89.8%, piperacillin/tazobactam 82%, ceftazidime 88.8%, cefepime 86.5%, imipenem and meropenem 80.5%, ciprofloxacin 76.4%, amikacin 53.9%,tobramycin 37.1%, netilmicin 56.2% and gentamicin 78.7%. Resistance to trimethoprim-sulfamethoxazole was 59.6%. There was no *A. baumannii* strain resistant to colistin and tigecycline.

Conclusion: Carbapenem resistance strains were 77.7% for *P.aeruginosa* and 80.9% for *A. baumannii. A. baumannii* showed no resistance to colistin, however, 3 strains of *P.aeruginosa* proved to be resistant to polypeptides.

Results could reflect the implication of some hospital multi resistant *Pseudomonas aeruginosa* and *Acinetobacter baumannii* strains in nosocomial infections. Carbapenems should be used with caution due to elevated percentage of resistance against this class of antibiotics. Antibiotic policy in combination with infection-control measures are needed to prevent the spread of multidrug resistant and panresistant strains in the hospital.

21.004 Antibiotic resistance of *Pseudomonas aeruginosa* strains isolated from nosocomial infections in Romania

S. L. Pandrea¹, L. Matros², M. I. Ciontea³

¹University of Medicine and Pharmacy, Cluj- Napoca, Romania, ²University of Medicine and Pharmacy, Cluj, Romania, ³Regional Institute of Gastroenterology and Hepatology, Cluj- Napoca, Romania

Background: *Pseudomonas aeruginosa* belongs to the nonfermenting gram-negative bacteria that are ubiquitous in nature and hospital environment, associated with opportunistic infections in critically ill or immunocompromised patients. One of the most difficult problems in hospitals is the appearance of an increased number of *P.aeruginosa* antibiotic resistant strains.

Objectives: The objective of this study was to determine antibiotic resistance and the resistance phenotypes to antibiotics of *P.aeruginosa* strains isolated from nosocomial infections.

Methods and Materials: During January–December 2008 we collected 8548 samples from pacients hospitalised in Regional Institute of Gastroenterology and Hepatology Cluj-Napoca. We monitorized 345 bacterial strains; of these, 45 strains were *P.aeruginosa*.

Strains were collected from nosocomial infections (NI), in a national surveillance program of NI.

Identification and sensitivity testing were performed using the automatic Vitek 2 Compact analyser with the corresponding GN and AST cards, according with CLSI criteria and using advanced expert system (AES), *P.aeruginosa* strains were classified in resistance phenotypes.

Results: Most NI have been reported by the hospital's intensive care units (ICU) to 205 patients (76.49%). All *P.aeruginosa* strains were collected from ICU.

For detecting the antibiotic resistance we used ticarcillin (TIC), ticarcillin/ clavulanic acid (TCC), piperacillin (PIP), piperacillin /tazobactam (TZP), ceftazidime (CAZ), cefepime (FEP), aztreonam(ATM), imipenem (IPM), meropenem (MEM), amikacin (AMK), gentamicin (G), tobramycin (TOB), netilmicin (NET), colistin (COL), ciprofloxacin (CIP), ofloxacin (OFL) and pefloxacin (PEF). The results are presented in the Table that follows.

	Antibiotics	% Resistance of <i>P.aeruginosa</i>
TIC/PIP	ticarcillin/piperacillin	80.9%
TCC	ticarcillin/clavulanic acid	78.5%
TZP	piperacillin/tazobactam	61.9%
CAZ	ceftazidime	71.5%
FEP	cefepime	73.5%
IPM	imipenem	61.9%
MEM	meropenem	61.9%
ATM	aztreonam	33.3%
CIP	ciprofloxacin	66.6%
OFL	ofloxacin	79.2%
PEF	pefloxacin	71.4%
AMK	amikacin	59.5%
G	gentamicin	69.9%
TOB	tobramycin	64.3%
NET	netilmicin	73.8%
COL	colistin	7.14%

We observed the maintenance of natural sensibility to all antibiotics in 14.28% (6 strains) from all the strains we have studied.

Three strains (7.14%) were resistant to colistin and two strains (4.98%) were resistant to all antibiotics.

Distribution of resistance phenotypes to beta-lactams in order of their frecquency was as follows: wild phenotype 14.28%, penicillinase producer 4.76%, cephalosporinase high level producer 26.19%, carbapenemase producer 54.76%.

The most frequently encountered phenotype to fluoroquinolones was IV (cross-resistance to all fluoroquinolones), 76.19%.

The most frequently encountered phenotype to aminoglycosides was GTNtA (resistance to gentamicin, tobramycin, netilmicin and amikacin), 57.14%.

Conclusion: Very high level of resistance was observed for all *P. aeruginosa* strains, only colistin is with low resistance. Carbapenems should be used with caution due to elevated percentage of resistance against this class of antibiotics.

21.005

JOS Antimicrobial resistance of gram-negative bacilli causing infections in intensive care units in Makkah hospitals, Saudi Arabia

A. Asghar

Umm Al-Qura University-Hajj Research Institute, Makkah, Saudi Arabia

Background: Nosocomial infections caused by antibiotic-resistant gram-negative bacilli that produce extended spectrum-β-lactamases (ESBL) and metallo-β-lactamases (MBL) are associated with higher mortality rates in hospitalized patients.

Objectives: This study aimed to determine the incidence and antimicrobial susceptibility patterns of the most common gram-negative bacteria causing infections in patients staying in the intensive care units (ICUs) of Makkah hospitals, Saudi Arabia, between September 2009 and March 2010.

Methods and Materials: A total of 509 gram-negative pathogens were isolated from clinical specimens and identified by routine microbiological methods. Antibiotic susceptibility was performed using automated instruments. ESBLs and MBLs were determined according to guidelines of Clinical and Laboratory Standards Institute (CLSI). Types of ESBLs and MBLs were detected by polymerase chain reaction (PCR).

Results: Acinetobacter baumannii was the most common bacteria (37%), followed by *Pseudomonas aeruginosa* (29.1%), *Klebsiella pneumoniae* (22.8%), and *Escherichia coli* (10.6%). *P. aeruginosa* and *A. baumannii* isolates were highly resistant to most antibiotics. ESBL was produced by 37.1% of *K. pneumonia* and 31.5% of *E. coli* isolates, while MBL was produced by 20.9% of *P. aeruginosa* and 68.6% of *A. baumannii* isolates. The most frequent ESBL type observed in *K. pneumoniae* was CTX-M (81.4%). The most frequent MBL type was IMP in both *P. aeruginosa* (22.6%) and *A. baumannii* (19.8%).

Conclusion: *P. aeruginosa, A. baumannii*, and *K. pneumoniae* cause several nosocomial infections in ICU patients in Makkah hospitals. Continuous monitoring of antimicrobial susceptibility is recommended to reduce antibiotic resistance.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

21.006 Inhibitory effects of *Lactobacillus plantarum* and Lactobacillus rahmnosus on the growth of Pseudomonas aeruginosa

S. Aminnezhad¹, K. Kermanshahi², R. Ranjbar³, O. Baghery³ ¹Research Center, Bagiyatallah University of Medical Sciences, Tehran, Iran, Tehran, Iran, Islamic Republic of, ²alzahra university, tehran, Iran, Islamic Republic of, ³Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran, Tehran, Iran, Islamic Republic of

Background: Increased use of antibiotics in treatment of infectious diseases resulted in development of antimicrobial resistance. Therefore there is a need to study and to evaluate other therapeutic approaches such as probiotics against pathogenic organisms.

Objectives: The aim this study was to evaluate the inhibitory effects of Lactobacillus plantarum and Lactobacillus rahmnosus on the growth of Pseudomonas aeruginosa.

Methods and Materials: The supernatant of culture of probiotic bacteria was provided by standard method. The inhibitory effects supernatants of probiotic bacteria against the growth of Pseudomonas aeruginosa was determined by well diffusion agar in Muller Hilton Agar. The minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) were tested by microdilution method. MIC of Azithromycin and Ciprofloxacin for Pseudomonas aeruginosa was also measured for comparison.

Results: The MIC and MBC of Ciprofloxacin on the tested strains were 0.25µg /ml and 0.5µg /ml respectively while the MIC of Azithromavcin were 128μ g/ml.The MIC and MBC of Gentamicin on the tested strains were $1\mu g$ /ml and $4\mu g$ /ml respectively while the MIC and MBC of Amikacin were 8 μ g/ml and 16 μ g/ml respectively.

The MIC and MBC of supernatant of culture of Lactobacillus plantarum on the tested microorganism were 6.25 μ l/ml and 12.5 μ l/ml. The MIC and MBC of supernatant of culture of Lactobacillus rahmnosus were 6.25 µl / ml and 12.5 µl/ ml respectively. Two week period storage of supernatant of probiotic bacteria did not affect the inhibitory effects of probiotic bacteria.

Conclusion: Our finding indicated that Lactobacillus strains as probiotic bacteria has a significant inhibitory effect on the growth of Pseudomonas aeruginosa.

21.007

Infection due to colistin-resistant Enterobacteriacae: A single tertiary centre experience in critically ill patients from Saudi Arabia

M. A. Garbati¹, A. Bin Abdulhak², A. I. AlGodair³, H. Sakkijha³ ¹King Fahad Medical City, Riyadh, Riyadh, Saudi Arabia, ²University of Missouri-Kansas City, Kansas City, MO, USA, ³King Fahad Medical City, Rivadh, Saudi Arabia

Background: Enterobacteriacae have continued to challenge infectious diseases physicians by evading current antibiotics. This return to the pre-antibiotic era has become a reality in many parts of the world, including Saudi Arabia. Colistin use has increased as a treatment option of last resort, with the emergence of resistance selective pressure and emergence of super-infection with pathogens intrinsically resistant to colistin (CIR), such as Proteus, Providencia, Morganella, Serratia, etc.

Objectives: To study the burden of infection due to colistin-resistant Enterobactriacae in the intensive care unit of King Fahad Medical City.

Methods and Materials: A retrospective review of infection due to colistin-resistant Enterobactriacae in the intensive care unit (ICU) of King Fahad Medical City (KFMC), Saudi Arabia, with a total bed capacity of 1095, is hereby presented.

All patients aged 13 years or older with infection due to colistinresistant Enterobacteriacae from inception till April 2012 were identified. E-test (AB Biodisk, Solna, Sweden) was used to determine susceptibility to colistin according to packet insert instructions, using Mueller-Hinton agar. Colistin resistance was defined according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) clinical breakpoint for Enterobacteriaceae and resistance to colistin was defined as an MIC of 4 µg/mL or higher.

Demographic and clinical data, admission source, co-morbid conditions, and prior antibiotic use were collected. Treatment given and outcome were also documented.

Results: Nine episodes of infection due to colistin-resistant Enterobactriacae were documented as presented in the Table; urinary tract infection (UTI) in five, blood stream infection (BSI) in two and malignant otitis media and surgical site infection in one patient each. Major risk factors were receipt of colistin, prolonged ICU stay and invasive procedures. All isolates had MICs above 4µg/mL.

Patient No.	Age/ Sex	Source of patient	Co-morbidities	Risk Factors	Isolate	MIC (MC/ mL)	Source of specimen	Duration of ICU stay at isolation	Prior antimicrobial exposure	Diagnosis	Treatment	Outcome
1	65/7	LTCF	DM, , DUP, Smaker	Smoker, CVC, IFC, CABG	K.P.	>4	Urine	4 days	AUG, IMP, VANC	Colonization	None	Good
2	69/81	Home	HTN, advanced NPC, Selbure disorder, pulmonary nocardiosis	Chemothe- rapy, CVC line, IFC, MV, PE9	K.P.	>4	Ear swab	Sweeks	PDN, CEP, CIPEO, CAEB, COL, VAN, ATT, TMP-SNOC MET, CAS	<u>Otitismedia</u>	Tepical Ciprofloxado	Cured
3	\$7/F	ICU	DIA, HTN, OSA, Hypathyraid,	CVC, IFC, MV, PEG,	К.Р.	>4	Blood	5 manths	PEN, CEP, , GEN, VAN, ALMK,	B.S.I.	AME +	Cured
4	\$7/F	100	DM, HTN, OSA, Hypothyroid,	CVC, IFC, MV, PEG;	K.P.	>4	Urine	6 menths	PDI, CP., GDI, VAN, AMK,	U.T.I.	AMK +	Cured
5	76/F	LTOP	DIA, HTN, IHD, DLP, COPD, Hypathyraid, ECRD	CRRT, CVC, ICD, TPN,	Serretia marcesc -ens	>4	Surgical site	4 months	PEN, CIPRO, , LIN, VAN, CTX	551.	Ciproflexade	Cured
5	77/8	Home	DIA, HTN, AF, GB stones, 05A hypothyroid, CED stones	ERCP, PICC, IFC, MV, cholecyste -stemy	K.P.	24	Urine	5 months	FIF-TAZ CAF8, CEF, COL	U.T.I.	Tigecycline + COL	Died
7	77/4	Home	DM, HTN, GB stones, OSA, hypothyroid	PICC, TPN, ERCP, MV, IFC, billiary stant	Serretia marcesc -ens	>4	Blood	1 month	PDN, CDP, CARB, VAN, , UN	0.5.1.	Ceftriaxone	Cured
8	75/F	LTOF	DM, HTH, IHD, DLP, COPD, Hypethyreid, ESPD	PICC, CVC, cystoscopy branchaso ogy, MV,	Enterob -acter aerogen #5	24	Urine	4 months	PEN, CEP, CIPRO, CARB, COL, VAN, UN, TMP-GADY, NTF	U.T.I.	Nitrofurantoi n	Died
9	45/M	LTCF	MS, Pseudabulbar palov	CVC, IFC, PEG, MV,	Previde- ntia rottgeri	>4	Urine	2 menths	PEN, CEP, CIPPO, TIG, PIP-TAZ, GEN,	U.T.I.	Cefepime	Cured
10	36/F	Home	HTH, DLP, Pan- hypopituitaris, Anaxic brain damage	CVC, IFC, MV, Tracheeo# omy	K.F.	>4	Tracheal aspirate	3 manths		Colonization	None	Died
11	\$3/#	Home	DM, HTN, CVD, Seizure, CNS viticulitis	CVC, IFC, MV, Endesceav	K.P.	>4	Urine	5 manths	PIP-TAZ, VAN, AZIT, CIPRO, METRO	U.T.I.	Cefepime	Cured

Table: Clinical characteristics and treatment outcome of patients with Colistinresistant Enterobacteriacae

Conclusion: Colistin resistance is an evolving global phenomenon especially in regions with extensive colistin use. Continued surveillance. hand hygiene and antimicrobial stewardship should be encouraged to halt the menace. More resources should be allocated to drug discovery for this fight to be won.

21.008 Infection with *Escherichia coli* and antimicrobial susceptibility

I. Zurak

Hospiral/University, Zagreb, Croatia

Background: E. coli species are normal inhabitants of the intestinal tract, but can cause infectious diseases in humans and animals, if they are in the middle of another centre organism. Thus, frequent diarrhea infections, urinary, abdominal and respiratory tract, blood sepsis, wounds and so on. All frequent uncontrolled use of antimicrobial therapy caused the emergence of resistance, and also a multiple resistance and the E. coli species. The aim of this study was to isolate E. coli species, and they determine the antimicrobial susceptibility in vitro using the diffusion method on Mueller-Hinton agar according to NCCLS standard method.

Objectives: *E. coli* types isolated from various clinical specimens of hospitalized patients in routine microbiological processing of the sample. Have trouble, misconception create with lactose negative of E. coli (the Escherichia inactive).

Methods and Materials: For isolation of E. coli species using the enriched MacConkey agar (add sugars, indicators), which is better differentiate types increased colony. Isolated suspicious colonies of E. coli been confirmed by more conventional biochemical. A panel of 120clinical isolates E. coli species (from: blood cultures 44; urines 48 and stools 28) was tests on antimicrobial susceptibility of these discs testing: AmC-30; AM-10; CZ-30; FEP-30; CTX-30; CAZ-30; CRO-30; CTB-30; CXM-30; CIP-5; GM-10; IPM-10; LVX-5; MEM-10; NA-30; NET-30; F/M-300; NOR-10; TZP-110; SXT.

Results: The obtained results were grouped according to the sensitivity of three kinds: a) E. coli is very sensitive to antibiotics, b) medium sensitive to antibiotics and c) insensitive, resistant species. E. coli is good sensitive on these antibiotics: Ceftibuten, Ceftazidime,

International Meeting on Emerging Diseases and Surveillance 2013

Meropenem, Nitrofurantoin, Piperacillin/Tazobactam, Imipenem and Cefepime. Medium sensitive is on: Amoxicillin/Clavunalic acid, Ceftriaxone, Ciprofloxacin and Norfloxacin. During this study, found 28 multiply resistant forms of *E. coli* (with insensitivity to more than three antibiotics).

Conclusion: Multidrug-resistant *E. coli* are rapidly emerging pathogen in healthcare setting. Because between of *E. coli* to have and multidrug resistant species are required, determine exactly antimicrobial susceptibilities test before medically antimicrobial treatment. All of these tests and the results may have important therapeutic target interventions.

21.009 Are the neurological rehabilitation wards at higher risk for multi-drug resistant microorganisms infections? A retrospective analysis from a rehabilitation center in Northern Italy focusing on clinical risk factors

M. Riccò¹, D. Nicolotti², C. Signorelli¹, P. Camia¹, S. Cattani¹,

V. Ciorba¹, F. Pezzetti¹, H. Cerrel Bazo² ¹Università degli Studi di Parma, Parma, Italy, ²AUSL Piacenza, Piacenza, Italy

Background: Patients admitted to neurological rehabilitation wards show high susceptibility to Urinary Tract Infections (UTI) by Multi-Drug Resistant (MDR) microorganisms (i.e. resistant to at least 1 antimicrobial in 3 or more antimicrobial classes). In particular carbapenem resistant Gram negative (CR-Gn) are globally associated with significantly increased morbidity and mortality.

Objectives: Here we present a retrospective analysis of the epidemiology and risk factors for UTI and MDR pathogens associated UTI in a specialized neurological rehabilitation ward in Northern Italy.

Methods and Materials: The retrospective analysis included all patients admitted to G.Verdi Hospital in Villanova sull'Arda (Piacenza-Italy) between 10/2009 and 04/2012. Personal and clinical data were retrieved from medical records. All urinary isolates were analyzed focusing on identified pathogens and pharmacological resistances. A regression analysis (binary logistic regression) was then performed in order to evaluate an association between clinical data and MDR infections.

Results: 543 patients were identified (Table 1); 222 of them had Spinal Cord Injuries (SCI) (40.9%), and 147 (27.1%) a previous diagnosis of stroke. In total, 462 urinary isolates (rate of 17.1 infections and 7.5 cases/1,000 hospital days) were retrieved (Table 2): 127 of them (23.3%) were MDR and 45 of them (10.7%) CR-Gn, with an increasing prevalence identified in linear regression analysis (r^2 =0.2022, p=0.0067; Figure 1). UTI were associated with hospital stay ≥60 days (Odds Ratio 2.72 95% Confidence Interval 1.7-4.2), urinary incontinence (UIn) (OR 2.13 95%CI:1.1-4.2) and SCI (OR 2.03, 95%CI:1.1-3.8). Patients with SCI or stroke, ≤65-year-old, of male sex resulted also at higher risk for MDR (p<0.001) and CR-Gn infections (p<0.001). Site of medullary lesion in SCI, ataxia, aphasia or spatial neglect were not associated with an increased risk for UTI and MDR-infections.

1			-		14.1	1.1		
		101		MEAN	alar	Mat	80	ft engre Qerejout,s i pou
	Mates	121	181%	12.03	14	28	18.44	a di mininy
Age at admission (years)	Parriale	322	42.9%	46.57	10	82	18.71	4,0-2007
	TOTAL (MLP)	.141	100.0%	58.52	10	88	18.35	
	Marine	321	38156	74.79	.0	125	80.7	
Monacilial Miny	Particile	322	40.9%	18.96	11	318	52.8	1.000
(spatia)	TOTAL (M+P)	540	100.0%	66.28	1.0.1	725	70.00	
	post-transitio	137	25.2%					
Revinal cond industries	ner tisuratic	. 85	15.7%					
	703AL	872	02.8%					
	Diroke	147	27.1%	1				
Pahabitisties at	for arthopaedic surgery	108	19.2%	1				
Autoimmune or degenerative CNII insiste		28	5.3N	1				
	24	4.8%						
Pergaharal deerysdinating polyneuropolity		1.0	3,7%	1				
	Afuitiple activosia	7	1.2%	10				
	10344	30	100%	1				

Table 1. Main personal and clinical data.

				Capitalosportes																					
	TUTAL	144	gari,	6 2nd p		300	3rd gan.		per.	Ami		Ang		AM.CL		Case		Ma		But		Pp		Carly.	
Activationactor beamared	6.4	4	105	4	1074	4	100%	4	100	2	.824	4	100	.4	784	4	100	1	328	4	100	2	1276	- 4	10
Obstactor sa	14	4	40%		-	14	100	10	-	9	γn		44		100	R.	100	1	108	.4	-	4	-		- 14
Enifortitie cal	218	14	373	58	.25	78	28%	77	274	2	1.96	212	1993	130	42%	163	676	105	82%	120	475	204	78%	.8	116
Snievsbacter soa	1.4	1.0	104	. 2	.76	2	10%	2	10.0	*	- 14	3	7919	4	-	ίŦ.	100	×.	27%	1	-			4	18
Kleiniella spai	78	28	.495	28	20%	24	10%	54	444	21	27%	27	-	40	215	44	619.	30	394	41	-01	均	69	14	184
Morganielo spe			7076		476	1.	10%	4	4.7%	4	- 14	.6	100		429	4	1/4	3	10%		178	3	104	2	314
Proteux retrabilit	- 12	#	194	28	675	26	HTS	26	204	+	174	28	80	27	10%	\$4	616	22	.12%	30	7.4	31	774	14	244
Providencia spa	. 4	4 22	100	4 20	24	1	,795 ,275	4	100	4	-78	4	100	4	100	2	77%	2	326	3	774	3.	29		28
Periodomonana ann'ogenera	47		40%		125			24	1.7%		-19	28	40	24	$\partial^{2} h$	19	100		104	28	42%	2	$\beta_i h \eta_j$	4	
Service au	4	1.2	-	÷.	- 24	- 2	78	4	. 04	2	3/5	2	,824	4	100	4	28	1	324	2	174	¢.	-	2	.28
TOTAL	.442	200	42%	\$8.1	214	164		180	,85%	41	.0%	374	A(r) =	247	104	208	1014	248	124	284	3,04	178	$^{\pm 4}$	48.	114
and beingsteit			00	-	-	_		-		Car.	_			-	~	-	-	112							
		agente Columnication agente Columnication								*															
2nd Gergenblang 2	-					nna anna rCatalana								No Toran											
that Generations C	all manager													Ponetogramity.datedrosamet											
4h Genjeraterij C	-								PM .				Operation												
Are			Ank	-						-					500	-	-								
Area		Argadir																							
Amdi	Aug die				Annual Ter Constant																				

Table 2. Isolates: microbiology and identified resistances.



Figure 1. Time trend of ratio MDR Isolates / Total Isolates with regression analysis (r2 =0.2022; p=0.0067)

Conclusion: With the limitations associated with a retrospective analysis, our data are consistent with the increasing prevalence of MDR-infections. In general, we identified higher risk for subjects with SCI, stroke or UIn. On the other hand, our data suggests that the Uin and prolonged hospital stays as the main risk factors for MDR and CR-Gn infections, whereas specific neurological impairment (i.e. level of the lesion in SCI, aphasia, ataxia, neglect) seems apparently unrelated.

21.010 Successful management of nosocomial ventriculitis and meningitis caused by extensive drug resistant *Acinetobacter baumannii*, Austria

M. Drescher¹, **M. Hoenigl¹**, G. Feierl², T. Valentin¹, K. Seeber¹, E. Leitner², G. Zarfel², W. Duettmann¹, R. Krause¹, A. J. Grisold¹ ¹Medical University of Graz, Graz, Austria, ²Intitute of Hygiene, Graz, Austria

Background: Nosocomial infections caused by the gram negative coccobacillus *Acinetobacter baumannii* have substantially increased over recent years. As *Acinetobacter* is a genus with a tendency to quickly develop resistance to multiple antimicrobials, therapy is often complicated requiring the return to old drugs. Resistance of *A. baumanii* poses a problem worldwide. We report a case of meningitis due to multidrug-resistant (MDR) *Acinetobacter baumannii* in an Austrian patient who had undergone neurosurgery in Northern Italy.

Objectives: To describe the successful treatment of a case of meningitis caused by MDR *Acinetobacter baumannii* and illustrate the limits of therapeutic options in CNS infections with pan-resistant pathogens.
POSTER PRESENTATIONS

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: We report a case of EVD (external ventricular drain) associated meningitis caused by MDR Acinetobacter baumannii in a critically ill 66-year-old Austrian female who had suffered from subarachnoid hemorrhage. Antimicrobial susceptibility testing was performed by Etest. For tigecycline interpretation was inferred from available breakpoints for Enterobacteriaceae issued by EUCAST. Antimicrobial synergy testing was performed using the relevant Etest method. Synergy was defined as a fractional inhibitory concentration index (FIC) of < 0.5.

Results: Multidrug-resistant (MDR) Acinetobacter baumannii was cultured from cerebrospinal fluid (CSF). Antimicrobial susceptibility testing showed susceptibility to colistin only (tigecycline MIC 2). Synergy was found for the combinations colistin/ciprofloxacin (FIC 0.0679) and for tigecycline/meropenem (FIC 0.25). Despite combination treatment with meropenem and tigecycline Acinetobacter baumannii was repeatedly cultured from cerebrospinal fluid (CSF). Therefore therapy was changed to intrathecal colistin plus intravenous ciprofloxacin. As a few days later the identical Acinetobacter baumannii isolate was cultured also from tracheal secretion intravenous colistin was added as a third agent. Intrathecal colistin was well tolerated and the patient did not develop seizures. After 64 days in hospital the patient was discharged into rehabilitation.

Conclusion: Meningitis caused by multi-resistant Acinetobacter baumannii poses great limitations in treatment and demonstrates the threatening development of antimicrobial resistance. A combination of intrathecal and intravenous colistin may be the best therapeutic option, dosages are limited, however, due to the potential side-effects. Synergy testing and subsequent initiation of synergistic antimicrobial substances may improve outcome as illustrated in this case.

21.011 Antimicrobial resistance of human Salmonella serovar Typhimurium U302 strains in Slovakia: Prevalence of R-type ASSuT

L. Majtanova, V. Majtan

Slovak Medical University, Bratislava, Slovakia

Background: In the last two decades, the emergence and spread of antimicrobial-resistant Salmonella serovar Typhimurium strains has become a serious health hazard worldwide, specifically associated with the certain phage types (DT104, DT193, U302).

Objectives: To determine the antimicrobial susceptibility in Salmonella serovar Typhimurium definitive phage type U302 strains isolated from humans over the last six years.

Methods and Materials: From 1779 phage typed human strains of Salmonella serovar Typhimurium over the period 2006-2011 total number of U302 phage type strains was 291 (16.4%). Antimicrobial susceptibility to ampicillin, ceftriaxone, ciprofloxacin, gentamycin, chloramphenicol, streptomycin, sulfizoxazole, sulfamethoxazoletrimethoprim, tetracycline, trimethoprim and nalidixic acid was determined using the disk diffusion method.

Results: Based on the antimicrobial susceptibility testing overall antimicrobial resistance was high when 244 (83.8%) of U302 phage type strains were multidrug-resistant (MDR). The most prevalent resistance to ampicillin, streptomycin, sulfizoxazole and tetracycline (R-type ASSuT) was verified in 87 (29.9%) strains. The annual rate of this resistance type was different but the highest number of these MDR strains in both 2009 and 2010 were identified. The classical pentaresistance phenotype (R-type ACSSuT), characteristic for strains of DT104 phage type, only in 40 (13.7%) U302 strains was found.

Conclusion: Although the prevalence of Salmonella serovar Typhimurium DT104 R-type ACSSuT in Slovakia decreased, ASSuT as well as ACSSuT resistance markers continue to circulate with emerging of new phage types. Therefore, the continual surveillance of the occurrence of these and similar multidrug-resistant phage types should be conducted.

This work was supported by Ministry of Health of the Slovak Republic under the project Molecular analysis of antibiotic resistance of nontyphoid salmonella serovars.

21.012 Inducuble clindamycin resistance in methicillin-susceptible and methicillin-resistant Staphylococcus aureus of inpatient, outpatient and healthy carriers

S. Uzunović¹, A. Ibrahimagić², F. Kamberović³, M. Kunarac², M. I. A. Rijnders⁴, E. E. Stobberingh⁴

¹Cantonal Public Health Institute Zenica, Faculty of Health Care and Nursing, University "VITEZ" Vitez, Zenica, Bosnia and Herzegovina, ²Cantonal Public Health Institute Zenica, Zenica, Bosnia and Herzegovina, ³Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia, ⁴School for Public Health and Primary Care (CAPHRI), Mastricht University Medical Center, Mastricht, Netherlands

Background: In vitro routine tests for clindamycin susceptibility may fail to detect inducible macrolide-lincosamide-streptogramin B (iMLCB) resistance resulting in treatment failure.

Objectives: To investigate the iMLSB prevalence in 142 methicillinsensitive (MSSA) and 48 methicillin-resistant (MRSA) in-patient (65), outpatient (75), and healthy carrier (150) Staphylococcus aureus isolates in Zenica-Doboj Canton, Bosnia and Herzegovina.

Methods and Materials: Disk diffusion testing by placing clindamycin (CLI) and erythromycin (ERY) disks 15 mm apart (edge to edge) on a Mueller-Hinton agar, as per CLSI guideline was performed. Two distinct induction phenotypes labeled as D (D-shaped clear zone of inhibition around CLI disk) and D+ (D-shaped zone containing inner colonies growing up to CLI disk), and four non-induction phenotypes designated as Neg (negative, no blunting of CLI zone), HD (hazy D zone, double zone of inhibition with an inner ring of reduced growth up to the edge of the disks), R (constitutive, cMLSB, solid growth around the CLI and ERY disks), and S (susceptible to both CLI and ERY). Methicillin-resistance was confirmed by the presence of mecA gene by PCR. The genetic characterization was performed using spa-typing and the algorithm based upon repeat patterns (BURP).

Results: iMLSB was detected in six (2.1%) isolates, of which five (3.5%) (two outpatients and three carriers) were MSSA, and one (2.1%) (outpatient) MRSA. One of them, D+ phenotype (iMLSB) was obtained from carrier (MSSA). None of inpatients had iMLSB. HD phenotype did not detect. One (MRSA) isolate has shown negative phenotype. Two strains with iMLSB originated from skin and soft tissue (MRSA) and eye infection (MSSA) were belonged to the same MLST CC8, with different spa-types (t451 and t008, respectively). R phenotype (cMLSB) was detected in two (inpatient) isolates (0.7%).

Conclusion: D test was identified 2% of wrongly reported isolates as clindamycin sensitive. Despite low prevalence of S. aureus with iMLSB, it is of a significance the finding that they mostly were MSSA, and all were isolated from outpatients or carriers. D-test becomes an imperative part of routine antimicrobial susceptibility test for all S. aureus isolates.

21.013 Serotype and clindamycin resistance of Streptococcus suis in diseased pigs and humans in upper northeast Thailand

S. Angkititrakul¹, T. C. Nutravong²

¹KHON KAEN UNIVERSITY, Khon Kaen, Thailand, ²Faculty of Public Health, Khon Kaen Univerfsity, Khon Kaen, Thailand

Background: Streptococcus suis is a zoononic agent that important causes severe infections between pigs and humans. Streptococcus suis serotype 2 is a frequent cause of diseases in pigs and humans worldwide including other serotype (5, 14, 16, 29 etc.). In Thailand, a lack of studies concerning epidemiological serotyping and clindamycin resistant in pig and human isolates in the same time period was reported. So our study collected data from both pig and human infections during 2007-2012.

Objectives: To know the distribution of antimicrobial resistant among serotype of Streptococcus suis in humans, healthy and diseased pigs.

Methods and Materials: These study was collecting of diseased pig isolates from the Veterinary research and development center (uppermost Northeast region) and human isolates from the hospital of upper Northeast Thailand, including healthy pig from slaughterhouse in upper Northeast Thailand, then isolated and identified performing

International Meeting on Emerging Diseases and Surveillance 2013

biochemical test with Gottaschalk method, confirmed for *S. suis* by PCR amplification of 16srRNA gene and cps 1, 2, 7, 9 gene, then performing antimicrobial susceptibility by NCCLS method.

Results: This study found that four of *S. suis* serotype2, three of type7 and type9 in pigs. Thirty *S. suis* serotype 2 was present in humans from upper Northeast Thailand. Half of pigs resist to erythromycin, but 20% in humans. All *S. suis* from pigs resist to tetracycline and clindamycin. Almost all humans resist to tetracycline, erythromycin and clindamycin. Humans have more resistant to antimicrobials than pigs, as gentamicin, chloramphenical. Every *S. suis* in all sources sensitive to penicillin and cefazolin while 8% of pigs resist to those. *S. suis* serotype2 has MIC 90 of clindamycin more or equal to 6.125 ug/ml and MIC50 > 800 ug/ml. Whereas MIC 90 of Penicillin G is less than 0.06 unit/ml and MIC 90 of cefotaxime < 4 ug/ml.

Conclusion: These indicated that clindamycin, tetracycline and erythromycin were not effective to all of *S. suis* isolates. While penicillin and cefotaxime are quite effective for *S. suis* both humans and diseased pig isolates.

21.014 *Escherichia coli* B2 and D virulent phylotypes carry extended-spectrum and pAmpC beta-lactamases in healthy dogs with no antimicrobial pressure

A. Belas, N. Couto, C. Pomba

Faculdade de Medicina Veterinária da Universidade Técnica de Lisboa, Lisbon, Portugal

Background: Phylogenetic analysis has shown that *Escherichia coli* is composed of four main phylogenetic groups (A, B1, B2, and D) and that virulent extra-intestinal strains mainly belong to groups B2 and D. Thus, canine commensal gastrointestinal *E. coli* may represent a reservoir of antimicrobial resistance and virulence.

Objectives: to analyze the antimicrobial resistance mechanisms and phylogenetic groups among amoxicillin-resistant *E. coli* isolates from healthy dogs under no antimicrobial pressure.

Methods and Materials: Fifty-five amoxicillin-resistant *E. coli* isolates were randomly selected from an on-going cross sectional study for this work. PCR-based screening for the presence of bla_{CTX-M} , bla_{SHV} , bla_{TEM} , and plasmid-borne genes encoding AmpC β -lactamase (pAmpC) was done using specific primers as previously described (Pérez and Hanson 2002, Edelstein et al 2003, Pomba et al 2006). Extended-spectrum beta-lactamases (ESBL) and pAmpC gene identification was accomplished by nucleotide sequencing. Phylogenetic groups of *E. coli* strains and clone O25-ST131 were tested by methods based on PCR multiplex (Clermont et al 2000, 2009).

Results: Classification of isolates into phylogenetic groups indicated that 41.8% belonged to commensal groups A (n=19) and B1 (n=4) and 58.2% belonged to virulent groups B2 (n=8) and D (n=24). Phylogenetic analysis of *E. coli* ESBLs and AmpC beta-lactamases producers revealed that: i) 5 single producer strains belonged to commensal groups A and B1; ii) 15 to virulent groups B2 and D, iii) 4 and 8 double enzyme producer strains belonged to the commensal and virulent phylotypes, respectively (Table 1). None of the *E. coli* isolates belonged to the pandemic virulent ST131-O25b clone.

Phylogeny	No of	ESBL genes (n)	AmpC genes (n)	ESBL+ AmpC genes (n)			
	strains						
A	19	$bla_{\text{CTX-M-32}}(1)$	$bla_{\rm CMY-2}(4)$	bla _{CTX-M-1} + bla _{CMY-2} (1), bla _{CTX-}			
				M-9 group+ blacMY-2(1), blacTX-M.			
				$_{15}+ bla_{CMY-2}(1)$			
B1	4	(0)	(0)	blactx-M-9 group+ blac MY-2(1)			
B2	8	<i>bla</i> _{CTX-M-32} (1)	(0)	blactx-M-32+ blacMY-2(1)			
D	24	bla _{CTX-M-1} (2),	$bia_{DHA-1}(1),$	bla _{CTX-M-1} + bla _{CMY-2} (1), bla _{CTX}			
		bla _{CTX-M-9} (1),	bla _{CMY-2} (7),	M-9+ bla _{CMY-2} (1), bla _{CTX-M-15} +			
		$bla_{CTX-M-15}(1),$	$bla_{\rm CMY-2-like}(1)$	$bla_{CMY-2}(2), bla_{CTX-M-32} +$			
		$bla_{\text{CTX-M-32}}(1)$		$bla_{CMY-2}(2), \ bla_{CTX-M-32} +$			
				$bla_{\text{CMY-2-like}}(1)$			

Table 1. Phylotypes and ESBL and pAmpC genes.

Conclusion: Our results show dogs as reservoirs for bacteria resistant to oxyimino-cephalosporins and cefamicins the majority of isolates belonged to virulent groups B2 and D. Additionally, virulent phylotypes produced more than one enzyme. This may have impact on human health due to the close and direct contact between pets and owners.

21.015 Antimicrobial resistance of *Salmonella* Stanley isolated from pigs, dogs and humans in northeast of Thailand

A. Polpakdee¹. S. Angkititrakul²

¹Khon Kaen University, Khon Kaen, Thailand, ²KHON KAEN UNIVERSITY, Khon Kaen, Thailand

Background: Food-borne disease caused by *Salmonella spp.* is an important public health problem in the world including northeast of Thailand. High incidence *Salmonella* contamination has been found in many species, such as pigs, dogs and humans. However, most infected animals show no clinical signs but can transmit to other animals. Infected animals can shed *Salmonella* to humans by contacting contaminated feces and environment. Antimicrobial resistance of *Salmonella* has an impact on the treatment in patients and animals including prolonged treatment duration, high cost and treatment failure. So, the use of many antimicrobials for prevention and control of the disease has no regulation for appropriate use.

Objectives: To know the distribution of antimicrobial resistance of *Salmonella* Stanley isolated from pigs, dogs and humans.

Methods and Materials: 50 isolates of *Salmonella* Stanley isolated from pigs (21), dogs (9) and humans (20) identified according to the standard ISO-6579 method. The antimicrobial susceptibility test for all isolates was determined. The following antimicrobials were tested: AML: amoxicillin 10 mg, CIP: ciprofloxacin 5 mg, CN: gentamicin 10 mg, NA: nalidixic acid 30 mg, NOR: norfloxacin 10 mg, SXT: sulphamethoxazole/trimethoprim 25 mg TE: tetracycline 30 mg.

Results: *Salmonella* Stanley isolated from pigs were resistant to amoxicillin (100%), sulphamethoxazole/trimethoprim (19.1%) and tetracycline (90.5%). Isolates from dogs were resistant to amoxicillin (33.3%) and tetracycline (22.2%). All isolates from humans commonly resistant to amoxicillin and tetracycline were 100%.

Conclusion: Salmonella Stanley in pigs and dogs are important risk factor to human salmonellosis especially people which close up them. Pattern of antimicrobial resistant from pig and dogs isolates are nearly to humans isolates due to important problem to used antibiotic for treat this disease.

21.016

Analysis of the plasmid profile in *Salmonella Typhimurium* strains isolated in the Republic of Uzbekistan

L. Tuychiev, G. Abdukhalilova, A. Ibragimov, I. Akhmedov Research Institute of Epidemiology, Microbiology and Infectious Diseases, Tashkent, Uzbekistan

Background: Food-borne salmonella poisoning is one of the most common and widespread diseases throughout the world. Outbreaks are normally caused by ingestion of contaminated food, meat or milk of domesticated animals or poultry. Recently, antibiotics have been intensively used to treat humans and animals infected with salmonella, resulting in salmonella strains that acquire a multidrug resistance (MDR) phenotype following intensive antibiotic therapy. In animal health care, antibiotics are used as prophylaxis and as a preventive measure against disease during animal production. Use of antibiotics disturbs animals' normal intestinal flora, resulting in the occurrence of antibiotic resistant salmonella strains, which are subsequently released into the environment in animal feces. Salmonella strains with acquired MDR phenotype cause significant problems in public health and animal health care, i.e. with limited options for available therapy and treatment. Resistance markers can be found in plasmids or chromosomes of resistant bacteria. Plasmids are the main factor of spread or transfer of antibiotic resistance among bacteria.

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: Analysis of R (resistance) plasmids in S. typhimurium strains.

Methods and Materials: We studied seven strains of *Salmonella enterica Serovar typhimurium* isolated from patients in Uzbekistan with acute intestinal infections. Salmonella isolates were tested for antibiotic sensitivity by a disc diffusion method on Muller-Hinton agar. Plasmid DNA was isolated from bacterial cells using the Kado & Lu method.

Results: *S. typhimurium* strains were demonstrated to be resistant to ampicillin, ceftriaxone, ceftazidime, nalidixic acid, ciprofloxacin, ofloxacin, and sensitive to imipenem and meropenem. Five strains had large plasmids with molecular weight of 67.5 kb and 140 kb. Two strains had three plasmids each, with molecular weight of 50 kb, 67.5kb and 140 kb.

Conclusion: Results of the research demonstrated that the resistance to ceftriaxone and ciprofloxacin in the *S. typhimurium* strains tested was related to the 67.5 kb R plasmid.

21.017 Characterization of uropathogenic *E. coli* and detection their ESBL TEM & SHV genes

S. N. El-Sukhon

Jordan University of Science & Technology, Irbid, Jordan

Background: Lack of strict control measures on the misuse of antibiotics, contributes prominently in emerging of resistant *E. coli* isolates. To trace their hazardous impact, determination of their virulence factors and the potential ESBL production become important requirements in combating them.

Objectives: This study aims at characterization of uropathogenic *E. coli* isolates and detection their TEM and SHV genes.

Methods and Materials: A total of 105 UTI *E. coli* isolates were studied to determine their: a- biochemical activities (Microgen GN-ID, Camberly, U.K., kit; b- HA-MRHA activity; c- resistance toward 16 antibiotics (CLSI); d- serum resistance; e- ESBL production (CLSI) and e- PCR-PCR products analysis and sequencing of beta lactamase TEM and SHV genes.

Results: All isolates were confirmed, biochemically, as E. coli. Their antibiotic resistance fluctuated between 10.4% and 95.2%. Serum resistance was recorded in 28 (26.6%) isolates. Of those, 24 isolates revealed count increment values of 0.3-1.54 logs, whereas other 4 isolates revealed no change. Of those, 10 were ESBL producers. A total of 31 isolates could agglutinate the group A+ human RBCs. Of those, 24 were mannose resistant. Phenotypically, ESBL was determined in 22.8%. It showed 10, 2, 15, 16, 2 frequencies toward the ceftriaxone, ceftazidine, cefotaxime, aztreonam, and cefuroxime, but none toward the imipenem. Genotypically, the TEM and SHV genes were detected in 75 and 3 isolates, respectively whereas additional 12 isolates were harboring both genes. The forward and reverse sequencing of PCR products of TEM of two samples revealed 99% similarity with the Escherichia coli strains: 2009EL-2071(O104:H4); 2011C-3493 (O104:H4) plasmid pESBL-EA11; 2009EL-2050 (O104:H4) transconjugant Tx098 plasmid pJIE098 multi-resistance region; HUSEC41 plasmid pHUSEC41-1; p838B-R transposon Tn2 plasmid, whereas the PCR product of one sample of SHV also revealed 99% similarity with the Escherichia coli plasmid pEco121 SHV type extended spectrum beta-lactamase (SHV-11) gene.

Conclusion: *E. coli* represents a serious public health threat and determination of its hazard based on their potential ESBL production becomes crucial in the planning of the remedial strategies.

21.018 Copper alloys beneficial effects on ICU operation

P. Efstathiou¹, E. Doe kouskouni², **S. Papanikolaou³**,

K. Karageorgou¹, Z. Manolidou¹, M. Tseroni², E. Logothetis¹, I. Agrafa¹

¹Ministry of Health, Greece, Maroussi-Athens, Greece,

²Medical School of the University of Athens, Athens, Greece,

³Peiraiko Therapeftirio"General Hospital, Maroussi Athens, Greece

Background: N/A

Objectives: The objectives of this study is to record the reduction of microbial flora in the ICU environment, and the effect on the financial operating parameters of the ICU after antimicrobial copper alloys' implementation.

Methods and Materials: Medical, epidemiological and economic data collected from a General ICU type (mixed/diverse) were recorded and analyzed into two periods, before and after antimicrobial copper Cu 63%-Zn 37% (Low Lead) copperization.

Parameters Assesed:

- Incidents severity upon admission, estimated along with

 APACHE II (Acute Physiology and Chronic Health Evaluation),
 - b. SAPS (Simplified Acute Physiology Score),
- 2) Monitoring/cultivation of microbial flora in the ICU before and after the implementation of antimicrobial copper and
- 3) The impact on epidemiological and economic parameters on ICU's operation.

Results: During the period between December 2010–March 2011 and December 2011–March 2012 respectively, comparative results showed statistically significant reduction not only on microbial flora (95%) but showed also a decrease on the use of antimicrobials by 30% (p = 0.014).

Conclusion: This innovative implementation of antimicrobial copper in ICU indicates: 1) Significant reduction of microbial flora in the environment of the ICU, and 2) Reduction on the use of antimicrobials with apparent positive effect (decrease) both on the length of hospital stay of patients in the ICU but also towards hospitalization costs for patients and the operation of the ICU. Under the present conditions of the economic crisis, the results of this research are considered to be of the highest importance and value.

21.019 Prevalence of drug-resistant tuberculosis in rural eastern China

Q. Zhao¹, Y. Hu¹, W. Wang¹, W. Jiang¹, T. Tao¹, B. Xu² ¹School of Public Health, Fudan University, Shanghai, China, ²Fudan University, Shanghai, China

Background: Multidrug-resistant Tuberculosis (MDR-TB) has become a major public health problem worldwide, which lays heavy burden to low and middle income countries. China, as one of the hot spots of MDR-TB epidemic, harbours the largest number of MDR-TB cases globally and perhaps the largest reservoir of individuals latently infected with MDR-TB.

Objectives: To descript the prevalence and risk factors of drugresistant TB and MDR-TB in rural eastern China

Methods and Materials: Population based cross-sectional study was carried out in 6 counties in Shandong and Jiangsu provinces in eastern rural China. All registered active TB patients, during May 2008 to July 2010, were investigated through questionnaire interview at the time of diagnosis. Three sputum specimens were collected from each patient for culturing. Bacterial Drug susceptibility test (DST) was performed for 1st-line anti-TB drug on all isolated TB bacilli.

Results: In total 2225 TB patients were recruited with one-fourth being female, and 14.7% having previous anti-TB treatment history. 1297 (58.3%) patients were diagnosed as smear positive TB. Finally 1275 isolates were obtained with 1222(95.8%) *M.TB, 40(3.1%) NTM and 2(0.2%) M.bovis. The overall drug resistant of these patients was 21.1%, while the rate of single drug resistant, MDR and PDR were* 9.7%, 6.4% and 5.1% respectively. The prevalence of resistant to isoniazid (INH), rifampicin (RIF), streptomycin (STR), and ethambutol (EMB) were 15.5%, 9.3%, 18.2% and 4.0% respectively. Adjusted by gender, age, health education years and health insurance, it was found that patients having previous treatment history had higher risk for resistance to 1st-line anti-TB medication (AOR=4.665,95%CI: 3.328-6.540) and MDR-TB (AOR=14.197,95%CI: 8.497-23.719). The prevalence of MDR-TB was much higher in Jiangsu province (AOR=1.718, 95%CI: 1.053-2.801) than Shandong province.

Conclusion: The prevalence of drug resistant TB and MDR-TB were higher in rural eastern China while the distribution was varied in different province and the different anti-TB treatment history patients. The standardized diagnosis and treatment strategies for drug-resistant TB are urgently needed for TB control. Furthermore researches should be carried out to understand the varied distribution of MDR-TB and the transmission model of drug-resistant TB.

International Meeting on Emerging Diseases and Surveillance 2013

21.020 Minced meat as a source for MRSA and ESBL-producing E. coli

C. Petternel, J. Posch, D. Haas, H. Galler, G. Zarfel, V. Strenger, E. Marth, F. Reinthaler, G. Feierl

Medical University of Graz, Graz, Austria

Background: Antimicrobial drug resistant bacteria are a common public health problem. Resistant bacteria present in animal food products can be a source for infections in humans. For resistant bacteria it is important to know the phenotype and genotype.

Objectives: This study was conducted to investigate the prevalence and genetic characteristics of resistant bacteria in mixed minced meat from pork and beef. Therefore special attention was paid to ESBL producers (Escherichia coli and Klebsiella spp), MRSA (Methicillinresistant Staphylococcus aureus) and VRE (Vancomycin-resistant Enterococcus).

Methods and Materials: 100 samples of minced meat were collected from supermarkets (n=70) and local butcher shops (n=30) in the city of Graz (Styria/Austria) between September 2011 and September 2012. After enrichment in liquid culture medium (peptone broth and Enterococcosel broth) and inoculation on selective media, bacteria were selected from chromeID[™] ESBL (bioMérieux), chromeID[™] VRE (bioMérieux) and OXA agar and subsequently identified with MALDI-TOF MS and Vitek2 systems. All isolated bacteria were tested for antibiotic resistance using disc diffusion test. The ESBL production was confirmed by double disc diffusion test according to current CLSI guidelines. Resistance-genes of ESBL producers and the spa-types of MRSA were detected with PCR and sequencing.

Results: In 20 of the 100 meat samples 22 ESBL positive E. coli strains were found. The most common ESBL-type, found in 16 E. coli strains, was CTX-M-1, one strain harbouring TEM-1 as an additional betalactamase. One E. coli strain with genes for CTX-M-32 and TEM-1 was found. Two strains contained CTX-M-14, two TEM-52 and one SHV-12. It is noteworthy, that from one sample three different types (CTX-M-1, CTX-M-14 and SHV-12) of ESBL-producing E. coli could be isolated. Moreover 10 samples were tested positive for MRSA and confirmed by spa-typing. Detected spa-types were CA (communityacquired) t3928, as well as LA (livestock-associated) t011, t034 and t2241. No VRE were found.

Conclusion: A contamination of beef and pork with resistant bacteria was confirmed in this study. It could be shown that ESBL and MRSA are present in meat samples. However it has to be investigated how much this bacterial pollution contributes to infections in humans and being responsible for the spread of antibiotic resistance.

SATURDAY • February 16, 2013

21.021 Prevalence of commensal ESBL-producing Escherichia coli strains isolated from piglets from birth to nursery on three Portuguese industrial pig farms.

M. M. Centeno¹, N. Couto¹, A. Belas¹, T. Nunes¹, V. Almeida¹, L. Alban², C. Pomba¹

¹Faculdade de Medicina Veterinária, Universidade Técnica de Lisboa, Lisbon, Portugal, ²Danish Agriculture and Food Council, Kobenhavn V Denmark

Background: Resistance to third generation cephalosporins (3GC) in animals is considered to be very important owing to the critical role these antimicrobials play in human medicine. Although recent EFSA reports state low 3GC resistance in animal bacteria, surveillance of commensal bacteria harbouring extended-spectrum β-lactamases (ESBL) genes is a priority specially when 3GC are used.

Objectives: To determine the prevalence of ESBL-producing commensal E. coli isolates from piglets at birth, weaning and during nursery on three Portuguese industrial pig farms.

Methods and Materials: For each farm 10 litters were randomly chosen and 7 piglets from each litter were ear-tagged. Fecal samples were collected from each piglet at birth before the administration of 3GC (n=209), at weaning (n=194) and during nursery (n=190). After enrichment in buffered peptone water, 100µl of bacterial suspension

IMED 2013

were inoculated on MacConkey agar supplemented with 1.5µg/ml of cefotaxime (CTX). Strains that showed resistance to CTX were identifiedas E. coli by gadA PCR. ESBL production was assessed by the double disk diffusion synergy test and isolates were screened for the $bla_{CTX-M-1Group}$ gene cluster.

Results: High prevalence of ESBL-producing E. coli from birth to nursery is shown in Table 1. Values varied between farms and sampling moments, demonstrating different ESBL-producing E. coli presence in the pig reservoir. Regarding the $\mathit{bla}_{\rm CTX-M-1Group}$ gene cluster, 97.2% (Cl_{95%} 95-98.4%) of all ESBL-producing E. coli isolates harboured this resistance gene group. The mechanism of resistance of the remaining eleven ESBL-producing isolates is still under study.

		Prevalence (%)	
	At Birth	After Weaning	During Nursery
	(a/N)	(n/N)	(a/N)
	72.5	93.4	57.6
Farm 1	Cl _{usts} 60.9-81.6%	Class, 84.3-97.4%	Class, 44.9-49.4
	(50/69)	(57.61)	(34/59)
	68.6	53.8%	69.2%
Farm 2	CI ₅₉₅ 56.9-78.2%	Clen, 41.9-65.4%	Class, 57.2-79.1
	(48/70)	(35/65)	(45/65)
	81.4%	19.1%	78.8%
Farm 3	CI ₈₀₅ , 70.8-88.8%	CI ₀₀₅ ,11.5-30%	Clan, 67.5-86.9
	(\$7/70)	(13/68)	(52/66)

Table 1. Prevalence (%) of ESBL-producing Escherichia coli strains in pigs from birth to nursery.

Conclusion: In this study we were able to demonstrate a high prevalence of ESBL-producing commensal E. coli throughout the first stages of the pig's life, possibly influenced by selective antimicrobial pressure and biosecurity measures. Furthermore, the bla_{CTX-M-1Group} gene cluster detected is also a prevalent one in humans. According to the results it is crucial to continue monitoring the presence of these resistance genes throughout the entire life cycle from pig to pork.

21.022

Relative activity over time of chlorhexidine and benzalkonium chloride against methicillinresistant staphylococci isolates from horses

N. Couto¹, A. Belas¹, P. Tilley¹, L. Telo da Gama¹, I. Couto²,

K. Kadlec³, S. Schwarz³, C. Pomba¹

¹Faculdade de Medicina Veterinária da Universidade Técnica de Lisboa, Lisbon, Portugal, ²Instituto de Higiene e Medicina Tropical, Lisbon, Portugal, ³Friedrich-Loeffler-Institut, Neustadt-Mariensee, Germany

Background: Methicillin-resistant staphylococci (MRS) from horses are a serious public health issue. Especially as antimicrobial therapy has become a challenge in the treatment of staphylococcal infections, biocides seem to be a reliable therapeutic option in veterinary medicine.

Objectives: To determine the relative activity over time of two biocides, chlorhexidine (CHA) and benzalkonium chloride (BAC), against methicillin-resistant staphylococci isolates from horses.

Methods and Materials: In total, 14 staphylococcal isolates were isolated from the anterior nares of healthy and diseased horses and used for determination of minimum bactericidal concentrations (MBC) of BAC and CHA according to NF1040. Briefly, each cell suspension was exposed to water containing the biocides for 5, 30 and 60 minutes at 20°C. The biocides were inactivated by a 5-minute neutralization step and the mixture was used for inoculating Mueller-Hinton broth. Bacterial growth was registered after 24h at 37°C. The relative activity over time of CHA and BAC was investigated. This was assessed by regressing the natural logarithm of MBC on time (minutes) with a statistical model, which also included the effect of biocide and its interaction with time. Individual regression equations on time were obtained for each biocide. Differences were considered significant if the p-value was ≤ 0.05 .

Results: The interaction between the effect of biocide and time was found to be significant (p<0.001), indicating that the activity of the two biocides differed over time (Figure 1). The results showed that, over

POSTER PRESENTATIONS

International Meeting on Emerging Diseases and Surveillance 2013

the whole period studied. CHA was more efficient than BAC. Moreover. CHA was almost as efficient at 5 minutes as it was at 60 minutes. Furthermore, to achieve the same efficiency, a higher concentration of BAC or a longer exposure to the biocide was necessary, when compared to CHA.



Figure 1. Activity of CHA and BAC over time (minutes).

Conclusion: Overall CHA was better than BAC at 20°C, since less time and a lower concentration was needed to kill all MRS. In order to use BAC for decolonization we would have to use a much higher concentration or increase the exposure time to achieve killing of MRS. Our results suggest that CHA may be the best antiseptic to decolonize horses carrying MRS when entering a veterinary hospital.

21.023 Detection of bacteria resistant to critically important antimicrobials from lower urinary tract infections in cats and dogs from Portugal

C. Pomba, D. Saial, M. M. Centeno, A. Belas, N. Couto Faculdade de Medicina Veterinária da Universidade Técnica de Lisboa, Lisbon, Portugal

Background: Cephalosporins, fluoroquinolones and aminoglycosides are classified as critically important antimicrobials by the OIE and also meet the WHO criteria 1 (sole therapy or one of few alternatives to treat serious human disease) and 2 (used to treat diseases caused by organisms that may be transmitted via non-human sources or that may acquire resistance genes from non-human sources).

Objectives: To detect critically important antimicrobial resistant bacteria among strains isolated from lower urinary tract infections originated from cats and dogs in Portugal.

Methods and Materials: Eight hundred and forty five uropathogenic bacteria were isolated from dogs (n=1160) and cats (n=553), between January1999 and November 2012, at the Veterinary Teaching Hospital of the Faculty of Veterinary Medicine and at veterinary private practices in the Lisbon area. Isolates were identified using standard commercial systems. Susceptibility testing was performed using the disk diffusion and broth microdilution methods. Extended-spectrum β-lactamases (ESBL) production was screened by double-disk synergy test. The ESBL, plasmid-mediated ampC and mecA genes were detected by PCR and gene enzymes were sequenced.

Results: Overall, among Enterobacteriaceae resistance to cephalosporins was 7.1%, 22% to fluoroquinolones (FQ) and 13.3% to aminoglycosides (AG). Thirty-three Enterobacteriaceae isolates were resistant to cefoxitin but only 12 produced plasmid-mediated cephalosporinases (11 bla_{CMY-2} and 1 bla_{DHA-1}). Seven E. coli isolates produced ESBL (3 bla_{CTX-M-15}, 3 bla_{CTX-M-32} and 1 bla_{CTX-M-14}) and were also resistant to ciprofloxacin. Eight staphylococci exhibited resistance to oxacilin (6.7%) and had the mecA gene (2 S. aureus, 3 S. pseudintermedius and 3 S. epidermidis). Staphyloccoci were 10.1% resistant to FQ and 8.5% to AG. Seven Enterococcus spp. were resistant to ampicillin and 3 strains also exhibited high-levelgentamicin-resistance.

Conclusion: These results demonstrate that the emergence of resistance to critically important antimicrobials among uropathogens from companion animals is a concerning fact. Furthermore the detection of uropathogens with antimicrobial resistance is not only an animal health issue but also a matter of public health, since companion animals may act as reservoirs of antimicrobial resistant bacteria or resistance genes for humans.

21.024 Trends in the prevalence of methicillin resistance in staphylococci isolated from companion animals

N. Couto, A. Belas, M. M. Centeno, C. Pomba

Faculdade de Medicina Veterinária da Universidade Técnica de Lisboa, Lisbon, Portugal

Background: In recent years, methicillin resistance has emerged in staphylococci isolates from animals, turning it to a serious public health issue. These days not only coagulase-positive staphylococci, but also coagulase-negative, are recognized as significant clinical pathogens, in which the mecA gene has been detected.

Objectives: To detect methicillin-resistant staphylococci (MRS) isolates from infections in companion animals in Portugal.

Methods and Materials: Six hundred and nine staphylococci were isolated from sick horses, dogs, cats and rabbits, between January1999 and November 2012, at the Veterinary Teaching Hospital of the Faculty of Veterinary Medicine and at veterinary private practices in the Lisbon area. Isolates were identified at the species level using BBL Crystal[™] Gram Positive Identification System and nuc-specific PCR. Susceptibility testing was performed using both the disk diffusion and broth microdilution methods, according to CLSI guidelines, and methicillin-resistance was confirmed by PCR amplification of the mecA gene. MRS isolates were subjected to SCCmec-typing.

Results: Forty-six staphylococci exhibited resistance to oxacilin and had the mecA gene (6 Staphylococcus aureus, 19 Staphylococcus pseudintermedius, 11 Staphylococcus epidermidis, 3 Staphylococcus haemolyticus, 1 Staphylococcus sciuri and 6 were Staphylococcus spp.). The first MRS detected was in 2001 and was a S. aureus strain. Since then the prevalence of MRS infections has increased and in 2012 MRS isolates accounted for 51% of the staphylococci strains. All MRS isolates were resistant to at least one more antimicrobial class other than β-lactam (fluoroquinolones or aminoglycosides). None of the isolates was resistant to vancomycin, guinupristin/dalfopristin or linezolid, drugs of choice for the treatment of MRS human infections. SCCmec-typing revealed type III (S. pseudintermedius, S. epidermidis and S. sciuri), type IV (S. aureus and S. epidermidis), type V (S. pseudintermedius and S. haemolyticus) and type VI (S. epidermidis) cassettes.

Conclusion: The prevalence of MRS infection in our companion animal population is increasing. This may compromise antimicrobial therapy and can become life threatening if not well diagnosed. Moreover, the presence of these MRS in sick animals highlights the importance of horizontal transfer of different SCCmec elements and might favor the transmission of resistance genes from animals to humans.

21.025 Isolation and characterization of anti-Pythium insidiosum compounds from Pseudomonas stutzeri isolated from aquatic environment

Y. Thongsri¹, C. Aromdee², S. Kanokmedhakul¹, C. Yeniai¹, A. Chaiprasert³, P. Hamal⁴, C. Prariyachatigul¹

¹Khon Kaen University, Thailand, Khon Kaen, Thailand, ²Khon Kaen University, Khon Kaen, Thailand, ³Mahidol University, Bangkok, Thailand, Thailand, ⁴Palacky University Olomouc and University Hospital Olomouc, Czech Republic, olomouc, Czech Republic

Background: Pythiosis is a granulomatous disease which mostly found in tropical, subtropical and temperate regions. Most cases of pythiosis have been found in animals and humans caused by a fungus-like Pythium insidiosum. Failure of drug treatment of pythiosis combined with a high rate of morbidity and mortality have drawn attention to search for new antifungal agents.



International Meeting on Emerging Diseases and Surveillance 2013

Objectives: To screened the bacterial flora for strains producing metabolites with inhibitory effect against human pathogenic oomycete, *P. insidiosum.* Separation and characterization of extract from *Pseudomonas stutzeri* with anti-*Pythium* inhibitory activity. Searching for genes with anti-*Pythium* effect within genome of *P. stutzeri*.

Methods and Materials: A total of 88 bacterial strains were isolated from water resources collected in northeastern Thailand. Two screening methods were performed to establish their inhibitory activity against *P. insidiosum*. Such activity was detected in 16 isolates (18.2%). One strain of them, *P. stutzeri* ST1302 was randomly chosen and its metabolite with anti-*Pythium* activity was extracted, separated to fractions using liquid column chromatography and purified by thin layer chromatography. Nuclear magnetic resonance (NMR) and mass spectrometry were used to identify this metabolite. Further, searching for genes involved in anti-*Pythium* activity was performed in this strain using five sets of primers reported in the literature.

Results: Fraction designated as PYK7 was assigned to diketopiperazines as cyclo(D-Pro-L-Val) based on results of Fourier transform infrared spectroscopy, nuclear magnetic resonance and mass spectrometry. One gene region only was successfully amplified, corresponding to pyrrolnitrin.

Conclusion: Presented data about the antimicrobial activity of environmental bacteria suggest the possibility to utilize their metabolites against *P. insidiosum*. This study is the first report about inhibitory activity of *P. stutzeri* against *P. insidiosum*. Our results may also contribute to developing of novel antimicrobial drugs or probiotics.

21.026 Detection of extended-expectrum β-lactamase (ESBL) producing *Enterobacteriaceae* in

organic bovine milk

A. K. Siqueira¹, M. M. G. Ferraz¹, T. Salerno², G. H. B. Lara², F. J. P. Listoni², C. Lambertini¹, A. V. da Silva³, A. C. Paes², M. G. Ribeiro², D. D. S. Leite⁴

¹UNICAMP, Campinas, SP, Brazil, ²FMVZ/Unesp, São Paulo, SP, Brazil, ³UEFS, Feira de Santana, 44036900, Brazil, ⁴Universidade Estadual de Campinas, Campinas, SP, Brazil

Background: Resistance to β -lactams has emerged worldwide as a great problem in both human and veterinary medicine. Antimicrobial resistance in pathogenic bacteria of animal origin is a significant threat to the public health. In organic dairy farms the prophylactic use of antimicrobials is not permitted. Therapeutic interventions must be based on alternative methods.

Objectives: The aim of this study was to identify the presence of ESBL-producing *Enterobacteriaceae* from a total of 259 organic milk samples collected from two organic farms in Sao Paulo state, Brazil.

Methods and Materials: The microorganisms were identified according to morphological, biochemical and culture characteristics. All isolates were submitted to the disc diffusion method and double disc approximation test. ESBL-producing *Enterobacteriaceae* were further analysed by PCR.

Results: A total of 13 *Klebsiella* spp. and seven *Escherichia coli* were isolated. Respectively 92.3% and 100% of *Klebsiella* spp. and *E. coli* were resistant to β -lactams and 46.1% of *Klebsiella* spp. to β -lactam inhibitor. PCR analysis revealed that 53.8% of *Klebsiella* spp. and 87.7% of *E. coli* strains harbored ESBL resistance genes. TEM-1 and TEM-2 were detected, respectively, in 46.1% and 38.5% of *Klebsiella* spp., and in 87.7% and 57.1% of *E. coli*. Four (30.8%) isolates of *Klebsiella* spp. and three (42.8%) of *E. coli* harbored TEM-1 and TEM-2 concomitantly.

Conclusion: Based on the results of this study, TEM-1 was the most commom β -lactamase among the isolates and clearly described the phenotypic and genotypic characterization of β -lactam resistance in *Enterobacteriaceae* isolates from organic milk. Evidence suggests that *Enterobacteriaceae* may act as a reservoir for the dissemination of antimicrobial resistance genes among organic farms in Brazil.

21.027 Antibiotic resistant urinary tract infections and *Zataria* multifolora Boiss: Can it help us?

Z. Sepehri¹, F. Javadian¹, E. Javadian², O. Aloosh³, M. Mohammadi¹, N. Keikhaee⁴, F. Rakhshani⁵

¹Zabol university of medical sciences, Zabol, Iran, Islamic Republic of, ²Zahedan university of medical sciences, Zahedan, Iran, Islamic Republic of, ³Hamedan university of medical sciences, Hamedan, Iran, Islamic Republic of, ⁴Mashhad university of medical sciences, Mashhad, Iran, Islamic Republic of, ⁵Ministry of health, Tehran, Iran, Islamic Republic of

Background: Hospital acquired infections usually are due to antibioticresistant strains that are mostly prevalent in many countries. There is growing so much effort to find new compounds and solutions to be used as a replacement for antibiotics in the world.

Objectives: The objective of present study was to evaluate the antibacterial effect of hydroalcholic extract leaves *Zataria* multifolora Boiss on bacterial pathogens of urinary tract infections.

Methods and Materials: A descriptive study on patients admitted in hospital with urinary tract infection was done in Bu-Ali and Ali-ebn-Abi Taleb hospitals in Zahedan, south east of Iran. Samples were collected from the patients who had positive urine cultures. Mining Zataria hydroalcoholic extract was performed using a rotary machine. One hundred and twenty samples of bacteria, including Staphylococcus aureus (14), Klebsiella (27), Citrobacter (2), Escherichia coli (18), Staphylococcus coagulase negative (40), Enterobacter (17) and Pseudomonas aeruginosa (2) were isolated from urinary tracts and the MIC (minimum inhibitory concentration) and MBC (minimum bactericidal concentration) of the plant (Zataria Multifolora) were studied by the micro titer plate method.

Results: The extract concentration of 10 mg per ml has the most inhibitory effect on bacterial growth and the concentration of 20 mg per ml was the most lethal effect. Significant relationship was found between concentration and bactericidal effect (P<0/05).

Conclusion: The results showed that low concentrations of the extract are less effective than high concentrations. It can be used in high concentrations as an alternative in antibiotic resistant bacterial pathogens of urinary tract.

21.028 Resistance phenotypes of *Staphylococcus aureus* strains isolated from intensive care unit in Romania

S. L. Pandrea¹, L. Matros², M. I. Ciontea³

¹University of Medicine and Pharmacy, Cluj- Napoca, Romania,

²University of Medicine and Pharmacy, Cluj, Romania, ³Regional Institute of Gastroenterology and Hepatology, Cluj- Napoca, Romania

Background: *Staphylococcus aureus* remains an important pathogen involved in nosocomial infections and creates difficulties in both treatment and prevention of this infections.

Objectives: The objective of this study was to reveal the distribution of antibiotics resistance/susceptibility phenotypes of *S. aureus* strains isolated from intensive care unit (ICU) in the Laboratory Department of the Regional Institute of Gastroenterology and Hepatology Cluj-Napoca, Romania.

Methods and Materials: Betweeen January–December 2011 was performed the identification and antibiotic susceptibility testing of *S. aureus* strains isolated from different pathological products: blood (12.09%), catheter tips (12.09%), tracheal secretions (29.03%), sputum (8.06%), urine (9.67%), peritoneal fluids (7,25%), pleural fluids (6.45%), conjunctival discharge (4.83%) and other secretions. Isolation of specimen was completed on appropriated and non-selective media. Identification was made by conventional methods and automated methods (Vitek 2 Compact). Sensitivity testing was performed by disk diffusion method and with the automatic Vitek 2 Compact analyser with the corresponding AST cards, according with CLSI criteria for a total of 124 *S. aureus* strains.

Results: Following beta-lactam antibiotics susceptibility testing of *S. aureus* isolated strains, it was noticed that 42.53% of strains were

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

MRSA. Testing to macrolides and lincosamides showed that, of the *S. aureus* tested strains 46.77% were resistant to erythromycin, 42.97% to clindamycin and that MLSBi resistance phenotype was predominated.

The study of the resistance to aminoglycosides showed 20.16% strains were resistant to to gentamicin and 48.38% to kanamycin. 51.61% of the strains had wild type phenotype and 48.38% were resistant resistant, showing phenotypes K/APH(3')-III, KT/ANT(4'') and KTG/APH(2'')+ AAC(6'). Resistance to tetracycline was high: 54.83%. Resistance to ciprofloxacin was 25.80% and to rifampicin was 19.35%. Low level of resistance were observed by testing the strains to fusidic acid (6.45%), chloramphenicol (4.83%) and trimethoprim-sulfamethoxazole (4.03%).

All *S. aureus* strains tested to second line antistaphylococcal antibiotics, linezolid, quinupristin/dalfopristin and glycopeptides were found sensitive.

There was no S. aureus strain resistant to tigecycline.

Conclusion: The most frecquent resistance phenotype was methicillin susceptibile penicillin resistant one.

42.53% of testing strains were MRSA, higher that reported by Romania in 2009 to the European network of resistance surveillance-EARS-Net (35.6%).

Trimethoprim/sulfamethoxazole might be a therapeutic option for multi-drug resistant S. *aureus*.

21.029 Evaluation of in-vitro anti-mycobacterial activity of some Indian medicinal plants: Isolation of active constituents from *Urtica dioica* L. and *Cassia sophera* (Linn.) Roxb.

S. H. Kelam

Bundelkhand University Jhansi, Jhansi, Uttar Pradesh, India

Background: Tuberculosis (T.B.) is a highly infectious disease with about one third of the world is population including 40 per cent fromIndia estimated to be infected. However, this problemhas become serious as Mycobacterium tuberculosis developed resistance against both the first line as also the second line drugs. Due to this, there is emergence of multi-drug resistant (MDR) and extensively-drug resistant (XDR) strains of M. tuberculosis all over the world including India. We evaluated the antimycobacterial activity of seven (7) medicinal plants including Senna sophera Linn. (Roxb.), Urtica dioica L., Momordica dioica (Roxb.), Tribulus terrestris L., Adhatoda vasica Nees., Coccinia indica L. and Glycyrrhiza glabra L.

Objectives: To determine the antimycobacterial activity Indian medicinal plants.

Methods and Materials: Plant materials were subjected to extraction process using soxhlet with different solvents. Extracts obtained were tested for antimycobacterial activity first aganist non-pathogenic strain Mycobacterium semegmatis by Disk diffusion test and Broth dilution test using Middle brook 7H11 agar and Middle brook 7H9 broth respectively.

Results: During antimycobacterial susceptibility testing several plant extracts showed a significant activity against Mycobacterium semegmatis. Among these hexane extract of Urtica dioica (HEUD) and methanol extract of Cassia sophera (MECS), Gl\c\rrhi]a glabra (MEGG) and Tribulus terrestris (METT) and ethyl acetate extract of Adhatoda vasica (EEAV) showed a significant activity against Mycobacterium semegmatis; while as hexane extract of Glycyrrhiza glabra (HEGG), hexane (HECI) and ethyl acetate (EACI) of Coccinia indica, Methanol extract of Momordica dioica showed moderate activity against Mycobacterium semegmatis. The ethyl acetate extract of Cassia sophera (EECS), hexane (HEMD) and Chloroform extract of Momordica dioica (CEMD), Chloroformextract of Glycyrrhi]a glabra (CEGG) and Adhatoda vasica (CEAV), ethyl acetate extract (EAUD) and methanol extract of Urtica dioica (MEUD) showed least moderate activity against Mycobacterium semegmatis. The drug sensitivity report reveledthat upto 90% inhibition by MECS, 85% by HEUD, 69% by MECI against these strains.

Conclusion: Our findings showed that several plant extracts exhibited the activity against mycobacterial strainsbut significant activity was found in MECS, HUED, MECI, EEAV.

21.030 Antibiotic resistance of uropathogens from community-acquired urinary tract infections in Besat University Hospital in Tehran, Iran in 2011

A. A. Saeedi, M. Aminianfar, E. Soleimani, M. Darvishi, S. Faraji AJA University, Tehran, Iran, Islamic Republic of

Background: The empirical therapy of urinary tract infections (UTI) relies on the predictability of the agents causing UTI and knowledge of their antimicrobial susceptibility patterns. The aim of this study was to determine the causative agents of community acquired urinary tract infections (UTIs) and their susceptibility patterns to commonly used antibiotics in patients from university hospital in Tehran, Iran.

Objectives: To collect routine susceptibility data for uropathogens from patients with community acquired urinary tract infections (UTIs) in Tehran, Iran and to relate them to bacterial identification and patient demographics with a view to guiding empirical therapy.

Methods and Materials: During 2010-2011, Over a 24-month period urine samples were collected from outpatients suspected of having a community acquired UTI. Isolated bacteria were identified by standard tests and antimicrobial susceptibility testing for 11 antimicrobials was performed by the disc diffusion method.

Results: According to our results, E.coli, klebsiella spp. and Staphylococcus saprophyticus were predominant uropathogen (cumulative 91.4%) in outpatients that suspect to have community acquired UTI. The resistance rate of most prevailing microorganism, E. coli for Nalidixic acid (60.5%), Nitrofurantoin (12.1%), TMP-SMX (42.07%), Ciprofloxacin (29.87), Amikacin (4.26%), Gentamicin (21.95%), Ceftizoxime (7.3%), Ceftazidime (10.97%), Cefepime (7.9%), Meropenem (7.3%), Imipenem (10.36%) were respectively.

Conclusion: The epidemiology of community-acquired antimicrobial resistance (caAMR) is poorly understood. The pattern of sensitivity of bacteria to antibiotics varies over time and in different geographical regions. The results show that the antimicrobial resistance patterns of the causes of community acquired urinary tract infections (UTIs) are highly variable and continuous surveillance of trends in resistance patterns of uropathogens is important.

21.031

Antimicrobial resistance surveillance of *Acinetobacter baumannii* isolated from Besat University Hospital in Tehran, Iran from 2009 to 2011

A. A. Saeedi, S. Faraji, F. Rahimi, M. Aminianfar, M. Khosravi, E. Soleimani, M. Darvishi

AJA University, Tehran, Iran, Islamic Republic of

Background: *A. baumannii* is an increasingly multidrug-resistant (MDR) cause of hospital-acquired infections, often associated with limited therapeutic options. In recent years, the increasing cumulative infection outbreaks involving *A. baumannii* have appeared worldwide.

Objectives: In addition, a perplexing trouble for clinical treatment is a severe drug-resistance problem with *A. baumannii*. In this study, we investigated the drug-resistance rates of *A. baumannii* in a university hospital in Tehran, Iran from 2009 to 2011.

Methods and Materials: 137 consecutive nonduplicate nosocomial isolates of *A. baumannii* were collected during the period from 2009 to 2011 in the Besat university Hospital in Tehran, Iran. Isolates were identified at the species level using standard biochemical tests and microbiological methods. The susceptibilities of *A. baumannii* to 10 antimicrobial agents were determined by the disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. The data were analyzed by WHONET 5 software according to CLSI.

Results: The resistance rates of Acinetobacter baumannii isolates in 2009 for meropenem(57.6%), imipenem (86.1%),cefepime (81.8%),ceftazidime (90.9%),ceftizoxime (63.6%), ciprofloxacin (84.8%),tetracycline(57.5%), TMP-SMX(81.8%), amikacin(51.5%), Gentamicin(90.9%) were respectively. The resistance rates of Acinetobacter baumannii isolates in 2011 for meropenem(28.07%),

IMED 2013

Poster Presentations I

International Meeting on Emerging Diseases and Surveillance 2013

imipenem (89.4%), cefepime (92.98%), ceftazidime (91.22%), ceftizoxime (66.66%), ciprofloxacin (92.98%), tetracycline (45.61%), TMP-SMX (68.42%), amikacin (70.17%), Gentamicin (66.66%) were respectively.

Conclusion: Today, while clinicians confront the worst situation trying to combat even pan-resistant isolates such as *Acinetobacter baumannii*, the industry curtails the development of new antibiotics. Due to the high antimicrobial resistance in the ICU, we must focus on both a wiser use of antimicrobials and the prevention of infection. Proper application of infection control measures and particularly of "hand hygiene" as well as better antibiotic stewardship in order to slow the development of resistance and to decrease high resistance rates.

21.032 Occurrence of plasmid-mediated enrofloxacin and tetracycline resistance determinants, among *Escherichia coli* isolated from lambs in Greece

G. Filioussis¹, E. Petridou¹, A. Tzivara², S. Kritas¹ ¹Aristotle University of Thessaloniki, Thessaloniki, Greece, ²Clinic of Medicine, Karditsa Thessaly, Greece

Background: In lambs less than 10 days of age *Escherichia coli is the agent of* an opportunistic disease associated with sloppy environmental conditions and poor sanitation. The disease usually presents itself as an outbreak called "scours or watery mouth," because affected lambs salivate and have a cold mouth. Adequate ingestion of colostrum by newborns and use of antibiotics for therapy and prevention decreases the incidence of the disease. Fluoroquinolones and tetracyclines are potential antimicrobial agents that are commonly used in cases of lambs' scours. The use of these compounds however, can result in the selection of resistant isolates.

Objectives: The aim of the study was to investigate the occurrence of the plasmid-encoded enrofloxacin and tetracycline resistance determinants (qnr and tet) among diarrhoeagenic *E. coli* isolates recovered from newborn lambs, in Greece, during the period January 2012 to April 2012.

Methods and Materials: One hundred *E. coli* isolates from equal number of lambs with symptoms of scours, born at open farms of Northern Greece were analyzed. Resistance of the isolates to the following antibiotics was screened using disk-diffusion (AB Biodisk): Enrofloxacin (5µg), tetracycline (30µg), amoxicillin (25 µg), gentamycin (10 µg), trimethoprim/sulphamethoxazole (1,29/23,75 µg), and cefixime (5 µg), according to methodology specified by CLSI. Acquired quinolone and tetracycline resistance was screened by PCR for *qnr*(A), *qnr*(B), *qnr*(S) tet(A), tet(B) and tet(M) genes.

Results: Sequencing of the amplicons showed that 10 of the isolates carried 3 resistance determinants *qnr(S)*, *qnr(B)*, *and tet(B)*. Additionally 5 other isolates were found to carry 2 resistance determinants, *qnr(S)* and *tet(B)*. Finally in the last 7 isolates tet(B) was the only resistance gene that was identified. Plasmid DNA samples from two *E.coli* isolates that carried the combination of *qnr*(S), *qnr*(B), and *tet*(B)genes, was extracted and further digested with the endonuclease *Eco*RI. The resulting fragments were loaded onto a 0.8% agarose gel and then subjected to Southern hybridization with the digoxigenin-labeled *qnr* and *tet* probes. As a result, only *qnr*(S)gene was identified on the plasmid.

Conclusion: This study demonstrates the presence of acquired enrofloxacin and tetracycline resistance among *E. coli* isolates in newborn lambs in Greece.

21.033 A Guide to the Diagnosis and Management of CDC Category A Bioterrorism Agents ("Be Past")

J. Varco, D. Lucey

Georgetown University Medical Center, Washington, DC, USA

Background: The US CDC "Category A" biothreat agents are characterized by high risk of mortality, the ability to cause social disruption, and the need for rapid public health and medical intervention.

While each outbreak is unique and requires a tailored response, it is of value to have a pre-event detailed and concise framework by which to better prepare for diseases due to Category A agents.

Objectives: To create a poster containing detailed and up-to-date information of Category A agents.

Methods and Materials: To address this issue of improved biodefense information against Category A biothreats, we reviewed and analyzed medical and public health literature and websites.

Results: We present a poster containing detailed information for the Category A agents, updated October 18, 2012, for Botulism, Ebola (and other Viral Hemorrhagic Fevers), Plague, Anthrax, Smallpox, and Tularemia (acronym "Be Past"). Information for each of these Category A agents is organized into the following six categories: Microbiology, Precautions (how to prevent infection), Clinical Features, Diagnosis, Prophylaxis/Vaccine, and Therapy (including some investigational therapies). Photographs are included throughout the poster as well as references. Links (URL) are provided to facilitate access to websites with updated information.

Conclusion: A color poster is presented in an easy-to-read format that serves as a concise and detailed tool upon which medical and public health personnel, first responders, and others can refer to prepare and respond better against the threat of Category A biothreats.

21.034

Antimicrobial susceptibility and molecular characteristics of *Bacillus anthracis* strains isolated in Slovenia

M. Ocepek¹, I. Zdovc¹, S. Duvnjak², U. Zajc¹, T. Pirš¹, M. Pate¹, M. Golob¹, S. Spicic², I. Racic², Z. Cvetnic²

¹Veterinary Faculty, UL, Ljubljana, Slovenia, ²Croatian Veterinary Institute, Zagreb, Croatia

Background: *Bacillus anthracis* is the causative agent of anthrax, an acute and often fatal zoonotic infection. It is also known as a bioterroristic agent. For clarifying the epidemiology of possible anthrax outbreaks, molecular typing of *B. anthracis* isolates is indispensable.

Objectives: The aim of our work was to determine the antimicrobial susceptibility and molecular characteristics of *B. anthracis* strains isolated from animals in Slovenia between 1960 and 2008.

Methods and Materials: A total of 23 *B. anthracis* animal isolates and 3 control strains were investigated. Antibiotic sensitivity (i.e. MIC) tests were performed using the commercially available microdilution plates for Gram positive bacteria (Sensititre Trek Diagnostic System) following the manufacturer's instructions for the 20 antimicrobials provided on the standard panel. Confirmation of virulence was carried out by PCR using the LightCycler® *B. anthracis* detection kit (Roche) according to the manufacturer's instructions. A six-loci-based (*vrrA*, *vrrB1*, *vrrB2*, *vrrC1*, *vrrC2* and CG3) multiple-locus variable number tandem repeat analysis (MLVA) was performed and the resulting fragment sizes interpreted according to Keim et al. (2000).

Results: The obtained MIC values for each antimicrobial were identical or similar for all the tested *B. anthracis* isolates, although they were obtained in different time periods and locations from Slovenia. The majority of MICs was low, except for the trimethoprim/ sulfamethoxazol where higher values were observed. However, the results could not be clearly interpreted, since there are no criteria for *B. anthracis* susceptibility given in the available standards. All the 23 animal isolates were positive. According to MLVA, *B. anthracis* isolates could be assigned to the following genogroups defined by Keim et al. (2000): seven isolates to cluster A1.a (comprising one genotype), four isolates to cluster B1 (comprising one genotype), and ten isolates to cluster B2 (comprising two different genotypes).

Conclusion: An overview of antimicrobial susceptibility and genetic diversity of *B. anthracis* animal isolates from Slovenia was obtained in the present study, which should prove beneficial for a rapid resolution of potential future cases/outbreaks of anthrax.

POSTER PRESENTATIONS I

International Meeting on Emerging Diseases and Surveillance 2013

21.035 Occurrence of the Asian tiger mosquito *Aedes* (*Stegomyia*) *albopictus* (*albopicta*) in Austria

B. Seidel¹, A. Rose², A. Indra³, P. Hufnagl³, **F. Allerberger³** ¹Technical Office, Persenbeug, Austria, ²Biogents AG, Regensburg, Germany, ³Austrian Agency for Health and Food Safety, Vienna, Austria

Background: Aedes albopictus, the Asian tiger mosquito, is a main vector of tropical human diseases.

Objectives: A model for predicting climatic suitability for pathogen transmission, commissioned by ECDC in 2009, assessed which areas in Europe could be most amenable for dengue transmission [1]. Much of Austria was diagnosed as potentially climatically suitable as a habitat for *Ae. albopictus*. According to the ECDC technical report the valley of the river Inn should lack climatic suitability. We evaluated these projections.

Methods and Materials: A mosquito surveillance network was established in Austria in 2011 (http://www.ages.at/ages/gesundheit/vektoruebertragene-krankheiten/gelsen-monitoring_1/).

Results: The Austrian mosquito surveillance network detected this invasive mosquito species *Ae. albopictus* initially in the most southern district of the Austrian province Burgenland (diagnosed as potentially climatically suitable as a habitat for *Ae. albopictus* by modelling) in May 2012. In September of 2012 however, a second record of the invasive species happened in the village of Angath in the lower river Inn valley in the Austrian province of Tirol, an area lacking—according to the ECDC technical report published in July 2012—environmental suitability for *Ae. albopictus*.



Conclusion: Whilst the first occurrence of the invasive species near the Hungarian and Slovenian border remained insular without showing a tendency of disperse in meantime, the second finding can be seen as the beginning of an expanding invasion, having its origin in established populations of northern Italy. Heavy transit traffic through the Tirol may have introduced this alien species, which seems to be already established, as German observations confirm occurrence of *Ae. albopictus* near the Austrian border at Kiefersfelden. Vector surveillance, including monitoring the spread of *Ae. albopictus*, provides a rational basis for developing public health measures that address the spread of dengue and its vectors. Suitability maps can be a useful tool for public health planning, but there are many potential sources of error that need to be properly understood. Projections on biotic trends should not be misunderstood as predictions.

[1] European Centre for Disease Prevention and Control. The climatic suitability for dengue transmission in continental Europe. Stockholm: ECDC; 2012 ISBN 978-92-9193-382-2.

21.036 The influence of the environment on anthrax in Ukraine

I. S. Kovalenko¹, O. B. Khaytovych²

¹Public Institution "Ukrainian Anti-Plague Station" Ministry of Health of Ukraine, Simferopol, AR Crimea, Ukraine, ²Public Institution "Ukrainian Anti-Plague Station" Ministry of Health of Ukraine, Crimean State Medical University named after S.I. Georgievsky, Simferopol, AR Crimea, Ukraine

Background: The influence of environmental factors has predominant importance for the circulation of natural focal infections in the environment.

Objectives: Determine characteristics of environment in the spatial distribution of anthrax permanently-unfavourable points in the territory of Ukraine.

Methods and Materials: The electronic database of anthrax permanently-unfavourable points in the territory of Ukraine was created and used. Creating digital maps was performed by using ArcGis 9.2 (License E 300 3/02, ESRI USA). Determining the level of anthrax risk was carried out by calculating the epizootic index.

Results: Ecological region (ecoregion) was selected for identify the characteristics of environmental influences on the distribution and maintenance of anthrax, because it is an integrated indicator that displays a set of biotic and abiotic factors (climatic, topographic, geobotanic, hydrologic and etc.).

There are identified six types of ecoregions in Ukraine (every type of ecoregions is characterized by certain features):

- Central European mixed forests;
- European forest steppe;
- Pontic Steppe;
- Sarmatic mixed forests;
- Carpathian ecoregion;
- Caucasian-Crimean broadleaf forests.

Anthrax permanently-unfavourable points found in all ecoregion of Ukraine.

Index, which showing the ratio of the number of fixed points during the troubled period when the disease detected to the total number of settlements in the analyzed region during monitoring period, was calculation for each type of ecoregions. We used ArcGIS (*Jenks' natural breaks method*) with a sufficient confidence level, for division of the territory of Ukraine on three groups according to the degree of anthrax infection risk: 1) ecological regions with high risk of anthrax infection: Pontic Steppe epizootic index-0.42, and the European forest-steppe-0.41; 2) ecological regions with an average risk of anthrax infection: Sarmatic mixed forests-an index of 0.3 and Central European mixed forests-0.28; and 3) ecological regions with low risk of anthrax infection: Carpathian ecoregion with epizootic index-0.04 and Caucasian-Crimean broadleaf forests-0.06

Conclusion: Zoning of the territory of Ukraine on the risks of anthrax gave an opportunity to identify the most important epizootic areas in which the complex of the environmental components is most favourable for the circulation of the anthrax in nature.

21.037

(1.037) Biome specific hanta epidemiologies in Europe H. Henttonen

Finnish Forest Research Institute, Vantaa, Finland

Background: Among emerging diseases, rodent-borne viral infections provide a prime example.

Objectives: In the large collaborative EU projects EDEN and EDENext (collaborators given in the presentation) our aim was to understand the human epidemiology of nephropathia epidemica, the most common hantaviral disease in Europe, caused by Puumala hantavirus (PUUV), between boreal and temperate Europe in different climatic conditions.

Methods and Materials: Intensive longitudinal vole monitorings were conducted to document PUUV transmission in different biomes and landscape systems.

International Meeting on Emerging Diseases and Surveillance 2013

Results: We documented differences in the transmission dynamics of PUUV between these two biomes. The patterns in temperate zone are affected by masting events, of which the frequency may increase due to warmer summers, while in the snowy boreal zone predator driven vole cycles shape the dynamics, and where warming winters can affect vole cycles. Consequently, the underlying top-down or bottom-up causes of rodent fluctuations and hanta outbreaks are different. We have further documented the role of landscape patterns (homogenous taiga vs. fragmented temperate forests) in rodent/virus dispersal, and in the presence or absence of host threshold densities for the PUUV occurrence. In addition, temperature and moisture affect the virus survival outside the host, affecting indirect transmission. Also, geographic differences in the immunogenetics of host rodents can affect their susceptibility. These results are essential for human risk evaluation with regard to both long-term and seasonal occurrence of PUUV in the environment.

Conclusion: In conclusion, it is important to realize that within the same host/virus system, *biome specific PUUV epidemiologies* occur, which highlights the importance of geographically comparative studies in Europe, or in any host/pathogen system.

21.038 West Nile Virus—Is Asia at risk?

G. Yap

National Environment Agency, Singapore, Singapore

Background: The unannounced entry and subsequent outbreak of West Nile virus (WNV) in USA 1999 caught health authorities by surprise, and the economic burden of the disease was enormous. Can this happen to Asia? Very little is known about WNV in Asia, with the exception of recent WNV reports from India. An isolate of Kunjin virus (KUN) from Sarawak, Malaysia in *Culex pseudovishnui*was reported previously in 1966. Apart from these studies, there is no other documented work to elucidate the presence of WNV in Asia. Singapore lies on the East Asian-Australasian flyway, and is a major pit stop for migratory birds.

Objectives: Since 2010, we initiated a series of surveillance studies. Using spatial and temporal data from migratory birds, other animal hosts (including humans), mosquito vectors, and combining with ecological factors, we aim to set up risk models for the quantification of WNV risk in Singapore.

Methods and Materials: Blood samples collected from migratory birds, together with mosquito samples collected from sites where migratory birds visit, were screened for WNV.

Results: WNV antibodies were present in some migratory birds, indicative of exposure at one/more pit stops along the flyway. No WNV was detected from the birds or mosquitoes during the migratory season.

Conclusion: The risk of WNV entry into Singapore is fairly low. However, data collected from just one country is not sufficient to assess the risk of WNV in Asia. A regional surveillance programme can be set up for such purposes.

21.039 Climate impact on the occurrence, distribution and activity of potential dipterans vectors in Eastern Slovakia

A. Kočišová, E. Bocková, A. Sarvašová, M. Halán

University of Veterinary Medicine and Pharmacy in Košice, Kosice, Slovakia

Background: In modern world, no country is safe from vector-borne diseases. Human and animal mobility has escalated dramatically in volume and speed between and within countries. Long-distance trade facilitates the geographical redistribution of pathogens and climate variations have been related to the new distribution and activity of vectors. Animal breeding and the forest nature of Eastern Slovakia provides a wide range and sufficient number of potential hosts.

Objectives: Our work deals with research of species diversity, distribution and capacity/competency of mosquitoes and biting midges from the climate point of view.

Methods and Materials: We focused our research on surveillance of mosquito species diversity in six inundation localities of East Slovakia. Mosquitoes were collected at weekly intervals between April and September during two years (2010-2012). Mosquitoes were identified using stereomicroscope (Nikon SMZ 1500) and keys according to Kramář (1958) and Becker et al. (2010). Collection of biting midges was performed according to a protocol adapted after Goffredo and Meiswinkel (1994) using the black light suction trap, model JW 1212. All Culicoides were identified to species using the morphological key according to Delécolle (1985).

Results: Prevalence, distribution and activity of biting midges and mosquitoes correspond to the meteorological situation in the spotted localities. In the season with floods the mosquitoes developed from spring to autumn and the most frequently determined were *Culex pipiens, Aedes vexans, Culiseta annulata* and *Ochlerotatus sticticus*. In dry and warm season mosquitoes usually developed only during the spring months, but on the other hand we first time confirmed the occurrence *Anopheles hyrcanus* in East Slovakia in 2012. The ascertained prevalence of biting midges is closely related with the extreme environmental situation during 2011-2012. Out of them, 65% belong to *Obsoletus* Complex, 15% to *Pulicaris* Complex and 20 % to other *Culicoides* species with usually two peaks of midge's activity in May and July.

Conclusion: Results of entomologic observation confirmed the presence of mosquitoes and biting midges as potential vectors of filariae and viruses in Eastern Slovakia farms.

The work was supported by the Slovak Grant Agency VEGA No. 1/0236/12 and under the basic research project NRL UVLF for pesticides.

21.040 Vector populations in different climatic conditions in Romania and the emergence of human cases of infection with West Nile virus (WNV)

L. Baltesiu¹, M. T. Gomoiu², R. Mudura³, G. M. Nicolescu⁴, V. Purcarea-Ciulacu⁵

 ¹Romanian Space Agency, Bucharest, Romania, ²R & D National Institute for Marine Geology and Geoecology, Constanta, Romania,
 ³Romanian Centre for Apply in Agriculture, Bucharest, Romania,
 ⁴National Institute of Research and Development for Microbiology and Immunology "Cantacuzino", Bucharest, Romania, ⁵National Institute of Research and Development for Microbiology and Immunology "Cantacuzino", Bucharest, Romania

Background: Since culicides are key elements in the transmission cycle of WNV in humans, the question is to analyze the occurrence of cases of WNV infection in Romania, under the influence of climate change.

Objectives: Our investigations took place during the years 2009–2011, when we identified 19 species of culicide in the Romanian Plain (11 species may be involved in the transmission of WNV) and 23 species in Dobrudja (floodplain and lagoon area), including 9 species involved in transmission of the virus.

In culicides fauna of Europe there are 17 species that may be involved in the WNV circulation. In Romania were reported 57 species of culicides and 16 of them there are in Europe and may also be involved in the transmission of this virus.

Dominant species in both study areas were *Culex pipiens* (the main vector for WNV in Romania) and *Anopheles maculipennis s.l. Culex modestus* and *Coquillettidia richiardi* there are in wetlands and reeds area and *Aedes vexans* in natural and anthropogenic ecosystems.

Methods and Materials: Analyzing meteorological data (temperature and humidity) from previous periods neurological infection with WNV epidemics known in Romania (Targu Mures–1955, SV Banat–1964 and the Romanian Plain, Dobrudja and Moldavia S–1996) were reported temperatures and precipitation higher than average values of reference (the last 60), thus increasing the populations of vectors, and hence the emergence of several cases of human infection

Results: The higher temperatures and the lower humidity, in the past 50 years had strong effects on culicide fauna by blocking and removing larvae and by decreasing the lifetime of adult mosquitoes, thus lowering culicide populations.

International Meeting on Emerging Diseases and Surveillance 2013

There have been risk maps according for temperature, humidity, elevationand land cover /land use for vectors and tangential host (human cases).

Conclusion: In these changing climatic conditions, although culicides populations declined, our team found annual occurrence sporadic human infections or epidemic, thus confirming the endemic presence of WNV in Romania.

These appearances of human infections with WNV is due to maintaining enzootic virus circulation in vectors, in the main hosts and in the tangential hosts (human) on very large territories.

21.041 Climatic anomalies and reemergence of West Nile virus in the United States

M. Wimberly¹, T.-W. Chuang², A. Lamsal¹

¹South Dakota State University, Brookings, SD, USA, ²Taipei Medical University, Taipei, Taiwan, R.O.C.

Background: West Nile virus (WNV) is the most widespread and important mosquito-borne pathogen in North America, and the national resurgence of human WNV cases during the summer of 2012 has highlighted the persistent threat posed by this potentially fatal disease. Environmental variability in temperature and moisture can affect WNV risk to humans through influences on mosquito populations, bird communities, human behavior, and the extrinsic incubation period of the virus. However, the degree to which these climatic factors influenced the reemergence of WNV in 2012 is unknown.

Objectives: The objectives of this study were to assess whether WNV oubreaks in 2012 were associated with temperature and precipitation anomalies prior to the main season of WNV transmission to humans and to determine whether these relationships varied seasonally and geogrpahically.

Methods and Materials: We computed county-level interannual relative rates of human WNV from 2004-2012 using public data from the CDC ArboNET surveillance program. We calculated monthly temperature and precipitation anomalies using interpolated data from the PRISM climate group. Nonparametric models were used to analyze the influences of climatic variability on WNV outbreaks.

Results: In most areas there were positive associations between temperature anomalies and WNV outbreaks. However, the seasonality of these relationships exhibited regional variation, with summer temperatures having a greater influence in the North and winter and spring temperatures being more important in the South. The effects of precipitation were generally weaker and more variable. Winter and spring preciptiation tended to have positive associations with WNV outbreaks, whereas late-spring and early summer precipitation had negative associations. In some areas, such as Colorado, these relationships were weaker and higher temperatures in 2012 did not result in WNV outbreaks.

Conclusion: This study provides initial evidence of an influence of temperature, and to a lesser extent precipitation, on the 2012 WNV outbreaks in several areas of the United States. Regional variability in these relationship likely reflects ecological differences in mosquito vectors, avian communities, and landscape characteristics. These results highlight potential effects of climate change on the WNV in the United States, but also emphasize the possibility of using environmental monitoring systems to project the risk of future outbreaks.

21.042 Implementation of an early warning system to predict Zoonotic Cutaneous Leishmaniasis epidemics in central Tunisia

H. Bellali¹, J. Daaboub², I. Nouiri³, A. Mrabet⁴, M. K. Chahed¹ ¹Medical university of Tunis, Tunis, Tunisia, ²Ministry of Public Health, Tunisia, Tunis, Tunisia, ³Ministry of agriculture, Tunisia, Tunis, Tunisia, ⁴Health Military Direction, Tunis, Tunisia, Tunis, Tunisia

Background: Zoonotic Cutaneous Leishmaniasis (ZCL) is an emerging vector born disease caused by L. major parasite. The onset of ZCL in humans is the result of the interaction between the different elements of a complex ecosystem. Transmission of ZCL is favored by climatic conditions and environmental factors, including climate change.

Objectives: The aim of this study was to Model ZCL transmission, point out variables closely correlated with outbreaks, test and validate an Early Warning System (EWS) to predict epidemics.

Methods and Materials: An active system of epidemiological surveillance of human cases of ZCL among the population of the area was established in July 2009 to collect the number of new cases per month. Data of climatic factors (temperature, rainfall, wind speed...) were collected through the installation of a weather monitoring station in the study area. Rodent's density was estimated from their monthly activities.

We calculated for each month the corresponding averages of these parameters 3, 6 and 9 months ago and 1, 2, 3, 4 and 5 years ago. Simple correlation and multiple linear regression were used to analyze the association between the number of cases of ZCL bioclimatic and environmental factors.

Results: Between July 2009 and June 2012, we collected 361 new cases of ZCL. Positive correlation between the number of cases of ZCL per monthly and the average temperatures of the three and six months ago, the average density of rodents of the three parcels in the previous six months and the average rainfall one year ago.

Higher correlation coefficients were observed with the parameters of the previous six months, especially for the minimum temperature (r=0.849, p<10⁻³). The average density of rodents for each month was correlated with average rainfall of the last year (r=0.443, p=0.013). Multivariate analysis showed that the average of the minimum temperature in the last 6 months would predict the occurrence of epidemics LCZ (R=0.87, p<10-3).

Conclusion: We demonstrated positive correlations between the number of cases of ZCL and bioclimatic factors. We intend to continue collecting data for a longer series and apply most appropriate analytical methods to identify the variables and their thresholds that could predict well in advance epidemics.

21.043 The ENHanCE project: A large scale risk assessment of the most likely human and animal pathogens to be affected by climate change

K. M. McIntyre¹, C. Setzkorn¹, P. J. Hepworth¹, S. Morand², M. Baylis¹ ¹Institute of Infection & Global Health, University of Liverpool, Chester, United Kingdom, ²CIRAD, Montpellier cedex 05, France

Background: Climate change is considered a major threat to human health and well-being, with increasing evidence of it impacting infectious diseases. But how large is this threat? Will many diseases respond to climate change or only a few? Is it possible that the most significant diseases in health or economic terms could be resilient to climate change, such that its overall influence on our health and wellbeing could be of relatively minor importance?

Objectives: Within the ENHanCE project we have developed an easily repeatable, bottom-up approach which allows the examination of many pathogens using multiple steps, enabling us to answer some of these questions.

Methods and Materials: Within the project, we have built a database, the open access ENHanCED Infectious Diseases (EID2) database, with which we first identified the main pathogens of man, domestic and companion animals. Second, a proxy for the impact of each pathogen upon man was then developed to ascertain those of the greatest importance to us. Automated literature searches of pathogen names and climate driver terms were then implemented to establish scientific literature which potentially contained evidence of the climate drivers of disease. It was thereafter necessary to examine the literature, for a short list of the pathogens with the highest 'impact', to verify the actual evidence of the effects of climate upon each pathogen. This was undertaken, finally, using a critical review tool which grades the quality of the data based on a number of factors including: the journals in which papers were published; whether they describe field or laboratory studies, analysis of collated data or review articles; and the significance of any statistical support for climate and pathogen associations.

Results: 66% high impact pathogens in Europe had some evidence of climate drivers

Conclusion: This presentation will demonstrate our methodologies, and present the main findings of our full bottom up assessment.

International Meeting on Emerging Diseases and Surveillance 2013

21.044 **Detection of morphological differences** between Batrachochytrium dendrobatidis **Brazilian strains**

C. Lambertini, D. D. S. Leite, A. K. Sigueira, L. F. Toledo Universidade Estadual de Campinas, Campinas, SP, Brazil

Background: Chytridiomycosis, an emerging infectious disease caused by the chytrid fungus Batrachochytrium dendrobatidis (Bd), is linked to the worldwide amphibian population decline, including extinction of species. The emergence of this pathogen is mainly related to climate change. Bd affects the keratinized cells of amphibian epidermis causing hyperkeratosis, a consequent osmotic imbalance and eventually death of infected individuals. Strains from worldwide were sequenced, including from Atlantic Forest in Brazil. One of the Brazilian strains showed to be genetically different of the others, while another was classified as putative hybrid and the others as global panzootic lineages (Bd-GPL). One study with European strains showed that genetic differences may be associated with morphological variations in zoosporangia, and another study showed that the zoospore size is correlated with DNA content, suggesting a variation in ploidy.

Objectives: Therefore, our objective was to investigate whether the Brazilian strains have morphological differences, both relative to zoospore size as in relation to zoosporangia size.

Methods and Materials: Nine strains were isolated from tadpole mouthparts in mTGH culture media, replicated in liquid media and incubated at 21°C for seven days. After growth, an aliquot of the cultures was viewed in optical microscope. Sixty zoospores and sixty zoosporangia were photographed and measured by the software TSView®. The results were analyzed by One-way ANOVA.

Results: We observed significant differences between zoosporangia size and between zoospore size in most strains.

Conclusion: Based on these results, we can suppose that genetic differences are associated with zoosporangia size. We detected differences among zoospore size, but further studies will be needed to associate this finding with variation in ploidy. It is known that genetic differences may result in differences in virulence. So, if we can establish a relationship between phenotype, genotype and virulence, it will be possible to identify the different strains by simple morphology analysis, and we could locate contaminated areas by more virulent and lethal strains, which could be used in conservation plans worldwide.

21.045 Climate change modelling of West Nile Virus and Avian Malaria in Madagascar

C. L. Risley¹, S. Goodman², M. Baylis¹

¹Institute of Infection & Global Health, University of Liverpool, Chester, United Kingdom, ²Field Museum of Natural History, Chicago, IL, USA

Background: Vector-borne pathogens are particularly sensitive to climate; and islands may be particularly sensitive to climate change. Here we used data from two vector-borne pathogens in a biodiverse tropical island (Madagascar) to and estimates of climate in 2055 predict the impact of climate on vector-borne disease in Madagascar.

Objectives: 1. Compare methods for estimating the relationship between disease prevalence and climate variables

2. Predict the current and future distribution of Avian Malaria in birds and west Nile in humans

Methods and Materials: SaTScan and Logistic Regression methods were used on WNV and AM datasets, with climate data from the CRU (climate research unit) and MODIS (MODerate resolution Imaging Spectroradiometer). Models were tested for predictiveness using Leave One Out regression. Methods were compared and predictions obtained

Results: The predictiveness of the Avian Malaria in wild birds model was adequate, whereas it was not for modelling West Nile in humans. CRU climate data were more appropriate than MODIS for this purpose. A 50-year prediction of Avian Malaria was carried out which indicated that five threatened birds may become newly at risk of Avian Malaria in Madagascar.

Conclusion: Predictiveness of models must be adequately tested before conclusions about future disease are drawn; and climate datasets and methods must be carefully chosen. In future, vector transmitted disease distribution in Madagascar is expected to expose new species to the threat of emerging disease.

21.046 Mass spectrometric approaches for the identification of candidate serum biomarkers for Schistosomiasis mansoni infected mice

M. I. H. I. Kardoush, B. Ward McGill, Montreal, Qc, Canada

Background: Schistosomiasis affects ~200 million people in >70 countries and causes >200,000 deaths/year. Early diagnosis typically depends on the detection of eggs that first appear in stool or urine between only 4-6 weeks post-infection. During the late stages of infection associated with liver fibrosis, eggs are often difficult to detect and diagnosis depends on immunoassays that are insensitive early in infection

Objectives: Proteomic profile analysis of the sera from infected mice: In order to detect new biomarkers of the early stage,

compare protein profiles in the acute and chronic stages of the disease

compare protein profiles among groups of mice infected with different doses of cercariae

Methods and Materials: Sera collected from 26 CD1 mice before infection and at 3, 6 and 12 weeks post infection were analyzed on a range of mass spectrometric (MS) approaches to identify candidate biomarkers

Results: Using SELDI TOF MS to compare uninfected and schistosomiasis-infected samples, 88 candidate biomarkers were obtained. Used in various combinations, these biomarkers could 1) reliably diagnose early-stage disease, 2) distinguish between acute and chronic infection and 3) differentiate between animals with lower vs higher parasite burdens. The most important contributors to these diagnostic algorithms were peaks at 3720, 7081 and 13407Da. Employing sample fractionation and differential gel electrophoresis, we analyzed gel slices either by MALDI-TOF MS or Velos Orbitrap MS. These approaches yielded 10 differentially-expressed host proteins in the serum at various disease stages and ~200 parasite-origin proteins during the acute stage respectively. Among the host proteins identified by MALDI, the presence of hemoglobin in (acute/chronic) disease was the most intriguing. The large number of parasite-origin proteins in acute serum was surprising, particularly the presence of proteins not thought to be associated with the parasite tegument (eg. Thioredoxin peroxidase 3, Fatty acid binding protein).

Conclusion: Our approach of using multiple proteomic platforms in parallel revealed that serum protein profiles differ extensively in infected and uninfected mice, offering a rich source of biomarkers. If similar differences are identified in human disease, this approach of may not only yield new diagnostic strategies but may also give insights into parasite biology and point to novel targets for treatment or prevention.

21.047

Improved collaboration at the animal-human interface-A European initiative to facilitate early detection and joint rapid risk assessments of outbreaks of non-foodborne zoonoses

A. Gervelmever¹, C. Gossner²

¹European Food Safety Authority, Parma, Italy, ²European Centre for Disease Prevention and Control, Stockholm, Sweden

Background: Close collaboration between the animal health and human health sector both at the national and the European level is paramount to the prevention and control of zoonotic diseases in Europe. Past examples of non-foodborne zoonotic or potentially zoonotic diseases challenging the EU are the newly emerged Influenza A/H1N1/pdm09 virus, the Q-Fever outbreak in the Netherlands and the recent Schmallenberg virus emergence.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: EFSA and ECDC take the lead in facilitating a closer collaboration between the animal health and the public health sectors in European Member States (MS) and at the EU level to increase European preparedness for outbreaks of non-foodborne zoonotic (and potentially zoonotic) diseases, to facilitate rapid, timely exchange of information and data using the one health approach to underpin rapid risk assessment and to coordinate cross border investigations of supranational outbreaks.

Methods and Materials: A European One Health network is being jointly established by EFSA and ECDC. Building on already existing networks run by EFSA and ECDC, the core group of the network will bring together representatives from the animal health and the human health sector of each EU MS, who coordinate ensuing activities within their sector and MS. Subject matter experts will be brought in from each MS and specific EU-funded network as and when needed. The network will meet several times per year and will operate an IT information exchange platform.

Results: The network will identify non-foodborne zoonotic diseases that need a supranational approach, research needs and priority questions on non-foodborne zoonotic diseases. The IT platform will provide a confidential space in which network members inform each other about new potential non-foodborne zoonotic threats, agree on data and information needs regarding outbreak investigations, exchange data and information on outbreaks and on ongoing surveillance activities.

Conclusion: It is anticipated that the One Health network will improve the capacity for joint assessments of and responses to non-foodborne zoonotic diseases at the European level, but also stimulate a better collaboration between the sectors within MS. Ultimately, it will increase the preparedness of the European Union for new zoonotic threats that are due to arise in the future.

21.048 Human interactions with wildlife associated with monkeypox in Tshupa District, **Democratic Republic of Congo**

B. Monroe¹, M. Reynolds¹, D. Tack¹, C. Moses², J. Malakani³, D. Carroll¹

¹US Centers for Disease Control and Prevention, Atlanta, GA, USA, ²International Conservation and Education Fund, Washington, DC, USA, ³University of Kinshasa, Kinshasa XI, Congo, Democratic Republic of

Background: Human monkeypox is a zoonotic infection capable of causing severe disease involving high fever and smallpox-like rash. The natural host of the disease has yet to be discovered, but is hypothesized to be a rodent. Contact with wildlife is believed to increase risk for human infection with monkeypox virus. The extent to which people in the affected area interact with wild game has not been properly studied.

Objectives: The objectives of this survey are to determine the extent of animal contact and daily activities that may lead to primary transmission of human monkeypox.

Methods and Materials: A sample of participants at community screenings of monkeypox films produced by the International Conservation and Education Fund (InCEF) were interviewed about potential monkeypox risk-associated behaviors. Outreach occurred in the Tshuapa District of the Democratic Republic of Congo between October 2009 and October 2011. Respondents were asked a panel of questions addressing basic demographic information, contact with domestic and wild animals, and frequent daily activities.

Results: Interviews were completed by 588 individuals from 21 localities. Interactions with animals included 419 (71.8%) persons reporting owning animals and 243 (41.3%) people hunting wildlife in the last 30 days. Ungulates (36.2%) and rodents (35.3%) were the most commonly hunted animal groups, followed by non-mammals, primates, other small mammals, and carnivores (21.9%, 12.7%, 6.9%, and 0.5% respectively). Consumption of rodents was high, with 68.2%, 63.8%, and 61.6% of people reporting eating Gambian rats, squirrels, and porcupines respectively. Attending school was the most frequent daily activity (65.1%), followed by entering the forest (39.7%); visiting a market was the least frequent activity (4.6%).

Conclusion: Human interactions with wildlife in Tshuapa appear to be a common occurrence. People in this area are reliant on entering forests for many daily activities and may lack access or financial resources to attend markets and purchase food. Several species of animals implicated in human monkeypox are commonly hunted and consumed in this area. The results of this survey should help to improve local health messaging and inform future monkeypox ecology research.

21.049 Epizootic situation and development tools for detection of Q-fever in Ukraine

L. Marushchak¹, A. Golovko², O. Deriabin³ ¹SSRILDVSE, Kiev, Ukraine, ²SSCIBMS, Kiev, Ukraine, ³IVM, Kiev, Ukraine

Background: Q-fever is a zoonotic disease caused by the ubiquitous pathogen Coxiella burnetii, and is responsible for acute and chronic clinical manifestations. C. burnetii is a category B bioterrorism agent and highly pathogenic to animals and humans.

Objectives: The aim of study was to analyze the distribution of Q-fever in the Odessa region of Ukraine and to review the methods of C. burnetii laboratory diagnostics employed within the veterinary system of Ukraine.

Methods and Materials: Investigations were conducted in the Odessa region due to the systematic registration of causes of this disease in people. Animals were tested serologically by complement fixation (CFT) and enzyme-linked immunosorbent assay (ELISA). Beginning from 2011 samples ware also tested by real-time PCR for the presence of C. burnetii (Genekam Biotechnology AG, Germany). For the purposes of conventional PCR design target outer membrane protein-coding gene (Com 1) was used. The gene sequences for the highly preserved single copy of outer membrane-associated com1 protein of C.burnetii from GenBank Accession #s: AB004712.

Results: In 2008 in the Odessa Region serum, samples of domestic animals were tested, resulted in 20.0% of seropositive samples detection, in 2009-41.2%, in 2010-37.4%, in 2011-24.5%. Geographic distribution analysis showed that in the Odessa region the existence of natural foci of Q fever was established in five southern districts (Artsizsky, Kiliyskiy, Tatarbunarsky, Bolgradsky and Tarutinsky). All attempts to identify the live agent via PCR have been negative.

Conclusion: Epidemiologic and serological investigations confirmed the transmission of C. burnetii in the Odessa region. Further systematic control efforts and more modern laboratory investigations are needed to conduct environmental and epidemiological research. The study of those infected using molecular and genetic techniques is critical for assessing the distribution of Q fever among animals.

21.050 Hepatitis E in Belgium: An imported disease or a viral zoonosis?

M. Wautier, V. Hutse, S. Van Gucht

Scientific Institute of Public Health, Brussels, Belgium

Background: In developed countries, hepatitis E (HE) occurs relatively infrequently and principally affects people who become infected while travelling in endemic areas for hepatitis E virus (HEV). HEV is mainly transmitted faeco-orally through contamination of drinking water. Nevertheless, HEV transmission by blood transfusion has also been described. Cases of HE in patients with no recent travel history are also reported sporadically in developed countries. For these cases, HEV subgenomic sequencing studies sometimes revealed a close relationship between the strains infecting humans and those infecting pigs. In Japan, HEV transmission was associated with consumption of raw or undercooked wild boar/deer meat.

HEV infection causes an acute self-limited or fulminate hepatitis that does not evolve into chronicity, except in organ transplant recipients. The mortality rate is low (1-3%), but in pregnant women the mortality is as high as 25%. The seroprevalence in blood donors from nonendemic countries ranges from 1 to 3%. A higher prevalence was seen in people working with swine.

Poster Presentations I

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: The major objectives of our study are to map and characterize the demographic, clinical and molecular features of HEV strains circulating in Belgium in humans and animals and to establish a risk profile in Belgium. The animal work is performed by the Veterinary Faculty of the University of Liège (Prof. Dr. Etienne Thiry). All analysis of human samples are performed at the National Centre for Viral Hepatitis of the Belgian Institute of Public Health. Methods and Materials: HEV IgM are detected by an ELISA and

confirmed by Western blot. HEV RNA is detected by real-time PCR. A genotyping assay is performed to determine the probable HEV origin.

Results: Since 2008, 2009, 2010, 2011 and until October 2012, respectively 8/210 (4%), 9/264 (3%), 18/206 (8.7%), 37/475 (7.8%) and 34/499 (6.8%) of suspected cases were HEV positive.

Conclusion: Epidemiological studies have shown that part of these infections was imported, but for some there were no travel history or contact with travellers, suggesting a locally acquired infection. Genotype 3 strains have been isolated from patients in Belgium. The sequence (ORF2 gene) of these isolates showed 88% homology with the strains of genotype 3 swine isolates in the Netherlands.

21.051 Evaluation of risk factors for autochthonous Leptospirosis in Austria

C. Wallner¹, H. Flick¹, F. Allerberger², T. Valentin¹, K. Seeber¹, I. Zollner-Schwetz¹, J. Wagner¹, W. Duettmann¹, R. Krause¹, M. Hoenigl¹

¹Medical University of Graz, Graz, Austria, ²AGES, Vienna, Austria

Background: In contrast to Germany and other European countries the majority of leptospirosis cases are autochthonous infections in Austria. High rates are particlary found in South- East Austria, however the reasons and associated risk factors are unknown.

Objectives: To evaluate risk factors for leptospirosis in South-East Austria.

Methods and Materials: We retrospectively analyzed risk factors for leptospirosis in South- East Austria. Patients admitted to hospitals in South-East Austria that had been tested positive for leptospirosis by serology/point of care test within a 8 year period (2004-2011) were included. Data concerning course of disease as well as recreational or residential risk factors (within 2 weeks before onset of infection) were collected via telephone questionnaires and/ or electronic databases.

Results: 103 adult patients (38 female, 65 male, median age 43.1 years) were included. 87/103 (84.5%) of patients had acquired leptospirosis within Austria and 16 (15.5%) had imported infections. Symptoms reported most frequently included fever (68/ 103; 66%), myalgia/ arthralgia (37%), abdominal pain/ diarrhea (31%), general weakness (26%), jaundice (24.3%) and headache (21.4%). Lab results at admission revealed that 23.3% had thrombocytopenia. Elevated liver transaminases (>2 times normal value) were found in 42.7%, and serum creatinine (≥ 1.5) in 32%. L. sejroe, L. bratislava and L. ballum were the serotypes identified most frequently. Risk factors were evaluated in cases that completed the telephone questionaire (n=70, all autochthonous). Concerning recreationel risk factors, activities in woods/ wet areas were reported by 40.8%, followed by gardening/ hunting (30%), and tidying up basement/ hut/ attic (22.3%). Rodents in surroundings (48.5%), followed by contact to pets (34%) and farm/animals (18.4%) were the most residential risk factors.

Conclusion: The vast majority of cases in South- East Austria are acquired autochthonously. The main risk factors for acquiring leptospirosis were activities in woods and wet areas as well as pets and rodents living in the surroundings.

21.052 VNTR-based molecular epidemiological study of Francisella tularensis ssp. holarctica biovar Il strains isolated from humans. European brown hares and red foxes in Austria from 1995 to 2010

S. Revilla-Fernández¹, K. Reisp¹, E. Hofer², H. Plicka³, F. Schmoll² ¹Austrian Agency for Health and Food Safety, Institute for Veterinary Disease Control Mödling, Moedling, Austria, ²Austrian Agency for Health and Food Safety, Institute for Veterinary Disease Control Mödling, Mödling, Austria, ³Federal Ministry of Defense, Vienna, Austria

Background: Francisella tularensis (Ft) is one of the most highly infectious bacteria known, affecting more animal species than other known zoonotic pathogens. The geographical distribution of tularemia in Austria is well known, however, the diversity and genetic relationships between strains isolated from humans and wild animals remained unknown.

Objectives: To study the population and the genetic relationships of 97 Ft isolates collected in endemic regions of Austria between 1995 - 2010

Methods and Materials: The 97 strains derived from 75 brown hares, 16 red foxes and 6 human cases. The six most discriminative VNTR markers within the Ft genome (M3, M6, M20, M21, M22 and M24) were amplified by specific SYBR-Green Real-time-PCR and directly sequenced. Then, the Simpson's Diversity-Index (SDI) was calculated for each individual marker. Sequences were analyzed with reference sequences of Francisella sp. with the Bionumerics software. Finally, to give a better overview about the relationships cluster analysis of discrete character sets was generated, including a Categorical Similarity Coefficient combined with a Neighbor-Joining (NJ) Method and a Multidimensional Scaling.

Results: All isolates were identified as F. tularensis ssp. holarctica biovar II. VNTR-loci displayed between 1 and 6 alleles (2 to 12 repeats), with SDI between 0 and 0.62 for M24 and M6 markers, respectively. Phylogenetically, 9 big clusters were distinguished. The NJ cluster analysis revealed 17 genotypes, in 9 cases even to individual strain discriminations level. Eleven out of the 17 genotypes were already present until 1997, so distribution seems to be in many little natural foci, also called "hotspots". Some genotypes from 1995 could be found in 2009-2010. Six new genotypes were detected after 2005. The 4 most affected regional districts had 15/17 of the genotypes. Redfox and human isolates were all clustered to previous hare isolates.

Conclusion: In Austria, Ft ssp. holarctica biovar II strains showed higher genetic diversity as reviewed in previous studies, possibly because they had been never included in any comparative study, and because of the numerous strains collected in a relative small geographical region. Since the natural reservoir remains still unclear, future investigation would be necessary, since end hosts do not appear to be responsible for the transmission between endemic regions.

21.053 Echinococcus multilocularis, etiological agent of alveolar echinococcosis, in Slovakia

D. Antolova, M. Miterpakova, G. Hrčková

Institute of Parasitology SAS, Kosice, Slovakia

Background: Alveolar echinococcosis is serious parasitozoonosis of men caused by larval stages of Echinococcus multilocularis, lethal in untreated or inadequately treated patients. The disease is characterized by development of cystic lesions almost exclusively in the liver; secondary lesions can form in the lungs, and other organs. The metacestode is tumor-like multivesicular, infiltrating structure consisting of numerous small vesicules embedded in stroma of connective tissue. Metastasis formation occurs after release of germinal layer cells into the blood or lymph system.

Objectives: The aim of the study was to compare the occurrence of alveolar echinococcosis in humans in Slovakia with the prevalence of parasite in red foxes its definitive hosts.

Methods and Materials: Serological methods (ELISA, Western Blot) and PCR where used for the confirmation of diagnosis in humans. In red foxes, modified sedimentation and counting technique was used for the parasite detection.

Results: In Slovakia, the first human case of alveolar echinococcosis was recorded in 2000 and till now, in total 20 cases has been confirmed. As many as 19 of them came from endemic northern Slovak regions (Prešov Region-8 cases; Žilina Region-10 cases; Trnava Region-1 case). The results of long term study in red foxes, realized between 2000 and 2012, revealed the existence of highly endemic foci of echinococcosis in northern Slovak districts, with the prevalence ranging from 20 % to more than 60 %.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: High prevalence of echinococcosis in red foxes. together with rising incidence of human cases suggest that the risk of infection is still very actual and alveolar echinococcosis could be considered in differential diagnostics of liver lesions.

Acknowledgement: The work was supported by the Science Grant Agency VEGA 2/0127/13 (0.5) and project "Application Centre for Protection of Humans, Animals and Plants against Parasites" (code ITMS: 26220220018), supported by the Research & Development Operational Programme funded by the ERDF (0.5).

21.054 Parasite circulation in the protected areas of the Tatra National Park, Slovakia

Z. Hurnikova¹, M. Miterpakova², B. Chovancova³ ¹Institute of Parasitology SAS, Kosice, Slovakia, ²Institute of Parasitology, Slovak Academy of Sciences, Kosice, Slovakia, ³Research Station and Museum TANAP, Tatranská Lomnica, Slovakia

Background: The northern part of Slovakia represents the main tourist and recreational area of the country. After the windstorm in 2004 that caused losses or changeovers of prime biotopes, migration of existing and immigration of new wildlife is expected, followed by growth of carnivorous predator populations that represents the risk of spreading parasitic infections.

Objectives: The aim of our work was to study parasite circulation in ecosystems that undergo dynamic changeovers. Distribution of zoonotic agents in carnivore hosts was analysed emphasizing the most important ones-echinococcosis and trichinellosis.

Methods and Materials: Small intestines of carnivores were examined for the presence of E. multilocularis using modified sedimentation and counting technique (Raoul et al., 2001). Muscle samples were examined for the presence of Trichinella spp. larvae by artificial HCI-pepsin digestion method (Kapel and Gamble, 2000). Fecal samples were investigated using coprological flotation method.

Results: The presented research work revealed the presence of Echinococcus multilocularis tapeworm, which causes severe alveolar echinoccosis in human, in almost 40 % of foxes from TANAP and adjacent areas. The parasite was also present in domestic cat, racoon dog and marten.

Trichinellosis harboured over 19% of foxed, parasite was also detected in wolf, brown bear, lynx, domestic cat and also in big proportion of predators from the family Mustelidae (19.4%).

In 2012, pilot research was initiated on parasite fauna of endemic sub-species Alpine marmot (Marmota marmota latirostris). Examination of 30 fecal samples revealed the presence of Eimeria spp. oocysts (16.7%) and eggs of Ctenotaenia marmotae tapeworm (53.3%).

Conclusion: Long-term examination of carnivores from the protected areas of TANAP revealed that these wild predators play a significant role in environmental contamination with parasites and may contribute significantly to the spread of parasitic zoonoses and play important roles in the structuring of parasite communities that provide opportunities for increased exposure of humans to parasitic infection.

The work was supported by the Science Grant Agency VEGA2/0011/12 (0.5) and project "Application Centre for Protection of Humans, Animals and Plants against Parasites" (code ITMS: 26220220018), supported by the Research & Development Operational Programme funded by the ERDF (0.5).

21.055 Contact with rodents in Khon Kaen Province, Thailand

K. Suwannarong¹, S. Woldehanna², Z. Rambeloson², R. Chapman³, S. Zimicki²

¹EPT/ PREVENT Project, FHI 360, Bangkok, Thailand, ²EPT/ PREVENT Project, FHI 360, Washington D.C., DC, USA, ³ Chulalongkorn University, Pathumwan, Thailand

Background: The incidence of zoonotic diseases (ZDs) has increased in the past 20 years and is projected to rise even more in the near future. One important reservoir of ZDs is rodents, which carry several significant diseases, e.g., hanta virus, plague, leptospirosis. Contact with rodents, and other characteristics, were measured in Khon Kaen province, Thailand, during November to December 2011.

Objectives: To characterize contact with rodents in 201 residents of Khon Kaen Province, Thailand.

Methods and Materials: This cross-sectional survey was conducted among villagers who lived in urban, forest and agricultural settings during November-December 2011. A two-stage cluster sampling procedure was used to select study population. Informed consent was obtained from all participants, who were informed of the objectives of the study. The selected respondents were interviewed by using questionnaires that included nine (9) sections of contact information with rodents.

Results: Two hundred-one (201) respondents (100 females and 101 males) were selected from 3 settings (urban, agriculture, and forest) within 4 districts of Khon Kaen province. Mean age of the respondents was 36.5 years old (range 18-50 years old). The results showed that 79.6% (160 persons) were always stayed at the areas while the rest, 39.15% (15) lived in country side, and 28.9% (11) lived in town and 31.6% (11) lived in city. Regarding to contact with rodents, 149 persons (74.1%) had eaten rodents in the past month while 11 persons (5.5%) were bitten by rodents in the past 12 months before the interview dates. One hundred eighty-four (91.5%) found left evidences of rodents inside and nearby their households. Surprisingly, 3 persons (2 from forest and 1 from agriculture settings) mentioned that they had raised rodents. Regarding to disease awareness, 151 persons (83.0%) had awareness toward leptospirosis.

Conclusion: There was substantial contact with rodents in Khon Kaen. The results raise concern about potential for significant risk of rodent-borne zoonoses. Futher research to chracterize risk factors for exposure is in progress. In order to obtain understanding of risky and protective practices and risk perceptions surrounding rats, we also plan to conduct participatory action research in selected communities in this province.



21.056 Orf virus infection in a hunter presumably transmitted by game in Western Austria

M. Kitchen¹, N. Romani¹, A. Zobl¹, A. Windisch¹, W. Glawischnig², M. Schmuth¹, H. P. Huemer¹

¹Med.U.Innsbruck, Innsbruck, Austria, ²AGES, Innsbruck, Austria

Background: Parapoxviruses exist in a variety of animals. Orf virus (ORFV) is prevalent in sheep and goats in the Tyrol region of Austria and Northern Italy and zoonotic infections in humans mostly occur after occupational exposure.

Objectives: Here we report a case of a hunter with a typical orf lesion (contagious ecthyma) on the finger without any history of direct contact with domestic animals. 3 weeks before he had been hunting chamois (Rupicapra rupicapra) and cut his finger while handling the carcass.

Methods and Materials: Parapoxvirus infection was confirmed by electron microscopy and PCR, and the species identification was obtained by DNA sequencing.

Results: The sequence was found highly homologous to prevalent sheep ORFV and rather distant to parapoxviruses found in red deer in Northern Italy. Our case indicates that ORFV may have been introduced into certain game species in Austria.

Conclusion: This could occur via roaming domestic sheep which share the range of the game in the high alpine areas during the summer months. To address this question a small sero-epidemiological survey in sheep and local game animals was initiated.

21.057 First description of Bartonella bovis in domestic ruminants in Israel

N. Rudoler

Hebrew University, Rehovot, Israel

Background: Bartonella are small, Gram-negative bacilli which have been isolated from a wide range of mammals including dogs, cats, rabbits, rodents and ruminants. To date, 13 Bartonella species or subspecies have been associated with diseases in humans. Transmission of Bartonella usually involves a vector, either fleas, lice or ticks. The main species isolated from cattle is B.bovis. B. schoenbuchensis, B.chomelii and B.henselae, have been sporadically isolated.

Objectives: To study the prevalence and characteristics of Bartonella bacteremia in cattle in Israel.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: Blood was collected from 2 beef cattle herds (each sampled thrice) and 1 dairy herd (sampled twice), subjected to freezing and thawing, and plated on chocolate agar plates for 6 weeks or until growth. Quantitative evaluation of colonies number was recorded. For species determination sequencing of a 379bp PCR product targeting the *glt*A gene was performed.

Results: During a period of 16 months 103 blood samples from 93 cows were collected. Of the 95 samples which remained after discarding contaminated plates, 71 (75%) grew *Bartonella* sp. The prevalence of *Bartonella* bacteremia was 82% and 74% among the 2 beef herds and 58% in the dairy herd (p100,000 cfu/mL) which was more prevalent among the beef herds compared with the dairy herd (29% of samples vs. 10%, pB.bovis blood concentration occurred in a bimodal fashion: 33% of positive cultures had high concentration (>100,000 cfu/mL), 60% had low concentration (Bartonella on the first visit as well as 60–120 days later. All isolates were found to have 100% homology to *B.bovis*. Ticks (mainly *Hyalomma* spp.) were found on vast majority of cows sampled in May, June and October.

Conclusion: This is the first description of *Bartonella bovis* from cattle in the Middle-East. The high prevalence bacteremia together with the previously un-reported high bacterial load in the presence of compatible vector make *B. bovis* a potential zoonotic agent.

21.058 Analysing phylogenetic relationships of *Pneumocystis carinii* f. sp. *suis* to other *Pneumocystis* species

C. Weissenbacher-Lang, N. Nedorost, H. Weissenboeck University of Veterinary Medicine Vienna, Vienna, Austria

Background: The opportunistic fungal pathogen *Pneumocystis* spp. causes a potentially life-threatening pneumonia in immune compromised humans with a mortality rate up to 60 per cent. Pneumocystosis has also been reported in a wide variety of animals, including pigs. *Pneumocystis carinii* f. sp. *suis* has not been investigated in detail. Cross infection experiments with rats and mice showed that *Pneumocystis* organisms generally are host-specific. However, as a close host species specificity for porcine *Pneumocystis* has not yet been proven, a potential risk originating from or for different species including humans cannot be ruled out.

Objectives: In the present study, the phylogenetic relationships of *Pneumocystis* derived from swine to defined *Pneumocystis* species or isolates was assessed by analysing ribosomal and mitochondrial DNA sequences.

Methods and Materials: As the analysis of sequences from different genetic loci of *Pneumocystis carinii* showed that isolates from different hosts were similar at some loci, but completely distinct at others, parts two different genomic regions, the 18S ribosomal small subunit (rSSU) and the mitochondrial large subunit (mtLSU) were amplified by PCR and sequenced from porcine lung samples. The phylogenetic investigation was performed with the MEGA4 program using the neighbour-joining method. Samples 5271/04 and 1816/08 (rat, rabbit) were used as positive controls. Samples 233/09 and 1313/11 were porcine *Pneumocystis* sequences established in the present study.

Results: Figure 1 shows the phylogenetic analysis of sequences of the 18S rSSU, Figure 2 of the mtLSU. Both trees support the assumption that *Pneumocystis* species are host specific and porcine *Pneumocystis* build a separate cluster.



Figure 1. Phylogenetic analysis of 18S rSSU



Figure 2. Phylogenetic analysis of mtLSU

Conclusion: Recently, the first two porcine *Pneumocystis* sequences have been published. Previously, no swine sequences were available for comparison. Sequences from other species and also humans are quite heterogeneous. According to this heterogeneity, alignments of published sequences from different species are often inexact. The present phylogenetic study shows a tendency for porcine *Pneumocystis* to build a separate cluster. Due to the low number of comparable sequences need to be characterized and phylogenetic studies with a higher number of datasets need to be carried out.

21.059

D9 *Toxoplasma gondii* detected in wild and captive European woodchuck (*Marmota marmota*)

S. Richter, Z. Bagó, S. Revilla-Fernández, H. Weinberger, F. Schmoll AGES, Inst. for Veterinary Disease Control Mödling, Mödling, Austria

Background: *Toxoplasma gondii* is an important zoonotic apicomplexan parasite with worldwide prevalence and great importance in veterinary and public health because it infects humans, a wide range of wild and captive warm-blooded mammals and birds. The life cycle of *Toxoplasma* includes definitive hosts (felids) and intermediate hosts (all other mammals, including humans, and birds). Hosts can become infected by ingestion of food and water contaminated with sporulated oocysts excreted by infected felids, by consumption of tissue cysts, or by congenital transmission.

Objectives: The current study reports for the first time a *T. gondii* infection in wild and captive *Marmota marmota*, an animal typically found in the Austrian alpine region.

Methods and Materials: The samples of the zoo and wild animals comprised liver, intestine and brain. Histological study was based on HE-sections, ultrastructural analyses on EPON- sections. Immunohistochemistry was performed by an Avidin-Biotinylated enzyme complex using polyclonal antibodies against *T. gondii* (Fermont, USA). Molecularbiological analyses included specific PCRs for *T. gondii* and *Neospora caninum*. Positive PCR results were further confirmed by sequencing.

Results: Histopathological changes in liver and brain were: presence of pseudocyts, multifocal or focal mononuclear inflammatory infiltrates and necrosis in the area of the lesions. Ultrastructural investigations showed characteristic tissue cysts in liver and brain tissue. The tissue cysts, respectively the cyst wall structure and bradozoite organization (apical conoid, rod-like structured micronemes, apicoplast, uniformly electron-dense rhoptries), resembled those of *Topxoplasma*. The tissue cysts contained bradyzoites of different generations—several of them were in various stages of producing progeny by endodyogeny. The diagnosis was confirmed by immunohistochemistry and by sequencing the B1 gene of *T.gondii*.

Conclusion: This report, besides confirming the possibility of *Marmota marmota* to be infected with *T. gondii*, confirms the transmission of toxoplasmosis in the alpine region. *M. marmota*, which inhabits like foxes and wild ruminants of the Italian, Swiss and Spanish mountain regions (roe deer, chamois and ibex) the European alpines, is one of the indicators for pasture contamination with *T. gondii* oocysts. Exposure to soil and water contaminated with oocysts shed in feces of infected domestic and wild felids (e.g. *Lynx lynx*) is suspected.

International Meeting on Emerging Diseases and Surveillance 2013

21.060 Monitoring of avian influenza and Newcastle Disease among wild birds of different ecological groups in Azov and Black Sea region of Ukraine in 2006–2011

D. Muzyka¹, B. T. Stegniy¹, M. Pantin-Jackwood², A. Stegniy¹ ¹National Science Center Institute of Experimental and Clinical Veterinary Medicine, Kharkiv, Ukraine, ²Southeast Poultry Research Laboratory, Athens, GA, USA

Background: Ukraine occupies a unique geographical position in central Europe and serves as a large area of transcontinental bird migration from Northern Asia and Europe to the Mediterranean, Africa and Southwest Asia. In particular, the Azov and Black Sea Basins have historically served as places of stops during migration and nesting, for many migratory bird species with a high level of biodiversity.

Objectives: Our primary objective was to survey populations of wild birds for AI and PMV.

Methods and Materials: During 2006 to 2011, scientists from NSC IECVM conducted a study of wild birds in Azov- and Black Sea region of Ukraine. Biological materials were collected from wild bird populations during periods of mass accumulation in AR Crimea, Kherson and Zaporigia region (Sivash Bay, Molochniy and Utlyukskiy estuaries); totaling 5091 samples of biological material from 66 species of birds (8 orders: *Pelecaniformes, Ciconiiformes, Anseriformes, Galliformes, Gruiformes, Charadriiformes, Coraciiformes*, and *Passeriformes*). Virological studies were conducted with the OIE recommendations.

Results: From these samples 79 hemagglutinated viruses were isolated. Fall migration, 28 hemagglutinated viruses were identified; influenza viruses of subtypes H3N8, H4N6, H5N2, H7N?, H8N4, H10N7, H11N9, H11N8, and paramixovirus serotypes PMV-1, PMV-4, PMV-6, PMV-7. Winter migration, 46 hemagglutinated viruses from birds were identified; including subtypes H1N1, H1N2, H4N?, H6N1, H7N6, H7N3, H7N7, H8N2, H9N2, H10N7, H10N4, H11N2, H1N6, H12N2, H15N7 and paramyxoviruses serotypes PMV-1, PMV-6, PMV-6, PMV-7. Spring migration, nesting, post-nesting movements 5 hemagglutinated viruses were identifed, including influenza A subtype H4N6, N6N4, N13N?, and N16N?. All influenza and paramixiviruses isolated from wild birds are low pathogenic.

Conclusion: Influenza remains an unpredictable infection for animals, birds and people. Moreover, the constant emergence of new strains and variants with novel properties and pathogenicity to new hosts require constant monitoring and careful research of new viruses. In this regard, we continue to monitor the constant circulation of influenza in wild bird populations in Ukraine. This will expand the understanding of the ecology of influenza viruses in nature and timely identification of new viruses.

21.061 Risk factors for acquiring nephropatia epidemica in Sweden, 2011–2012: A case control study

A. M. Gherasim¹, M. Hjertqvist², Å. Lundkvist³, S. Kühlmann-Berenzon³, J. Verner Carlsson³, A. Wallensten³

¹EPIET Fellow-European Centre for Disease Prevention and Control, Stockholm, Sweden, ²Swedish Institute for Infectious Disease Control, SOLNA, Sweden, ³Swedish Institute for Infectious Disease Control, Solna, Sweden

Background: Nephropatia epidemica (NE) is a haemorrhagic fever with renal syndrome caused by Puumala virus (PUUV), a hantavirus transmitted to humans by inhalation of aerosolized excreta of infected rodents. Although in Sweden the disease has the highest incidence in the four northernmost counties (Northern Sweden), associated risk factors have not been investigated locally.

Objectives: We aimed to identify risk factors for NE in Northern Sweden, in order to recommend control measures.

Methods and Materials: We conducted a matched case-control study comparing laboratory-confirmed NE cases, identified in Northern Sweden between July 2011 and March 2012, with randomly selected controls. Cases and controls were matched by age, sex and location (postal code). Anticipating a 50% response rate among controls, we contacted six controls for each case.

We collected data on potential exposures for the six weeks prior symptoms onset (six weeks prior to receiving the questionnaire for controls). Controls were offered to test for the presence of PUUV IgG. We estimated adjusted odds ratios (aOR) and 95% confidence intervals (95%CI) for various exposures through multivariable conditional logistic regression

Results: Of the 166 cases surveyed, 123 cases replied (74% response rate). We surveyed 996 controls, of which 379 controls replied (38% response rate). Only 193 controls tested, 33 being positive, while for 13 the result was inconclusive. We included in the final analysis 114 cases and 300 controls. For cases, male-female ratio was 1.5, and median age was 56 years. Cases were more likely to have seen rodents (aOR=5.6, 95%Cl=1.8-16.5) or rodent droppings (aOR=9.4, 95%Cl=1.7-49.5), mown the lawn (aOR=5.8, 95%Cl=1.7-19.3) or made house repairs (aOR=4.6, 95%Cl=1.3-17.2). Cases were also more likely to have stayed in a dwelling with an open space underneath (aOR=4.8 95%Cl=2-11.5). Smoking (aOR=3.1, 95%=1.1-9.7) was also associated with the disease.

Conclusion: We identified several environmental, occupational, and behavioural risk factors for acquiring NE in Northern Sweden. Based on these findings, the national and the local public health authorities should adapt the public health recommendations in order to raise awareness towards these risk factors.



Case report: Outbreak of *Salmonella Dublin* in wildlife associated with infection in cattle

W. Glawischnig¹, A. Wallner¹, C. Kornschober², K. Schoepf¹ ¹Austrian Agency for Health and Food Safety, Innsbruck, Austria, ²Austrian Agency for Health and Food Safety, Graz, Austria

Background: Since summer 2012 an increased death rate in a defined population of chamois (*Rupicaprae rupicaprae*) could be observed by local hunters in the Tyrolean district of Kufstein. At the same time cattle were grazed on alpine pastures within this region. In two grazing cattle with clinical symptoms of severe diarrhoea *Samonella Dublin*-infection could be confirmed as the causative agent. We suspect that waterponds located on the mentioned pastures, contaminated by infected manure, acted as a source of infection for the chamois.

Objectives: The objective of our investigations was to proof an infection chain between domestic and wild animals and if contaminated waterponds act as a transmitter for the disease.

Methods and Materials: Environmental water samples from five different ponds on these alpine pastures, pooled faeces sample from foxes collected in direct neighbourhood to chamois skeleton and pooled faeces samples from cattle grazing in the summer time on the mentioned pastures where examined microbiological for the presence of *Salmonella* spp. Furthermore 3 chamois terminally ill and shot by hunters underwent post mortem examination.

Results: Three out of five water samples proofed positive for *S. Dublin*. Additionally *S. Dublin* could be confirmed in pooled faeces samples from 3 cattle holdings. Furthermore the fox faeces were positive for these bacteria. In post mortem one of the examined chamois showed severe diarrhoea and *S. Dublin* was isolated out of the liver and the intestine. Microbiological analyses of the different isolates confirmed that only one strain of *S. Dublin* was involved in the outbreak.

Conclusion: Our results gave strong evidence that cattle from endemically infected holdings shed bacteria into the environment of alpine pastures. These contaminated relevant water ponds act as a route of infection to wildlife. The positive faeces from foxes collected nearby the skeletons from chamois give strong evidence that the cause of death of theses observed chamois was a highly invasive *S. Dublin* stain. Furthermore the post mortem diagnosis of the examined clinically ill chamois confirmed our hypothesis of this interesting infection dynamics.

International Meeting on Emerging Diseases and Surveillance 2013

21.063 Using wildlife surveillance to provide evidence of freedom from Echinococcus multilocularis in Northern Ireland,

E. Courcier¹, S. Fee², F. Malone², K. McBride¹, I. McKeown³, D. Abernethy⁴, F. Menzies¹

¹Veterinary Epidemiology Unit, Belfast, United Kingdom, ²Veterinary Sciencies Division, Omagh, United Kingdom, ³Veterinary Service, Belfast, United Kingdom, ⁴Department of Veterinary Tropical Diseases, Pretoria, South Africa

Background: Alveolar echinococcus (Echinococcus multilocularis) is an emerging zoonosis of major public health importance. Currently, the British Isles is considered free of the tapeworm despite having suitable hosts and environmental conditions. Praziguantel treatment of dogs entering the United Kingdom and Ireland (under derogation to EU Regulation No.998/2003) is a fundamental control measure to prevent entry of the parasite. In order to maintain this derogation, the European Union required the United Kingdom to demonstrate freedom of disease in the definitive host (the fox-Vulpus vulpus) (Regulation 11152/2011).

Objectives: This abstract describes how Northern Ireland, as a separate epidemiologically relevant geographical unit from Great Britain, demonstrated freedom from Echinococcus multilocularis.

Methods and Materials: The majority of fox carcasses were shot by pest controllers, farmers, and landowners while a minority were reported through the wildlife road traffic accident survey. The intestinal tract was examined for parasites by the sedimentation and counting technique specified under Regulation 11152/2011.

Results: Two hundred and forty seven fox carcases were collected between the May 31, 2011 and March 31, 2012 throughout Northern Ireland. All foxes tested negative for *E multilocularis* and *E. granulosus*. The probability of *E.multilocularis* being present in the fox population above a prevalence of 1% was calculated at around 90 to 95% using the method described by Hadorn et al (2002).

Conclusion: This study demonstrated that the fox population of Northern Ireland is highly likely to be free of *E.multilocularis*. This concurs with the finding from the Republic of Ireland. It may be useful to consider conducting surveillance of the definitive host on an all-island basis.

21.064 Zoonotic Poxviruses isolated from symptomatic cattle in Sirajganj District, Bangladesh

E. Lederman¹, S. U. Khan², S. Luby³, H. Zhao⁴, Z. Braden⁴,

K. Karem⁴, I. Damon⁴, M. Reynolds⁴, Y. Li⁴

¹San Diego State University, San Diego, CA, USA, ²ICDDRB, Dhaka, Bangladesh, 3Stanford University, Stanford, CA, USA, 4US Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Bovids have been implicated in the transmission of Poxvirus infections to humans for centuries. Dairy cattle in Brazil and India-and buffalo in India-have been observed to harbor zoonotic poxviruses from both the Orthopoxvirus and Parapoxvirus genera. In bovids, vaccinia and buffalopox virus infections (orthopoxviruses) often engender high morbidity, with symptoms including malaise, anorexia, and pustular or ulcerated lesions or nodules on the teats and muzzles of adult and juvenile animals, respectively. Symptoms of infection with Bovine papular stomatitis virus (BPSV) and Pseudocowpox virus (PCV) (parapoxviruses) are similar to each other, and to the symptoms associated with orthopoxvirus infections, however, BPSV may be most recognizable in young animals as a papular rash on oral mucosa or as an inflammation of the gingiva. In most instances human infections are the result of direct contact with infected animals, via milking, feeding or from animal bites.

Objectives: Objectives: To identify zoonotic poxviruses of significance to public health in domestic bovid species in Bangladesh.

Methods and Materials: Whole blood, oral swabs and/or lesion specimens were collected from 9 symptomatic cattle from the Sirajganj District and 4 buffalo from Bhola. For animals that had evidence of scarring, but no active lesions, only blood was collected. Blood specimens were assayed for the presence of orthopoxvirus antibodies by ELISA and lesion and oral swab specimens were examined by gPCR for the presence of genus and species level DNA signatures from zoonotic orthopoxvviruses and parapoxviruses.

Results: Evidence of BPSV DNA was obtained from lesion material (teat) and an oral swab collected from a single adult cow and her calf (respectively). PCV DNA signatures were obtained from a scab and oral swab collected from a second cow and her calf. No evidence of prior or current orthopoxvirus infection was detected in any of the 13 animals examined.

Conclusion: Two species of zoonotic parapoxviruses were identified in specimens obtained from symptomatic cattle in Bangladesh. Humans who have occupational exposure to bovids -through dairy or meat production or other husbandry activities-are at risk for infection with these viruses and should take precautions when handling animals with lesions or gingival symptoms.

21.065 Surveillance of West Nile Virus in birds in Los Angeles County-A successful and proactive program to anticipate human outbreaks

G. Lamielle, K. Ehnert, E. Beeler, T. Scott

County of Los Angeles, Department of Public Health, Los Angeles, CA. USA

Background: Mosquito-borne West Nile virus (WNV) emerged in the Americas in 1999, affecting both human and wild bird populations in New York City, and prompting authorities to use a One Health approach to disease surveillance integrating all species. While the virus usually causes mild symptoms in people, rare neuroinvasive forms can result in life-threatening disease. WNV is now established in wild birds of North America where significant outbreaks have recently occurred. During periods of increased mosquito activity, peaks in crow mortality usually precede human infections. Significant attention should therefore be placed on monitoring disease status in wildlife in order to predict outbreaks in people

Objectives: This presentation aims to validate the WNV surveillance system in Los Angeles County, California, which uses an integrated, species-spanning approach and promotes inter-professional collaboration between the human and veterinary medical fields.

Methods and Materials: Mandated by the California Department of Public Health (CDPH), veterinarians at the County of Los Angeles Department of Public Health (LADPH) test dead crows using an antigen assay all year. During periods of increased virus activity, animals are also submitted to CDPH for further testing using PCR technique. Results are combined with data from collaborating agencies to include human cases and infected mosquito pools. The public is promptly notified of results and public health services are able to publish up-todate reports educating the population about the risk posed by the virus.

Results: In the past two years, WNV virus has generally increased in Los Angeles County in both animals and people. Thus far, the number of WNV positive wild birds has increased from 226 to 274 between 2011 and 2012. Likewise, human cases have risen from 58 to 149 cases including 5 deaths, during the same time period.

Conclusion: The importance of multidisciplinary cooperation has become increasingly recognized under the One Health banner. The WNV monitoring program at the County of Los Angeles is a perfect example of how an integrated surveillance system can provide a more complete understanding of disease status and ecology in an affected population, and also highlights the risks caused by reducing disease surveillance in wildlife.

21.066 Survey of infectious disease agents of zoonotic or epizootic significance in Austrian wildlife

A. Steinrigl¹, Z. Bago¹, S. Revilla-Fernández¹, E. Hofer¹, M. Dünser², E. Wodak³, A. Loitsch³, J. Hofrichter⁴, A. Deutz⁵, F. Schmoll¹ ¹AGES, Institute for Veterinary Disease Control, Mödling, Austria, ²AGES, Linz, Austria, ³AGES, Mödling, Austria, ⁴AGES, Graz, Austria, ⁵Steiermärkische Landesregierung, St. Lambrecht, Austria

Background: The potential significance of wild animals as indicators or reservoirs of infectious diseases potentially affecting livestock and/

International Meeting on Emerging Diseases and Surveillance 2013

or humans is increasingly acknowledged. Furthermore, infectious disease monitoring in wildlife can provide timely information regarding introduction of emerging diseases. Despite their potential significance, infectious diseases in wildlife are not well studied, probably due to difficulties to sample wild animals in a representative manner.

Objectives: The aims of the work presented here were to implement a representative sampling strategy and to estimate prevalences of selected infectious diseases in several wild animal species in Austria.

Methods and Materials: A survey design was implemented in cooperation with the Austrian Hunters' Association, aiming at representative sampling of red fox (*Vulpes vulpes*), red deer (*Cervus elaphus*) and wild boar (*Sus scrofa*). Foxes and red deer were tested for *Mycobacterium tuberculosis* complex (MTBC), red deer was additionally tested for *Mycobacterium avium* ssp. *paratuberculosis* (MAP). Wild boars were tested for *Brucella suis*, Suid herpesvirus 1 (SuHV-1), Classical swine fever virus (CSFV) and African swine fever virus (ASFV). In addition, wild boar sera were tested for presence of antibodies to SuHV-1, CSFV and ASFV.

Results: In total, 318 red foxes, 275 red deer and 298 wild boars were sampled from April 2011 to January 2012. Prevalences for infectious disease agents were as follows: MTBC in red fox: 0.0%; MTBC in red deer: 0.5%; MAP in red deer: 1.6%; *Brucella suis* in wild boar: 1.0%; SuHV-1 in wild boar: 1.0%; CSFV and ASFV in wild boar: 0.0%. Prevalences of antibodies to SuHV-1, CSFV and ASFV were 22.8, 0.0 and 0.0%, respectively.

Conclusion: This survey is the first reliable estimate of selected disease prevalence in Austrian wildlife. Prevalences found in this study mainly confirm results of previous studies and provide information concerning possible transmission between wildlife, domestic animals and humans.

21.067

JO7 Ecology of hemorrhagic fever with the renal syndrome (HFRS) in the West Kazakhstan Oblast (WKO)

T. Ayazbayev, F. Bidashko, A. Grazhdanov, M. Pak, V. Surov,

L. Belonojkina, A. Andriushenko, A. Zakharov, B. Kdyrsikh,

A. Kuspanov

Uralsk Anti-Plague Station, Uralsk, Kazakhstan

Background: Many Hantaviruses, a genus of the Bunyaviridae Family, are known to cause hemorrhagic fever with renal syndrome (HFRS) in humans exposed to rodent excrements. Since 2000, Hantavirus has been documented in the West Kazakhstan Oblast (WKO) with little understanding of the ecology in which this virus flourishes.

Objectives: The objective of this work was to study and understand the ecology of Hantavirus associated with HFRS that are known to circulate in the WKO by screening small field mammals.

Methods and Materials: Lung tissue from rodents trapped in the field were collected, identified, and tested for Hantaviruses, Puumalla and Dobrava, via ELISA and immunofluorescent assays. A total of 11 rodent species were collected including voles (*Clethrionomys glareolus, Microtus arvalis*) and mice (*Apodemus silvaticus, Mus musculus*). Hospital data showing rates of human HFRS were also collated.

Results: Out of 55,000 small mammals screened, 594 tissue samples tested positive via an antigen capture ELISA assay. The number of *C. glareolus* (bank vole) ELISA positive results inversely correlated with the sum of those obtained from three other species. Pearson' correlation coefficient is -0.852; p<0.01. The same statistical analysis between *C. glareolus* and *M. arvalis* (common vole) show highly inverse correlation number (-0.714; p<0.01).

Conclusion: The results suggest seasonal epizootic activity associates with the four species *C. glareolus*, *M. arvalis*, *A. silvaticus*, and *M. musculus*. Specificially, *C. glareolus* have been found to be more active in the cold months whereas the three other species are more active in the warmer seasons. The *C. glareolus* activities correspond with the seasonal distribution of human cases, which would suggest that this bank vole species is one of the main sources for Puumalla hantavirus infection of people in WKO.

21.068 Epidemiological and clinical manifestations of Crimean-Congo hemorrhagic fever (CCHF) in the Southern Kazakhstan Region (SKR)

R. Egemberdiyeva¹, Z. Shapiyeva²

¹Kazakh National Medical University, Almaty, Kazakhstan, ²Scientific Practical Center of Sanitary Epidemiological Expertise and Monitoring, Almaty, Kazakhstan

Background: CCHF cases are registered in the SKR almost every year. Since the official registration of CCHF cases only notes patients with hemorrhagic signs, which define a clinical CCHF diagnosis in Kazakhstan, we believe there is evidence that the actual number of CCHF cases is higher than that being registered.

Objectives: To study epidemiological and clinical manifestations of CCHF, and standardize diagnostics and case definitions.

Methods and Materials: Epidemiological outbreaks of CCHF from the SKR (2005–2011) were studied. In this period there were 67 cases diagnosed by an ELISA test (Vector Best antibody capture) on (i) the blood serum samples collected from 165 individuals exposed to tick bite and (ii) from 55 acute febrile patients.

Results: The majority of officially registered CCHF patients (79%) had a severe form of the disease manifesting as shock and disseminated intravascular coagulation (DIC),and hemorrhagic signs.

Early clinical manifestations of CCHF infection in patients, often described as the pre-hemorrhagic period, typically include: flu-like symptoms such as fever, weakness, loss of appetite, headache, chills, body pain (32.8%), nausea (47.8%), vomiting (44.8%), abdominal pain (35.8%), and diarrhea (34.3%). For patients who progress to the hemorrhagic period, dyspeptic symptoms become stronger including: hematemesis (49.3%), diarrhea (53.7%), and the appearance of hemorrhagic syndromes such as rash (60%), hematomas (82.1%), bleeding of nose (61.2%), bleeding of gums (51.7%), gastro-intestinal bleeding (52.2%), renal bleeding (29.9%), and uterine bleeding (14.9%).

During outbreak response activities (Zhambyl oblast), we tested all patients with fever, and determined that 66.6% of CCHF cases were without shock and DIC syndrome, and only 33.3% had hemorrhagic manifestations.

ELISA results of 165 tick bite individuals (2005–2011) and 55 acute fevers patients not diagnosed with clinical CCHF showed that 12.7 and 30.8% of cases respectively had IgM to the CCHF virus, indicative of a recent infection with CCHF virus.

Conclusion: The official registration of CCHF cases notes only patients with hemorrhagic signs. The process of improving standardized diagnostics, case registration, and epidemiological mapping will increase the understanding of the scale of CCHF prevalence among people residing in endemic areas.

21.069 Building capacity in ecohealth in Asia: Impact on research activities.

D. Hall¹, M. Lunney², Q. B. Le¹, J. Davidson³

¹University of Calgary, Calgary, AB, Canada, ²Consultant, Santiago, Chile, ³University of Prince Edward Island, Charlottetown, PE, Canada

Background: To assist the Southeast Asian region in reducing the risk of emerging infectious diseases, a three year project (the Building Ecohealth Capacity in Asia project, or BECA) was implemented with emphasis on increasing understanding of ecohealth concepts and encouraging researchers to engage in ecohealth research, particularly at a transdisciplinary level. Asian countries participating were Cambodia, China, Indonesia, Laos, Thailand, and Vietnam.

Objectives: Objectives of the BECA project were:

- contribute to building a network of ecohealth researchers in SEAsia

develop an ecohealth monitoring and evaluation (M&E) framework
 develop methodologies for measuring impact of sustainable ecohealth applications

- inform and influence local and regional policy formulation related to ecohealth.

POSTER PRESENTATIONS

International Meeting on Emerging Diseases and Surveillance 2013

This presentation reports on the recent evaluation of this project. This information should be of interest to anyone aiming to increase transdisciplinary health research capacity.

Methods and Materials: The methods used to implement the BECA project were a combination of consultation and planning with key focal points in the six Asian project countries, workshop planning and participation, technical support and mentoring, network development, and monitoring and evaluation.

The project was evaluated using a combination of: 1) an extensive in-country evaluation process trialed in Vietnam; 2) an online questionnaire; 3) a questionnaire distributed prior to the final workshop; 4) semi-structured interviews with participants; 5) a SWOT analysis exercise; 6) gap analysis; and 7) performance indicator identification.

Results: More than 100 participants benefitted from attending workshops and focused meetings. The M&E process revealed that participants used new ecohealth knowlede in academic curricula, scholastic articles, and application to new ecohealth research projects. Participants preferred to learn from case studies and presentations from their peers rather than academic based presentations. The development of policy briefs was particularly helpful in understanding the policy formulation process. Main areas of concern were lack of project initiation funds with which to apply new knowledge, difficulty in maintaining communication after meetings, and the small number of participants (about 6) per country per meeting.

Conclusion: Efforts to develop capacity in transdisciplinary health research were successful in increasing ecohealth knowledge and encouraging researchers to include ecohealth principles in their work. Weaknesses include expectation of donors to fund their research programs.

21.070 Animal bites and the prevention of rabies in Albania

E. Tomini¹, K. Mersini², J. Sulo¹, S. Tobli³, S. Bino¹ ¹Institute of Public Health, Tirana, Albania, ²Food Safety and Veterinary Institute, Tirana, Albania, ³Public Health Directory, Kukes, Albania

Background: The last reported human rabies cases were reported in 1976 and mandatory rabies vaccination in confined areas for domestic animals and wildlife population control where carried out. Since 1976 Albania has been a Rabies-free country due to many factors but since 1990 Albania faced an uncontrolled influx of pet dogs from dog rabies countries and many wild animals crossed the border due war in Kosovo.

Objectives: The main objective is to evaluate the surveillance of animal rabies and dog bites, rabies prevention program in Albanian during the last ten years and future risk factors.

Methods and Materials: The data provided from national registry of dog bites, outbreak investigation database from National Surveillance Unit, Veterinary Wild Animal Health Surveillance and National Rabies Vaccination Registry were compiled and analysed based on the time, place and persons. Also the wildlife movement and other geographic characteristics were analysed to identify further risk factors.

Results: The disease in animals has reoccurred in Albania in March 2001 in Kukes district (Morine village) in north-east Albania, bordering Kosovo. Up to now there have been recorded sporadic cases in domestic and wild animals and outbreak in cows occurring in 2001, 2006, 2009 and 2012 mainly in north east part of the country. These outbreaks have been controlled by eliminating contact animals and by implementing ring vaccination in susceptible animals. From 2001–2012 outbreaks, 6 people have been bitten by confirmed rabid animals. Post exposure prophylactic measures have been applied to all of them. Pre-exposure vaccination has been administered to 151 persons present at the outbreaks. Rabiesprophylaxis it was administered in all 103 dog bitten cases and based on a risk assessment only 11% received immunoglobulin and vaccination scheme.

Conclusion: The current data shows the integrated human and health surveillance, identification of rabies risk areas and risk factors and immediate provision of human vaccination has prevented human rabies cases in Albania. Based on the current disease patterns, wildlife movement, lack of animal vaccination programs it could be assumed

21.071 Evaluation of cross-reactivity of human influenza antibodies against H1, H2 and H3 avian influenza virus subtypes

M. S. Pizzuto¹, I. Monne¹, S. Maniero¹, A. Burattin¹, M. S. Beato¹, V. Valastro¹, M. Mancin¹, E. Vicenzi², G. Cattoli¹, I. Capua¹ ¹Istituto Zooprofilattico Sperimentale delle Venezie, Padua, Italy, ²San Raffaele Scientific Institute, Milan, Italy

Background: To date, only viruses of the haemagglutinin (HA) H1, H2 and H3 subtypes have caused pandemics in humans, and all pandemic viruses emerging in the 20th century had an avian progenitor virus donating at least the HA gene. So far, avian H1, H2, and H3 subtype viruses have been excluded from priorities aiming at the development of pandemic vaccine candidates as the human population was considered sufficiently immune to H1 and H3 viruses due to exposure or vaccination against homosubtypic human influenza viruses. A preliminary study (Capua et al, 2009) has highlighted the possibility that post-seasonal influenza vaccination antibodies may be not cross-reactive with contemporary avian H1 and H3 subtype viruses underlining the need to further explore human intrasubtypic immunity against H1, H2 and H3 avian influenza viruses.

Objectives: The aim of this study was to evaluate the crossprotective activity of antibodies generated for human H1, H2 and H3 viruses against contemporary homosubtypic avian viruses.

Methods and Materials: Human serum specimens were collected in the frame of 2006 seasonal and 2009 pandemic vaccine studies. Fifty human sera from each study were tested by virus microneutralization (MN) assay for cross-reactivity with a panel of 21 representative avian influenza viruses of the H1, H2 and H3 subtypes.

Results: The results showed that antibodies present in human sera, induced by vaccination do not significantly cross-react with contemporary Eurasian lineage avian influenza viruses of the H1, H2 or H3 subtypes as of the 2100 tests performed only 270 resulted in MN titres \geq 40 and merely 39 of them presented seroprotective MN titres \geq 160 referable to just 13 human sera. The statistical analysis of the median of differences between the titres confirmed that MN titres against H3 strains were higher than those obtained for H1 (p<0.01) and H2 (p<0.05).

Conclusion: Seasonal influenza vaccination antibodies do not appear to be cross-reactive with contemporary avian H1, H2 or H3 subtype viruses of Eurasian lineage.

21.072 Detection and phylogeny of coronavirus in Costa Rica neotropical bats

A. E. Moreira-Soto¹, L. M. Taylor¹, B. Rodriguez¹, E. Corrales-Aguilar¹, C. Jimenez²

¹Universidad de Costa Rica, San Jose, Costa Rica, ²Universidad Nacional, Heredia, Costa Rica

Background: Bats have been involved as reservoirs in outbreaks of zoonotic emerging diseases that can cause spillover events to other mammals. After the 2003 SARS outbreak and its putative bat origin, several research groups have found alpha- and betacoronavirus in different bat species throughout the world.

In Costa Rica, several genera of bats previously detected with Coronavirus are present. Thus, the screening for coronavirus in this country is of utmost importance due to its high bat biodiversity, its geographical role as species crossing bridge, and will provide valuable clues concerning virus evolution.

Objectives: Screening of different Costa Rican bat species for coronavirus presence and the phylogenetic analysis of the sequences found.

Methods and Materials: Fecal samples were collected form bats captured at different locations in Costa Rica. RNA was extracted using TRIzol reagent and retrotranscribed into cDNA. RT-PCR for a conserved region of RdRp was done and correct size-bands were purified for sequencing. RdRp sequences were analyzed using ClustalW (http://workbench.sdsc.edu). Phylogenetic trees were constructed using the neighbor-joining method (PAUP* 4.0, Sinauer Associates, Inc., USA).

International Meeting on Emerging Diseases and Surveillance 2013

Results: 145 anal swabs/fecal samples were screened for coronavirus RdRp gene sequences. 4 families, 11 genera, and 19 species of bats were analyzed. Low total prevalence (1.3%) for the targeted sequence of the bat CoV genome was found. Surprisingly the prevalence for *Artibeus jamaicensis* was 3%, and an urban location presented a 4,7% prevalence. Furthermost, CoV prevalence for *Carollia perspicillata* was 4,16%.

Poster Presentations I

Analysis of nucleotide sequences showed that all CO-Bt-CoVs found belong to alphacoronavirus and have some similarities to those published for the Asian bat alphacoronaviruses. Nevertheless, there is enough dissimilarity found suggesting that Costa Rican samples may represent unique coronaviruses.



Map of Costa Rica showing the locations of bat collection sites.

Bat Species (Family)	Location	Total tested (total positive)	
Pteronotus parnellii (Mormoopidae)	PV	7 (0)	
Carollia subrufa (Phyllostomidae)	PV	2 (0)	
Carollia perspicillata (Phyllostomidae)	PV, Ti	24(1)	
Carollia sowelli (Phyllostomidae)	PV, VS, TI	13(0)	
Carollia castanea (Phyllostomidae)	VS, TI	8 (0) 34 (1)	
Artibeus jamaicensis (Phyllostomidae)	PV,VS,UCR,TI		
Artibeus lituratus (Phyllostomidae)	PV,UCR	2 (0)	
Desmodus rotundus (Phyllostomidae)	PV,TI, MAG1	6 (0)	
Glossophaga soricina (Phyllostomidae)	UCR	6 (0)	
Glossophaga comissarisi (Phyllostomidae)	UCR	3 (0)	
Noctilio albiventris (Noctilionidae)	PV	5 (0)	
Sturnira Iudovici (Phyllostomidae)	VS	10 (0)	
Sturnira lilium (Phyllostomidae)	PV,VS,UCR	5 (0)	
Sturnira mordax (Phyllostomidae)	VS	1(0)	
Lampronycteris brachyotis (Phyllostomidae)	PV	2 (0)	
Trachops cirrhosus(Phyllostomidae)	PV	3 (0)	
Eptesicus brasiliensis (Vespertilionidae)	TI	10 (0)	
Eptesicus furnalis (Vespertilionidae)	TI	3 (O)	
Myotis nigricans (Vespertilionidae)	TI	1(0)	
Total		145	

Total number and location of bat species collected and tested during 2012, showing bat coronavirus positivity.

Conclusion: Two different bat species, from urban locations, were found positive for the detection of coronavirus. None presented obvious signs of disease suggesting subclinical or persistent disease. Though sequence similarity was found with a bat coronavirus from China, we suggest that the viruses found may represent a unique group of coronavirus due to subtle sequence differences observed.

21.073 Genetic diversity of *Brucella* isolates in Georgia

E. Zghenti¹, M. Zakalashvili¹, L. Malania¹, L. Sanodze¹, T. Akhvlediani², N. Kokaia³, E. Mamisahsvili⁴, N. Trapaidze² ¹National Center for Disease Control and Public Health, Tbilisi, Georgia, ²WRAIR-USAMRIID Clinical Research Unit, Tbilisi, Georgia, ³Medical Parasitology and Tropical Medicine Research Institute, Tbilisi, Georgia, ⁴Laboratory for the Ministry of Agriculture, Tbilisi, Georgia

Background: Brucellosis is a highly contagious zoonotic disease caused by the genus *Brucella* thatremains endemic in Georgia causing substantial human morbidity and significant agricultural economic loss. In addition, *Brucella* species are considered potential biological threat agents. Precise genetic characterization of *Brucella* isolates by molecular typing methods can provide useful tools for the description of strain diversity, detection of clonal groups, trace-back to sources

of infection and discrimination of naturally occurring outbreaks from a bioterrorist event. Recent studies have demonstrated that multiplelocus variable-number tandem-repeat analysis (MLVA) is a high resolution genetic subtyping tool that can provide valuable information for epidemiological investigations.

Objectives: The aim of this study was to describe the genetic variability of 86 *Brucella* isolates obtained in Georgia from humans (N=48) and domestic ruminants (N=38) and preliminary identified as *Brucella melitensis* or *Brucella abortus*.

Methods and Materials: Genotypes were revealed bycapillary electrophoresis basedMLVA-8 and MLVA-15 typing systems, targeting eight markers with good rapid subtyping capability and seven markers providing greater resolution. Selected isolates were also characterized by a gel-based MLVA-16 typing system.

Results: Initial MLVA-8 analysis revealed four clusters of *B. abortus* and a single cluster of *B. melitensis* that was further disaggregated into two clusters by application of more highly discriminatory MLVA-15 approach. In addition, the latter revealed three outlying isolates, two *B. melitensis* and one *B. abortus*. Data were utilized for construction of the phylogenic tree and evaluation of geographical distribution of various *Brucella* genotypes countrywide.

Conclusion: Human isolates in this study were more widely geographically distributed than animal isolates. The presence of three genetic outliers suggests that diversity of *Brucella* strains in Georgia is greater than captured in this study. Revealed clonal relationships support the hypothesis that mixed herding allows transient infection of bovines with *B. melitensis* that in turn could be ingested by humans through milk. An indication of the existence of this type of transmission was only revealed by using the MLVA subtyping approach that was introduced in this project. Establishment of MLVA-16 genotyping capability will allow comparison of Georgian and European community strains.

21.074 Human brucellosis in Georgia: Prevalence and distribution of the infection

N. Trapaidze¹, T. Akhvlediani¹, L. Sanodze², N. Garuchava², N. Kokaia³, N. Chitadze², S. Saghinadze², L. Malania², M. Ramishvili² ¹WRAIR-USAMRIID Clinical Research Unit, Tbilisi, Georgia, ²National Center for Disease Control and Public Health, Tbilisi, Georgia, ³Medical Parasitology and Tropical Medicine Research Institute, Tbilisi, Georgia

Background: *Brucellosis* is an ancient zoonotic disease that still persists as significant threat to the public health and economy of Georgia. The brucellosis incidence rate increased from 2.9 to 4.5 cases per 100,000 population in last five years. As elsewhere, passive surveillance systems do not reveal the true disease burden.

Objectives: This study aims to assess the burden and regional distribution of human brucellosis with the final goal to improve the brucellosis surveillance system in Georgia.

Methods and Materials: Adult volunteers (>18 years) with symptoms consistent with brucellosis were recruited at the Virsaladze Research Institute of Medical Parasitology and Tropical Medicine. Household members of confirmed cases and community controls were also offered participation and screened for the presence of brucellosis determinants. Clinical, epidemiological information and blood specimens were collected at initial and follow-up visits. The samples were subjected to serological tests such as agglutination and ELISA. Blood culture testing was conducted.

Results: A total of 80 suspected cases, 50 household members and 20 community controls for confirmed cases were enrolled and tested. The routine serological laboratory test, tube agglutination was positive in 50% (n=40) of suspected cases, 4% (n=2) of household members and 5% (n=1) of controls. Nevertheless, 15% (6/40) of initially serologically negative cases were later found positive by culture and detectable seroconversion. Thus, 57.5% (46/80) of enrolled suspected subjects had a laboratory confirmed diagnosis of brucellosis. Anti-*Brucella* total immunoglobulin or IgG was also detected in 12% (6/50) of asymptomatic household members and 25% (5/20) of community

Poster Presentations I

International Meeting on Emerging Diseases and Surveillance 2013

controls. The majority of symptomatic as well as laboratory confirmed human brucellosis cases were inhabitants of Kakheti (43% and 23.75%) and Qvemo-Qartli (38% and 22.5%) regions.

Conclusion: Our results demonstrate the existence of undetected human brucellosis cases in Georgia. The similar rate of brucellosis found among household members and the surrounding population suggests that brucellosis is also prevalent in these groups. Based on these findings, we propose the implementation of an active surveillance program for brucellosis with sensitive and effective laboratory diagnostic testing to significantly increase the early detection of these unrecognized brucellosis cases in Georgia.

21.075 Evidence for transfer of West Nile Virus between African countries by migrating birds: Comparing migratory connectedness with West Nile phylogenetic connectedness

C. L. Risley, A. Rich, M. Baylis

Institute of Infection & Global Health, University of Liverpool, Chester, United Kingdom

Background: West Nile virus is currently invading Southern Europe and the role of bird migration in its spread is not currently well known. We attempted to detect the signal of introduction of West Nile to new coutries via bird migration by comparing volume of migrating susceptible birds with West Nile Virus strain sequence similarity.

Objectives: 1) Classification of migratory bird species with regard to West Nile susceptibility; 2) Quantification of migration of these species between African countires where West Nile strain data are available; 3) Quantification of strain sequence similarity between African countries; and 4) Correlation of strain sequence similarity and migratory connectedness, adjusting for covariates associated with human activity.

Methods and Materials: Nine authoritative bird encyclopedia detailing migration in Africa by species were searched through, in addition to online sources of bird migration information. For those species living in countries where West Nile strain data were available and susceptible to the virus, population size estaimates by country and migration routes by species were used to estimate migratory connectness by species where this was not explicity given.

West Nile Virus strain sequences were obtained from NCBI's nucleotide database and compared using BLAST to give values for strain sequence similarity between countries.

Strain sequence similarity was compared to migratory connectness correcting for distance between countries and international flights connecting them.

Results: We detected a signal of bird migration in the similarity of strains between countries; a regression by country of strain sequence similarity on bird migratory connectedness, adjusted for international air traffic connectedness, produced a significant positive correlation.

Conclusion: Africa is the continent of emergence and early evolution of West Nile and therefore the deepest diversity of West Nile strains are found between African countries. The detection of the signal of intercountry bird migration within Africa indicates that bird migration may have played a significant role in the early spread of the disease.

21.076 Avian influenza H5 subtype antibodies in apparently healthy local poultry in live bird markets in Jigawa State, Nigeria

R. Miko¹, A. Assam², P. A. Abdu² ¹Ministry of Agriculture, Dutse, Jigawa, Nigeria, ²Ahmadu Bello University, Zaria -Nigeria, Zaria, kaduna, Nigeria

Background: Jigawa State with over 90% of its poultry being extensively managed local poultry has a vast wetland, the Hadejia Nguru wetland, which serves as a center for aggregation of migratory' birds from Europe and Asia. The wetland provides a point of interaction between migratory wild birds, resident wild birds and local poultry which are of great significance in the ecology of avian influenza. Avian influenza outbreak in Jigawa State involved local poultry usually traded in live bird markets and constitutes the bulk of the poultry population in the State.

IMED 2013

Objectives: The study surveyed for avian influenza antibodies in local poultry in live bird markets.

Methods and Materials: Three hundred and ninety six sera were collected and tested by haemagglutination inhibition test.

Results: Overall avian influenza H5 subtype antibody prevalence and mean titre were 12.1 % and 7.73±0.35 log, respectively. The prevalence and mean titre were 12.15% and 7.30±0.50 log, respectively for chickens; 16.39% and 9.90±0.10 \log_2 and 9.92%/ 6.92±0.58 \log_2 for ducks and guinea fowls respectively. Taura live bird market had the highest prevalence of 39.1% with a mean titre of $9.9 \pm 0.11 \log_{2}$

Conclusion: Chickens, ducks and guinea fowls in live bird markets in Jigawa State were exposed to H5 subtype antigen and are likely to maintain avian influenza virus in the markets. There is a need for continuous active surveillance for avian influenza virus in live bird markets especially in States where there are high likelihoods of poultrymigratory wild bird interaction.

21.077 Perils of pigs and PICCs: Septic shock secondary to two plant pathogens in a pig farmer

H. Yadav, D. Manning Mayo Clinic, Rochester, MN, USA

Background: Increasingly, patients are receiving outpatient parenteral intravenous therapy though peripherally inserted central catheters (PICC). We describe a case of polymicrobial septic shock in a 54-yearold nurse from Pantoea sp. and Tsukamurella pulmonis. The patient was an avid gardener and pig farmer, two plausible sources of the polymicrobial infection.

Objectives: Increase awareness of atypical blood stream infections that result from increased use of long-term intravascular catheters.

Methods and Materials: Case report.

Results: A 54-year-old female was evaluated for a second opinion for a multifocal inflammatory CNS vasculitis, currently being managed with monthly infusions of intravenous immunoglobulins (IVIG) via PICC line. During her outpatient evaluation, she developed fevers, chills and felt generally unwell. She presented to the Emergency Room and was found to be hypotensive and tachycardic. She underwent aggressive fluid resuscitation, and was started on broad spectrum antibiotic therapies with ciprofloxacin, cefepime and vancomycin. Chest X-ray and urine analysis were negative. Her PICC line was removed. Once stabilized, further history was obtained. She was a full time nurse currently living on a farm where she was involved with gardening (growing fruit and vegetables), as well as caring for the farm swine livestock.

After initial resuscitation, her clinical status improved rapidly. After 9 hours peripheral and catheter blood cultures grew a gram negative bacterium, later speciated to Pantoea sp. (sensitive to beta-lactams, quinolones and aminoglycosides). After 28 hours, blood cultures also grew a gram positive coccus, later speciated to Tsukamurella pulmonis (sensitive to quinolones and aminoglycosides, resistant to beta lactams).

She continued to make improvements and was discharged from hospital on day 3 with a 14 day course of ciprofloxacin.

Conclusion: Long-term indwelling vascular catheters increase risk of blood stream infections. We describe an unusual case of polymicrobial septic shock from two rare human pathogens, both plant pathogens, in an avid farmer. In patients who absolutely need long-term indwelling vascular catheters, counseling should take place on appropriate hygiene measures to minimize risk of bacterial contamination.

21.078

Two outbreaks of hemorrhagic fever with renal syndome in Albania

P. Biberaj¹, M. Kota², N. Como³, E. Koreta², E. Tomini², D. Kraja⁴, A. Ndreu⁵, S. Bino²

¹Faculty of Medical Sciences. University of Tirana. Tirana. Al. Albania. ²Institute of Public Health, Tirana, Albania, ³UHC "Mother Teresa", Tirana, Albania, ⁴U.H.C. "Mother Teresa", Tirana, Albania, ⁵UHC "Mother Teresa", Tirane, Albania

Background: Hemorrhagic fever with renal syndrome (HFRS) have been identified in northern Albania in 1986. Most of the case shave been related to Dobrava-Belgrade virus (DOBV) hosted by different

International Meeting on Emerging Diseases and Surveillance 2013

rodent species, *Apodemus flavicollis* and *Apodemus agrarius* also present in Albania. Since then several case have been identified almost every year but not outbreaks. DOBV has been identified as the most virulent one found in Europe.

Objectives: We want to analyze common risk factors and differences of two main outbreaks of HFRS that were identified in Albanian in 2011. Also we want describe the importance of case definition and its adaptation during the investigation.

Methods and Materials: We have made a retrospective analyses of HFRS cases admitted at the Infectious Diseases and Nephrology Department of Tirana University Hospital. Also we analysed data obtained during contact tracing provided by the Institute of Public Health. Blood samples were tested with ELISA(Vector Best, Rusi) and IFA (Euroimmune, Germany) to discover IgM and IgG antibodies.

Results: From June to September 2011, seven cases of HFRS were identified in Tirana University Hospital Center. Hemorrhagic fever and jaundice predominated in 5 cases and later were accompanied with acute renal failure. All cases belonged to a group of miners in central north Albania where hantavirues were found nearby in *Apodemus agrarius* rodents. The index case had jaundice and hemorrhagic fever but also pulmonary hemorrhage and had a fatal outcome. Three other cases were identified during the investigation of all jaundices and unexplained fever as well as all acute renal failure cases coming from the same area as the index case. The other outbreak was related to another index case of jaundice and thrombocytopenia and acute renal syndrome. Two other cases were identified during contact tracing related to place, time and person. All were shepherds and operating in South East of Albania, an area where few cases of HFRS were identified in the past.

Conclusion: HFRS can be found in different areas of Albania and it is related to selected professions such as shepherds and miners. Other syndromes than hemorrhagic fever and contact tracing are important for identification of outbreaks

21.079 Pathogenic *Leptospira* in wild rodents in Cape Verde

A. Martín-Alonso¹, P. Foronda¹, A. Fernandez-Alvarez¹,

G. Bonnet¹, C. Feliu², B. Valladares¹

¹University Institute of Tropical Diseases and Public Health of the Canary Islands, University of La Laguna, Santa Cruz de Tenerife, Spain, ²University of Barcelona, Barcelona, Spain

Background: Cape Verde is an Archipelago situated at the NW off Senegal. Although leptospirosis is a disease that has been found in humans, no previous data about the presence on definitive hosts has been reported. Humans are infected by close contact with animals and contaminated water with the urine of infected animals. Rodents, *Mus* species and rats (*Rattus norvegicus* and *Rattus rattus*), are the most important reservoir hosts.

Objectives: The aim of this study was the identification of the reservoirs of pathogenic leptospiral species.

Methods and Materials: Urine samples and the urinary bladder of wild rodents (*R. rattus* and *Mus musculus domesticus*) from Cape Verde were preserved in 100% ethanol. DNA extraction was carried out using the Fast DNA (BIO 101 Systems) kit. Samples were analyzed by PCR. *L. interrogans* serovar Icterohaemorragiae was used as a positive control. Amplicons of interest were sequenced.

Results: Positive cases for *Leptospira* species were detected in rodents. These samples amplified for a genomic fragment present only in pathogenic *Leptospira* species, which targets the *Leptospira* lipL32 region. Some areas showed prevalences even higher than 10%. A distribution map was carried out in order to highlight the presence of these bacteria in the Archipelago. A χ^2 test was performed and the differences between areas and hosts were studied.

Conclusion: The lipL32fragment is useful since it only amplifies in pathogenic *Leptospira* species. In Cape Verde, and from the public health point of view, it is relevant the identification for first time of pathogenic *Leptospira* species in rodents, since leptospirosis is an important zoonotic emerging infectious disease. It is characterized by fever, renal and hepatic insufficiency, pulmonary manifestations and reproductive failure.

Furthermore, the high incidence of *Leptospira* among rodents, suggests that rodent population could play an important role in the transmission of human leptospirosis via environmental contamination in Cape Verde.

Supported by a grant of the Canary Government, A1/035356/11 and CGL 2009-07759BOS.

21.080 *Brucella abortus* in cattle and buffaloes in Bangladesh

M. S. Rahman

Bangladesh Agricultural University, Mymensingh, Bangladesh

Background: Brucellosis is an important zoonotic disease distributed worldwide including Bangladesh. Prevalence of brucellosis has been widely investigated on the basis of serological test in livestock but no study was devoted to identify the specific *Brucella* species prevalent in Bangladesh using the molecular tools.

Objectives: The objective was to determine the prevalence of *Brucella* species in cattle and buffaloes in Bangladesh through qRT-PCR.

Methods and Materials: A total of 799 serum samples of cattle and buffaloes were collected from the different districts of Bangladesh. The sera samples were analyzed by screening test such as Rose Bengal Test (RBT) and then the RBT positive sera were re-tested with SAT, CFT, ELISA and quantitative real time PCR (qRT-PCR). *Brucella abortus* specific DNA was confirmed by qRT-PCR.

Results: Out of 799 serum samples, 44 serum samples reacted positive in the Rose Bengal test (RBT); among the RBT positive serum, 24 sera were found to contain *Brucella* DNA by genus specific IS711 screening using quantitative real time PCR (qRT-PCR); and out of 24 qRT-PCR positive samples, 19 samples found to contain specifically *Brucella abortus* DNA.

Conclusion: This is the first proof that *Brucella abortus* is endemic in cattle and buffaloes in Bangladesh. A combination of RBT and PCR could be effective for future eradication programmes.

21.081 Evolution of U.S. foot-and-mouth disease response strategy

H. Allen, A. Taylor LMI, McLean, VA, USA

Background: Throughout the 20th century the primary response strategy of the United States to an outbreak of foot-and-mouth disease (FMD)—one of the most devastating diseases of livestock—was stamping-out. Stamping-out is the depopulation of clinically affected and in-contact susceptible animals. Improved veterinary countermeasures, changing social norms, and the speed and magnitude of commerce require that the United States reevaluates this policy for the 21st century.

Objectives: To examine the experiences of the United States and other nations with developed veterinary infrastructure in order to identify the critical factors that led the evolution of the U.S. response strategy.

Methods and Materials: A thorough literature review, which included official reports of U.S. FMD outbreaks from 1914-1929; documentation on vaccine bank creation; and careful examination of peer-reviewed articles on outbreaks in previously FMD-free countries. Additional textual analysis was conducted on past and current U.S. FMD response plans, identifying the use of the term 'vaccination' or 'emergency vaccination' indicating the potential use of strategies other than stamping-out.

Results: The United States has shifted from a strategy of exclusively stamping-out to a response strategy that would consider emergency vaccination in *any* FMD outbreak. This evolution was punctuated by the creation of FMD vaccine banks, and a focus on using vaccine as a strategy of last resort. This shift was due to technical and industry/ economic factors: improved biologics, in the form of vaccine-antigen concentrate, which enabled lower cost and more feasible vaccine storage; and the likely inability to effectively execute a stamping-out strategy, due to the magnitude of the U.S. livestock industry.

Conclusion: A U.S. FMD outbreak is likely to rapidly outpace the

International Meeting on Emerging Diseases and Surveillance 2013

current capacity for stamping-out. With rapid livestock movement, any delay in detection-as evidenced in other countries-could create a widespread outbreak; emergency vaccination as a response strategy would assist in containing and ultimately eradicating FMD. Though the United States' policy states that emergency vaccination will be considered in any FMD response, additional work must be completed to develop transparent and executable vaccination response plans so emergency vaccination is a viable strategy in practice.

21.082 Health problems on the pig farm and detection of antibodies against Mycoplasma

hyopneumoniae (case study) M. Prokeš, A. Ondrejková, R. Ondrejka, Ľ. Korytár, E. Slepecká, P. Čechvala, A. Récky

University of Veterinary Medicine and Pharmacy in Košice, Kosice, Slovakia

Background: The health status of pigs is one of the key success factors in pigmeat production. Enzootic pneumonia of pigs is caused by the bacterium Mycoplasma hyopneumoniae, as most mycoplasma disease of pigs is of great economic importance, particularly in terms of low weight gain in animals that carried disease in mild form.

Objectives: The aim of our study was to detect antibodies against M. hyopneumoniae in pigs with respiratory diseases and to suggest preventive precautions.

Methods and Materials: The samples were collected in October 2012 on the pig farm in district of Trebišov in Slovakia with a closedherd production system. The number of samples was proportional to the number of pigs on farm (5%). A total of 20 blood samples were collected from two to three months old growing pigs, from a population of White Improved pig breed with signs of respiratory disease. We observed a dry and non-productive cough as a typical symptom of enzootic pneumonia. The herds were not treated with antibiotics in this time. They were not vaccinated against infectious diseases either. Blood samples from pigs were obtained by jugular vein puncture. Serum was analysed for the presence of antibodies to M. hyopneumoniae using a blocking ELISA (OXOID Ltd, UK).

Results: Using an ELISA assay we detected from sera 100% (20/20) positive samples for the presence of antibody against M. hyopneumoniae. Our results are comparable with findings from neighboring states, Europe and beyond. In Poland it was 91.3% (Dors at al. 2012). In Germany, seropositivity was 65% from 2578 tested sows (Grosse-Beilage at al. 2009). Mattsson at al. (1995) detected by ELISA in Sweden a prevalence of antibodies against M. hyopneumoniae in 90% of pias.

Conclusion: Ideal detection of M. hyopneumoniae is suitable extend with using ELISA, which gives us a broader view of the emergence and development of disease. The presence of enzootic porcine pneumonia had a negative impact on the health and productivity of farm pigs. Preventing direct contact of newborn piglets with the sow and other contaminated pigs, or contact between different age groups of animals, vaccination, welfare also belong to preventive measures. This work was supported by KEGA 009UVLF-4/2011.

21.083 Prion expression inhibition by antisenseoligodeoxynucleotides for Transmissible Spongiform Encephalopathy (TSE) treatment and prevention

L. Ivanytska¹, A. Zaichenko², V. Vlizlo¹

¹Institute of Animal Biology NAAS, Lviv, Ukraine, ²Lviv Polytechnic National University, Lviv, Ukraine

Background: It was ascertained that presence of normal PrPc is absolutely necessary for prion infection development. Targeting PrPc has the potential to remove substrate for the TSE pathogenesis so this is a promising strategy for development of safe and effective means for treatment and prevention prion infections.

Objectives: In accordance to this aim of our study was to decrease the cellular prion expression level in vivo by antisense oligodeoxyribonucleotides (asODNs) toward prion mRNA.

Methods and Materials: 5'-TCTGCTGCTCTGACAACGC-3', 5'-AGTAGCCAAGGTTCGCCAT-3', 5'-ATGCTTGAGGTTGGTT-3' asODNs were used to decrease prion expression level. As a carrier for asODNs novel dimethylaminoethylmethacrylate oligoelectrolite 1D was tested. AsODNs-binding ability was studied using UV-spectroscopy and turbidimetry. Size of polyplexes was measured by light scattering. Sensitivity of asODNs molecules complexed with oligoelectrolyte 1D against serum nucleases was assessed by PAAG electrophoresis. Level of PrP^c expression in rat prion-replicating organs was evaluated by western blotting and immunohistochemistry. Toxicity testing of novel oligoelectrolite 1D in vivo included hematology, blood biochemistry and histological investigations as well as functional observation battery examination to evaluate potential toxicity to the nervous system.

Results: Selected asODNs incorporated in cationic immunoliposomes have decreased expression of the prion to 40 % of control level in the spleen and intestine of rats but haven't in the brain. So in order to gain inhibition of PrP^c expression in brain we have used alternative asODN delivery system. Formation of highly stable nanoscale (35-95 nm) intermolecular complexes between 1D and asODNs protects asODNs from nucleases degradation in serum up to 24 hs. These complexes were capable to overcome the blood-brain barrier and decreased PrP^{c} expression in brain to 48.1 \pm 6.1 % for 48 hours. Higher priondecreasing activity of asODNs-1D complexes was ascertained in the spleen and intestine. Testing in vivo showed very low toxicity of oligoelectrolite 1D.

Conclusion: There were developed effective asODNs and their delivery system for inhibition prion expression in rat brain. This gives a ground for future investigations of asODNs as drugs for prion infections prevention and treatment.

21.084 Associations between intestinal lesions and detection of Clostridium perfringens type A or beta-2 toxin in neonatal piglets with diarrhoea

H. Kongsted¹, B. Jonach², B. Kokotovic², J. P. Nielsen³ ¹Danish Agriculture & Food Council, Kjellerup, Denmark, ²Technical University of Denmark, Copenhagen, Denmark, ³University of Copenhagen, Copenhagen, Denmark

Background: The etiological significance of *Clostridium perfringens* type A (CpA) in piglet neonatal enteritis is unclear. Experimental data have shown an association between infection with this bacterium and intestinal lesions (Johannsen, et al., 1993), however, these findings need to be confirmed in natural outbreaks. Furthermore, since beta-2 toxin is expected to play a role in the pathogenesis of disease (Bueschel, et al., 2003), associations between the presence of this toxin and pathological findings need to be evaluated.

Objectives: To evaluate associations between gross- and histopathological lesions and the presence of CpA and beta2 toxin in piglets from outbreaks of diarrhoea in 4 herds.

Methods and Materials: A total of51 diarrhoeic piglets aged 3-7 days were macroscopically and microscopically examined. CpA was cultured anaerobically and typed by PCR. A Clostridium perfringens spp targeted probe was used for flourescent in situ hybridization (FISH) of intestinal tissue. Detection of beta-2 toxin in intestinal contents was performed by ELISA. Associations between intestinal lesions and detection of the bacterium (by culture or FISH) / beta2-toxin were evaluated using two-sided Fisher's exact tests (a=0.05).

Results: No positive associations between intestinal lesions and detection of bacterium/beta-2 toxin were seen. In contrast, with respect to certain lesions, negative associations were seen. These are presented in Table 1

International Meeting on Emerging Diseases and Surveillance 2013

	% CPA positive samples				% Beta-2 toxin positive samples		
	CultureFISH(n=51)(n=51))	ELISA (n=45)			
Intestinal lesion	Lp	Lnp	Lp	Lnp	Lp	Lnp	
Dilatation of small intestine	24%	64%					
Dilatation of large intestine	19%	54%			32%	83%	
Villous atrophy	22%	58%					
Small intestinal epithelial lesions			60%	90%	25%	65%	

Table 1. Associations between intestinal lesions and detection of *CpA* and beta-2 toxin. Lp=Lesion present, Lnp= Lesion not present. Only statistically significant associations are presented.

Conclusion: Demonstration of CpA or Beta-2 toxin was not associated with intestinal lesions. On the contrary, occurrence of CpA or Beta-2 toxin was associated with reduced risk of intestinal lesions. The biological significance of this finding needs further investigation.

21.085 Prevalence of *Toxoplasma gondii* in Greek swine industry

V. Papatsiros¹, D. Stougiou², S. Boutsini², L. Athanasiou¹,

G. Christodoulopoulos¹, P. Tsampalis³, A. Bisias²

¹University of Thessaly, Karditsa, Greece, ²Center of Athens

Veterinary Institutions, Ministry of Rural Development and Food, Greece, Athens, Greece, ³Veterinary Directorate of Thessaly Region, Greece, Larissa, Greece

Background: Toxoplasmosis is a globally distributed zoonosis. Most species of livestock, including sheep, goats, and pigs, are susceptible to infection with *Toxoplasma gondii*.

Objectives: The aim of the present study is to investigate the seroprevalence of *Toxoplasma gondii* infection in Greek swine population.

Methods and Materials: Total 371 blood samples were collected at slaughterhouses form 55 different swine farms in Central Greece, including samples from fattening pigs and sows. The Central Greece is one of the main areas of high-density commercial swine production in Greece. The samples were collected from different capacity (small, medium and large-scale) and biosecurity level commercial farms as well as from a few organic farms.

The samples were tested for the detection of Anti-Toxoplasma gondii antibodies using indirect commercial ELISA kit (ID Screen® Toxoplasmosis Indirect ELISA–IDvet).

Results: The results indicated that the presence of *Toxoplasma gondii* in Greek swine industry is not an important risk factor. Only 5.4% (20/371, 8 sows and 12 fattening pigs) of tested samples were positive, derived from 7 positive swine farms (12.7%). Most positive samples came from farms that are located close to semi-mountains areas, with wealthy wildlife

Conclusion: Based on the results of the present study, the prevalence of *Toxoplasma gondii* is low for swine industry in Greece up to now. However, wildlife, as rodents remain the main risk factor for transmission of *Toxoplasma gondii* in Greek swine farms.

21.086 Serosurveillance of foot and mouth disease virus in Asian elephants in Thailand

D. Ounpomma¹, **W. Linchongsubongkoch**², P. Charoenphan³, W. Pintawong⁴, T. Yano⁵

¹Vetrinary Research and Development Center, Meung, Khon Kaen, Thailand, ²National Institute of Animal Health, Pakchong, Nakhonratchasima, Thailand, ³ National Institute of Elephant Research and Health, Meung, Surin, Thailand, ⁴National Institute of Elephant Research and Health, Meung, Surin, Thailand, ⁵Faculty of Veterinary Medicine, Meung, Chiang Mai, Thailand **Background:** Foot and mouth disease (FMD) is highly contagious viral disease in cloven-hooved livestock and wildlife, There was only single reported of FMD in elephant in Thailand in 1993. Serotypes O and A are considered endemic in Thailand, there has been national strategic plan to control and eradication of FMD for establishment the FMD free country under the Southeast Asia and China FMD Control Campaign (SEACFMD). The disease surveillance and monitoring of susceptible animals including elephants were investigated. Recently, many elephant camps were located in tourist places and were used for working or tourist riding. Therefore, this might be a risk in receiving FMD from other animals near by.

Objectives: To study serosurveillance of FMDV in Asian elephants, due to no information of FMD was reported.

Methods and Materials: Total 689 bloods were used to determine antibody to FMDV type O, A and Asia1 by liquid phase blocking ELISA (LP ELISA), parellel with the detection of antibody to 3ABC non structural protein of FMD (3ABC NSP) and virus infection associated antigen (VIAA) by agar gel immunodiffusion (AGID).

Results: The result of antibody to FMDV type O, A and Asia1 were indicated as 100% of sero-negative to all 3 serotypes. Similarly results were found as 100% negative by 3ABC NSP and 100% negative by VIAA-AGID test in the same samples. There was an accidental case of FMD type O infected in one elephant at elephant camp, tracing back to the source of infection was by oral route from congestion contaminated feed from infected cattle excretion in that area.

Conclusion: Serosurveillance of FMDV in Asian elephants during 2010-2012 were studied, totally 689 serum samples were collected from 13 provinces in Thailand where elephant camps were located and used for working or tourist riding. The LP ELISA was used to determine antibody to FMD type O, A and Asia1, the result was found no antibody obtained in all elephnat sera or 100% sero-negative. The NSP result was 100% negative to 3ABC NSP and 100% negative to VIAA. In conclusion, those elephants have not been infected with FMDV and also they have never been vaccinted with FMD vaccine before. This information would be useful in supporting the control and eradication of FMD in Thailand.

21.087 Chemical decontamination of live animals contaminated with African swine fever virus

Y. Selyaninov¹, I. Egorova¹, V. Balishev¹, **O. Tatarchuk**² ¹National Research Institute for Veterinary Virology and Microbiology of Russia (NRIVVaMR), Pokrov, Russian Federation, ²KRKA FARMA, Moscow, Russian Federation

Background: Since 2007, when the first outbreak of African swine fever (ASF) in the Russian Federation has occured, the disease has spread to 26 of 83 federal districts across the country resulted in disposal of >600,000 pigs. While carrying out of ASF eradication measures, it was found that target animals for ASF virus (domestic pigs) on 45 ASF-affected sites and 309 ASF-threatened sites were confinely reared with various animals of non-target species—such as cows, horses, sheeps, chickens, dogs, cats, and rabbits. Being unaffected by ASF contagion, these non-target animals can serve as fomites, thus require decontamination before displacement from ASF-affected territories.

Objectives: To evaluate the efficacy of chemical decontamination procedures addressed to live animals of various non-target for ASF species contaminated superficially with ASF virus.

Methods and Materials: Due to the absence of any local guidance addressed to decontamination of live animals, the selection of germicides was made upon meta-analysis of their chemical and biological properties. Selected biocides were subjected to skin and eye irritation studies on rabbits. Samples of the hair coats having either <2000 hairs/cm² and >2000 hairs/cm² were employed for preliminary study with *Staph. aureus* applied at a rate of 10⁹ CFU/cm³ followed with germicidal treatments and bacteriological evaluation of decontamination efficiency. At the next stage of the study, the samples of different hair coats were contaminated with ASF virus at the rate of 7,0 lg HAU₅₀/cm³, and then subjected to germicidal treatments followed with bioassay evaluation of decontamination efficiency.

International Meeting on Emerging Diseases and Surveillance 2013

Results: Live animals having low-density hair coat (<2000 hairs/ cm²) contaminated with ASF virus and washed with 6% solution of peroxymonosulfate-based germicide Ecocid S by spraying at a rate of 500 cm³/m² became free from ASF contagion after 1-hour exposure. Anumal species having dense hair coat (>2000 hairs/cm²) required the same exposure time, but two subsequent applications of 6% Ecocid S solution at a rate of 700 cm³/m² should be performed with 30-minutes interval between applications.

Poster Presentations I

Conclusion: This study confirms the efficacy of chemical decontamination addressed to live animals contaminated with ASF virus. Implementation of such procedures would prevent pathogen from being mechanically spread by those animals which are non-target for ASF contagion.

21.088 Detection of AsHV-5 in a herd of 266 Lipizzaners throughout a period of two years

J. O. Rushton, J. Kolodziejek, N. Nowotny

Viral Zoonoses, Emerging and Vector-Borne Infections Group, Vienna, Vienna, Austria

Background: Herpesvirus infections are species specific, however recently two case reports on the detection of asinine Herpesvirus 5 (AsHV-5) in horses with pulmonary disease have been published. AsHV-5 is classified as a Gammaherpesvirus, related to equid Herpesvirus -5 and -2 To date there is little information about the pathogenicity of AsHV-5 in donkeys and horses.

Objectives: To describe the detection of AsHV-5 in a closed herd of 266 Lipizzaners—free of clinical symptoms with no reported contact with donkeys.

Methods and Materials: All Lipizzaners (266) distributed among three federal states in Austria were sampled four times over a period of two years, with six month intervals, for the detection of Herpesviruses as part of a health surveillance programme. All horses were sampled by an experienced equine veterinarian, no clinical symptoms of disease were evident in any of the horses. Quantified EHV-2 and -5 PCRs of PBMCs, nasal and conjunctival swabs of all horses were performed. Samples negative in type-specific qPCRs were subjected to nested Herpesvirus consensus PCR and sequence analysis of positive samples was carried out.

Results: Fifty one samples of 39 horses were positive for AsHV-5, seven of which were positive more often than twice. Twenty four positive results were identified in PBMCs, 22 in nasal and five in conjunctival swabs. The rate of infection was 4.5%, 5.0%, 3.6%, and 6.5% of the total study population at the first, second, third, and fourth sample period, respectively. The overall mean age of AsHV-5 positive horses was nine years (SD± 5.9); 21 mares, 16 stallions and two geldings were distributed among Styria, Vienna and Lower Austria with 29, seven and three cases respectively. No statistically significant association between gender and location of positive horses was identified.

Conclusion: Based on the results of this study AsHV-5 is ubiquitous in the equine population with an average infection rate between 3-7%. A close genetic relationship of AsHV-5 to EHV-5 exists. Further genomic research is needed to determine whether AsHV-5 is an individual Herpesvirus or a variant of EHV-5 since the longest nucleotide sequence within the DNA polymerase gene available in GenBank consists of 881bp only.

21.089 Occurrence of *Clostridium perfringens* type A and its toxins in neonatal piglets from four Danish pig farms.

B. Jonach¹, B. Kokotovic¹, H. Kongsted², M. Boye¹, T. Kåre Jensen¹ ¹Technical University of Denmark, Copenhagen, Denmark, ²Danish Agriculture & Food Counsil, Kjellerup, Denmark

Background: *Clostridium perfringens* type A is considered a common pathogen involved in neonatal diarrhea in pigs and its ability to cause disease is associated with toxin production (1). However, the pathogenesis of *Clostridium perfringens* type A diarrhea is unclear and the prevalence and significance of this disease in Denmark is unknown.

Objectives: The objective of this study was to investigate the occurrence of *Cl. perfringens* type A and its toxins (alpha and beta2) in healthy and diarrheic pigs in order to determine its association with diarrheic condition.

Methods and Materials: The study included 51 diarrheic and 50 non-diarrheic piglets aged 3-7 days from 4 Danish farms with outbreak of neonatal diarrhea, which was not due to either ETEC, rotavirus, *Clostridium perfringens* type C, *Clostridium difficile* or parasite infection. Jejunum and colon contents were examined for the presence of *Clostridium perfringens* type A by standard methods of bacterial culturing followed by typing using PCR. For detection of *Clostridium perfringens* in the intestinal tissue fluorescence in situ hybridization (FISH) was carried out with 16S rRNA-targeting oligonucleotide probe on tissue sections from duodenum, jejunum, ileum and colon. For detection of alpha and beta2 toxin ELISA tests were performed on intestinal contents from the small intestine.

Results: *Clostridium perfringens* type A was cultured from 35% of diarrheic and 70% of non-diarrheic piglets. Bacterial cells were detected by FISH in the intestinal tissue of 84% of diarrheic and 88% of non-diarrheic piglets. 78% of diarrheic and 76% of non-diarrheic piglets were positive for alpha toxin and 58% of diarrheic and 46% of non-diarrheic piglets were positive for beta2 toxin.

Conclusion: In this study the prevalence of *Clostridium perfringens* type A was higher in non-diarrheic piglets compared to diarrheic piglets and the occurrence of toxins was similar in both groups of piglets. No association between the presence of the bacterium or the examined toxins and diarrhea was observed, although there was a slightly higher occurrence of beta2 toxin in diarrheic piglets. Further investigations are necessary in order to determine the role of beta2 toxin in neonatal diarrhea.

21.090

.090 Seroepidemiology of Contagious Bovine Pleuropneumonia in Kaduna State, Nigeria

A. Suleiman, M. Bello, L. T. Zaria, A. A. Dzikwi Ahmadu Bello University, Zaria, Nigeria

Background: Contagious Bovine Pleuropneumonia, a respiratory disease of cattle caused by *Mycoplasma mycoides* subspecie *mycoides* Small Colony (*Mmm*SC) type, is the most economically important livestock disease in Africa. Nigeria suffers from the disease through deaths of cattle and exclusion from livestock products trade. The disease has presently assumed endemic stability in the country with most outbreaks occurring in the Fulani pastoral herds of the North where majority of the cattle are located. CBPP control is particularly difficult in Nigeria due to lack of epidemiological data for sustained measures which are currently estimated to cost 1.5 million US Dollars annually.

Objectives: Astudy was designed to determine CBPP seroprevalence in cattle herds by competitive Enzyme Linked Immunosorbent Assay (cELISA), assess the level of awareness of herdsmen about CBPP and identify possible risk factors associated with transmission of the disease among herds.

Methods and Materials: Five hundred and sixteen animals from 190 cattle herds in Kaduna state, North Western Nigeria were tested for antibodies to CBPP by cELISA. Questionnaires were administered to herdsmen to identify risk factors to CBPP transmission among herds.

POSTER PRESENTATIONS I

International Meeting on Emerging Diseases and Surveillance 2013



Map of Kaduna state showing the 6 local government areas involved in a study of CBPP seroepidemiology.

Results: 58.4% of the herds had at least one seropositive animal and 50 (45%) of the seropositive herds had 40-59% seropositive cattle. Odds Ratio analyses showed that CBPP seroprevalence was associated with herd size, livestock contacts (animals brought into herds) and herd dynamics (mixing at grazing and watering points). Prompted recall of CBPP clinical signs and control measures revealed that the likelihoods of having a seropositive herd significantly decreased with increasing level of awareness about the disease by the corresponding herdsmen.

Variable	Variable Level	Herds Sampled	Positive Herds	Prevalence (%)	OR	95% CI on OR
New animal brought into herd	Yes	44	42	95.5	65.63	12.90- 334.0*
	No	33	8	24.2		
Herds mixing at grazing/ watering points	Yes	47	42	89.4	23.10	6.744- 79.11*
	No	30	8	26.7		
Significant at 95% C.I						

 Table 1. Distribution of CBPP herds according to herd contacts and dynamics in Northern and Central parts of Kaduna State.

Conclusion: It was recommended that more grazing and watering facilities should be made available to cattle herds especially in dry seasons when pastures are not available.

21.091 Efficiency of *B. anthracis* detection in soils having different physicochemical properties

I. Egorova, Y. Selyaninov

National Research Institute for Veterinary Virology and Microbiology of Russia (NRIVVaMR), Pokrov, Russian Federation

Background: Current epizootic situation for anthrax in the Russian Federation is considered as a stationary problem due to existence of more than 35,000 contaminated soil foci across the country. Expansion of either urban and rural areas requires the safety evaluation of the soils suspected for contamination with anthrax spores. Significant

differencies of physical and chemical properties among different soil types may lead to a false-negative results compromising the efficiency of anthrax detection in soils.

Objectives: Evaluation of different approaches of *B. anthracis* detection in soils having different physical and chemical properties.

Methods and Materials: Different soil samples with neutral and acidic pH levels having variable clay, silt and sand content at different moisture rates were used in the study. The samples were enriched with the spores of vaccine strain STI-1 of *B. anthracis* at a rate of 1000 spores/g and kept at controlled conditions allowing the formation of "soil particle + spore" aggregates. The samples were processed for routine bacteriological examination using surface-active reagent to disaggregate the soil particles with following concentration of the samples.

Results: The lowest detection rate of *B. anthracis* spores was find in soils with acidic pH (3.0 to 5.0), high clay and/or silt particles content, and in samples with low humidity (<5%). To improve the effectiveness of *B. anthracis* spore detection in soils having the abovementioned characteristics, new approaches based on the environmental hydrogenion value shift was evaluated. It has been found that pH shifted towards a neutral level triggered in the period of the samples being prepared for microbiological investigations resulted in a destruction of the micro- and/or macroaggregates containing the pathogen spores, thus increasing the detection efficiency. The similar phenomenon was also observed with the saturation of the soil samples with the vater for prolonged time (3 hours), which was also resulted with more than 10% increase in the detection efficacy.

Conclusion: Detection of *B. anthracis* spores in soils with different physical and chemical characteristics requires special and differentiated approaches to ensure the detection efficiency is appropriate for each case of safety evaluation.



Sero-prevalence of foot and mouth disease in small ruminants of Pakistan

U. Farooq¹, A. Ullah¹, A. Latif², K. Naeem³, A. Bin Zahur⁴, M. Hussain⁵ ¹National Agricultural Research Center, Islamabad, ICT, Pakistan, ²NARC, iSLAMABAD, ICT, Pakistan, ³National Agricultural Research Center, Islamabad, ICT, Pakistan, ⁴National Agricultural Research Center, Islamabad, ICT, Pakistan, ⁵Food and Agriculture Organizatin, Islamabad, ICT, Pakistan

Background: Foot and mouth disease (FMD) is a contagious viral disease endemic in Pakistan with huge economic losses.

Objectives: This study was conducted to estimate sero-prevalence of FMD in small ruminants kept in proximity to large ruminants with a recent history of FMD outbreak. Initially, eight districts of Pakistan were selected randomly. Within each district, serum samples were collected from sheep and goats from 2010 to 2012.

Methods and Materials: A total of 1486 sera were collected; 74.16% (1102) were goat and 25.84% (384) belonged to sheep. Over half of the samples, 53.36% (793) belonged to female animals, while the rest 46.64% (693) were from male animals. Serum samples were tested for the presence of antibodies against non-structural protein (3ABC) of FMD virus using CHEKIT FMD-3ABC bo-ov kit (IDEXX laboratories, USA).

Results: The data were analyzed using χ^2 test and multiple logistic regression methods. The sero-prevalence of FMD was 22.75% (338 in small ruminants. This was significantly (χ^2 =30.93; p<0.001) higher in goats (85.80; 290) than sheep (14.20%; 48). After adjusting for other factors, the goats were 5.19 times (Odds Ratio: 5.19, 95% CI; 3.15-8.56) more likely to test sero-positive for FMD than sheep. The sero-prevalence was significantly (χ^2 =6.55; p=0.01) higher in female animals; of 338 FMD sero-positive animals 59.47% (201) were females. After adjusting for other factors, the female animals were 1.36 times (Odds Ratio: 1.36, 95% CI; 1.04-1.77) more likely to test sero-positive for FMD than male animals. The sero-prevalence in district Islamabad was significantly lower than other districts (p<0.01), there were no differences in the sero-prevalence of FMD in small ruminants in other districts.

Conclusion: The finding indicates that small ruminants kept in close contact with large ruminants can be reservoirs of FMD virus and can transmit FMD to susceptible livestock.

International Meeting on Emerging Diseases and Surveillance 2013

21.093 Persistence of equine piroplasmosis in polo and pleasure horses in Nigeria

P. W. Mshelia

Ahmadu Bello University, Zaria, Nigeria

Background: The continuing prevalence of Equine Piroplasmosis (EP) in Nigeria has important implications in the health and welfare of horses. The non-specific clinical signs commonly seen in horses in Nigeria including weight loss, lack of appetite and poor performance have raised questions of the possible causes of these signs.

Objectives: A total of 156 horses were sampled from 2007 to 2012 from four widely separated states of Nigeria in order to determine the prevalence of piroplasmosis among polo and pleasure horses, and the clinical correlation of EP with the impending non-specific signs. The breeds of horses sampled include West African dongola, Arabian, Sudan country-bred and Argentine Thoroughbred horses.

Methods and Materials: A detail history was taken and a thorough physical examination was performed. A direct examination of all the sampled blood was carried out using giemsa stain where *Theileria equi* and Babesia caballi was demonstrated. Tick infestation was seen in some cases. All the horses had a history of extensive travelling within the year of study. Out of the 153 blood samples tested 16(10.5%) were positive for *Theileria equi* while 4(2.6%) were positive for *Babesia caballi*.

Results: Out of the 153 blood samples tested 16(10.5%) were positive for *Theileria equi* while 4(2.6%) were positive for *Babesia caballi*. This demonstrated that 20(13%) out of 153 was positive for piroplasmosis. The presence of a bilateral purulent ocular discharge was common among all the horses at the onset of EP infection and relaxation of the anal sphincter was common among the Argentine Thoroughbred especially in acute and subacute forms of EP.

Conclusion: The nationwide distribution of EP could be related to the presence of the vectors. Also, there is a clear indication that the non-specific signs have a positive clinical correlation with EP. Finally, some of the horses that were negative for piroplasmosis could actually be positive considering the fact that "carrier horses" and in most cases of *Babesia caballi*, parasetemia is very low and determination on giemsa stain is usually a difficult task.

21.094 Real-time PCR for diagnosis of contagious equine metritis (CEM)

S. Artiushin¹, U. Balasuriya¹, M. Erdman²

¹University of Kentucky, Lexington, KY, USA, ²National Veterinary Services Laboratories, Ames, IA, USA

Background: The national and international movement of horses and semen considerably increases the risk of spread of several infectious diseases including contagious equine metritis (CEM).CEM caused by *Taylorella equigenitalis* (Teq) is a highly transmissible, acute venereal disease leading to infertility, endometritis and abortion in mares. Since there is no vaccine to prevent CEM the diagnosis and subsequent quarantine along with sanitation and antibiotic treatment of affected horses are the only options for control of this disease. Several PCR and real-time PCR assays targeting 16S ribosomal RNA gene of Teq with same gene of *T. asinigenitalis* (Tas) and other bacteria may lead to false-positive results.

Objectives: Develop a novel more specific TaqMan real-time PCR assay for the identification of Teq in samples from horses.

Methods and Materials: A panel of primers and probes specific for Teq was designed following comparative analysis of Teq and Tas gene sequences available in GenBank. Specificity and sensitivity of real-time PCR with these primers and probes were evaluated using DNAs from type strains and isolates of Teq and Tas.

Results: Eighteen Teq specific genes were selected as potential targets for real-time PCR assay. Primers and probes specific to these sequences were produced and evaluated in real-time PCR using DNAs from Teq, Tas and other bacteria that are commonly present in the

reproductive tract of horses. Real-time PCR assay targeting sequence encoding Hep_Hag repeat-containing protein of Teq was selected as the most specific and sensitive. An artificial DNA sequence, primers and probe were designed and incorporated into the Teq specific TaqMan PCR assay as internal control (IC). No inhibition of Teq specific real-time PCR was evident in presence of IC primers and probe. Amplification of IC template was also not depended on the presence of DNA from Teq or other bacteria.

Conclusion: The highly specific and sensitive real-time PCR assay was developed for detection and differentiation of Teq and Tas which will enhance the capability to control and eradicate CEM.

21.095 Understanding the pig backyard sector for realistic prevention and control of African swine fever

D. Beltrán-Alcrudo

FAO, Rome, Italy

Background: First introduced in Georgia in 2007, African swine fever (ASF) spread rapidly throughout the Caucasus and the Russian Federation. The disease is now endemic in several areas and continues spreading. Both endemicity and spread are mainly associated to backyard farming, a very common and traditional practice in rural areas that predominates in most countries in Eastern Europe and the Caucasus, representing an important source of meat and cash income. However, these production systems do not receive much institutional support. Moreover, disease prevention and control is most challenging in these settings due to the lower levels of awareness among the rural communities, low biosecurity, poor compliance to livestock related regulations (reporting, movement control, certifications, vaccination, etc) and unknown numbers and locations. Also, veterinary services often lack the personnel, equipment and funding to control ASF. Because of this, currently utilized prevention and control approaches are not being effective to control the disease at the backyard level, particularly the traditional stamping out approach.

Objectives: There is a need to engage all stakeholders at the village level (pig keepers, butchers, middlemen, wild boar hunters and private veterinarians) and empower them to deal with ASF and other pig diseases. Such approach needs to be based on a thorough and detailed understanding of the predominantly informal, largely unknown pig sector, which is highly diverse, even within a country.

Methods and Materials: To gather such information in a quantifiable manner, questionnaires were developed for pig keepers and butchers covering biosecurity and husbandry practices, market chains, wild boar interactions, awareness status and socio-economic aspects. Georgia was selected to pilot this new approach. Veterinary associations in four distinct regions across Georgia were used to collect 600 questionnaires (450 pig keepers and 150 butchers) in 178 villages.

Results: The analysis of questionnaires allowed to quantify biosecurity gaps and risky behaviours, develop risk profiles, and identify critical control points across the market chain where to implement mitigation measures.

Conclusion: Ultimately this will allow the design of realistic and sustainable prevention, surveillance and control strategies based on simple and inexpensive interventions, largely based on awareness campaigns and trainings. The same approach could be easily adapted to Africa.



Study on effect of acetic acid spray on *Escherichia coli* load and meat PH at an export abattoir, Modjo, Ethiopia.

T. J. Beyene, A. W. Wudie, G. Zewude, T. Ali Addis ababa University, Debre Zeit, Ethiopia

Background: According to a recent estimation, food-borne illnesses cost the U.S. \$152 billion in health-related expenses each year. Worldwide, *Campylobacter, Salmonella* and Shigatoxin-producing *E. coli* (STEC) are among the most important bacterial food-borne

International Meeting on Emerging Diseases and Surveillance 2013

pathogens (Loretz, 2010). Ministry of Agriculture of Ethiopia has approved abattoirs to use acetic acid spray on carcasses. So, some export abattoirs in Ethiopia are using 2%-3% acetic acid with the intention of improving early darkening of the carcass. However, the effect of acetic acid spray has not been assessed in any of the export abattoirs

Poster Presentations I

Objectives: Therefore, this study was conducted with the objectives of determining the effect of 2.5% acetic acid spray on E. coli load, the combined effect of acetic acid spray and chilling on E. coli load and the effect of acetic acids spray on pH and color of goat carcass.

Methods and Materials: A total of 144 sample's swabs were taken from 24 carcasses. 48 swabs were from front leg and hind leg areas before acetic acid spray, immediately after acetic acid spray and after 24 hrs of chilling at 2±1°C. Following incubation of on media at 37 °C for 48 hrs, E. coli CFU/cm² was counted. A portable hand pH meter was used to measure pH of carcass at 15 minutes after slaughter and 24 hrs of chilling at 2±1°C.

Results: The log mean of E. coli count before acetic acids spray, immediately after spray and after chilling were 2.53Log, CUF/cm², 1.35Log₁₀ CUF/cm² and 1.97Log₁₀CUF/cm², respectively. The number of E. coli counts before acetic acid spray was higher in samples from front leg than hind leg area. The mean pH value of goat carcasses at 15 minutes after slaughter was found to be 6.38.

Conclusion: The means of E. coli counts before and after acetic acid spray showed significant difference. Relatively lower pH were measured in sprayed chilled carcasses (with mean pH=5.77) than nonsprayed chilled carcasses (Mean pH=5.98). Goat carcasses after spray and chilling showed less darkness. Acetic acid has been shown to be effective against E. coli O157:H7 by reducing the pathogen.

21.097 Study of Listeria monocytogenes contamination in raw milk and some Moroccan traditional dairy derivatives (Lben and Jben)

B. El Marnissi¹, L. Bennani², A. El ouali lalami², R. Belkhou¹ ¹Ecole Supérieure de Technologie, Fès, Morocco, ²Laboratoire Régional de Diagnostic Epidémiologique et d'Hygiène du Milieu de Fès, Fès, Morocco

Background: Listeria monocytogenes is the causative agent of listeriosis, a serious food-borne disease primarily associated with the consumption of processed foods that require no further cooking by the consumer. Milk and dairy products have been implicated.

Objectives: The objective of this study was to determine the incidence of Listeria monocytogenes in raw milk and its two traditional drives, the "Lben" (traditionally fermented skimmed milk) and "Jben" (traditional soft white cheese) commercialized in Fez city situated in the center northern Morocco throughout a year.

Methods and Materials: A total of 288 samples of three dairy products were collected from eight dairies traditional belonging to various sectors of Fez City throughout a year. Isolation and identification of Listeriamonocytogenes were carried out according to Moroccan standards NM 08.0.110 (2004). Selected physicochemical parameters were also carried out in parallel. The L. monocytogenes strains that were isolated in this study were tested against eleven antimicrobial discs.

Results: The overall incidence of Listeria monocytogenes contamination was 17.70%. It was present in the three dairy products. The results of this study revealed also a variation of contamination from one sector to another with a higher incidence of contamination in milk and dairy product samples collected in the autumn and winter, suggesting a link between management practices feed, poor hygienic conditions and Listeria monocytogenes contamination. The physicochemical results show an acidic pH in the "Lben" and "Jben" that in raw milk, indicating a significant lactic fermentation of these two products.

Conclusion: The levels of contamination found justify the control of the feeding cattle, milk pasteurization and enforced the general principles of food hygiene in order to reduce consumer's exposure to Listeria monocytogenes

21.098 Rapid cessation of acute diarrhea in pediatric patients using a novel plant extract

A. S. Dover¹, T. Noguera²

¹Aptos Travel Clinic, Aptos, CA, USA, ²Universidad CentroAmerica CE, Managua, Nicaragua

Background: Supportive care with oral rehydration solution (ORS) is standard treatment for acute diarrhea, although its use does not shorten the duration of illness. There is a need to investigate new approaches to diarrhea treatment, such as phytobiologic agents with active elements that show anti-microbial activity.

Objectives: Assess the effectiveness of a novel plant extract (LifeDrops, LiveLeaf Inc.) to restore bowel homeostasis in patients with acute diarrhea

Methods and Materials: With IRB approval, pediatric patients in a Nicaraguan community clinic with uncontrolled diarrhea in the previous 48 hours were enrolled, with parental consent. Patients were randomized to receive either ORS with the plant extract on day 1 and then ORS alone on day 2 (study arm) or receive ORS alone on day 1 and then ORS plus the extract on day 2 (control arm). Patients were observed under standard of care (ORS) for 24 hours after administration of fluids and time and number of bowel movements noted; stools in each bowel movement were ranked using the Bristol Stool Scale (BSS).

Results: 61 patients were enrolled (30 in the study arm, 31 in the control arm). In the first 24 hours after consumption of the fluids, study arm patients reported BSS stool 4 or less in a mean time of 3.1 hours contrasted to mean time of 9.2 hours in control arm (p=0.002); 66% of patients in study arm had BSS ranking of 4 or less the first bowel movement after drinking ORS+extract fluid. During the second study day, patients given the ORS+extract on day 1 and then ORS alone on day 2 continued with a BSS stool of 4 or less while crossed over patients who received the plant extract on day 2 achieved a BSS of 4 within 24 hours of extract consumption. For patients in control arm, mean number of bowel movements on day 1 (receiving ORS alone) was 4 but only 2 after given the extract on day 2 (p=0.0001). No adverse events were observed during the study.

Conclusion: Decreased stool frequency and rapid normalization of stool consistency were observed with ORS containing LifeDrops compared to ORS alone.

21.099

Occurrence of Echinostoma revolutum metacercariae and other larval trematode infections in freshwater snails from Chiang Mai, Thailand

K. Chantima¹, J. Y. Chai², C. Wongsawad¹

¹Faculty of Science, Chiang Mai University, Chiang Mai, Thailand, ²Seoul National University College of Medicine, Seoul, Korea, Republic of

Background: Echinostomes and larval trematodes have previously been reported in Thailand. However, no complete epidemiological data existed regarding its infection in freshwater snails, an important epidemic factor for Echinostomiasis and snail borne parasitic zoonoses in Northern Thailand.

Objectives: This study is aimed to investigate the presence and epidemiology of Echinostoma revolutum metacercariae and other larval trematode in freshwater snails.

Methods and Materials: 10,692 snails belonging to 12 species were examined for assesse larval trematode infections in Chiang Mai province from November 2011-October 2012. The larval trematode infections in snails were studied by crushing methods. The 37-collar spined echinostome metacercariae were force-fed to experimental hosts, and adult worms were recovered. The adult worms were identified based on biological features for confirming metacercarial species.

Results: Out of total 12 freshwater snail species, 40.3% (4,312/10,692) were infected with larval trematodes. From these, 3 metacercarial species (E. revolutum, Asymphylodora sp. and 1 unidentified species) and 7 morphologically distinguishable cercariae (monostome cercariae,

International Meeting on Emerging Diseases and Surveillance 2013

distome cercariae, xiphidiocercariae, gymnocephalus cercariae, furcocercous cercariae, parapleurolophocercous cercariae and parapleurolophocercous cercariae) were recorded. Seven snail species were infected with both cercariae and metacercariae of *E. revolutum*, namely, *Clea helena* (1.0%), *Eyriesia eyriesi* (16.4%), *Bithynia funiculata* (6.8%), *B. siamensis siamensis* (2.6%), *Filopaludina doliaris* (63.1%), *F. sumatrensis polygramma* (61.0%) and *F. martensi martensi* (55.7%) respectively. In addition,this metacercariae have been found to infect in *C. helena* for the first time in Thailand. Seasonal variation of prevalence was also observed by revealing that it was quiet high during the hot-dry and rainy seasons but relatively low in the cool (*P*>0.05).

Conclusion: The present study is the first report of *E. revolutum* metacercariae in the molluscan intermediate host, *C. helena*, and also confirmed that 12 freshwater snails species were served as both the first and second intermediate hosts of larval trematodes under natural condition, which are indigenously distributed in Chiang Mai province. The discovery of these larval trematodes in this epidemic area is a starting point for some comprehensive studies on snail-related transmission aspects and for monitoring its dispersion in Northern Thailand.

21.100 Characterization of *Salmonella enterica* subsp. *enterica* monophasic variant 4,[5],12:i:- human isolates in Slovakia V. Majtan, L. Majtanova, J. Majtan

Slovak Medical University, Bratislava, Slovakia

Background: In the mid-1990s a monophasic *Salmonella enterica* subsp. *enterica* with the antigenic formula 4,[5],12:i:-, represents the monophasic variant of serovar Typhimurium started to emerge in Europe. In Slovakia the incidence of serovar 4,[5],12:i:- has been increased from 2006.

Objectives: The phenotypic (phage type, antimicrobial resistance, markers of virulence) and genotyping (PFGE) characterization of a collection of 104 *S. enterica* serovar 4,[5],12:i- strains isolated from sporadic human cases of salmonellosis.

Methods and Materials: The relatedness of the isolates was determined by phage typing and *Xbal*-PFGE analysis. All isolates were tested for susceptibility to 11 antibiotics by the disk diffusion method. Surface hydrophobicity was assessed using bacterial adhesion to xylene. Virulence plasmid was characterized by alkaline lysis and the biofilm production was determined spectrophotometrically at 570nm.

Results: According to the phage typing the isolates belonged to 7 different phage types with predominance of U302 (19.2%), U311 (13.5%) and DT193 (12.5%) phage types. Forty-six isolates (44.2%) were untypable. Based on the antimicrobial testing, 90 (86.5%) isolates were multidrug resistant and the most frequent resistotype was ASSuT, which was expressed by 68 (65.4%) isolates. On the basis of virulence markers investigation, 22.1% of isolates were hydrophobic in the assay of bacterial adherence to xylene and 77.9% of isolates produced biofilm. The 90-kbp virulence plasmid in 26.9% of isolates was found. Studied virulence markers did not always correlate with the predominant phage types, nevertheless the strong biofilm production can suggest increased adhesion ability to the host. PFGE typing of isolates by (90.4%) of studied isolates were distributed in cluster (X1,X1a,X2,X2a).

Conclusion: Phenotypic analysis showed that four main lineages of *S. enterica* serovar 4,[5],12:i- are currently spreading in humans which are characterized by phage types U302, U311, DT193 and by untypable strains. PFGE analysis suggested a close clonal relationship among human isolates of this monophasic variant in Slovakia.

This work was supported by Ministry of Health of the Slovak Republic under the project *Molecular analysis of antibiotic resistance of nontyphoid salmonella serovars.*

21.101 Fresh fish as a potent vehicle for the transmission of Salmonellosis in Egypt

A. A. Tayel¹, W. El-Tras², O. A. Abdel-Monem¹ ¹Genetic Engineering & Biotechnology Research Institute- Minoufiya Univ, El-Sadat City, Egypt, Egypt, ²Faculty of Veterinary Medicine, Kafrelsheikh, Egypt

Background: Salmonella sp. is from the most disastrous foodborne pathogens in the world. Nile tilapia, *Oreochromis niloticus*, is the most consumed fresh fish type in Egypt.

Objectives: Current study was designed to investigate the role of Nile tilapia in carrying and transmitting *Salmonella* sp. to human.

Methods and Materials: Wild and farmed Nile tilapia fishes were screened for the presence of *Salmonella* sp. on their surfaces and muscles, swaps from fish handlers and sellers' hand were also collected and examined for the presence of *Salmonella* spp.

Detailed questionnaire was conducted to investigate the recurrence of salmonellosis among fish dealers.

Results: Results indicated that *Salmonella* spp. was isolated from wild and farmed fish with percentages of 62.2 and 48.4%, respectively. The existence of *Salmonella* spp. in surfaces and muscles of positive carrier fish was 98.6 and 42.2 % in wild fish and 97.4 and 56.4% in farmed fish. *Salmonella* spp. was isolated from 74.8 % of fish dealers' hand swabs, whereas the appearance of recurring salmonellosis was recorded in 32.4% from them.

Questionnaire indicated that fish handling was the merely route to transmit *Salmonella* spp. to 18.6% from the positive human cases.

Conclusion: The results of this study strongly evidenced that fresh fish in Egypt, especially Nile tilapia, could be considered as a potent carrier for salmonellosis transmission and infection among fish dealers.

21.102 Evaluation of completeness of the mandatory notification system for salmonellosis and shigellosis, Greece, 2011.

K. Mellou, T. Sideroglou, A. Kallimani, M. Potamiti-Komi,

E. Lillakou, T. Georgakopoulou, C. Hadjichristodoulou

Hellenic Center for Disease Control and Prevention, Athens, Greece

Background: Surveillance of laboratory confirmed salmonellosis and shigellosis cases in Greece is based upon a combination of Mandatory Notification System (MNS) and surveillance through the National Reference Laboratory for *Salmonella* spp. and *Shigella* spp. (NRLSS). Underreporting of both diseases has been postulated but there has not been any study to estimate the actual size of the problem.

Objectives: The objective of this study was: a) to estimate underreporting of salmonellosis and shigellosis to the MNS in 2011 in Greece with a capture recapture study and b) compare the estimated total number of cases to the actual one documented at the hospital registries.

Methods and Materials: The MNS and NRLSS databases were used in the capture recapture analysis. Data were checked for duplicates and cases were matched using the variables "name" and "date of birth". The total number of salmonellosis and shigellosis cases was estimated with Chapman's formula developed for two-list capture recapture studies. The actual number of cases was calculated through a retrospective review of the registries of the microbiological laboratories of the hospitals.

Results: The estimated underreporting of salmonellosis and shigellosis to MNS was 49.0% and 52.0% respectively. Based on the hospital records underreporting was similar; 53.5% for salmonellosis and 58.4% for shigellosis.

Conclusion: Underreporting of salmonellosis and shigellosis to the MNS was high and enhancement of notification is needed. The capture recapture study led to an estimation of underreporting close to the actual one which indicates that the four assumptions of capture recapture studies were not seriously violated. However, a positive dependence between the data of MNS and NRLSS cannot be excluded.

International Meeting on Emerging Diseases and Surveillance 2013

21.103 Viral gastroenteritis outbreaks in school settings in a Greek village. January 2012

K. Mellou¹, T. Sideroglou¹, M. Potamiti-Komi¹, E. Lillakou¹, P. Kokkinos², P. Ziros², A. Vantarakis², T. Georgakopoulou¹ ¹Hellenic Center for Disease Control and Prevention, Athens, Greece, ²University of Patras, Patras, Greece

Background: Viral gastroenteritis outbreaks in school settings are underreported and hence, under-investigated. In January 2012, two outbreaks, in an elementary school and a kindergarten, in a village of 1,531 inhabitants in Central Macedonia were notified.

Objectives: To identify the extent of the outbreak at each school, the possible common source of the outbreaks, the possibility of an extensive community outbreak and possible risk factors.

Methods and Materials: Background and current data regarding the occurrence of gastroenteritis in the community were gathered. Two retrospective cohort studies were conducted, one at each school. For both studies, a case was defined as any student or staff member who presented vomiting and/or diarrhoea between 9 and 22 January 2012. Staff members and children's guardians completed a structured questionnaire. Tap water samples from schools were tested for adenoviruses and noroviruses GI and GII. Collection of stool samples was requested. Recommendations regarding prevention and control measures were made.

Results: A parallel gastroenteritis outbreak in the community was not verified. Attack rate at the elementary school and the kindergarten was 57.5% and 60.9% respectively. Regarding elementary school, the shape of the epidemic curve was compatible with a common point source outbreak; according to the multivariable analysis, consumption of tap water was the only statistically significant risk factor for gastroenteritis (RR=9.37, 95% C.I: 3.45-25.46); Noroviruses GI and GII and adenoviruses were detected with RT-PCR in five clinical samples while testing of water was negative. For kindergarten, the shape of the epidemic curve supported a person-to-person transmission; no statistically significant risk factor was identified; Adenoviruses were detected in one water sample, but clinical samples were not collected.

Conclusion: The attack rate was high in both schools and there was strong evidence that the outbreak in the elementary school was of mixed viral waterborne origin. The aetiological agent was not verified probably because of the delayed water sampling. Even though both schools had the same water supply system, clinical samples were not collected at the kindergarten and we cannot conclude that the two outbreaks were of the same origin.

21.104 Early detection of severe complications with Escherichia coli O111 in a large outbreak in Japan

T. Misaki¹, Y. Yahata¹, M. Nagira¹, Y. Tada¹, K. Taniguchi¹, K. Oishi¹, N. Okabe²

¹National Institute of Infectious Diseases, Tokyo, Japan, ²National Institute of Infectious Diseases, Infectious Disease Surveillance Center, Tokyo, Japan

Background: In 2011, a large outbreak caused by Enterohemorrhagic Escherichia coli O111 infection occurred on the regional scale in Japan among people who ate raw beef meet at some branches of chain BBQ restaurant A.

Objectives: To determine the predictors for early detection of severe complications such as HUS and acute encephalopathy with E coli O111 infection.

Methods and Materials: We conducted a retrospective cohort study among 86 cases who developed one or more digestive symptoms and isolated E coli O111 or a detected LPS antibody of E coli O111.

Results: Of 86 confirmed cases, 34 (40%) were associated with HUS. Of 34 HUS cases, 21 (62%) developed encephalopathy and 5 (15%) died. All of fatal cases were associated with encephalopathy.

The incubation period in HUS cases was shorter than that in non-HUS. Markedly thickening of descending colon wall and constant proteinuria were observed at the early stage in severe cases. Decline in serum Na level and elevated blood-glucose, fibrin/fibrinogen degradation products (FDP) and D-dimer level were also observed in HUS cases at the time of admission.

A rapid decrease in platelet counts and increases in serum lactate dehydrogenase (LDH) and creatinine (Cr) levels during 24 hours before the onset of HUS were observed in patients with encephalopathy. Abnormal findings were observed in thalamus and/or basal ganglia in the brain imaging, especially in MRI imaging, of patients with encephalopathy.

Conclusion: An increased level of FDP or D-dimer at the time of admission is possible indicator of HUS. Rapid changes in platelet counts, serum LDH and Cr levels during admission were indicative of encephalopathy, and brain MRI studies are useful to detect the acute stage of encephalopathy.

21.105 Prevalence and risk association for Trichinella infection in domestic and free range pigs in Greece

S. Boutsini¹, D. Stougiou¹, V. Papatsiros², A. Panteli¹, M. Bisia² ¹Center of Athens Veterinary Institutions, Ministry of Rural Development and Food, Greece, Athens, Greece, ²University of Thessaly, Karditsa, Greece

Background: Trichinellosis is among the most common food-borne parasitic zoonoses. The European Commission adopted a regulation stating specific rules aimed at the detection of *Trichinella* spp. in fresh meat.

Objectives: During 2009-2011 routine testing for the detection of Trichinella larvae at slaughterhouses and the Greek National Reference Laboratory for Parasites (NRL), a total of 3.339.961 pigs were tested for Trichinella spp., including 2,892 samples from free-range pigs of organic farms (Table 1).

Methods and Materials: These samples were examined with the new official reference method for Trichinella spp. detection as foreseen and described in the Annex 1 of the Commission Regulation 2075/2005 (Magnetic stirrer method for pooled sample digestion).

Results: The results of present study are shown in Table 1. The positive farms are located very close to the Greece-Bulgaria borderline. It is possible to be a connection between the outbreaks of T. britovi cases in Bulgaria and the trichinellosis outbreak in Greece. Around this border line lives a significant population of wild boars and it is possible that they come to direct or indirect contact with the environment of local Greek free range pig farms.

Animals	Year	No of tested samples	No of positive farms	T. spiralis	Trichinella spp. (unspecified)	T. britovi
Fattening pigs	2009	820.512	0	0	0	0
	2010	1.269.894	0	0	0	0
	2011	1.189.691	0	0	0	0
Breeding stock	2009	3.022	0	0	0	0
	2010	20.981	0	0	0	0
	2011	25.427	0	0	0	0
Free range pigs	2009	2.892	2	0	1	1
	2010	4.159	5	0	5	0
	2011	3.383	4	0	0	14
Total	2009	826.426	2	0	1	0
	2010	1.295.034	5	0	5	0
	2011	1.218.501	4	0	0	14
TOTAL		3.339.961				

Table 1. Number of tested samples for Trichinella spp and positive samples during 2009-2011.

Conclusion: Based on the results of the present study, Trichinella spp. is a high risk factor for free-range pig farming in Greece.

POSTER PRESENTATIONS I

International Meeting on Emerging Diseases and Surveillance 2013

21.106 Sorbitol-fermenting VTEC 0157 caused an outbreak via unpasteurized milk and farm visits, Finland 2012

S. Salmenlinna¹, R. Rimhanen-Finne¹, H. Lundström²,

A. Jaakkonen³, A. Pihlajasaari³, A. Vainio¹, S. Toikkanen¹,

O. Lyytikäinen¹, A. Siitonen¹, S. Hallanvuo³

¹National Institute for Health and Welfare, Helsinki, Finland, ²City of

Turku, Turku, Finland, ³Finnish Food Safety Authority, Helsinki, Finland

Background: In Finland, the annual number of human verocytotoxinproducing *Escherichia coli* (VTEC) cases ranges from 20 to 40 (incidence 0.37-0.75/100000) and outbreaks are rare. In June 2012, a VTEC outbreak occurred among persons who had visited or consumed unpasteurized milk purchased from a recreational farm offering theme visits.

Objectives: is to evaluate the extent of the outbreak among persons possibly exposed in relation to milk, animal and environmental contamination at the farm.

Methods and Materials: A web-based questionnaire was launched to regular customers purchasing unpasteurized milk and to persons who visited the farm during June. Human stool samples were cultured at, and VTEC isolates obtained for further typing, from two clinical microbiology laboratories. To investigate animal and environmental contamination, samples for VTEC, *Salmonella*, and *Campylobacter* culture were taken at the farm. Both culture and PCR methods were used.

Results: Of 146 persons who answered to the questionnaire study, 11 reported diarrhea; six had consumed unpasteurized milk and five of them had a laboratory confirmed VTEC. Altogether, VTEC isolates were received from eight persons. All were of serotype O157:H7, phage type 88, positive for *stx2, eae, hlyA*, fermented sorbitol, and shared an identical pulsed-field gel electrophoresis (PFGE) pattern. Of the farm samples, 4/16 cattle, 0/1 lamb, 4/8 milk and 7/23 environmental samples were culture positive for VTEC. Three of four culture positive milk samples were negative in the PCR assay. The human and farm isolates shared otherwise the same microbiological characteristics, but PFGE patterns of farm isolates were heterogeneous. Several environmental and faecal cattle isolates shared an identical PFGE pattern with human isolates. Farm samples for *Salmonella* were negative, but 4/15 cattle faecal samples were positive for *C. jejuni*. Two animals had both VTEC and *Campylobacter*.

Conclusion: The VTEC outbreak was caused by consumption of contaminated, unpasteurized milk. Cattle and farm environment was widely contaminated with VTEC strains and also *Campylobacter* was found. The detection of VTEC from farm samples is challenging; PCR alone for milk samples is prone for false negatives and possibility of sorbitol-positive strain should be taken account. The same animals may also be a source for both VTEC and *Campylobacter*.

21.107

Characterization of *Staphylococcus aureus* producing biofilm isolated from food and clinical samples

G. La Salandra¹, M. G. Basanisi¹, R. Pedale¹, A. Di Taranto², D. Chiocco³

¹Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata, Foggia, Italy, ²Azienda Ospedaliera Universitaria Ospedali Riuniti, Foggia, Italy, ³Istituto Zooprofilattico della Puglia e della Basilicata, Foggia, Italy

Background: *Staphylococcus aureus* is the first bacterium implicated in nosocomial infections due to the capacity to form biofilm. Biofilms are complex microbial communities attached to a surface and embedded in an extracellular matrix. This ability is regulated by expression of polysaccharide intracellular adhesion (PIA), which mediates cell to cell adhesion and is the product of *ica*ADBC.

Objectives: This study investigates the virulence properties of *S. aureus* strains encoding *ica*A isolated from food samples and human clinical specimens such as the enterotoxin(s) genes, Panton-Valentine Leukocidin (PVL) toxins, antibiotic susceptibilities and the ecological origin.

Methods and Materials: 395 *S. aureus* strains isolated from milk and cheese produced in Apulia region (South Italy) and 88 *S. aureus* strains isolated from human clinical specimens were examined for the presence of *ica*A gene. Isolates encoding *ica*A were investigated for the presence of staphylococcal enteroroxin(s) genes (*sea, seb, sec, sed, see, seg, seh, sei, sej, sem, sen, seo*) and PVL-encoding gene (*lukF-PV* and *lukS-PV*) by PCR. The antibiotic resistance was tested using Kirby-Bauer method. The biotype of *S. aureus* strains isolated from food samples was determined by Devriese method.

Results: Overall out of 395 strains isolated from food samples, 297 (75,2%) were found to be positive for *ica*A. Among these strains, 13,5% encoded *sec* and 12,5% *sed* associated to *sej*,40% resulted susceptible and 5,9% showed multidrug resistance proprieties (MDR). Non host-specific (NHS) biotype results to be the most representative (27,3%). For 88 strains isolated from human clinical specimens, 70 (79,5%) carried *ica*A gene. 43 (61,4%) of them harbored enterotoxin(s) genes, 11,4% resulted susceptible and 34,6% were multiresistant. Furthermore all analyzed strains lacked the PVL-encoding gene.

Conclusion: *ica*A gene has high occurrence and comparable rate between food samples and clinical specimens. Biofilm formation increases multidrug resistance especially in human isolates and reduce the host immune response. The prevalence of NHS biotype in food samples shows a cross contamination along food chain due to the presence of food handlers as principal source of contamination. In terms of risk analysis, it is very important a better sanitary education to prevent nosocomial infections and foodborne diseases.

21.108 The Italian survey on prevalence of *Listeria monocytogenes* in RTE meat products and cheeses

V. A. Prencipe, S. Antoci, R. D'Aurelio, D. Neri, G. A. Santarelli,

F. Cito, S. lannetti, F. De Massis, P. Calistri Istituto Zooprofilattico sperimentale dell'Abruzzo e del Molise "G.Caporale", Teramo, Italy

Background: As established in the Decision 2010/678/EU, the Member States carried out a coordinated monitoring programme to assess the prevalence of *L. monocytogenes* in certain ready to eat (RTE) food categories in European Union. Since the number of samples allocated to Italy by this survey was not sufficient to estimate prevalence of *L. monocytogenes* at national level, the Ministry of Health established in 2011 a national survey.

Objectives: The survey was put in place to evaluate the prevalence of *L. monocytogenes* in two specific RTE products at retail in Italy.

Methods and Materials: Two RTE food categories were sampled: soft and semi-soft cheeses and heat-treated meat products. Three hundred and seventy-nine municipalities were randomly selected and a stratified proportional sampling was carried out based on the number of inhabitants. The sample size considered was of 900 units for each RTE food categories under the survey. Both soft and semi-soft cheeses and heat-treated meat products were tested immediately after sampling. Meat products were also tested at the end of the shelf-life. Concerning cheeses, if rinds were present they were separately analysed. Each sample collected was examined qualitatively according to ISO 11290 part 1 (ISO, 1996).

Results: A total of 1795 units (894 cheeses and 901 RTE meat products) were collected and tested by the National Reference Laboratory. *L. monocytogenes* was isolated in 19 units of rind-cheeses out of 475 units collected. *L. monocytogenes* was detected in both rind and paste samples (0.6%; 95%CI 0.2-1.8%) and only in rind in 16 samples (3.4%; 95%CI 2.1-5.4%). *L. monocytogenes* was also isolated in 21 units out of 901 RTE meat products (2.3%; 95% CI 1.4-3.4%). Among them, 4 were positive only when immediately tested, 6 only when tested at the end of shelf life and 11 in both.

Conclusion: This study shows the prevalence of *L. monocytogenes* in some RTE products in Italy. Main outcome is that rind-cheeses are more frequently contaminated by *L. monocytogenes*, rather than norind cheeses. The survey confirms that the food categories considered were among the most frequently contaminated with *L. monocytogenes* and that they may represents the most important risk for consumers.

International Meeting on Emerging Diseases and Surveillance 2013

21.109 Detection of monophasic *Salmonella* Typhimurium and its antimicrobial susceptibility throughout pigs' life cycle from three industrial pig herds in Portugal

M. M. Centeno¹, L. Fernandes¹, A. Belas¹, N. Couto¹, T. Nunes¹, V. Almeida¹, L. Alban², C. Pomba¹

¹Faculdade de Medicina Veterinária, Universidade Técnica de Lisboa, Lisbon, Portugal, ²Danish Agriculture and Food Council, Kobenhavn V, Denmark

Background: Monophasic *Salmonella* Typhimurium has become an emergent and rapidly disseminated variant among food-animals, companion animals and humans worldwide. Little is known on the characteristics of this *S.* 4,[5],12:i:- in the pig reservoir.

Objectives: Detect the presence of monophasic *Salmonella* Typhimurium and characterize its antimicrobial resistance in randomly selected pigs followed throughout their life cycle.

Methods and Materials: Three farms that shared biosecurity measures were selected conveniently. In each farm, 10 litters were randomly chosen and 7 piglets from each litter were ear-tagged. Each pig was sampled six times throughout its life: at birth, after weaning, at 10 weeks of age, at 4 months of age, before leaving the farm for slaughter and after slaughter. Fecal samples were obtained from live pigs and after slaughter sponges were used to swab the carcass (100cm²). Detection, isolation and serotyping of *Salmonella* spp. were achieved according to the ISO 6579:2002 Annex D and the Kauffmann-White-Le Minor scheme. Confirmation of genus was attained by *invA* PCR and the serotyping results validated through PCR for the *IS*200 fragment and the absence of the 2nd flagellar phase. Susceptibility testing was performed using disk diffusion and broth microdilution methods. PCR was used to screen for resistance genes and clonality was assessed by PFGE according to the Pulsenet protocol.

Results: A total of 37 *Salmonella* spp. strains were isolated and identified as monophasic *S*. Typhimurium. All isolates were detected in pigs from farm 2: seventeen *S*. 4,[5],12:i:- were obtained at birth, 1 after weaning and 19 at 4 months of age. Fifteen different resistance patterns were identified and 5 resistance genes detected as shown in Table 1. In contrast to the diversity of resistance patterns found in *Salmonella* during the fattening process, a predominant resistance profile AmITeStrS3NKNaCt with the *bla*_{TEM}, *tet*(B) and *sul2* genes occurred at birth. PFGE analysis showed considerable genetic similarity among all *S*. 4,[5],12:i:- isolates.

	Nr. of Isolates	Antimicrohial Resistance Pattern	Antimicrobial Resistance Genes
	14	AmiTeSuS3NKNaCt	
Al Birth	2	AmITeStr53NKNaCtAmc	blambic ser(B), sul2
(A = 10)	1	AmITeSuS3NKNaCtTob	
After Weaning (n = 65)	1	AmITeSuS3NKNgCi	bla _{ruth} set(B), mil2
	1	AmiTeStr53NK	
	1	AmiTeSuS3NKXnl	Mo. Lot III and 2
	1	AmITeStr53NKCt	condition and off our
	1	AmiTeSuS3NKXniCt	
	1	AmiTeStrS3NKCnTobNet	
4-months old	2	AmiTeSuS3NKCnTobNerCt	
(n = 65)	1	AmJTeStrS3NKCnTobNetXnl	All second and second to the
	1	AmITeStrS3NKCaTobNgtNa	States, into), succ. ancis pro-
	1	AmITeStrS3NKCnTobNetNaC1	
	1	AmlTeStrS3NKCnTobNetNaCtXnl	
	3	AmiTeSuS3NKCnTobNetCiFfeC	bla
	3	AmiTeSuS3NKCnTobNetCtFfcCNa	flox

Logens: Anno = nerocorrino, Anno = amosticititivitavitanis and; C = cannatitission; CA = genaminin; CA = obliciti; Fit = floreferencel; K = isanastryain; N = netonyoin; Na = nalidinic acid; Net = netilinicis; S3 = ndphonamides; Str = streptomysin; Ta = setting-peline; Tob = tobenryocit; Xai = ceffoolar

 Table 1. Characterization of monophasic Salmonella Typhimurium isolates obtained from fecal samples from pigs from Farm 2.

Conclusion: This study demonstrates the emergence of a *Salmonella* serovar similar to the European resistant monophasic *S*. Typhimurium spreading clone. Further studies are needed to fully assess the dynamics of thisserovar and its impact on food-safety and human and animal health.

21.110

.110 *Kudoa septempunctata* caused outbreak in humans with raw flounder ingestion

Y. Yahata¹, T. Ohnishi², Y. Sugita-Konishie³, T. Toyokawa⁴, N. Nakamura⁵, K. Taniguchi¹, N. Okabe⁶

¹National Institute of Infectious Diseases, Tokyo, Japan, ²Natinal Institute of Health Science, Setagaya, Japan, ³Natinal Institute of Health Science, Setagaya-ku, Japan, ⁴Okinawa Prefectural Nanbu Medical Center & Children's Medical Center, Haebaru-cho, Japan, ⁵Astellas Pharma Global Development, Cyuo-ku, Japan, ⁶Kawasaki City Institute for Public Health, Kawasaki, Japan

Background: The consumption of raw fish (e.g. Sushi, Sashimi and so on) is increasing worldwide. The World Health Organization mentioned raw fish consumption is one of the high risks for gastrointestinal infection all over the world. Since around 2000, western parts of Japan have reported unknown cause of foodborne disease that occurred after consumption of the raw flounder. However, a sufficient number of cases for epidemiological investigation have not been reported.

Objectives: In October 2010, a large outbreak occurred from the western part of Japan. All illness people consumed the raw flounder fish. This flounder fish distributed form same food processing company. We investigated the cause of outbreak and the estimation of threshold of intake of the agent.

Methods and Materials: This outbreak investigation conducted the case-control study. Statistical analysis used Fisher's exact test, logistic regression analysis and Monte Carlo simulation.

Results: The median incubation period was 5 hours (range: 1-22 hour[s]). The most frequently symptom was diarrhea (80%). The flounder consumption was significantly higher than the development of symptoms (P=0.0041, Fisher's exact test). The amount of flounder consumption was not significantly different between the cases (median: 66.7g; range: 33.3-300.0g) and controls (median: 77.5g; range: 20.0-300.3g). Regarding preserving, the use of a refrigerator (OR=0.5, 95% CI: 0.3-1.0) and a preservde of chilled room (OR=2.5, 95% CI: 1.3-4.7) was significantly associated with the onset of symptoms. A Polymerase Chain Reaction (PCR) test detected Kudoa septempunctata. Moreover, the median amount of K. septempunctata was 0.5×104 (range: 0.1×104-9.6×10⁶). All of the flounder fish were grown through aquaculture. A Monte Carlo simulation estimated that the threshold of the development of gastrointestinal symptoms illness was 7.2×107 of K. septempunctata. Attempt to Public Health measure, our results should refer to prevent for the flounder ingestion related the gastrointestinal symptom.

Conclusion: This outbreak caused by consumption of flounder fish which was contaminated by the *K. septempunctata*. The estimation number of threshold of *K. septempukctata* was 7.2×10^7 . Ministry of Health, Labor and Welfare has been disseminated this study result through the web site and notification for public relation to the local governments.

21.111 High prevalence of antibodies against Leptospira in Austrian adults: A nationwide cross sectional survey

W. Poeppi¹, M. J. Orola², H. Herkner³, A. Faas⁴, G. Mooseder⁴, M. Müller⁵, F. Allerberger⁶, H. Burgmann¹

¹Medical University Vienna, Vienna, Austria, ²University of Applied Sciences, Vienna, Austria, ³Medical University of Vienna, Vienna, Austria, ⁴Military Hospital Vienna, Vienna, Austria, ⁵AGES, Institute for Veterinary Disease Control, Mödling, Austria, ⁶AGES, Vienna, Austria

Background: Leptospirosis is a worldwide zoonotic disease caused by bacteria belonging to the genus *Leptospira* and has been recognized as an emerging global public health problem because of it's epidemic proportions and increasing incidence in both developing and developed countries. Military personnel is historically regarded as an established high risk group for contracting leptospirosis.

Objectives: To assess the distribution of specific antibodies against *Leptospira spp.* in Austrian adults and the exposure among military personnel and civilians.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: Serum samples and epidemiological data were obtained from adults volunteering for international military employments between April and June 2009 at the Military Hospital Vienna. 400 healthy adults from all federal states of Austria were included. Antibody titres against Leptospira were determined by microscopic agglutination test using a panel of cultures with 14 different serovars. Samples with titres ≥1:100 were considered positive. Variables surveyed included professional soldier or civilian, previous foreign military assignments, residential area, occupational animal contact and regular outdoor activities. Differences in proportions were tested using Fisher's exact test. A two-sided p value <0.05 was considered statistically significant.

Results: 18 participants were excluded from the statistical analysis because of impurities in the serum. The remaining 382 participants were between 18 and 57 years and consisted of 166 professional soldiers and 216 civilians.

Overall, 88 (23%) individuals tested positive in serologic screening. Subject sera were most commonly reacting with organisms of the serovars Canicola (16.5%) and Hardjo (11.8%). Epidemiological information was obtained with a questionnaire: no correlation was found for different residential areas, travel activities abroad, regular outdoor activities, occupational animal contact, or pet ownership. The proportion of seropositive samples was significantly lower among professional soldiers (15.7%) than among civilians (28.7%) (P = 0.003).

Conclusion: Our data demonstrate serologic evidence of a high exposure rate to *Leptospira* spp. among the Austrian population. No increased risk of exposure to *Leptospira* spp. could be detected for military personnel.

21.112 Seasonality of diarrhea in children of Gilgit, northern Pakistan: Nastier episodes and shift to older ages as summer unfolds

Z. Rasmussen¹, **B. McCormick¹**, W. J. Alonso¹, N. Samji², J. Baker¹ ¹National Institutes of Health, Bethesda, MD, USA, ²Consultant, Hamilton, ON, Canada

Background: The burden of diarrheal mortality, the second most frequent cause of childhood death, and the widespread morbidity associated with enteric infection is particularly concentrated in impoverished populations and continues despite considerable advances in therapeutic care and improved living conditions.

Objectives: To explore the differential experience of enteric infection across age groups and the calendar year in order to better identify seasonally relevant risk groups for appropriate stratification of treatment.

Methods and Materials: Using seasonal analysis we explore the burden of diarrheal disease in different age groups and the duration of episodes throughout the calendar year in a rural population of 1857 children (0-59months old) from Oshikhandass Village, Gilgit in northern Pakistan studies 1990–1996. Data were collected through weekly active surveillance.

Results: The burden of diarrhea was highest in children aged 6–11 months old and decreased in older age groups. The timing of peak diarrhea burden for different ages were not, however, evenly distributed throughout the year with the peak burden earlier in younger children (0–23 months peaked in May/June) than older children (24–60 months, peaking in July). Furthermore, shorter duration diarrheal episodes tended to occur earlier than later episodes: 1 day episodes tended to peak in mid-May, acute and prolonged episodes (65% and 24% of all episodes respectively) in mid-June and chronic episodes (>30 days long) tended to start in July.

Conclusion: The seasonal burden of diarrheal disease changes as children age. Consequently the need for age-stratified therapeutic treatments is not constant throughout the year. Preventive measures need to be targeted at different groups at different times, with an emphasis on management of diarrhea of longer duration.

21.113 Molecular characterization and epidemiological trend of Hepatitis A virus isolates in a tertiary care hospital in North India

M. P. Singh¹, M. Majumdar¹, B. R. Thapa², P. K. Gupta², J. Khurana², B. Budhathoki², R. Ratho³

¹Postgraduate Institute of Medical Education and Research, Chandigarh, India, ²Post Graduate Institute of Medical Education

and Research, Chandigarh, India, ³Postgraduate Institute of Medical Education and Research, Chandigarh, Chandigarh, India

Background: Hepatitis A usually causes acute viral hepatitis (AVH) in the pediatric age group. However, recent studies have shown a shift in the age distribution to older age group and disease manifestations like acute liver failure (ALF) have also been reported. This has been attributed to mutations in 5'non-translated region (5'NTR) which affects the viral multiplication.

Objectives: The present study was aimed to determine the epidemiological trends of Hepatitis A and to carry out the molecular characterization of the isolates over the years

Methods and Materials: Serum samples from patients with clinically suspected AVH patients were tested for anti Hepatitis A virus (HAV) IgM antibodies during 2007–2011 and were included in the study. Acute sera were subjected to nested PCR targeting the 5'NTR region followed by sequencing of the representative strains. These were then analysed for the presence of mutations in this region.

Results: Anti HAV IgM antibodies positivity was found to be 21.7%. Children < 15 years of age accounted for majority (94%) of the cases with highest seropositivity during the rainy season. Of the 78 acute sera, HAV RNAwas detected in 37(47.4%) samples. Sequencing of 15 representative strains was carried out and the circulating genotype was found to be III A. The nucleotide sequences showed high homology among the strains with a variation ranging from 0.1-1% over the years. Comparison with wild strains showed that the acute strains (n=11) had higher substitutions compared to strains from ALF cases (n=4).

Conclusion: Hepatitis A is still a disease of children in our region and the circulating genotype is genotype III A. The mutations at 5'NTR region warrant further analysis as they affect the structure of Internal Ribosomal entry site which is important for viral replication.

21.114 Food safety requires public-private partnerships

T. Wilke ¹, V. Raab¹, O. Breuer², M. Hamer², B. Petersen¹ ¹University of Bonn, Bonn, Germany, ²GIQS e.V., Bonn, Germany

Background: During the last two decades the political and regulatory framework of food safety, consumer protection changed and roles were reallocated with a sharp swift towards self-responsibility of the private sector. In crisis situations the deficiencies in the interaction between public and private actors become obvious.

Objectives: Objective of our study was to analyze and to subsume these developments in order to derive thereof the strategy of public-private partnerships (PPP) as well as to formulate recommendations for the successful implementation of PPP-structures in the agri-food chain.

Methods and Materials: Based on a thorough review of literature about public and private efforts in food safety and crisis management, we analyzed example cases of public-private interaction (minimization of chemical residues, data exchange in animal disease control, crisis management exercises for bioterrorist attacks, agri-food research and development platform).

Results: Analysis of the dynamics of shared responsibility revealed that there exists a growing gap between steadily increasing safety requirements and the amount of shared responsibility in the food chain. Organized co-operations in the form of public-private partnerships are able to fill this gap.

In practice PPP-structures can be organized in different ways (clusters, consortia, alliances, agencies) and at different formal levels. Members of a PPP-structures need to formulate an common overall goal and goal conflicts must be recognized Scientific partners play an important role in successful PPP-structures because they can act as moderator and knowledge providerPPP-structures require the development and usage

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

of appropriate information and communication systems. This requires mutual trust and the consideration of privacy, data ownership and data security. In order to maintain and refine sustainable PPP-structures the establishment of a neutral long-term organization (PPP-platform) has proved to be successful.



Dynamics in responsibility and opportunity for public-private partnerships.



Three main groups in public-private partnerships for food safety.

Conclusion: From our results we conclude that public-private partnerships between private, public and scientific actors are the most promising approach to cope with the steady increasing requirements of food safety, consumer protection and crisis management.

21.115 Knowledge attitude and behavior of medical students towards safety in student laboratory

K. Chaicom, B. Palaeng, P. Kungsang

Medcine Facculty, Khon Kaen university, Thailand, Khon Kaen, Thailand

Background: Risks in medical students laboratory were frequently found such as accident, needle injuries, exposures to body fluids etc. They were causes of injury and blood borne infection.

Objectives: The purposes of this research were to study knowledge, attitude, and behavior of medical students towards safety in student laboratory.

Methods and Materials: The quantitative and qualitative data were collected during May–June 2012. The research instruments were the questionnaire answered by 100 medical students who practice at medicine department, Khon Kaen University, Thailand. The statistics for analyzing the data were arithmetic mean and correlation coefficient.

Results: The results showed that the 100 medical students were female as 58.50% an average age was 22 years, maximum age 23 years, minimum age 20 years. 88.55% use to working in laboratory and 38.25% have a experiments of laboratory accidents. They have a high level, moderate and low of knowledge were 70.33%, 28.17% and 1.50% respectively. High level, moderate and low of attitude were 84.3%, 15.7% and 0% respectively. High level, moderate and low of behavior were 35.75%, 58.75% and 5.50% respectively.

Conclusion: When looking at relationship between each category, it was found that knowledge was positive relative to attitude and behaviors. Attitudes were positive relative to behavior with statistical significance at the level of 0.01. It is necessary to have a course on safety in the laboratory for medical students before practice.

21.116 A 20-years retrospective cohort study of HIV/ AIDS situation among hill tribe vulnerable population, Thailand

T. Apidechkul

Mae Fah Luang University, Chiang Rai, Thailand

Background: Thailand has been reported as the highest HIV/AIDS epidemic area in the world last few years. Most of HIV/AIDS had been reported from the north ofThailand. Northern Thailand is the favorite living places of hill tribe people who migrated from the south ofChina through Myanmar last 150 years ago. Nowadays almost 600,000 people were living in these areas with differences of culture and life styles.

Objectives: To investigate the situation of HIV/AIDS among hill tribe marginalized and vulnerable population.

Methods and Materials: The retrospective cohort study was conducted. The systematic data extraction from the medical records in 16 hospitals in northernThailand during 1990-2010 was performed. The six main hill tribe people: Akha, Lau, Karen, Yao, Kmong, and Lisu were the target population. Chi square test was analyzed.

Results: Totally 3,130 cases were recruited into the study. 54.6% were male, the first case had been reported in 1990, and the highest incident case had been reported in the year 2004 with 461 cases followed by 2005 (343 cases), and 2006 (302 cases) respectively. The highest cumulative case had been reported from Mae Fah Luang Hospital (25.8%), followed by Mae Suai hospital (18.8%). 46.0% were Akha, 19.7% were Lahu, and 9.5% were Yao. 38.8% were 31–40 years old, followed by 21–30 years old (33.6%), and 41–50 years old (13.4%). 44.4% were agriculture, 32.0% were employee. 91.6% were infected by sexual intercourse, 5.7% were mother to child. 24.0% were receiving ARV, 30.7% were receiving OI treatment, and 9.5% were tested CD4 level. Male had higher of survival rate than female (p-value>0.001), and male were younger than female at the age of infection (p-value>0.001). There was statistically significant difference of mode of infection by tribe (p-value>0.001).

Conclusion: Specific health education programs and empower them for using condom are needed to setting up for HIV/AIDS prevention and control among hill tribe people in Thailand.

21.117 Prevalence of human metapneumovirus infection in hospital wards comprising patients with severe motor and intellectual disabilities

S. Matsuda¹, M. Noda²

¹National Hospital organization, Tohon, Ehime, Japan, ²National Institute fou Infrctious Diseases, Tokyo, Japan

Background: Epidemics of infectious diseases often occur in hospital wards comprise patients with severe motor and intellectual disabilities. However, the causative pathogens are not identified in half of these epidemics.

Objectives: Three epidemics occurred in 3 wards consecutively in National Hospital Organization Ehime Hospital in 2010–2012. We tried to detect the causative agent and compared it with the clinical symptoms.

Methods and Materials: Respiratory viruses were detected by PCR, cell culture and genome-sequencing.

Results: In the first epidemic, 18 of 40 patients in one ward and 14 of 60 patients in another ward showed symptoms, and human metapneumovirus (HMPV) was detected from pharyngeal and/or nasal swabs of 4 patients. Phylogenetic analysis of the viral genomes showed that the virus belong to subgroup B2, and the same virus had spread consecutively in 2 wards. High fever lasted for 5.3 days on an average in the 32 inpatients, and was mostly over 38°C and accompanied by productive coughs. In the 4 patients in whom human HMPV was detected, the number of peripheral blood lymphocytes decreased but that of monocytes increased. Two patients were found to develop pneumonia as shown by chest radiography, and they showed increased number of peripheral blood neutrocytes and elevated CRP levels. Of the 151 inpatients, anti-human HMPV antibody was found in the sera of 143 inpatients (95%), and the relationship between high fever and

International Meeting on Emerging Diseases and Surveillance 2013

antibody titer was not significant, indicating that HMPV infection could recur in spite of the presence of specific antibodies. Additionaly, other two epidemics of the same virus that occurred afterwards in the wards will be descrived.

Conclusion: Because human HMPV is highly prevalent, and causes high fever and pneumonia, hospital staff should be vigilant of this virus in hospital wards and take steps to prevent infection in long-term inpatients.

21.118 The first report of *Mycobacterium riyadhense* lung infection with HIV and CMV co-infection

M. A. Garbati¹, A. M. Hakawi²

¹King Fahad Medical City, Riyadh, Riyadh, Saudi Arabia, ²King Fahad Medical City, Riyadh, Saudi Arabia

Background: *Mycobacterium riyadhense*, named after Riyadh, is gradually becoming an emerging infectious agent of clinical significance. Discovered only in 2009, it has continued to be isolated from both pulmonary and extra-pulmonary sites. Four previous cases of infection with this agent have been published, but none had co-infection with HIV, making our case the first to be reported in the literature.

Objectives: We hereby present the first documented case of *M. riyadhense* lung infection in a patient with HIV/AIDS and Cytomegalovirus viremia in the literature.

Methods and Materials: Case report.

Results: We hereby present the case of a 54-year-old male, with diabetes who presented to the emergency room (ER) with chronic cough, diarrhea, odynophagia and dysphagia for solids and progressive weight. He looked wasted with oro-pharyngeal thrush, and herpes zoster lesion affecting the left first and second thoracic dermatomes. Chest x-ray revealed consolidation on the right.

Complete blood count revealed lymphopenia (absolute count of 0.864 x 109/L (1.5-3.5). He had transaminitis with elevated alanine aminotransferase (ALT)-70 U/L (30-65), aspartate aminotransferase (AST)-73 U/L (15-37), alkaline phospahatase (ALP)-357 U/L (50-136), and a gamma glutamyl transpeptidase (GGT) of 94 U/L (11-50). Serum albumin was 23 g/L (34-50). His stool was positive for *Clostridium difficile* toxins by PCR. HIV test was positive with high viral load (Table 1). Sputum culture yielded *M. riyadhense* from Bioscientia laboratories (Ingelheim, Germany), however DNA Probe-detection assay for MTB complex was negative.

The patient was successfully treated with a combination of clarithromycin, ethambutol and rifampin for one year. The patient also received Truvada (Emtricitabine and tenofovir) and Efavirenz. He also received fluconazole, and valganciclovir, for the oro-pharyngeal candidiasis and CMV viremia respectively.

Prophylaxis with trimethoprim-sulphamethoxazole was initiated until CD4 count became more than 200 x 109/L for consecutive 3 months. Repeat sputum smear and culture after two months into his therapy were negative.

Parameter	Ar baseline	é monthe	12 months	Reference value
CD3				
almufiste (x \$9"/L)	8.17	11.12	2.34	2010/01/02/02
A4.	17	387.4	76.6	NA
CBA				
alsobite (x 107/L)	0.002	43.040	0.29	0.869 ± 0.310
No	2	25	4.5	NA
CD8				
almostate (x 101 E)	0.12	6.96	1.00	8012-0.278
AL.	72	10	145	NA
CD4-CD8 ratio	0.02	41.06	0.70	1.6 = 0,
CD19	and the second se	and the second sec		and the second second
absolute in 10° T.1	60.00	0.10	0.28	0.230 a.0.1M
Au	17	73	37	29.4
CB19				
absolute (s. 10° L)	70.0	0.15	0.25	0.230 ± 180
46	- 17 -	7.5	8.7	N/A
HADS ou B	and the second se	and the second se	and the second se	
bughacter				
absolute to 10" La	41.03	0.34	0.24	N/A
56	-100	100	100	WA.
IIIV Ostantibality	237 (61	Ciskerecokle	Undergraphie	20-10000000
Vical load import				
ad.i.				
PCRCM	37,800	Lindenuide		600-100000
to and an owned at				

Table 1. Virologic and Immunologic characteristics of the patient.

Conclusion: We presented the case of a patient with acquired immune deficiency syndrome (AIDS) and opportunistic CMV viremia and *M. riyadhense* infection lung making this the first to be documented in the literature.

21.119 Prevalence of B6, B12 and folic acid deficiency in HIV positive patients

B. Achappa, D. Madi

Kasturba Medical College (affiliated to Manipal University), Mangalore, Karnataka, India

Background: Deficiency of certain vitamins and trace elements are associated with altered immunological and neurological status among HIV positives. There are very few studies from India evaluating this issue in India.

Objectives: To identify vitamin B6, B12, folic acid deficiency in: a) HIV positive patients with tuberculosis (Group I); b) HIV positive patients with neuropsychiatric manifestations (Group II); and c) HIV positive patients without tuberculosis or neuropsychiatric manifestations (Group III).

Methods and Materials: 150 HIV positives were included and divided into above 3 groups.

Pyridoxine estimation was done using of high performance liquid chromatography. Reference range was 5–30 ng/mL.

Folate estimated using carbonyl metallo immunoassay method (CMIA) and reference range was 2.7–34.0 ng/mL

Vitamin B12 estimated using carbonyl metallo immunoassay method (CMIA) and reference range was 189–883 pg/mL.

HIV cohort containing 150 subjects were followed regularly for 6 months. Out of 150 subjects 74 completed study, 33 expired and 43 were lost for follow up.

Results: Baseline median pyridoxine levels (in ng/mL) in HIV cohort groups I, II, III were 8.23; 8.5 and 11.12 respectively. The prevalence of Vitamin B6 deficiency in various groups was group I–18.8%, group II–28.3%, group III–10%.

Median baseline folic acid levels in groups I–III were 5.91; 3.64; 5.08; Prevalence of Folic Acid deficiency in various groups was group I–27.1%, group II–31.9%, group III–23.4%.

Median serum B12 levels in groups I–III were 380; 555; 460.5; The prevalence of Vitamin B12 deficiency in various groups was group I–8.16%, group II–6.12%, group III–4.16%.

Conclusion: Pyridoxine deficiency, folate deficiency and B12 deficiency is common in HIV infected patients irrespective of the stages of disease.

The results showed that median pyridoxine levels were significantly lower in HIV positive patients with tuberculosis and neuropsychiatric manifestations in comparison with asymptomatic HIV positives.

The median folic acid levels were lowest among neuropsychiatric patients and nearly a third of these had folate deficiency. However nearly a quarter of HIV positive patients who were asymptomatic or had tuberculosis also had folate deficiency.

Median B12 levels were lowest in tuberculous HIV patients and higher in neuropsychiatric patients probably because of supplements received.

21.120 TB/HIV among hill tribe marginalized vulnerable population, Thailand

T. Apidechkul

Mae Fah Luang University, Chiang Rai, Thailand

Background: Since 1982, Thailand had been reported 372,874 cases of HIV/AIDS, and 98,153 deaths. The north of Thailand has been report as the highest prevalence areas. There were almost 600,000 hill tribe populations live there as a marginalized and vulnerable people under lacked of access to health care and limited education. Most of them emigrated from China last 200 years ago. Chiang Rai Province is the most favorite living area of hill tribe people.

Objectives: To explore the TB/HIV co-infection among the hill tribe marginalized population northern, Thailand.
Methods and Materials: The retrospective cohort study design aimed to investigates the TB and HIV situation among hill tribe marginalized and vulnerable population. The systematic data collection with the completed questionnaire was conducted in the 12 hospitals, Chiang Rai Province. All questionnaires had been tested for reliability and validity before use. Survival and Cox's regression were analysis.

Results: Of 629 cases of TB reported during 2009-2011 form 12 hospitals were recruited into the study. 60.7% were male 23.8% aged 51-60 years old, and followed by 41-50 years old (20.2%) (min=1, max=93). Of 84.6% were pulmonary TB and extra pulmonary 15.4%, 44.6% recieving AFB testing, 77.4% new cases. The results of treatment found that 22.7% were cure, 28.6% complte, 4.3% defults, 8.1% death, and 1.9% failure. Prevalence of HIV/AIDS among hill tribe TB cases was 17.2%. Of 88.1% had treatment on CAT1, and 4.6%CAT2, and 2.3% CAT4. Male had greater pulmonary TB (p-vale=0.044), and HIV+ than female (p-value=0.023). Survival analysis found that being male (p-value=0.01), non-HIV (p-value<0.01), and CAT1 had greater success treatment. Cox's regression found that only aged 11-20 years old had related to success treatment (HR=2.11, 95%CI=1.05-4.26).

Conclusion: Active screening program and increasing the rights of access to care are immediate needed for hill tribe vulnerable people for coping TB problem in Thailand.

21.121 Highly active antiretroviral therapy maintains the population of Langerhans cells in the tongue from Human Immunodeficiency Virus -1 infected patients

R. Gondak¹, F. V. Mariano¹, T. Mauad², O. P. Almeida¹, P. A. Vargas¹ ¹University of Campinas, Piracicaba, SP, Brazil, ²University of São Paulo, São Paulo, SP, Brazil

Background: Langerhans cells (LCs) may have important roles in the course of Human Immunodeficiency Virus (HIV) infection, including the probable initial uptake of HIV, transmission to the lymph nodes and subsequent transfer to T cells. Highly active antiretroviral therapy (HAART) administration that is effective in controlling HIV-1 replication should be associated with improvement in innate immune parameters. However, the effect of HAART on innate immune cells has not been well established.

Objectives: To quantify and compare the expression of LCs in the tongue mucosa of HIV-1 patients on HAART, HIV-1 patients without HAART and HIV-negative patients, using autopsy material.

Methods and Materials: CD1a and CD83 antibodies were used to identify and quantify LCs in tongue tissue by immunohistochemistry of 15 HIV-1 patients (5 on HAART and 10 without HAART), and 10 tongues from HIV-negative control patients. Quantification was performed by means of conventional morphometry and the results were expressed as positive cells per area of epithelium.

Results: The HIV-1 patients without HAART presented a lower density of CD1a+ cells (P < 0.001) and CD83+ cells (P = 0.001) in the tongue compared to the HIV-1 patients on HAART. However, no differences in any of the markers were found when HIV-1 patients on HAART were compared with the control group [CD1a+ cells (P = 0.229) and CD83+ cells (P = 0.547)].

Conclusion: HAART administration to HIV-1-infected patients maintained the population of Langerhans cells in the tongue and consequently led to an improvement in immune function.

21.122 Outbreak of tuberculosis among elderly in geriatric home

B. Achappa, D. Madi, P. Adhikari, S. Raj, M. Tripathy Kasturba Medical College (affiliated to Manipal University), Mangalore, Karnataka, India

Background: India has the highest Tuberculosis (TB) burden with World health Organization (WHO) statistics for 2010 giving an estimated incidence figure of 2.3 million cases of TB for India out of a global incidence of 9.4 million cases. The geriatric population has four times the risk of TB as that of the general population. Nursing home residence doubles the age-adjusted risk of developing TB. However, not much data is available from India on the problem of tuberculosis in elderly.

Objectives: To study the outbreak of tuberculosis among elderly and its predisposing factors.

Methods and Materials: All the inmates were screened for TB using chest x-ray. Mantoux test and ESR.

After detecting those with tuberculosis based on radiological evidence, the inmates were divided into two groups. The first group consisted of those with active and latent tuberculosis and those without tuberculosis were classified into the second group.

Possible factors contributing to the outbreak such as age, gender, presence of co-morbid illnesses, nutritional status as assessed by BMI, duration of stay in the home were studied and compared in these two groups.

Results: 23 out of 34 (67.64%) inmates had tuberculosis. Mean weight, BMI and ESR of patients with TB were 46.42kg, 19.7 and 43mm/1st hour respectively and 56.7kg, 21.7 and 23mm/1st hour in those without TB. Mantoux test showed mean induration of 23 mm among patients with TB and 13mm in inmates without TB.

None of the inmates showed classical symptoms of TB like fever, night sweats, cough and hemoptysis.

Conclusion: Elderly living in the home for the aged are at higher risk of developing TB. Classical clinical features of TB such as fever, cough, hemoptysis are not present and hence the diagnosis may be missed. Malnutrition, overcrowding are the major risk factors for TB in the elderly. Care of the elderly living in the home for the aged must include periodic screening for TB using chest x-ray.

21.123

Prevalence of Clostridium difficile among cases of antibiotic associated diarrhea in hospitalized patients in an Egyptian hospital

M. M. AbdelHaleim, N. Nawar, R. Elsherif, A. Farouk Cairo University- Faculty of medicine, Cairo, Egypt

Background: C. difficile is one of the commonest causes of PMC and AAD. It remains the most commonly recognized cause of HAI and is increasingly important as a community pathogen. A more virulent strain of C. difficile has been identified and has been responsible for more-severe cases of disease worldwide. Although CDI is not a reportable condition in Egypt, patients are often elderly and has been exposed to antimicrobials, suggesting that rates of disease and/or colonization could potentially be high. Definitive diagnosis of C. difficile infection is accomplished by detection of toxigenic C. difficile. A few reliable techniques for toxin detection are available in Egyptian clinical laboratories.

Objectives: In this work we aimed to determine the prevalence of toxigenic C. difficile among cases of AAD in Cairo University hospitals in Egypt using specific PCR protocols.

Methods and Materials: The study was conducted on 100 adults, admitted in Cairo University hospitals, suffering from AAD and 20 healthy individuals as control group. All included cases were subjected to full history taking, clinical examination and laboratory investigations of stool samples including; direct microscopic examination, culture on blood agar and chromogenic media. Molecular detection of C. difficile DNA in stool samples using multiplex PCR of the triose phosphate isomerase gene tpi, specific for this bacterial species, tcdA and tcdB genes coding for toxin A and B respectively and cdtA and cdtB genes of binary toxin.

Results: Two out of 100 cases were positive for tcdB gene and tpi gene, and one of these two positive cases were also positive for cdtA and cdtB genes. No cases were positive for tcdA toxin A. No samples of the control group were positive for any of the tested genes.

Conclusion: This study confirms the usefulness of PCR in the detection of toxigenic C. difficile and suggests that it is responsible for a small, but under-appreciated proportion of AAD cases in our country. Further studies on larger scale are warranted.

IMED 2013

21.124 Tuberculous meningitis at the Hospital Nacional Dos de Mayo, Lima, Peru: 2005–2010

POSTER PRESENTATIONS

T. Metcalf¹, J. Soria², S. Montano³, E. Ticona², M. Kasper³, J. Zunt⁴ ¹Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand, ²Hospital Nacional Dos de Mayo, Lima, Peru, ³U.S. Naval Medical Research Unit No.6, (NAMRU-6), Callao, Peru, ⁴University of Washington, Harborview Medical Center, Seattle, WA, USA

Background: Tuberculous meningitis (TBM) is considered the most severe form of tuberculosis—causing substantial morbidity and mortality. It is commonly found to occur in developing countries endemic to tuberculosis. HIV-infected persons are particularly vulnerable which, even when not fatal, often results in very poor clinical outcomes.

Objectives: To describe clinical and laboratory correlates of clinically diagnosed TBM and identify demographic and clinical risk factors associated with increased mortality in a cohort of clinically diagnosed TBM adults in Lima, Peru.

Methods and Materials: We performed a retrospective cohort study of 101 adults (≥15 years old) clinically diagnosed with TBM at the Hospital Nacional Dos de Mayo in Lima, Peru. Data was extracted from medical records and risk factors associated with mortality were assessed using Cox regression analysis and bivariate calculations. Our case definition for clinical tuberculous meningitis included: headache, neck stiffness, altered mental state or fever and pleocytosis or other CSF abnormalities. Positive cultures for *M. tuberculosis* confirmed the diagnosis of TB infection.

Results: Twenty-one patients were aware of their HIV positive status prior to admission. At time of admission 10 (10%) of the patients were in BMRC clinical stage III. The clinical diagnosis of TBM was confirmed by culture in 26 (26%) patients. Culture and susceptibility testing identified six TB isolates as drug resistant; three were MDR-TB, of which two were in HIV-infected patients. Twenty percent of the patients died during hospitalization. In-hospital mortality rate was higher for HIV patients where 12 (35%) died during hospitalization, compared to 8 (12%) non-HIV patients (p=0.002). HIV co-infection (HR: 2.1), previous TB history (HR: 2.2), and previous MDR-TB history (HR: 3.0) were significantly associated with mortality. All HIV-infected patients receiving ART showed a detectable viral load at time of TBM diagnosis; 90% reporting poor adherence.

Conclusion: Our study detected greater disease severity and shorter survival from TB meningitis in patients who either had a previous history of TB and/or HIV infection—especially those with poor adherence to antiretroviral therapy.

21.125 The epidemiology and burden of Q fever in the UK 1999–2011

H. Kirkbride, A. Walsh, K. Halsby, D. Morgan

Health Protection Agency, London, United Kingdom

Background: Approximately 50–100 cases of Q fever are reported in the UK each year. However, accurate data on the number of cases are difficult to obtain through routine surveillance systems due to under-ascertainment. We used an enhanced dataset to give a more comprehensive description of Q fever in the UK.

Objectives: To describe the epidemiology and burden of Q fever in the UK.

Methods and Materials: Databases of routine laboratory reports were supplemented with data from Q fever reference laboratories to describe laboratory confirmed cases of Q fever in the UK from 1999-2011. The number of Q fever hospital admissions in England and deaths in England and Wales for 1999–2008 were identified from the Hospital Episode Statistics database, and the Office for National Statistics Infectious Disease Deaths dataset respectively.

Results: Between 1999 and 2011 in the UK there were a total of 1298 "new diagnoses" of Q fever consistent with either acute or chronic infection. The number of new diagnoses decreased from 1999 to 2010 across the UK but doubled in England and Wales from 2010–2011.

The mean annual incidence of Q fever in the UK was 0.17 cases/100,000 population/year, with substantially higher rates in Northern Ireland than in England, Wales and Scotland.

IMED 2013

The median age of cases in England and Wales was 47 years, with

more than 2/3 cases in males. During 1999–2008, 13% (94/720) of new Q fever cases in England were hospitalised, with a mean length of stay of 2 weeks. The mean age of admitted cases was 10 years older than laboratory diagnosed cases, which may indicate that a high proportion of hospital admissions were for chronic disease. Only one death was reported in England and Wales over this period.



Figure 1. Q fever new diagnoses (excluding outbreaks in the UK, 1999-2011).

	UK		E	&W		Northern	
Year	Cases	IR	Cases	IR	Scotland	Ireland	
1999	143	0.24	76	0.14	0.28	3.08	
2000	121	0.20	80	0.15	0.12	2.03	
2001	95	0.16	66	0.12	0.04	1.57	
2002	184	0.31	151	0.28	0.12	1.57	
2003	96	0.16	79	0.15	0.12	0.64	
2004	61	0.10	53	0.10	0.02	0.41	
2005	61	0.10	53	0.10	0.04	0.35	
2006	200	0.33	43	0.08	2.83	0.76	
2007	71	0.12	63	0.12	0.06	0.29	
2008	68	0.11	56	0.10	0.02	0.64	
2009	31	0.05	27	0.05	0.04	0.12	
2010	55	0.09	52	0.10	0.06	0.00	
2011	112	0.19	104	0.19	0.14	0.06	
Mean annu 1999-	al incidence 2011ª	0.17		0.13	0.30	0.89	

^a calculated at the midterm population (2005) and average annual number of cases

Table 1. Incidence rates (per 100,000) for Q fever new diagnoses 1999-2011.

Conclusion: This study shows that Q fever has a considerable burden of infection in the UK even with significant under-reporting. There is some evidence that the substantial increase in numbers of new diagnoses in England and Wales during 2011 may be explained by increased testing, and further investigations are being undertaken.

21.126

20 Role of antiplatelet antibodies in the development of trombocytopenia in patients with chronic hepatitis C

N. Pshenichnaya, G. Kuznetsova, E. Romanova

Rostov State Medical University, Rostov-on-Don, Russian Federation

Background: One of the key position in hemostasis belongs to surface platelet receptors (SPR)-glycoproteins (GP) la/lla (collagen receptor), lb/IX (Von Willebrand factor receptor) and Ilb/IIIa (fibrinogen receptor). Antibodies to SPR can lead to development of thrombocytopenia in patients with chronic HCV-infection via its destruction in spleen and disorders in the primary hemostasis. However the role of different types of antibodies in this process is unknown.

POSTER PRESENTATIONS

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: The objective of research were to estimate the role of different types of antibodies to surface platelet receptors in HCVassociated thrombocytopenia.

Methods and Materials: The detection GP Ia/IIa, Ib/IX and IIb/ IIIa was made by the ELISA technique in HCV-infected patients with thrombocytopenia (group 1, n=29), HCV-infected patients without thrombocytopenia (group 2, n=28) and healthy people (group 3, n=32). All patients were PCR(+), untreated with interferon, 20-55 years old with F0-F2 stage of liver fibrosis.

Results: Anti-GP Ia/IIa were detected in 44,8±9,2 % in 1st group, 3,6 ± 3,5% in 2nd group, 12,5±5,8% in 3rd group, p1-2<0,01, p1-3<0,05. Anti-GP lb/IX were indicated in 55,2±9,2% in 1st group, 10,7±5,8% in 2nd group, and 28,1±7,9% in 3rd group, p1-2<0,01, p1-3<0,05. Anti- GP IIb/IIIa were recorded in the same groups in 24,1±8,0%, 17,8±7,3% and 25±7,6% accordingly without any statistical difference. Mean optical density (MOD) of anti-GPIa/IIa in 1st group also was more significant than in 2nd and 3rd group (0,331±0,035, 0,208±0,015 and 0,217±0,012 accordingly, p1-2<0,01, p1-3<0,01). More high level of anti- GPIb/IX TOD was also recorded in 1st group than in 2nd group (0,280±0,025 and 0,215±0,010 p<0,05), no statistical evidence was found between 3rd group and patients in 1st and 2nd groups. Investigation of anti-GP IIb/IIIa MOD also did not find any statistical difference between patients with HCV (both groups) and healthy people.

Conclusion: High frequency of revealing and significant level of MOD of anti-GP Ia/IIa и Ib/IX in HCV-infected patients with thrombocytopenia demonstrated the evidence of damage in the first stages of primary hemostasisas well as more high risk of destruction platelets binding with anti-GP la/Ila and anti- GP lb/IX in spleen. Detection of anti-GP Ia/IIa и Ib/IX can serve as prognostication criteria for developing thrombocytopenia in patients with chronic HCV-infection.

21.127 The outcome of chronic hepatitis C (CHC) depends of degree of intensity and rate of progression of fibrosis in liver tissue

E. Romanova¹, N. Pshenichnaya¹, G. Kuznetsova¹, M. Ladychuk², T. Belashova¹

¹Rostov State Medical University, Rostov-on-Don, Russian

Federation, ²Central City Hospital #1, Rostov-on-Don, Russian Federation

Background: The semi-quantitative methods (SQM) such as Desmet and Metavir scores most often used for assessment the stage of fibrosis. The subjectivism of such methods is obvious. The morphometric method (MM) can be offered as an alternative approach for estimation the stage of liver fibrosis.

Objectives: The aim of investigation is evaluation the degree of equivalence of the fibrosis stage assessment according to the data of SOM and MM

Methods and Materials: The study included 42 patients with CHC in the age from 25 to 37 years with positive HCV RNA PCR.

Trans-skin puncture of liver was performed to all patients by Mengini needles. According to Desmet SQM it was marked out the following stages of fibrosis: F0-absence of fibrosis, F1-weak fibrosis (portal or periportal), F2-moderate (porto-portal-septal), F3-severe (portocentral septal) and F4-cirrhosis. Simultaneously the samples of liver tissue was investigated by MM using program Sigma Scan Pro 5.0.

Fibrosis index (FI) was determined as ratio of the area of fibrosis to the square of tissue sampling.

The frequency of significant liver fibrosis (F2-F4) was 54,5%. The formation of thin collagen fibers along of sinusoids with generation of perihepatocellular sclerosis was registered even at the weak stage of fibrosis.

Results: It was established that the stage of the F1 correspond to 0,01-0,02 value of FI, moderate fibrosis stage (F2) to 0,03-0,06 FI, the severe liver fibrosis (F3 and F4) to 0.07–0.2 and ≥0.3 FI accordingly.

Significant differences were revealed when compared the results of the fibrosis stage assessment by the SQM and MM in 35,7% patients.

So, the fibrosis was absent in 4 patients (9.5%) according to the assessment by SQM, although MM revealed the moderate stage of fibrosis (F2) in these patients.

Conclusion: The MM allows to objectify the assessment of severity of liver fibrosis. It has significant importance in the case of necessity of morphological monitoring for the natural course of disease and during the combined antiviral therapy.

21.128 The efficiency of Helicobacter pylori eradication therapy in prevention of thrombocytopenia in patients with HCV and Helicobacter pylori co-infection

N. Pshenichnaya, G. Kuznetsova, E. Romanova Rostov State Medical University, Rostov-on-Don, Russian Federation

Background: Several investigations revealed the possible influence of Helicobacter pylori-associated diseases (Hp) on the platelet level.

Objectives: To investigate the prevalence of Hp in HCV-infected patients, its influence on the platelet level and to estimate the efficiency of Hp eradication therapy for prevention of thrombocytopenia in patients with HCV-Hp co-infection.

Methods and Materials: Screening for revealing Hp was implemented in 108 persons without HCV and in 187 HCV-infected patients. Hp was diagnosed in 67,6±4,5% persons without HCV and in 77,0±3,1% (p>0.05) patients with HCV. In PCR(+) HCV-infected patients (n=102) Hp was indicated more frequently (80,4±3,9%) in comparison with persons without HCV.

PCR(+) HCV-infected patients before start of combined antiviral therapy (CAT) were randomized in 3 groups. The 1st group included patients without Hp (n=34). 2nd (n=37) and the 3rd (n=31) groups of patients consisted of HCV-Hp co-infected patients. Patients of the 2nd group passed the triple eradication therapy against Hp before starting of CAT, the 3rd group of patients did not receive this type of therapy.

Results: The main clinical and laboratory indicators before starting CAT were comparable between groups. For example, thrombocytopenia was revealed 11,8±5,5% in 1st group, 18,9±6,4% in 2nd group and 19,4±7,1% in 3rd group (p1-2-3>0.05).

The patients were observed within 1-6 months of CAT. The decline of platelet level below 150000 cells/mcl or more than 25000 cells/mcl (if thrombocytopenia were registered initially) was observed in 28.4% of patients. In the 1st group of patients thrombocytopenia was registered in 20,6±6,9%, in the 2nd group-in 21,6±6,8% of cases (p>0.05). In the 3rd group the reduction of platelets was observed in 45,2±8,9% of patients, that was statistically significant in comparison with patients of the 1st and 2nd group (p<0.05).

Conclusion: Hp is revealed more frequently in HCV-infected patients with positive PCR than in persons without HCV. CAT in patients with HCV-Hp co-infection is associated with an increased risk of developing or worsening thrombocytopenia. Eradication therapy against Hp before the CAT can reduce the risk of thrombocytopenia in patients with HCV-Hp co-infection.

21.129 Epidemiological evaluation of spatio-temporal and genotypic clustering of Mycobacterium tuberculosis in Ontario, Canada

A. Tuite¹, D. Fisman¹, D. Alexander², J. Guthrie², A. Marchand-Austin², K. Lam², J. Ma², M. Whelan², B. Lee², F. Jamieson² ¹University of Toronto, Toronto, ON, Canada, ²Public Health Ontario, Etobicoke, ON, Canada

Background: Although tuberculosis (TB) burden is at a historically low level in Canada, recent experience suggests that de novo transmission events should be closely monitored to identify emerging (often drugresistant) strains. The tendency of latent TB infections to reactivate, often years or decades after primary infection, complicates the study of TB epidemiology. Genetically identical TB isolates from different cases can be used to detect recent transmission events.

Objectives: To describe the epidemiology of tuberculosis in the province of Ontario, Canada and to characterize risk factors associated with transmission events.

Methods and Materials: We analyzed trends in TB epidemiology using the Ontario Universal Typing of Tuberculosis (OUT-TB) database.

which contains comprehensive genotypic and epidemiologic data for all culture-positive cases of tuberculosis in Ontario between August 2007 and December 2011. We used logistic regression models to evaluate both apparent clustering of cases using standard spatiotemporal methods and actual case clustering using genotypic data. We conducted analyses of temporal trends, drug resistance, and risk of genotypic clustering in frequently observed strain lineages.

Results: TB incidence over this time period was highest in individuals aged 65 or older and born outside of Canada. Adjusting for differences in the distribution of foreign-born individuals across the province, being in a spatio-temporal cluster was associated with homelessness (adjusted odds ratio (AOR): 2.3, 95% CI: 1.4-6.3). By contrast, cases in genotypic clusters were more likely to be homeless (AOR: 2.8, 95% CI: 1.7-4.7) or male (AOR: 1.3, 95% CI: 1.1-1.7) and were less likely to be older (AOR: 0.7, 95% CI: 0.5-0.8) or born outside Canada (AOR: 0.3; 95% CI: 0.2-0.4). Although overall annual rates of TB incidence remained unchanged, the Beijing lineage had an annual rate of increase of almost 10% (*P*-value=0.047) and was significantly associated with genotypic clustering (AOR: 2.9, 95% CI: 2.3-3.7) and multidrug-resistant TB (AOR: 4.7, 95% CI: 2.4-9.5).

Conclusion: Genotypic information can provide novel insights into tuberculosis transmission by identifying clusters of active tuberculosis cases. In particular, the emergence of novel drug resistant strains via person-to-person transmission is readily identified using genotypic data, but difficult to identify using traditional space-time epidemiological methods.

21.130 Has the epidemiology of bacterial meningitis changed in a limited-resource country (Kosovo)

S. A. Namani¹, R. Koci¹, B. Koci², E. Qehaja¹, L. Ajazaj³,

M. Mehmeti⁴ ¹University Clinical Center of Kosovo, Prishtine, Kosovo, Republic of (under UNSCR 1244/1999), ²Private Pahrmacy, Prishtine, Kosovo, Republic of (under UNSCR 1244/1999), ³University clinical center of Kosovo, Prishtine, Kosovo, Republic of (under UNSCR 1244/1999), ⁴Univesity clinical center of Kosovo, Prishtine, Kosovo, Republic of (under UNSCR 1244/1999)

Background: The epidemiology of bacterial meningitis has changed since the introduction of the protein conjugate vaccines against common meningeal pathogens. Vaccination against meningeal pathogens has not been implemented into national immunization programs in Kosovo except for the Hib vaccine in 2010.

Objectives: This study was carried out to analyze the epidemiologic features of bacterial meningitis in a limited-resource country (Kosovo).

Methods and Materials: Data were collected from active surveillance of bacterial meningitis cases treated in Infectious Diseases Clinic during years 2000-2010. Also were analyzed the epidemiologic features and the outcome of bacterial meningitis cases during two study periods, in the year 2000 (first post war year) and 2010.

Results: Comparison of the annual incidence in 2000 with 2010, showed a significant decline by 35.5% (from 4.8 to 3.1 cases per 100 000 population). The case fatality rate has decreased from 10% in 2000 to 5% in 2010. In children there was a lower recorded mortality rate (5% vs 2%) and a lower incidence of neurologic complications(13% vs 16%) as compared to adults (32% vs 10%; 16% vs 35%). *N. meningitidis* was the most common pathogen of bacterial meningitis in both study periods. Bacterial meningitis continues to affect most frequently children, with increase of the median age of bacterial meningitis cases from 3 years in 2000 to 7 years in 2 010. We recorded a steady number of bacterial meningitis cases in adults throughout last decade.

Conclusion: During the last decade gradual changes have been observed in the epidemiology of bacterial meningitis, unrelated to the introduction of new vaccines but partly due to the improvement of living conditions. After a decade we evidenced a reduction of the bacterial meningitis incidence and case fatality rate.

21.131 Identification of bacterial community in biofilms formed in biliary stents retrieved from patients C. Vaishnavi¹, P. Kapoor², R. Kochhar³

¹Post Graduate Institute of Medical Education and Research, Chandigarh, India, ²Post Graduate Institute of Medical Education and Research, Chandigarh, Chandigarh, Chandigarh, India, ³Post Graduate Institute of Medical Education and Research, Chandigarh, Chandigarh, India

Background: Biofilms are matrix enclosed bacterial population adherent to each other and to surfaces. They have an enormous impact on medicine as they can form on many implants such as stents and catheters. Owing to their increased resistance to antimicrobial agents, these infections can often only be treated by removal of the implant, thereby increasing the trauma to the patients and the cost of treatment. **Objectives:** We quantified the biofilm mass and matrix proteins and identified some of the micro-organisms responsible for biofilm formation in biliary stents retrieved from patients with biliary diseases.

Methods and Materials: The study population comprised of 30 biliary disease patients who required removal of their biliary stents. Clinical details of the patients were recorded in a pre-printed proforma. Biliary stents were collected in sterile containers from these patients during their ERCP procedure and processed for biofilm mass, protein concentration and micro-organisms responsible for the biofilm formation. Quantification of biofilm mass was done by the tetrazolium reduction assay and read in an ELISA reader. Protein estimation was done by the biuret method. Micro-organisms responsible for biofilm formation were identified by polymerase chain reaction using their 16S rRNA sequences for different bacteria.

Results: There were equal number of males and females (n=15 each) with age range 20 to 81 years. The clinical diagnosis of patients was pancreatitis (n=8), CBD stone (n=16) and CBD stricture (n=7). The range of the biofilm mass in the biliary stents was 0.07 O.D. to 0.50 O.D. with a mean of 0.18 O.D. as compared to 0.04 O.D. in control unused stents. Protein concentration ranged from 0.07 to 1.6 g/dl with a mean of 0.47 g/dl. Micro-organisms identified were Pseudomonas aeruginosa (n=15), Citrobacter sp. (n=12) and *Escherichia coli* (n=5). Investigation for other common bacteria is ongoing and will be presented.

Conclusion: High concentration of biofilm mass and protein along with different bacteria was detected in the biliary stents. This is an ongoing work and other organisms are also being studied and will be presented.

21.132 Risks factors and level of awareness of bovine tuberculosis in Kaduna metropolis, Nigeria

E. G. Haruna, C. A. Kudi, M. Bello, I. Ajogi

Ahmadu Bello University, Zaria, Zaria, Nigeria

Background: Bovine tuberculosis (BTB) is endemic in Nigeria, a leading cause of deaths. Despite its zoonotic importance and obvious public health concern, little has been done in raising awareness of the community to prevent the disease.

Objectives: The study was designed with the aim of assessing the risk factors to and level of awareness of Bovine tuberculosis amongst small ruminants' handlers/owners in Kaduna Metropolis, Nigeria.

Methods and Materials: A total of 300 opened and closed ended questionnaires were randomly distributed amongst small ruminants' handlers (viz: livestock marketers, butchers and professionals like the veterinarians and animal health workers) and a randomly sampled populace. The questionnaire was divided into the following sectors: basic demographic information, animal husbandry and practices, lifestyle and habits and knowledge of zoonotic tuberculosis.

Results: A 76.3% (229/300) return rate for the questionnaire was recorded. Amongst the respondents 64.6% indicate awareness of the disease tuberculosis; 41.9% were aware of BTB while 39.7% were aware that BTB is zoonotic. Out of the 39.7% that were aware BTB is zoonotic, 11% gave the route of transmission is as inhalation; 48.4% through ingestion; 28.6% via direct contact with infected sources and 2.2% via the environment. Level of education was however found to be associated with the degree of awareness of BTB as zoonoses among the respondents (P<0.0001). The risk factors to the disease were identified as co-habitation of owners with small ruminants,

SATURDAY • FEBRUARY 16, 2013

POSTER PRESENTATIONS

International Meeting on Emerging Diseases and Surveillance 2013

sharing of utensils and consumption of ruminants' meat and milk. Out of the 72.5% respondents that keep livestock, 53% of them do so in close proximity with the animals and 52% have a preference for small ruminant as source of meat.

Conclusion: In view of the common livestock management practices in Nigeria, small ruminants could play an important role in the transmission of the disease. Lack of knowledge about the disease and its risks, with increase in debilitating infections like HIV& AIDS, consuption of raw milk/meat and poor ventilation of houses, may increase the risk of zoonotic tuberculosis. Consequently, there is a need to educate the populace on zoonotic implication of BTB and targeted control measures involving population at risk should be put in place.

21.133 Multidrug-resistant tuberculosis: A review of diagnosed cases over a 5-year period in a Portuguese hospital

D. Póvoas, J. Machado, F. Maltez

Hospital de Curry Cabral, Lisbon, Not US/Canada, Portugal

Background: The emergence of multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant tuberculosis (XDR-TB) represents a serious worldwide threat with a yet unknown prevalence. MDR-TB is caused by strains of Mycobacterium tuberculosis resistant at least to isoniazid and rifampicin; XDR-TB refers to additional resistance to any fluoroquinolone and any injectable second-line antituberculous drugs (amikacin, capreomycin and kanamycin).

Objectives: To characterize demographic and clinical data as well as the pattern of drug-susceptibility of all cases of MDR-TB and XDR-TB admitted to our Infectious Diseases unit since 2008.

Methods and Materials: All patients with M. tuberculosis identified in fluid samples by fluorimetric Bactec MGIT-960 were included. Medical and laboratory records were reviewed.

Results: During this 5-year period, 19 patients had MDR-TB. Most were male (14; 73.7%), aged from 24 to 67 years of age. Most were African-origined (9; 47%). Among the 11 HIV-positive patients, 3 had had TB previously and 3 of them had HIV-revealing MDR-TB. Among the 8 HIV-negative patients only 2 had previous history of tuberculosis. Most of them had symptoms for more than 30 days (16; 84.1%), mainly cough (14; 73.7%), weight loss (13; 68.4%) and fever (13; 68.4%). Chest x-ray was abnormal in 16 patients (84.2%), 6 presented pulmonary cavitation (31.6%), 5 patients had milliary TB (26.3%) and only 1 patient had no pulmonary involvement (5.3%). 15 patients (78.9%) had acid-fast bacilli on microscopic examination of stained smears of sputum. Apart from resistance to isoniazid and rifampicin in all samples, the rates of resistance to other agents were as follows: streptomycin, 14 (73.7%); etambuthol, 13 (68.4%); pyrazinamide, 12 (63.2%); ethionamid, 12 (63.2%); capreomycin, 9 (47.4%); amoxicillin, 10 (52.6%); kanamycin, 7 (36.8%); PAS, 2 (10.5%); linezolid, 1 (5.3%). Of all the samples tested, 5 (26.3%) were XDR.

Conclusion: Most of the patients diagnosed with MDR-TB and XDR-TB had no previous history of TB, suggesting a persistent risk of drug resistance transmission in the Portuguese community. Accurate drug-resistance surveillance data can be used to assess and improve national tuberculosis programs against the serious threats of MDR-TB and XDR-TB.



W. Krammer¹, J. Wagner¹, R. Raggam¹, E. Leitner², F. Prüller¹, A. J. Grisold¹, K. Seeber¹, W. Duettmann¹, R. Krause¹, M. Hoenigl¹ ¹Medical University of Graz, Graz, Austria, ²Intitute of Hygiene, Graz. Austria

Background: Soluble urokinase plasminogen activation receptor (suPAR) levels reflect inflammation and may predict mortality in hospitalized patients. Small studies have reported that suPAR levels may also correlate with renal function. While most studies concentrated on the role of suPAR as a prognostic marker in infectious diseases, studies elucidating a possible role of suPAR in prediction/diagnosis of infection are rare.

Objectives: The objective of this cohort study was to correlate suPAR with renal function and to evaluate the diagnostic potential of suPAR for bacteraemia in SIRS patients.

Methods and Materials: This prospective cohort study was performed between November 2010 and November 2012 at the Hospital of the Medical University of Graz, Austria. Patients presenting symptoms of SIRS at the emergency room were screened for study inclusion. Blood cultures and serum samples (suPAR, CRP, glomerular filtration rate andcreatinine) were simultaneously taken and clinical data was collected. Median, interguartile range (25%-75%) and standard deviation were calculated for scaled data. Mann-Whitney-U-Test, Kruskal-Wallis Test and Spearman's rank correlation coefficient (2-tailed) were performed.

Results: A total number of 663 patients were included. 468 had a positive blood culture. Results of suPAR values are depicted in Figure 1. SIRS patients with a positive blood culture showed higher levels of suPAR than SIRS patients with negative blood cultures (p<0,001). A negative correlation was found between suPAR and GFR (-0,483; p<0,001) and a positive was found between suPAR and creatinine (0,456; p<0.001). ROC curve analysis revealed an AUC of 0.768 for suPAR levels at admission for predicting 30-day mortality (71patients died). AUCs for age (0.567 and 0.522) and CRP (0.563 and 0.532) were significantly lower. Using multivariate regression analysis suPAR (p<0.001; OR 1.154, 95%Cl 1.108-1.202) and bacteraemia (p=0.015; OR 3.028, 95%CI 1,237-7,407) remained significant predictors of 30-day mortality.



Figure 1. Correlation suPAR with glomerular filtration rate

Conclusion: We found that suPAR levels may predict mortality in SIRS patients and correlate with renal function. Nevertheless and independent of renal function initial suPAR levels may predict bacteremia in SIRS patients. Data indicate that suPAR may be a useful diagnostic and prognostic marker for evaluation of SIRS patients in clinical routine.



Mycobacterial infection in cosmetic surgery: A case report and review of the literature

L. Frye¹, S. Hasan², K. J. Leneweaver², P. Dilanchian², N. Bray¹, D. Droller¹

¹Broward Health Medical Center, Fort Lauderdale, FL, USA, ²Nova Southeastern University, Fort Lauderdale, FL, USA

Background: The rapid growing mycobacterium (RGM) M. chelonae, M. fortuitum, and M. abscessus are emerging infectious agents associated with common cosmetic procedures. We report a case of a severe M. abscessus infection following facial cosmetic injections, and a review of the literature.

Objectives: A 49-year-old Hispanic female presented with multiple non-draining facial pustules after receiving subcutaneous "vitamin E" injections 4 weeks prior to admission (Figure 1). During her 3-month hospitalization she underwent multiple debridements and antibiotic therapy including IV vancomycin, piperacillin/tazobactam,

SATURDAY • FEBRUARY 16, 2013

International Meeting on Emerging Diseases and Surveillance 2013

amikacin, clarithromycin, cefoxitin, and clofazamine. Three weeks after admission, cultures revealed Mycobacterium species that was subsequently identified as *M. abscessus* by rpoB gene sequencing at the National Jewish Hospital in Denver, Colorado, USA. Histology showed granulomatous inflammation with multinucleated giant cells in the muscle tissue (Figure 2). The patient was discharged on IV cefoxitin, amikacin and oral azithromycin as per susceptibility testing with clinical improvement. Of note, amikacin was discontinued due to ototoxicity.

POSTER PRESENTATIONS I



Figure 1. Patient, 49-year-old Hispanic female. Figure 2. Muscle tissue showing granulomatous inflammation with multinucleated giant cells. Image provided by Naoimi Montague, M.D. via FirstPath.

Methods and Materials: A literature search of adult cases with RGM skin infections secondary to pedicures, cosmetic injections, tattoos, cosmetic surgery and acupuncture in immunocompetent hosts published in the English language was conducted. PubMed data base was searched with no limitations regarding date, journal, author, or type of article. The following MeSH terms were used: Rapid growing mycobacterium; Cosmetic skin infections; *M. abscessus; M. chelonae; M. fortuitum.*

Results: A total of 388 cases were identified during the years 1983-2012. Invasive procedures including acupuncture, lidocaine injections, mesotherapy, and tattooing were the most common source of RGM infections (81%), followed by non-invasive procedures (11%), and surgical procedures (8%) (Figure 3A) *M. abscessus* was the most common RGM isolated (74%), followed by *M. fortuitum* (15%) and *M. Chelonane* (11%) (Figure 3B). Seventy eight percent of cases had a favorable outcome, although 21% had residual effects (Figure 3C). *M. abscessus* is the most resistant of the RGM species¹, responding poorly to commonly used antibiotics. Though some studies depict susceptibility to amikacin (95%) and clarithromycin (92.5%)^{3.4}.



Conclusion: RGM should be considered as etiologic agents in cosmetic procedure infections. Early suspicion for RGM infections will prompt the appropriate diagnostic studies and empiric treatment where indicated potentially preventing irreversible damage in patients.

21.136 Prevalence of *S. hematobium* infection among school children living along the south-western shores of Lake Malawi

S. A. Kayuni¹, R. Peeling², P. Makaula³

¹MASM Medi Clinics Limited, Blantyre, Malawi, ²London School of Hygiene and Tropical Medicine, London, United Kingdom, ³Research on Health, Environment and Development, Mangochi, Malawi

Background: Malawi is one of the countries in sub-Saharan Africa where both *Schistosoma hematobium* and *Schistosoma mansoni* are present. These are more prevalent along the shores of Lake Malawi and most water bodies. Previous studies showed *S. hematobium* prevalence of 23.7% among children living in the lakeshore areas, with re-infection rates of 30% to 40%.

This study was conducted to determine the current prevalence and distribution of *S. hematobium* infection in school children along the south-western shores of Lake Malawi and the control interventions present in the area.

Objectives: 1) To assess prevalence and distribution of *S. hematobium*infections in school aged children of south-western shores of Lake Malawi in Mangochi. 2) To assess the available control interventions for schistosomiasis in the area. 3) To determine the impact of these control interventions on prevalence and distribution of schistosomiasis in the area.

Methods and Materials: This prospective cross-sectional study was conducted in 7 primary schools, enrolling 400 children (attached map). They provided health information and submitted urine samples for analysis on macrohematuria, microhematuria and *S. hematobium* eggs. A questionnaire was administered to 3 health facilities on diagnosis, treatment and control interventions of schistosomiasis.

Results: 174 male and 226 female children were enrolled, aged 7–12 years (mean age: 9.57 years). 50 children (12.5%) had *S. hematobium* eggs. The mean egg count was 14.6/10ml and highest infection intensity was seen in 10 children (2.5%).

The prevalence in schools was significantly different, ranging 0–20%. Schools with higher prevalence rates were located farther away from public hospital, providing free treatment. The prevalence rates correlated with previous history of mass chemotherapy in schools.

Mass chemotherapy, health education, improved water supplies and sanitation are some interventions which contributed to lower prevalence rates in some areas.



Conclusion: S. hematobium prevalence in south-western Lake Malawi was lower than previously reported, owing to control interventions focussing on health education, improved water supplies, sanitation and mass chemotherapy.

POSTER PRESENTATIONS

Consistent and uniform interventions can reduce prevalence further and sustain control. As prevalence falls, diagnostics can identify high transmission areas, monitor disease trends and guide evidence-based control strategies.

21.137 The duration of effects of antibiotic exposures on the risk of Clostridium difficile infection (CDI): A cohort study

K. A. Brown¹, N. Daneman², R. Moinedden¹, D. Fisman³ ¹University of Toronto, Toronto, ON, Canada, ²Sunnybrook Health Sciences Center, Toronto, ON, Canada, ³University of Toronto, Toronto, Canada

Background: The rising incidence of Clostridium difficile infection (CDI) could be lessened by reducing exposures to high risk antibiotics. However, the effect of reducing duration of exposure is less well understood.

Objectives: We sought to assess both the duration of CDI risk after the cessation of antibiotic therapy and the cumulative risk, and whether these differed between antibiotic classes.

Methods and Materials: The source cohort consisted of all patients hospitalized at Sunnybrook Health Science Centre in the April 1, 2010 to May 31, 2012 period. Cases of CDI were identified prospectively, and their acquisition source and symptom onset timing were determined. Patient age, gender and hospital pharmacy records were obtained from electronic hospital administrative records. Antibiotic receipt was classified into 9 broad classes in accordance with the Anatomical Therapeutic Chemical Classification System (ATC); penicillins and non-penicillin beta-lactams were further subdivided, for a total of 14 classes. Receipt of a specific class of antibiotic or any antibiotic therapy was measured for each patient-day in a 20 day retrospective window. Cox regression with lagged effects parameterized as constant, linear and inverse sequences were compared.

Results: Over the 26 month study period, a total of 47,241 patients were identified as having been admitted, of which 144 had new onset nosocomial CDI while hospitalized. When risk was modeled as an inverse function of time since cessation of antimicrobial therapy (Figure 1, red lines), fit was improved relative to a model that assumed constant risk in the 20 day window (black lines). After adjustment for age and hospitalization history, the cumulative effect of each additional day of therapy was to increase CDI risk 4.14-fold (95%CI: 2.43-7.07). Daily effects were largest on the day of antibiotic receipt (HR=1.48, 95%CI: 1.27-1.71) and decreased rapidly (for example, HR of lag day 10=1.04, 95%CI: 1.02-1.05). Only 10 antimicrobial classes had exposure levels permitting risk estimates (Table 1); antibiotic associated risks were consistent with the literature.



Figure 1. Estimated risk of CDI due to any antibiotic exposure, based on Cox proportional hazards models. The plots demonstrate the estimated effects through time for a hypothetical patient receiving: (A) 1 day of antibiotics, (B) 3 days antibiotics.

Antibiotic (ATC code)	HR	95% CI
Any	4.14	2.43-7.07
Penicillins (J01C)	2.70	1.07–6.82
Broad-Spectrum	2.88	1.00-8.26
Narrow-Spectrum	2.08	0.32-13.55
Cephalosporins (J01D)	5.91	2.76-12.67
1 st & 2 nd Generation	9.94	3.10-31.84
3 rd & 4 th Generation	4.27	1.28-14.24
Carbapenems	3.76	0.50-28.33
Quinolones (J01M)	3.92	1.49-10.34
Macrolides (J01F)	2.69	0.12-60.86
Other (J01X)	1.89	0.53-6.71

Table 1. Cumulative hazard ratios (HR) associated with a single day of antibiotic therapy, by antimicrobial class.

Conclusion: The risks associated with antibiotic exposure decrease rapidly after the end of antimicrobial therapy. Judicious use of antibiotics and shorter antibiotic courses would substantially reduce CDI risk inhospital.

21.138 Tuberculosis-Major killer of adult urban women: Demographic and Health Survey (DHS) from Pakistan

S. Awan

Aga Khan university hospital karachi, Pakistan, Karachi, Pakistan

Background: Overall, almost 3.8 million cases of tuberculosis were reported in the world in 1990. of which 49% were in Southeast Asia. The World Health Organization (WHO) has estimated that there are approximately 8.8 million new cases of tuberculosis (TB) each year with an annual mortality of over 1.6 million.

Objectives: To study mortality patterns amongst women between 12-49 years of age in Pakistan.

Methods and Materials: DHS in Pakistanwas conducted from September 2006 till February 2007. A total of 1,125 adult female deaths were identified through the household questionnaires as occurring since January 2003. Verbal autopsies were successfully completed for 1,062, for a response rate of 94 percent.

Results: Most of the respondents were parents (24.9%), Brother/ sister in law (19.2%) and husband (17.3%). About 91% of the respondents were present at the time of death of the deceased.

Out of 1,022, 103 (10.1%) death were due to Tuberculosis in women between 12-49 years of age. Tuberculosis was the number three cause of death in women between the ages of 12-19 years (10.8%), 25 to 29 years (7.3%) and 35 to 39 years (10.2%). Between the ages of 30-34 years tuberculosis (16%) was number two cause of death after complication of pregnancy, child birth and puerperium.

Death from tuberculosis fluctuated eratically by age groups. However, middle age 30-34 yers women are more likely to die from tuberculosis. Considerablry more urban women die of tuberculosis (11.7%) than rural women (9.5%).

Conclusion: Cancer, tuberculosis and other infectious diseases are the next most important causes of death after complication of pregnancy, child birth and puerperium among women in reproductive ages. The prevention of TB, the extension of WHO DOTS programs, and a focused effort to control TB in are matters of great urgency.

21.139

Healthcare-associated infections due to carbapenemase-producing Enterobacteriaceae in Hungary

R. Szabó, K. Böröcz, A. Szönyi

National Centre for Epidemiology, Budapest, Hungary

Background: Healthcare-associated infections (HAIs) due to carbapenemase-producing Enterobacteriaceae (CPE) are emerging as an important challenge in public health worldwide. Recent studies show that infections with CPE are associated with higher rates of



International Meeting on Emerging Diseases and Surveillance 2013

mortality and prolonged length of hospital stay. The prevalence of CPE is exactly unknown, because only a few countries have protocol for detection. In response to the increasingly trends, the National Centre for Epidemiology issued a national guideline for screening and contact precautions of patients with CPE.

Objectives: Our study objective was to describe demographics, bacteria and resistance mechanisms, clinical characteristics and outcomes of CPE episodes.

Methods and Materials: Patient-based data on CPE episodes were collected through the National Reference Laboratory (NRL) and the National Nosocomial Surveillance System between September 2011 and September 2012.

We defined an episode as a patient infected or colonised by a CPE that was confirmed by the NRL. The clinical diagnosis of infection or colonisation was made by the physician based on CDC definitions.

Results: A total of 98 infections and colonisations were identified during the study period. The median age was 66.5 years (range, 0–92 years). Overall, 59 (60%) of all patients occurred in males.

The reported CPEs were mainly *Klebsiella pneumoniae* (n=83), *Enterobacter cloacae* (n=5), *Serratia marcescens* (n=3), *Klebsiella oxytoca* (n=2), *Enterobacter aerogenes* (n=1) and *Citrobacter freundii* (n=1). The carbapenemases involved in the 83 episodes were VIM (n=81) and OXA-162 (n=2).

A total of 98 cases are comprised 35 infections and 30 colonisations. In 33 cases, these data are not available.

Of the 35 infected cases had at least one affected site: urinary tract (n=12), bloodstream (n=8), surgical site (n=7), respiratory tract (n=4), gastrointestinal tract (n=2) and gynaecological tract (n=2).

Among all the cases, 14 deaths were reported (case-fatality 14%).

Conclusion: Our results represent that CPE are a serious public health problem in Hungary. Although few cases were identified, many hospitals were affected. Therefore it is an important task to increase adherence to national guidelines and to extend surveillance in hospitals to prevent the spread of CPE. We recommended continued screening, aggressive infection control practice and prudent antibiotic use against spread of CPE.

21.140 The discovery of EMRSA-15 in environmental *staphylococci* isolates

H. Mkrtchyan, R. Cutler Queen Mary University of London, London, United Kingdom

Background: The spread of antibiotic resistance within bacterial pathogens is an increasing problem throughout the entire World. The current measures used to control this threat seem ineffective and few novel antimicrobial agents are being developed in response to this threat. A major example of drug resistant microbial pathogens is community acquired methicillin resistant *Staphylococcus aureus* (CAMRSA) which has gradually increased to similar levels of antibiotic resistance as hospital associated MRSA (HAMRSA).

Objectives: We have found that environmental *Staphylococci* may act as a potential reservoir for methicillin resistance in non-hospital environments and report for the first time on the molecular characterization of EMRSA-15 isolated from public restrooms.

Methods and Materials: Six strains of *Staphylococcus aureus* were isolated from public washrooms. The minimum inhibitory concentrations (MIC) of these isolates against 30 antibiotics were determined using the MicroScan Walkway 96 plus automated system and disc diffusion methods. Genomic DNA was prepared using QIAamp DNA mini kit. SCCmec type was determined by detecting *mec* and *ccr* complexes using appropriate primers. Panton Valentine leukocidin (PVL) detection was performed for all *Staphylococci* strains using *luk-PV-1* and *luk-PV-2* primers. MLST and the x-region of the protein A *spa* gene was amplified by PCR using appropriate primers. Purified PCR products were sequenced using an ABI 3730XL DNA analyser.

Results: MLST and SPA typing revealed that two of the 6 MRSA strains (SCC*mec* type IV) belonged to the internationally disseminated EMRSA-15 clone with spa type t032 and MLST ST22. These isolates were also classified as *SCCmec* subtype IVh positive but PVL-negative.

These strains were resistant to 14 out of 30 antibiotics including oxacillin. Oxacillin MICs for these strains were determined to be 2 mg/l.

Conclusion: Despite all efforts that have been undertaken to control antimicrobial resistance it is still on the increase.

We report that public restrooms are potential reservoirs of EMRSA-15. The characterization of EMRSA-15 in our study is evidence that infection control measures both in the hospitals and in public places have failed to limit the spread of such clones highlighting the importance of good hygiene control in these environments.

21.141

A1 Risk factors associated with seropositivity against Lyme borreliosis: Results from a representative serosurvey of adults in Germany

H. Wilking¹, V. Fingerle², C. Klier², M. Thamm³, K. Stark¹ ¹Robert Koch-Institute, Berlin, Germany, ²Bavarian Food and Health Safety Authority, Oberschleissheim, Germany, ³Robert Koch Institute, Berlin, Germany

Background: Lyme borreliosis (LB), caused by *Borrelia burgdorferi* (*Bb*) sensu lato is the most common tickborne disease of the northern hemisphere. Major clinical manifestations include Erythema migrans, Neuroborreliosis and Lyme arthritis. Central Europe including Germany is regarded a highly endemic area; however, data on the extent of endemicity and on risk factors are limited.

Objectives: Our objectives were to conduct a representative seroepidemiological survey among adults in Germany to assess the seroprevalence (anamnestic titer) of LB in different geographical regions and to identify potential risk factors for seropositivity.

Methods and Materials: Sera from a nationwide representative survey for adults (DEGS) (2008 to 2011) were analysed by ELISA to assess the prevalence of anti-Bb IgG-antibodies in adults (18-79 years). Data collected by interview were used to evaluate possible associated factors. Univariable and multivariable statistical analyses used sampling weights and accounted for the cluster structure of the survey design.

Results: Out of a total of 6,965 individuals 852 were seropositive. Seroprevalence in men (14.5%; 95%-confidence interval (95%-Cl:13.1-15.9%)) was twice as high as in women (7.6%; 95%-Cl: 6.6-8.8%). Seropositivity increased from 6.8% in the 18–29-year-age-group to 22.6% in the 70–79 age-group without effect modification by sex. The largest increase was observed in the elderly (60–79 years). Residence in rural areas (Odds ratio (OR)=2.15; 95%-Cl:1.66-2.79) and living in Southern Germany (OR=1.52; 95%-Cl:1.23-1.86) were independent risk factors for seropositivity.

Conclusion: LB is endemic in all over Germany. The seroprevalence seen in the different age-groups reflects the cumulative incidence proportion. A previous study recognized children and adolescents (1–17 years) as a risk-group, this study identified elderly (60–70 years) as a second risk-group. This is compatible with recreational behaviour. Alternatively, this might be explained by a birth cohort effect of a previous time frame of lower risk of seroconversion in Germany resulting in less increase in 18–59 years-old. Seropositivity is not equivalent with clinical manifestation. Thus, differences between groups may not necessarily be reflected by the real disease burden. Identified risk factors are useful for targeted campaigns. Furthermore, the knowledge on seroprevalence in the population is a basic requirement to adjust pre-test probabilities in context of clinical diagnoses.

21.142

Pulmonary involvement of Brucellosis in patients treated in Kosovo

E. Qehaja Bucaj¹, S. A. Namani², L. Ajazaj Berisha³, M. Mehmeti⁴ ¹University Clinical Center of Kosova, Prishtina, Kosova, Kosovo, Republic of (under UNSCR 1244/1999), ²University Clinical Center of Kosovo, Prishtine, Kosovo, Republic of (under UNSCR 1244/1999), ³University Clinical Center of Kosovo, Prishtine, Kosova, Kosovo, Republic of (under UNSCR 1244/1999), ⁴Univesity clinical center of Kosovo, Prishtine, Kosovo, Republic of (under UNSCR 1244/1999)

Background: Brucellosis is a zoonotic infection transmitted to humans by direct or indirect contact with infected animals or their products. Kosovo remains a region with persistence of the infection in domestic animals and frequent transmission to human population.

IMED 2013

Objectives: The objective of the study was to analyze the respiratory involvement during the course of brucellosis in patients treated at the Infectious Diseases Clinic in Prishtinë (Kosova) during years 2006-2011.

Methods and Materials: In this retrospective study were collected data from medical records of 124 patients treated for brucellosis. We analyzed 30 patients with respiratory involvement confirmed with pulmonary pathologic findings with their pulmonary symptoms, physical examination and chest radiography.

Results: Of the 124 patients confirmed for brucellosis, 80 of them (64.5%) were male, the average age was 30.8 (range 2-74 years). The infection was mostly prevalent among people aged 15-34 years, 65 patients (52.4%). The highestincidence of patients with brucellosis was recorded from June to September (74/124,75%). Among 124 patients, socio-epidemiological data were gathered for 74 patients, where 58 (78.4) of them worked on farms with sheep, goats and cattle, 14 (18.9%) have consumed milk products from the market. Of the 124 patients, 30 (24%) were diagnosed for pulmonary involvement of brucellosis, 22 males (74%) range 4-74 years. Paroxysmal dry cough manifested ten patients, fever twelve and dyspnoea two patients Radiologic findings were pneumonia, bronchopneumonia, paratracheal lymphadenopathy and pleural effusion. The Wright's titer was 1/2560 (10 patients), 1/1280 (10 patients), 1/640 (5 patients) and 1/320 (5 patients). On abdominal ultrasound, in 23 patients were seen hepatomegaly, hepatosplenomegaly or splenomegaly, with high rate of ESR and CRP in 19 patients and elevated liver enzymes in 10 patients. At the end of the treatment of brucellosis, clinical findings of pulmonary involvement were recovered.

Conclusion: Pulmonary involvement was not a rare event among the patients treated for brucellosis in Kosovo and should not be forgotten as a causative agent in patients with pulmonary symptoms.

21.143 Clostridium difficile infection in a private hospital of Mexico City. Incidence rate and epidemiological features during 2011-2012

J. Reyes Mar, L. Rojo Gutierrez, P. Leal Moran, L. Cabrera Ruiz, N. Perez Hernandez, C. Y. Ruiz Hernandez, G. Santillan Lopez. M. D. L. Robles Hernandez, E. Aleman Aguilar, L. E. Soto Medica Sur, Mexico City, Mexico City, Mexico

Background: Clostridium difficile Infection (CDI) is an increased worldwide health-care associated problem. Recently, CDI has become a cause of community acquired diarrhea. Little it is known about CDI epidemiology and incidence in Mexican hospitals.

Objectives: Clinical and epidemiological description of CDI cases at Medica Sur during 2011 and 2012.

Methods and Materials: It is a retrospective review of CDI cases recognized among 2011 and 2012 at our Hospital. It is a 170 beds graduate teaching private hospital. The CDI cases were identified from toxin A&B detection by EIA commercial test positive in stool samples. The clinical charts were reviewed.

Results: From January 2011 to November 2012, a total of 51 CDI cases (5.67%) were detected by toxin-test from 898 clinical samples from patients with diarrhea. Of these, 29 (56.8%) were nosocomial cases including 8 cases (28% from nosocomial cases) with CDI diagnosis within 4 weeks after discharge. All cases had presented fever beside diarrhea. The incidence rate was 3.11 nosocomial cases / 10,000 patient-days. Mean of age was 60 years (19 to 95 years), 37 cases (72%) happened on female patients. In 49 cases (96%) there was an antibiotic use within previous 30 days. The main antibiotic used were one cephalosporin in 15 cases (30%), carbapenem in 9 cases (18%) or quinolone in 8 cases (16%). The kind of antibiotic was unknown in 16%. The common comorbidities were diabetes, cancer and heart disease in 13 cases (25%). In 28 cases (55%) there was not comorbidity. Three patients died but the attributable cause was the ongoing disease.

Conclusion: Despite of diagnostic limitations of Clostridium difficile toxin assays, unexpectedly, we found a high proportion of community acquired CDI cases even in healthy people. Typically, in the majority there was the background of antibiotic use, specially, cephalosporins, carbapenems or quinolones. This information is important for the approach of diarrhea associated to antibiotic use regardless the epidemiological scenario.

21.144 Human parasitic ova and cyst in local food drinks sold in open markets in Enuqu municipality, South-East, Nigeria

C. A. Ekwunife¹, C. I. Okafor¹, D. N. Aribodor¹, M. N. Ezeunala², C. N. Ukaga³

¹Nnamdi Azikiwe Univeristy, Awka, Nigeria, ²National Institute of Pharmaceutical Research and Development, Abuja, Nigeria, ³Imo State University, Owerri, Nigeria

Background: The consequences of human infection with parasites is of major health concern in developing countries. The transmission of most parasites are promoted by poor sanitation and personal hygiene such as insanitary handling of fruits, vegetables and locally made drinks.

Objectives: This work is to determine the level of parasitic infections of local food drinks hawked in open markets of Southeast Nigeria.

Methods and Materials: A cross sectional study on the prevalence of parasitic ova and cyst in local food drinks (Soya milk, Kunu-zaki and Zobo) from four open markets in Enugu municipality, Southeast Nigeria was carried out in March, 2012. Fifty (50) bottles of each drink were bought from hawkers from four different markets, making a total of 600 drinks. Formol-ether concentration technique was employed to concentrate the parasites in the drinks. Sediments observed were placed on a glass slide and observed microscopically using x10 and x40 objective lens, for possible parasite ova.

Results: Of the 600 bottles of drinks whose content were examined 254 (42%) were contaminated with ova and cysts of parasites. Parasites isolated were protozoan (Entamoeba histolytica, Giardia lamblia, Balantidium coli) and helminthes (Ascaris lumbricoides and Trichuris trichiura). More protozoan parasites 431 (78.6%) than helminthes 117 (21.4%) were observed. E. histolytica was the highest (27.6%) type of parasite recorded. The highest number of parasites 166 (30.1%) was recorded in food drinks collected from Ogbete main market while the lowest number of parasites 117 (21.4%) was from Artisan market. Kunu-zaki drink recorded the highest number 192 (31.9%) of parasites. However the number of parasites isolated from the different drinks and from different markets did not differ significantly (P>0.05)

Conclusion: Study indicated that most of the locally made food drinks being hawked in Nigerian markets and environ are contaminated. Such drinks which are cheap with high nutritional values are beverages from beans, leafs and sorghum. Unhygienic environment and poor handling could be the sources of contamination. Health education involving the food drink producers as well as monitoring the activities and the environment of such producers by health workers is advocated.



Seroprevalence of lassa fever and infection control practice among health workers in an endemic suburban community in Nigeria

E. A. Tobin¹, D. A. Asogun¹, G. Akpede¹, P. Okokhere¹,

S. Gunther², C. Happi³

¹Irrua Specialist Teaching Hopital, Irrua, Edo, Nigeria, ²Bernhard notch Institute of Tropical medicine, Hamburg, Hamburg, Germany, ³Harvard University, Boston, MA, USA

Background: Lassa fever (LF), an acute viral hemorrhagic illness is endemic in parts of West Africa can be transmitted to man through food contaminated with infected rodent excreta and by contact with body fluid of a patient, particularly in health care settings. Nosocomial epidemics are often associated with high case fatality rates. In Nigeria at least 5 Health workers died from LF in year 2012 alone. The level of knowledge of LF and infection control practices among health workers has not be assessed in recent times. This information will be useful in the design of programs to reduce occupational exposure and deaths from LF.

Objectives: To investigate the knowledge and seroprevalence of LF and infection control practices among health workers in an endemic area of Nigeria.

Methods and Materials: In an endemic community, 182 Health workers were selected by a stratified random sampling technique and

International Meeting on Emerging Diseases and Surveillance 2013

interviewed on their knowledge of LFand infection control practices using a pretested structured interviewer administered questionnaire. Their serum levels of IgG and IgM were determined using ELISA developed by the Bernhard Notch Institute of Tropical medicine, Hamburg.

Results: Knowledge of LF was poor for 74 (40.7%), fair for 75 (41.2%) and good for 33 (18.1%). Majority of the doctors and nurses regularly wash their hands after examining a patient(61.5% and 47.5%), wear hand gloves when touching body fluids (100% each), use face mask when doing procedures (53.8% and 64.4%) and do not recap needles after use(92.3% and 84.7%). However, majority of them regularly pass used syringes and needles from one person to another (53.8% and 81.4%). Although one hundred and eighteen (64.8%) of respondents have heard of infection control, only 39 (28.1%) had received some formal training in infection control, while 87 (71.9%) had never been trained. IgG was detected in 12(6.5%) and IgM in 3(1.6%) of respondents.

Conclusion: There is a need to improve on the level of knowledge and infection control practices of the health workers. This can be achieved through seminars and placement of posters on LF and standard precaution practices in all health facilities in Nigeria.

21.146 Status of TB indicators in Austria

E. J. Simons, A. Indra, S. Pfeiffer, F. Allerberger, D. Schmid Austrian Agency for Health and Food Safety, Vienna, Austria

Background: The WHO and ECDC recommended a series of indicators in an effort to fight TB and MDR-TB in the European region in 2010.

Objectives: The objective of our study was to evaluate Austria's current progress in efforts to achieve TB indicator targets.

Methods and Materials: TB data from 2002–2011, collected by the national surveillance system, were analyzed by indicators and compared to indicator targets: mean five-year decline in the trend of the TB case notification rate and of the MDR-TB case notification rate, mean ten-year decline in child-to-adult ratio of notification rate and increasing trend over ten years of mean age of TB cases, achievement of 80% culture confirmation among new pulmonary cases, 100% drug-susceptibility testing (DST) results among new pulmonary culture-positive cases and 70% treatment success rate in new pulmonary dDR-TB cases. Trends were measured using annual average percentage change (AAPC).

Results: The annual TB case notification rate steadily declined (AAPC: -7.1%) and the MDR-TB case notification rate increased (AAPC: +16.5%) between 2007 and 2011. Over the past ten years, the child-to-adult ratio of notification rate declined (AAPC: -1.8%) and the mean age of TB cases slightly increased (AAPC: +0.3%). Over the past five years, culture confirmation among new pulmonary cases increased by 6.5%, not fulfilling the target of 80% (2011: 71%); DST results were completed for 95–99% of pulmonary, culture-confirmed cases, not reaching the target of 100%. From 2004-2008, treatment success rates among new pulmonary, culture-positive cases ranged between 58-76%, compared to a target of 85%. Among MDR-TB cases, the treatment success rate decreased from 78% in 2004 to 47% in 2008, with a steep decline in 2007 (13%), compared to a target of 70%.

Conclusion: The steady decline in both overall TB case notification rates and ongoing TB transmission activity align with targets. Indicators failing to meet targets include the trend of the MDR-TB case notification rate, percent of culture-confirmed cases among new pulmonary cases and treatment success rates for all culture-confirmed cases and, in more recent years, for MDR-TB cases. The true success rate, however, is likely underestimated due to poor outcome data completeness.

21.147 Increasing incidence of pertussis in Austria, 2005–2011

S.-W. Jian, D. Schmid

Austrian Agency for Health and Food Safety, Vienna, Austria

Background: Resurgence of pertussis has been repeatedly reported in different regions around the world, even in the countries with sustained high vaccine coverage such as the UK and the US. In Austria, pulmonologists raised the concern of an increasing incidence of pertussis among adolescents since 2006 in one of the nine provinces.

Objectives: To describe the annual incidence of pertussis in Austrian total population by province from 2005 to 2011 and by age group from 2009–2011.

Methods and Materials: The national surveillance data including monthly reporting of aggregated data by province from 2005 to 2008 and a cases-based dataset from 2009 to 2011 were used. We described trends in the annual pertussis incidence from 2005–2011 by province. We analyzed the frequency distribution of cases by month of onset and age group and the distribution of cases by hospitalisation and vaccination status among aged <1 year from 2009 to 2011.

Results: Since 2006, the annual incidence increased steeply and reached 5.5/100,000 persons in 2011 ascribed to increasing trends in four provinces: Styria, Salzburg and Upper Austria from 2006–2011 and in Tyrol from 2009 to 2011. The incidence increased mainly among aged <15 years in Salzburg (9.6-39.6/100,000), Upper Austria (10.8-32.8/100,000) and Tyrol (1.8-20.4/100,000), whereas in Styria both age groups experienced the increase. In the age group <1, 1–4 and 5–9 years, highest proportion of cases (29–33%) occurred in August/ September. In the age group 10–19 years, the highest monthly proportion (29%) was observed in September/October. In aged ≥ 20 years old, a total of 31% of cases were distributed across September-December. The highest proportion of hospitalised cases in aged <1 year was aged 0–2 months (84%) followed by aged 3–5 months (82%) and decreased with age. The proportion of cases aged 1–5 years fully vaccinated (basic vaccines) was 39%.

Conclusion: Based on the national surveillance data, four of nine Austrian provinces recognized an increasing incidence of notified cases and affected mainly aged <15 years from 2006 to 2011. Investigations of causes for the province specific differences such as notification behaviour of clinicians, misclassification of cases, laboratory diagnostic methods and province specific vaccine coverage are currently ongoing.

21.148

Assessment of awareness and practices of secondary school students on lassa fever in Nigeria

D. A. Asogun¹, E. A. Tobin¹, N. Akpede¹, G. Akpede¹, S. Gunther², S. Okogbenin¹

¹Irrua Specialist Teaching Hopital, Irrua, Edo, Nigeria, ²Bernhard notch Institute of Tropical medicine, Hamburg, Hamburg, Germany

Background: Lassa fever (LF) is one of the viral hemorrhagic fevers commonly found in West Africa caused by the lassa virus, which has the multimammate rat as its natural host. Fatality rate can be as high as 60–80% during outbreaks. High risk behavior and practices that facilitate transmission include hunting and processing of rats for food by teenagers. Sensorineural hearing loss is one of the sequelae of clinical infection. This has the potential to affect academic performance of children in school, as LF occurs across all age groups.

Objectives: To determine the knowledge level and practices of secondary school students on LF

Methods and Materials: In a descriptive cross-sectional survey, 524 secondary school students selected by stratified sampling technique from 2 secondary schools in 2 local government areas of Edo State, Nigeria, were interviewed by means of a pretested structured self administered questionnaire on their knowledge and practice of LF. Knowledge and practice of LF was graded based on summation of scores allotted for responses to questions on LF.

Ethical clearance and informed consent were obtained prior to study. **Results:** Mean age of respondents was 16.35 + 1.6 years. 284 (54.2%) were males, 240 (45.8%) were females. Two hundred and fifty nine

International Meeting on Emerging Diseases and Surveillance 2013

(49.4%) had poor knowledge, 216 (41.2%) had fair knowledge and 49 (9.4%) had good knowledge. Knowledge was significantly associated with sex, family type, educational status of mother and father. Age had no relationship with knowledge ($X^2 = 1.14$, p = 0.89). Three hundred and eleven (55.4%) scored below the mean for good practices while 250 (44.6%) scored above the mean. Key house hold practice most performed was the washing of plates and utensils before use (72.0%). The performance in food hygiene practices was significantly associated with educational status of mother and father. (p =0.002 and p = 0.003respectively)

Conclusion: The knowledge of the students on LF is low and have significant high risk behavior that favors transmission. Health education seminars designed as part of the school health program should be given a priority in LF endemic communities.

21.149 Potential outbreak of rabies in bats in Los **Angeles County, USA**

T. Scott, G. Lamielle, K. Ehnert, E. Beeler

County of Los Angeles, Department of Public Health, Los Angeles, CA, USA

Background: Rabies symbolizes the guintessential zoonotic disease and while dog bites have largely been recognized as risk factors, bats represent another risk for both animal and human populations. In Southern California, the virus can be present in several species of bats, whose bites can often go unnoticed. Humans who have been exposed to bats must receive prompt post-exposure prophylaxis to prevent progression of the disease. Likewise, pets that come in contact with bats should be guarantined for a specific period of time. During an average year, 10 to 12 bats usually test positive for rabies in the County of Los Angeles, however, there has been an increase in rabid bats in the past two years.

Objectives: This presentation aims to report a dramatic rise in the number of rabid bats during the years 2011 and 2012 and to evaluate the concurrent risk of transmission of the disease to local populations of Los Angeles and their pets.

Methods and Materials: Dead and dying bats are reported to the County of Los Angeles' veterinary public health and then tested using a fluorescent antibody assay. Any interaction with potential human or animal victims is consistently recorded. Individuals reporting the bats are promptly contacted to inform them of the disease status of the animal and the procedure to follow in case of positive results.

Results: A sharp increase in the number of rabid bats has been noticed in Los Angeles, with 38 and 55 positive animals in 2011 and 2012, respectively. More bats have also been submitted for testing during the same amount of time, which can falsely increase positive results, however, the rate of positive bats also rose from 8-10% to 20%, demonstrating a true increase in disease prevalence.

Conclusion: This outbreak of rabies in bats is a cause for concern for the safety of residents of Los Angeles and health officials must remain vigilant in order to prevent cases in humans. Pets are at higher risk of contact with bats and should remain vaccinated. Possible causes for this increase are not evident, but may include changes in environmental factors or disease dynamics.

21.150 Performance of QuantiFERON TB Gold in the detection of latent tuberculosis infection among healthcare workers (HCWs) in Akwa Ibom State, Nigeria

A. N. Umoh¹, A. E. Asuquo², L. N. Abia-Bassey², E. O. Ibeneme² ¹University of Uyo, Uyo, Nigeria, ²University of Calabar, Calabar, Nigeria

Background: Identification and treatment of Latent Tuberculosis infection in high risk individuals is a priority in TB control and requires methods that provide accurate results to avoid wrong therapy in false-positive individuals. The interferon gamma (IFN-y) assay principle based on the ESAT-6 and CFP-10 which are more specific to M. tuberculosis is reportedly more accurate than the tuberculin skin test (TST).

Objectives: This study determined the prevalence of Latent TB infection among health-care workers in an endemic population using TST and Quantiferon TB-gold.

Methods and Materials: A total of 609 HCW from TB healthcare facilities across Akwa Ibom State, Nigeria were studied. The IFN-y release assay was performed using 3mL of whole blood by ELISA according to the manufacturer's instruction (Cellestis Ltd., Carnegie, Australia) after which 0.1mL of 5 tuberculin units of PPD was administered intra-dermally on each subject. TST results were read after 72 hours by measuring the size of indurations in millimetres. Data were analysed using SPSS version 17 (SPSS Inc., Chicago, Illinois).

Results: At the threshold of 10mm, the prevalence of LTBI by TST was 279 (45.8%) and 151 (24.8%) at the IGRA diagnostic value of ≥0.351IU. Mean TST induration values of 5.23mm and 6.65mm were obtained respectively for the 151 IGRA positive and 458 IGRA negative subjects. Laboratory staff and ward orderlies as well as being in service for >10 years, were more significantly associated with LTBI. A moderate agreement of 76.7%, k=0.51 was obtained between TST at 10mm, and QFT. Neither previous exposure to TST nor BCG vaccination affected the prevalence of LTBI in the study population.

Conclusion: The difference of 54% prevalence of LTBI between TST and QFT may be due to non-tuberculous mycobacterium (NTM) since TST is non-specific. This may have grave implications of drug toxicity and development of anti-TB drug resistance in individuals harbouring NTM, but receiving anti-TB drugs. The 76.7% agreement between the 2 tests suggests that the 10mm cut-off indurations for TST is still relevant in the diagnosis of LTBI. Despite the advantages of the QuantiFERON TB Gold test over TST, the prohibitive cost may limit its use in resourcelimited settings.

21.151

Prevalence of Methicillin-resistant Staphylococcus aureus (MRSA) in high-density livestock farming areas along the Dutch-German border.

H. Aangenend¹, R. Köck², K. Velden van der ¹, J. Hautvast¹, A. Friedrich³, A. Voss⁴, J. W. Paget¹

¹Radboud University Nijmegen Medical Centre, Nijmegen, Netherlands, ²University Hospital Münster, Munster, Germany, ³University Medical Center Groningen, Groningen, Netherlands, ⁴Canisius Wilhelmina Hospital, Nijmegen, Netherlands

Background: MRSA poses a considerable public health threat to the community, especially in high-density livestock farming regions. It is therefore very important that the prevalence of MRSA is monitored and risk factors are identified so that targeted public health actions can be initiated.

Objectives: The objectives of the PreMA study were: 1) assess the prevalence of MRSA in community patients who had taken antibiotics in the previous three months, 2) assess differences in the prevalence of MRSA in high-density livestock farming areas in the two regions, 3) determine risk factors for MRSA.

Methods and Materials: Cross sectional prevalence study carried out between October 2011 and May 2012 in the Netherlands (Brabant, Gelderland, Limburg) and Germany (North Rhine Westphalia). Nasal swabs and questionnaires were collected in patients (>4 years) from twelve Dutch General Practitioners (GPs), seven German GPs and two German outpatient urologists. Nasal swabs were analyzed using selective MBSA agars after broth enrichment

Results: Data were collected from 512 persons in the Netherlands and 461 persons in Germany. The prevalence of MRSA in the Netherlands was 0.8% (95% CI 0.2-1.9%; n=4) and 1.5% (95% CI 0.7-3.0%; n=7) in Germany. Livestock-associated MRSA was almost equal in both countries (n=4 (0.8%); 4x t011) and Germany (n=3 (0.7%); 2x t032, t011), whereas healthcare-associated MRSA was only present in Germany (n=4 (0.9%); t068, t032, t003, t1023). Persons who were farmers or who lived on a farm had the highest MRSA prevalence on both sides of the border: 12.5% in the Netherlands (3 out of 24) and 9.5% in Germany (2 out of 21). All cases were nasal carriers without MRSA infection.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: Despite sampling from a population that had used antibiotics in the previous 3 months and who lived in high-density livestock farming areas, the prevalence of MRSA was low in both regions. The prevalence of MRSA was significantly higher in Germany compared to the Netherlands, and 65% of cases in Germany carried healthcare-associated strains versus 0% in the Netherlands. These data suggest a different spread of MRSA in the two regions: in Netherlands the spread is livestock-associated whilst in Germany it is livestock- and healthcare-associated.

21.152 Lassa fever control: Assessment of food hygiene practice among market traders in Nigeria

E. A. Tobin¹, D. A. Asogun¹, N. Akpede¹, E. Ogbaini¹, C. Happi², G. Akpede¹

¹Irrua Specialist Teaching Hopital, Irrua, Edo, Nigeria, ²Harvard University, Boston, MA, USA

Background: Lassa fever(LF) is a viral haemorrhagic fever found in West Africa transmitted primarily to man through the contamination of food by the urine and droppings of infected rodents. An estimated 250,000 to 2million people are infected annually with a fatality rate of between 5 and 10,000. Improperly stored food items sold in the market are recognized sources of infection. Ignorance and lack of awareness of the disease as well as low educational status and poor hygienic practices are contributory factors to community transmission.

Objectives: To assess the awareness and practices of market traders on lassa fever

Methods and Materials: By means of a pretested structured interviewer administered questionnaire, 385 market traders selected by means of a stratified random sampling from each of the 3 senatorial districts in Edo State were interviewed on knowledge and practices on lassa fever.

Data was analysed using SPSS version 15 for quantitative variables and the mean, median and standard deviation for continous variables. Ethical approval and informed consent were duely obtained prior to study commencement.

Results: Majority of respondents, 272(70.6%) were females. Mean age was 30.1+11.9 years. Two hundred and ninety three (76.1%) had heard of Lassa fever. One hundred and forty two (48.5%) had poor knowledge, 151 (51.5%) good knowledge. Good knowledge was significantly associated with higher educational status (p = 0.025) and being of male gender (p = 0.005). Religion, age and marital status were not significantly associated with grade of knowledge (p = 0.631, 0.128 and 0.203 respectively).

One hundred and ninety (49.4%) engage in practices that favours spread of Lassa fever, while 195 (50.6%) had good food hygiene practices. Good food hygiene practices was significantly associated with being of female gender (p = 0.039) and within the age range 38-47 years (0.018)

Conclusion: About half of the Market traders had good knowledge and good food hygiene practices with respect to LF. More enlightenment campaign by appropriate organ of government with support from NGOs is imperative to halt community transmission of the virus and reverse the present high morbidity and mortality in Nigeria.

21.153 Active tuberculosis in patients under therapy with TNF-a inhibitors

L. Mejdoubi¹, T. Barisani-Asenbauer², R. Rumetshofer³ ¹Medical University of Vienna, Vienna, Austria, ²Medical University of Vienna, Wien, Austria, Austria, ³SMZ Otto Wagner Spital, Vienna, Austria

Background: Although tuberculosis screening and exclusion of active disease is mandatory prior to initiation of treatment with biologics, TNF- α inhibitors in particular, active diseases are reported worldwide in this context.

Objectives: Aim of our study-in a case series of 8 patients with tuberculosis activated during treatment with $TNF-\alpha$ inhibitors-was to

Methods and Materials: The Otto-Wagner Hospital in Vienna is specialized in tuberculosis infections. Yearly around 150 tuberculosis patients are admitted. We identified 8 patients with active tuberculosis during TNF- α inhibitor therapy by retrospective review of the clinical charts.

The indication for treatment was rheumatoid arthritis in 4 patients, Behcet's disease in 2 patients, Erythema nodosum in 1 patient and Crohn's disease in 1 patient. 4 Patients received infliximab, 2 adalimumab, 1 certolizumab and one patient a series of TNF- α inhibitors including adalimumab, etanercept, abatacept and golimumab.

Results: The patient group consists of 7 women and 1 man. Mean age at manifestation is 52.12 (min 24y; max 64y). The mean time to diagnosis of active infection was 35.75 days (min 1d; max 75d). The symptoms found were FUO in 4 cases, night sweats in 4 cases, cough in 2 cases, weakness in 2 cases and dyspnoea in 1 case.

Quantiferon test was performed and positive in 5 out of 8 patients, PCR was positive in 4 out 8 patients, Mycobacterium tuberculosis was identified by culture in 7 out of 8 cases (bronchial lavage samples, sputum, thoracentesis and lung biopsy).

Conclusion: Active tuberculosis infection occurs during therapy with TNF- α inhibitors although patients and treating physicians are aware of the risks and potential fatal sequels. Our cases show that not only screening failures are possible, but also follow-up of tuberculosis infection status is necessary, to diagnose tuberculosis reactivation and de novo infections in a timely manner. Furthermore clinical symptoms and manifestations differ from classical tuberculosis infections making diagnosis more difficult.

21.154

D4 Evaluation of acute flaccid paralysis suspected cases reported to the surveillance system in Akwa-Ibom State April 2006–April 2012.

W. E. Nwachukwu¹, B. E. Bassey², J. G. Ebuk³, P. Nguku⁴, M. N. Aghaji⁵

¹University of Nigeria Teaching Hospital, Enugu., Enugu, Enugu State., Nigeria, ²WHO Surveillance Office, Uyo, Nigeria, ³Akwa Ibom State Ministry of Health, Uyo, Nigeria, ⁴Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ⁵University of Nigeria Teaching Hospital, Enugu., Enugu, Enugu, Nigeria

Background: Nigeria is a polio-endemic country. Active surveillance of Acute flaccid paralysis (AFP) in children under 15 years of age is crucial in monitoring suspected cases of paralytic poliomyelitis which is an important component of the World Health Organization (WHO) global polio eradication campaign. No information on the charateristics/ attributes of suspected cases of AFP in Akwa-Ibom State.

Objectives: To determine the demographic, clinical and epidemiological charateristics/attributes of AFP surveillance system in Akwa Ibom State.

Methods and Materials: This is a 6 year secondary data analysis of suspected poliomyelitis cases reported and verified by the WHO surveillance system.AFP case verifying investagation form was adopted. Univariate and bivariate data analysis were done in Epi Info software. Statistical significant level was p-value = 0.05 at 95% confidence interval (CI).

Results: Total of 574 cases were reported between 2006–2012. Female:male ratio was 1.03. Median age was 1.75years (range 1–14 years).Under-five children were 91.3%. About 75.8% were of rural setting. Oral polio vaccination (OPV) status was low in 57.5% (1-3 doses of OPV) and was associated with hot case criteria (fever, under 3 years of age and OPV less than 3 doses) p-value=0.000. Clinically, 31.2% (Cl 27.4–35.2%) had history of injection, 90.9% (Cl 88.2%–93.1%) had fever, asymmetric 91.3% (Cl 88.6%–93.4%), progression to paralysis after 3 days 77.9% (Cl 74.2%–81.2%), muscle tenderness 26.5% (Cl 23.0%–30.3%). History of injection is associated with hot case criteria p-value 0.00 and residual paralysis p-value = 0.04. Trend of case reporting increased from 2.6% in 2006 to 40.4% in 2011 with avarage of 144 cases per year. Polio focal person reported 43.9% cases and 93.9% of the stool specimen arrived the reference laboratory within 72hours.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: Increasing level of OPV doses, strengthening polio surveillance and reducing frequency of injection in this under-15 age group are critical to polio eradication.

21.155 Evaluation of Acute Flaccid Paralysis surveillance system- Zamfara State, Nigeria, 2011

K. I. Getso¹, S. Gidado¹, P. Nguku¹, O. Biya¹, S. H. Idris², K. Sabitu² ¹Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ²Ahmadu Bello University, Zaria, Nigeria

Background: Poliomyelitis still remains a serious public health problem in Nigeria and presents constant threat to child survival and development. Zamfara State, North-West Nigeria is one of the polioendemic States.

Objectives: We evaluated Zamfara State's AFP surveillance system to assess its key attributes and performance.

Methods and Materials: Between May and August, 2011; we used Centers for Disease Control and Prevention's Updated Guidelines for Evaluating Public Health Systems (2001) to evaluate the State's AFP surveillance system. We identified and interviewed 48 key stakeholders using semi-structured questionnaires and telephone interviews and reviewed relevant documents. We analyzed the State's AFP surveillance data from 2009 to 2011 using MS excel and Epi Info Software 3.5.3 (CDC Atlanta).

Results: The system uses simple case definition, has clear reporting mechanism and information generated was used to implement targetted interventions. In 2011, the system had an annualized Non-Polio AFP rate of 12.6/100,000 (target ≥ 2/100,000), stool adequacy of 93% (target \ge 80%), timeliness of 90% (target \ge 80%), completeness of reports of 100% (target ≥ 90%) and Predictive Value Positive (PVP) of 2.6%. All (100%) stakeholders interviewed expressed willingness to participate in the system. Gaps identified included poor documentation of surveillance activities, inadequate supervisory visits by State Ministry of Health (5%), poor knowledge of AFP case definition among Healthcare workers (only 46% of Disease Surveillance and Notification Officers, 22% of Doctors and 10% of Primary Healthcare workers know AFP case definition) and 92% of funding for the system comes from donor agencies.

Conclusion: The system has achieved most of its set targets. It is simple, sensitive and acceptable but has low PVP. We recommended that the State should scale up supervision, improve documentation, train staff periodically and provide budgetary allocation for AFP surveillance.

21.156 KAP, housing standards and risk factor analysis for seroprevalence to Lassa fever in a rural community of Edo state, Nigeria

D. A. Asogun¹, G. Akpede¹, E. A. Tobin¹, S. Gunther², N. Akpede¹ ¹Irrua Specialist Teaching Hopital, Irrua, Edo, Nigeria, ²Bernhard notch Institute of Tropical medicine, Hamburg, Hamburg, Germany

Background: Lassa fever (LF) is a viral haemorrhagic fever estimated to cause 300,000-500,000 infections annually with 5,000 to 10,000 deaths across West Africa. The natural hosts for the virus are Mastomys natalensis which stay within close rangeof houses. Humans are infected primarily by contact with rodent excreta or urine in food or water and through direct contact with infected body fluids of a patient. Possible relationship between risk factors for LF such as housing standards against the background of knowledge and behavior is yet to be documented in endemic communities of Edo State.

Objectives: To document the association if any, between LF and risk factors in an endemic community.

Methods and Materials: By means of a pre-tested interviewer administered structured questionnaires 54 subjects 18 years and above resident in the community for at least 6 months prior to the study were interviewed on their knowledge and attitude towards LF, and practices that favour spread of the disease. Five (5) mls of blood was collected to determine presence of IgG and IgM antibodies using ELISA.

Ethical clearance and written informed consent was obtained from all participants before the study.

Results: Majority, 49 (90.7%) had poor knowledge, 4 (7.4%) fair knowledge and 1 (1.9%) good knowledge. Knowledge was not associated with age (p = 0.61), marital status (p = 0.72), education (p = 0.28), sex (p = 1.00) and religion (p = 1.00). All 54 (100.0%) respondents were at risk of direct contact with rodents and their excrement. Forty-eight (88.8%) were engaged in practices that favour transmission of LF through food, 6 (11.1%) having practices that do not promote spread of the virus.

Forty nine (90.7%) had seen rats in their homes, 31(57.4%) had seen faecal droppings in their foodstuff.

Majority, 43(79.6%) of the respondents were IgG positive and 8(14.8%) were positive for IgM. Majority of the houses with poor standard and other risk factors were IgM positive

Conclusion: Houses with poor environmental conditions and other risk factors had evidence of LF infection in endemic communities.

21.157 A study of viral load and genotype association among HCV infected patients in a tertiary care hospital of Pakistan

S. Aslam¹, T. Ijaz², B. Munir Ahmad³, S. Ali Raja⁴, S. Ijaz⁵ ¹College of Ophthalmology and Allied Vision Sciences, King Edward Medical University, Lahore, Pakistan, ²Mayo Hospital, Lahore, punjab, Pakistan, ³Mayo Hospital, Lahore, Pakistan, ⁴UVAS, Lahore, Pakistan, 5Services Institute of Medical sciences, Lahore, Pakistan

Background: Hepatitis C virus (HCV) is a principal cause of chronic liver diseases including liver fibrosis, liver cirrhosis and hepatocellular carcinoma. Identification of HCV genotype is extremely important clinically before prescribing therapy because different HCV genotypes require different duration and dose of anti viral therapy. Beside HCV genotypes, pre-treatment viral load has also been shown to be prognostic indicator of response to antiviral therapy.

Objectives: To identify the distribution of different HCV genotypes and their correlation with pre-treatment HCV RNA viral load among infected patients.

Methods and Materials: A prospective study including a total of 286 patients was conducted at Mayo Hospital, Lahore, Pakistan. Anti-HCV ELISA was performed on the blood samples of the patients and positive samples were tested for HCV RNA quantification performed using SmartCycler II, Real-Time amplification and detection system. HCV genotyping was also performed using nested-type specific primers. Data was analyzed through SPSS version 16.

Results: The study population comprised of 286 patients, 139 (48.6%) males and 147 (51.4%) females. Out of total samples, 214 (74.8%) were found to be positive for HCV-RNA status. The viral load was recorded to be less than 0.1 million IU/ml in 90 (31.5%) samples, 0.10-0.50 million IU/ml in 40 (14.0%), 0.51-1.0 million IU/ml in 38 (13.3%) and more than 1 million IU/mI in 46 (16.1%) samples. Among detectable genotypes, 1a was accounted for 14 (4.9%) patients, 1b for 4 (1.4%), 3a for 109 (38.1%), 3b for 28 (9.8%), 1a and 1b for 2 (0.7%), 1a and 3a for 6 (2.1%), 1a and 3b for 3 (1.0%), 1b and 3a for 8 (2.8%) and genotype 3a and 3b for 3 (1.0%) patients. The pi square values showed that there was a significant association between HCV genotype and viral load (p<0.001), locality and viral load.

Conclusion: HCV genotype 3a is the most prevalent genotype circulating in this region of the world. Baseline viral load is significantly high in patients infected by HCV genotype 3 as compared to the other genotypes such as 1 and untypeable genotypes.

21.158

Immune-based therapy against Clostridium difficile infection

J. A. Steele, J. Sponseller, S. Tzipori, D. Schmidt

Tufts University Cummings School of Veterinary Medicine, North Grafton, MA, USA

Background: Although Clostridium difficile infection (CDI) has been recognized as a cause of diarrhea for decades, it has emerged as an increasing cause of morbidity and mortality since 2000. CDI is now the most common cause of antibiotic associated diarrhea in humans in many

IMED 2013

developed countries and is also a frequent cause of neonatal diarrhea on swine farms. Treatment options for CDI are still limited, and we have developed a gnotobiotic piglet model for evaluation of novel therapeutics.

POSTER PRESENTATIONS

Objectives: We investigated a novel CDI therapy using hyperimmune bovine colostrum (HBC) against TcdA and TcdB in the piglet model.

Methods and Materials: The HBC was generated by immunization of a dairy cow during the final 10 weeks of gestation with recombinant, atoxic TcdA and TcdB, resulting in high titers of IgG against TcdA and TcdB in the colostrum. A total of 10 piglets were inoculated with *C. difficile* spores at 5 days of age and then divided into two groups: 5 piglets received HBC and 5 piglets were controls, receiving non-immune colostrum, with treatment initiated at the onset of diarrhea and continuing twice daily for 7 days.

Results: All control piglets developed clinical signs of CDI including moderate-severe diarrhea, and 3/5 developed fatal disease with systemic clinical signs before the experimental endpoint. Control piglets had typical gross large intestinal lesions, including pseudomembrane formation, and neutrophilic infiltration on histopathology. In the piglets treated with HBC, all had improvement of clinical signs after initiation of treatment, with diarrhea graded as mild or resolved in 5/5 piglets at the experimental endpoint, and no severe systemic signs of illness. Piglets in this group had no or mild gross large intestinal lesions, with no lesions or mild inflammation noted on histopathology.

Conclusion: While further investigation is warranted, this initial study indicates that HBC is an effective treatment for CDI and could be evaluated for use in human patients in the future. Development of a cost effective immunization for use in sows prior to farrowing could also provide a means of protecting piglets from CDI via hyperimmune colostrum.

21.159 Cross-sectional survey on seroprevalence of hepatitis E virus in Austria: Pilot study at the Austrian armed forces

H. Lagler¹, W. Poeppl¹, H.-M. Winkler¹, H. Herkner², A. Faas³, G. Mooseder³, H. Burgmann¹

¹Medical University of Vienna, Austria, Vienna, Austria, ²Medical University of Vienna, Vienna, Austria, ³Military Hospital Vienna, Vienna, Austria

Background: Hepatitis E Virus (HEV) seroprevalences of 0.3– 52.5% were reported from different European countries. Nationwide seroprevalence data from Austria are missing.

Objectives: To assess risk factors and exposure to HEV in Austrian adults and the occupational exposure of military personnel.

Methods and Materials: Study design: Explorative nationwide cross-sectional seroprevalence survey.

Setting: Serum samples and epidemiological data were obtained from adults volunteering for international military employments between April and September 2009 at the Military Hospital Vienna.

Participants: Healthy adults (from all 9 federal states) of Austria between 18–60 years were included.

Variables: Anti-HEV specific IgG antibodies were determined by enzyme-linked immunosorbent assay (Fortress Diagnostics Limited, Antrim, United Kingdom) according to the manufacturer's instructions. Variables surveyed included professional soldier or civilian, previous foreign military assignments, residential area, occupational animal contact and regular outdoor activities.

Statistical methods: Differences in proportions were tested using Fisher's exact test. A two-sided p value <0.05 was considered statistically significant.

Results: Participants: 1003 participants (980 men, median age 26 years) consisted of 407 professional soldiers and 596 civilians.

Main results: Overall, anti-HEV IgG was found in 136 (13.6%; 95% CI 11.5% to 15.8%) blood samples and correlated significantly with age (Fig.1; p<0.001) and frequency of previous foreign military assignments (p<0.001). The proportion of seropositive samples was significantly higher among professional soldiers than among civilians (16.5% vs. 11.5%; p=0.016). There were no significant associations with any of the remaining variables surveyed.



Figure 1. Seroprevalence of Anti-HEV IgG in 1003 adults by age group in Austria 2009

Conclusion: Our data showed an unexpectedly high seroprevalence in the Austrian adult population and indicate that military activities represent a significant exposure risk.

21.160 Incidence of tuberculosis after initiation of antiretroviral therapy in Georgia; Risk factors of mortality among HIV-infected patients

A. Abutidze¹, T. Tsertsvadze¹, R. Kempker², L. Sharvadze¹,

N. Chkhartishvili¹, M. Magee³, C. del Rio³

¹Infectious Diseases, AIDS and Clinical Immunology Research Center, Tbilisi, Georgia, ²Emory University School of Medicine, Atlanta, GA, USA, ³Rollins School of Public Health, Emory University, Atlanta, GA, USA

Background: There is a lack of data on the impact of antiretroviral therapy (ART) on the incidence of Tuberculosis (TB) and survival of HIV/ TB co-infected patients in high TB burden countries of Eastern Europe.

Objectives: The study objective was to determine TB incidence rate among HIV-infected individuals receiving ART and to estimate the independent association between ART use and mortality among HIV-infected individuals in Georgia in years 2008-2009.

Methods and Materials: Retrospective cohort study among all HIVinfected patients entering clinical care at National AIDS Center, Tbilisi, Georgia between 01/2008-06/2009. Factors associated with mortality including ART use were assessed utilizing a logistic regression model.

Results: Of 410 HIV-infected patients, 110 (26.8%) had TB at initial presentation and 49 (11.9%) had a prior history of TB. CD4 count at time of HIV diagnosis among the 410 HIV-infected patients was less than 200 cells/mm³ in 180 (45.9%). The mean baseline CD4 count was lower in HIV/TB co-infected patients compared with HIV-infected patients without TB (156.9 cells/mm³ vs. 339.9 cells/mm³, P<0.0001).

During a total of 776.6 person-years of observation, 4 new cases of TB were diagnosed. The overall TB incidence rate was 5.15/1000 person-years (95% CI=1.64-12.42). The overall mortality rate among HIV/TB co-infected patients was 27.9% in the ART+ group (n=93) and 82.3% in the ART- group (n=17).

After controlling for factors associated with death, not receiving ART was independently associated with increased mortality (OR=13.9, CI= 2.54-76.44).

Survival rates at 1, 2 and 3 years after TB diagnosis were approximately 77%, 75% and 75% in ART+ group, compared to 15%, 0% and 0% in ART- group (long-rank test, p<0.0001).

Conclusion: TB is the presenting opportunistic infection in over a quarter of HIV-infected patients in Georgia. Recently published randomized trials suggest that starting ART during TB treatment is associated with significantly increased survival. Implementation of ART during TB treatment is critical to improve outcomes for HIV/TB co-infected patients.

21.161 Trends in the clinical features and mortality in hospitalised Lassa fever patients in Nigeria

P. Okokhere¹, D. Asogun², G. Akpede¹

¹Irrua Specialist Teaching Hopital, Irrua, Edo, Nigeria, ²Irrua Specialist Teaching Hospital, Irrua, Nigeria

Background: Lassa fever, a re-emerging disease of public health concern in Nigeria has caused yearly outbreaks in the last decade. The pattern of clinical features and mortality may differ among sexes and age groups.

Objectives: To determine the frequency of the major clinical features and the mortality pattern of Lassa fever over a three year period, and to determine if age, sex and severity of disease significantly influence the clinical features and mortality

Methods and Materials: A retrospective, hospital based study, involving 160(84 males, 76 females) RT-PCR confirmed cases of Lassa fever managed at our health facility from January 2008 to December 2010. The duration of fever before treatment, the ages and sexes as well as the clinical features (bleeding, central nervous system manifestations, vomiting, diarrhoea, sore-throat, conjunctivitis and proteinuria) were retrieved from patients' records. The frequencies and severity of the clinical features and mortality were determined. These were compared among the sexes and age groups (<20 years (A); 20-49 years (B); \geq 50 years(C)), using relevant statistics to determine significance.

Results: Mean duration of fever before treatment was Group A : Male =6.27±3.23; Female=6.55±5.36; group B : Male=10.85±5.89; Female=11.29±11.03; group C: Male=9.70±6.1; Female= 8.94±5.14; p>0.05.

Vomiting (63.1%; Male vs Female: 63.1% vs 63.2%), Proteinuria (54.4%; Male vs Female: 53.6% vs 55.3%), CNS manifestations (41.3%;66: Male vs Female: 40.5% vs 42.1%), sore-throat(29.4%; Male vs Female: 28.6% vs 30.3%) and bleeding (28.8%;46: Male vs Female: 27.4% vs 30.3%) were the most frequent clinical features in the 3 years under review. The overall case fatality rate (CFR) was 35.6% (Male vs Female: 36.9%vs34.2%; p>0.05).

CNS features were 53.45%,51%,33.7% in A, C, B groups.The CFR was 61.5%,27.4%,26.9% in C,B,C groups; p<0.001.

CFR with severe clinical features: bleeding alone (mucosal and venepuncture sites) 19.1%; CNS alone (coma, seizures, tremors) 82.6%; bleeding plus CNS: 84.6%.

Conclusion: The clinical features which were of similar occurrence in the sexes show severe multi-systemic disease in majority of patients, and when present in individuals with fever in endemic areas may increase the likelihood of Lassa fever. Mortality is high, especially in older individuals and those with severe CNS manifestations.

21.162 Detection and genetic characterization of a Brucella infection in Saudi patients

T. Uzzaman¹. M. Elfakhei²

¹National Guard Health Affairs, Riyadh, Saudi Arabia, ²King Faisal Specialist Hospital and Research Centre, Riyadh, Saudi Arabia

Background: Brucellosis remains a major concern for the public health as well as for the economy of any country. In Saudi Arabia the national seroprevalence of brucellosis is 15-19%. In spite of such an alarming incidence of the disease, no serious effort has been done to molecular characterize the pathogen.

Objectives: No report is available on molecular characterization of bacteria involved in the pathogenesis of Human/bovine brucellosis in Saudi Arabia.

Methods and Materials: Patients attending the King Faisal Specialist Hospital and Research Center, Riyadh were subject of this study. We first screened the patients (n=23), who were positive for anti-brucella antibodies, by serum-PCR method using Bailey's primers. A duplex PCR was then employed to select patients positive only for B.melitensis and negative for B.abortus in a single reaction tube. Patients who were positive for B.melitensis and negative for B.abortus were further investigated. Isolated bacterial DNAs were evaluated by Southern hybridization for Brucella specific restriction patterns (EcoRI) using rRNA gene probe. Prototype isolates of Brucella abortus (BA544) and Brucella melitensis (16M) from ATTCC were used as positive controls

Results: The use of serum-PCR screening of the Brucella patients using Bailey's Primers showed a good sensitivity. As little as 40ul of serum was sufficient to give a positive PCR reaction. The duplex PCR established the infection to be involving B.melitensis strain in 17 out of 23 positive patients. The 16S rRNA gene sequence matched with the reported B.melitensis sequences. The Ecorl restiction patterns confirmed the brucella infection and the strain (melitensis sps.) specificity respectively.

Conclusion: Serum can be a safer and reliable source for detection of brucellosis. Duplex PCR can be employed for the charecterization of species in Brucellosis. B.melitensis is the major species affecting these patients. Involvement of other species is not ruled out.

21.163 Serologic evaluation of Crimean-Congo hemorrhagic fever in human population of endemic and non endemic areas in Albania

S. Bino¹, E. Tomini¹, M. Kota¹, S. Tobli², J. Sulo¹, A. Simaku¹, N. Como³, A. Papa⁴

¹Institute of Public Health, Tirana, Albania, ²Public Health Directory, Kukes, Albania, ³UHC "Mother Teresa", Tirana, Albania, ⁴Medical School, Aristotle University of Thessaloniki, Thessaloniki, Greece

Background: Crimean-Congo hemorrhagic fever (CCHF) first human case was recognized in Albania in 1986 and since then outbreaks are reported almost every year. Recently most of CCHF cases have been identified in northeastern past of the country and near Kosovo border. Before 2000, CCHF cases were recorded in different areas of the country such as central or southeastern part, bordering Greece. In a seroprevalence small study in 2003 no cases with IgG antibodies were identified in southeastern part of the country. In 2010 Albania experienced another outbreak of CCHF in Kukes and Has in northeastern area bordering Kosovo that experienced also another outbreak

Objectives: The main objective of the study was to evaluate circulation of CCHF virus in human population in areas with CCHF cases, previous areas and other areas without cases and analyze possible related risk factors.

Methods and Materials: A cross sectional survey with random sampling was used to collect 1762 samples in 2010 -2011 from all over Albania. Serum samples were tested for CCHFV immunoglobulin (Ig) G by ELISA (Vektor-Best, Koltsovo, Novosibirsk, Russia). A multivariate analyses of risk factors such as place of living tick bites and contacts. patient contacts, family contacts, animal slaughtering, agricultural activities, animals hosted next to the living house etc was performed.

Results: The overall national seroprevalence was 2.1%, with significant differences among different districts, ranging from 0.8 to 12 %. The highest prevalence was in northeastern districts of Has and then Kukes and in the southeastern district of Kolonja. The general population form non endemic areas had a seroprevalence of 0.5% Multivariate analysis revealed that slaughtering, family contacts and animals hosted next to the living house were significant risk factors for CCHFV seropositivity. The number of seropositive samples were much higher in areas experiencing the recent outbreaks of 2010 and 2011.

Conclusion: CCHF continues to densely circulate along northeastern border of Albania with Kosovo but also there is an re introduction of the disease in south eastern areas bordering Greece. Low prevalence in general population shows the low possibility to find CCHF cases in other areas of the country.



Epizootic and laboratory diagnostic methods of anthrax within the scope of CBR GG-18 project

M. Zakareishvili, M. Donduashvili, M. Kokhreidze, M. Nikolaishvili Laboratory for the Ministry of Agriculture, Tbilisi, Georgia

Background: Bacillus anthracis, the causative agent of Anthrax, is a zoonoses of concern throughout many countries of the world, including Georgia. Anthrax diagnostics and surveillance has been carried out since 1907 in Georgia by the LMA.



International Meeting on Emerging Diseases and Surveillance 2013

Objectives: As part of the CBR (Cooperative Biological Research) GG-18 project, the LMA team was tasked to improve the surveillance capabilities and diagnostic microbiology infrastructure in Georgia, in order to properly monitor the prevalence and distribution the *B. anthracis.*

Methods and Materials: Within the GG-18 project implementation period, a total of 130 animals and environmental (soil) samples were tested from multiple regions of Georgia. According to the TADR algorithm the following tests have been used for identification of *B. anthracis:* Gram Stain test, Lysis by gamma Phage, Motility test, Detection of poly-D-glutamic Acid Capsule by Direct Fluorescent Antibody (DFA), Detection of Cell-Wall Associated Polysaccharide by Direct Fluorescent Antibody (DFA), Malachite Green, PCR; GIS techniques were also developed within CBR GG18.

Results: The results of the tested samples are as follows: 36 were positive and 94 negative. A majority of infected animal samples and positive results were from the Kvemo Kartli Region. The isolated cultures (36) were stored as museum stocks. All the diagnostic procedures were carried out at biosafety level two laboratories using BSL-3 practices. Positive and negative samples were entered into the Electronic Integrated Disease Surveillance System (EIDSS) as soon as each result was available.

Conclusion: The project provided an opportunity to apply existing and already certified methods more widely and intensively across Georgia. Testing data indicated that 44% (35 samples) out of 80 specimens were positive

21.165 Opportunistic infections in HIV/AIDS patients in Jayapura City Papua Province, Indonesia

Y. Y. R. Mirino¹, A. Oktavian², A. M. Juliana¹

¹Institute of Research and Development for Biomedicine Papua, Jayapura, Indonesia, ²National Institute of Health Research and Development for Biomedicine, Papua Province, Jayapura, Indonesia

Background: Opportunistic infections in HIV/AIDS patients are infections that arise due to decreased immunity. These infections can be caused by microbes (bacteria, viruses, fungi) that comes from outside the body, as well as existing in the human body, but normally controlled by the immune system. Opportunistic infections often lead to death. There were 2381 HIV/AIDS cases cumulatelively until September 2012, but no information about opportunistic infections.

Objectives: The purpose of this study was to obtain an overview of opportunistic infections in the Jayapura City, include characteristics of HIV-AIDS patients, the types of opportunistic infections and the proportion of HIV-AIDS patients with opportunistic infections.

Methods and Materials: The study was conducted at two central hospitals in Jayapura City : through medical records of HIV/AIDS in 2010 and 2011

Results: The results showed the proportion of HIV/AIDS patients with opportunistic infections in 2010 was 61.8% and 68.1% in 2011.

there are no statistically significant relationship between age with opportunistic infection p value: 0.661 (2010), p value: 0.323 (2011), with sex in 2010 (p value: 0.100), in 2011 (p value: 0.118), with level of education in 2010 (p value: 0.214), in 2011 (0.681).

The highest number of opportunistic infections HIV/AIDS in Jayapura City is Tuberculosis

Conclusion: Early diagnosis and management of opportunistic infections in HIV/AIDS are needed to decrease the severity of the diseases

21.166 West Nile Virus is moving eastward in North Eastern Italy

P. D'Agaro¹, V. De Angelis², D. Franchi³, T. Gallo⁴, **P. Martelli**⁵, M. Palei⁶, A. Perosa⁷, M. Ruscio⁸, D. Santon⁹, M. Stecchina³ ¹University, Trieste, Italy, ²Azienda Ospedaliero-Universitaria "S. Maria della Misericordia", Udine, Italy, ³Hospital of Gorizia, Gorizia, Italy, ⁴ASS.4 "Medio Friuli", Udine, Italy, ⁵Az. Ospedaliera "Santa Maria degli Angeli", Pordenone, Italy, ⁶Regione Friuli Venezia Giulia, Trieste, Italy, ⁷Hospital of Latisana, Latisana, Italy, ⁸Hospital of San Daniele, San Daniele, Italy, ⁹Institute for Maternal and Child Health-IRCCS "Burlo Garofolo", Trieste, Italy **Background:** In Italy the first human case of WNV neuroinvasive disease (WNND) was observed on September 2008 in the Emilia-Romagna region and six cases of WNND were demonstrated retrospectivelly in the Veneto region. In 2009, the endemic area spread in northern Italy and 17 cases of WNND were notified from three regions (Veneto, Emilia-Romagna and Lombardia). Since then a larger geographic area in north-eastern regions was involved. Since 2009, Italy applies nucleic acid amplification technology (NAT) screening on all blood donations from residents in endemic areas. Since 2001, a veterinary WNV surveillance programme has been activated in Italy and is based on wild bird mortality, sentinel chicken, and WNV seroconversion in horses residing in risk areas. It was implemented in 2010 with the entomological surveillance. In the Friuli Venezia Giulia (FVG) only two cases had been reported before 2012 and one was epidemiologically linked to the Veneto region.

Objectives: To evaluate the incidence of WNND in the FVG in 2012 and to compare data on human animal and vector surveillance for WNV.

Methods and Materials: In 2012, the FVG region activated a regional surveillance for WNND: Possible cases were referred to the Regional Reference Laboratory. Diagnosis of infection includes serological diagnosis (IgG, IgM, Avidity test and PRNT) on serum and CSF samples and NAT on blood, CSF and urine samples.

Results: Eight cases of WNV infection were demonstrated in FVG between September and November 2012; six presented a WNND and two, asymptomatic, had been detected by NAT in blood donors. They were residents in the Udine, Pordenone and Gorizia provinces. The animal surveillance in 2011 could demonstrate the infection in horses living in the three provinces and the entomologic surveillance demonstrated viruses of lineages 1 and 2 in pools of mosquitoes collected in two provinces. Urine samples of the patient from the Gorizia province resulted positive at NAT and the sequence was identified as a lineage 1 WNV.

Conclusion: The surveillance of human cases could demonstrate the eastward progression of the WNV endemic area that is now reaching the Slovenian border. The animal and entomologic surveillance is a reliable predictor of the infection in humans.

21.167 Challenges in the management of patients with leprosy in Msambweni District, Kenya

S. K. Kazi

FELTP, Nairobi, Kenya

Background: Leprosy is a chronic disease caused by *Mycobacterium leprae*, andcan result in permanent disability. In Africa the prevalence is 0.8 per 10,000 persons. Msambweni district in coastal Kenya noted an increase in leprosy cases during recent years. We conducted an investigation to characterize the cases and provide recommendations for control.

Objectives: To assess the challenges of the management of leprosy patients in Msambweni district.

Methods and Materials: We reviewed the leprosy register from Msambweni District in Kenya from 2007-2012. A case of leprosy was defined clinically using leprosy cardinal signs (skin patches and enlarged peripheral nerves). Demographic and clinical data were extracted from the register.

Results: We captured 111 cases, resulting in a prevalence rate of 7.4 per 10,000 persons. The median age was 42 years (range: 5–80 years); 73 (66%) were males. Multibacillary leprosy was reported in 103 (95%) patients, and 6 (5%) had paucybacillary leprosy. Majority of the cases reported lacked information on laboratory confirmation of the diagnosis. In terms of treatment, 87 (78%) were new patients, 15 (14%) were relapses, 8 (7%) had resumed treatment, and 1 (1%) was a transfer. Forty-four (41%) had grade two disability at the start of treatment, 31 (29%) had grade one, and 32 (30%) had no disability. Sixty-one (68%) recovered, 20 (22%) were lost to follow-up, 7 (8%) were transferred out, and 2 died (case fatality rate of 2%).

Conclusion: The burden of leprosy in Msambweni is exceedingly high, reflecting that leprosy continues to be a problem in Kenya. Majority of patients sought treatment after developing disabilities, and many

are lost to follow-up. Public health efforts should increase community and healthcare worker knowledge of the disease to improve detection and timely treatment. Defaulter tracing efforts should be enhanced to minimize patients lost to follow-up.

21.168 Disaster medical assistance team (DMAT) activity and infectious disease and control in 2011 Great East Japan earthquake

Y. Kohayagawa, Y. Koido, H. Kondo

National Health Organization Disaster Medical Center, Tachikawa, Tokyo, Japan

Background: Disaster Medical Assistance Team (DMAT) in Japan was established in 2004 for the purpose of reducing preventable disaster death. After the establishment, many disaster occures in Japan. In 2011 Great East Japan Earthquake, 383 DMATs worked to operate hospital support, patients' transportation in local- and wide-area, and hospital evacuation. National Police Agency reported that the number of death in the earthquake was about 16000 and the most of them were instant death by drowing.And Reconstruction Agency reported that the number of earthquake-related death was about 2300.Now on survey of the cause of earthquake-related death, it is possibele that main cause of the dealth is infectious disease.

Objectives: To reveal the activity of DMAT regarding to infectious disease and control.

Methods and Materials: To check scripts in activity reports submmitted to DMAT secretariat from each DMAT.If there is any script about infectious disease and the control in activity report, the team was counted as a team worked for infectious disease and control.

Results: There is almost no script about infectious disease and control in activity reports for medical management.

Conclusion: In general, Infectious disease is not a main problem in acute phase in catastrophe. In sub-acute and chronic phase of disaster, infectious control become to be more important. DMAT is a medical tearm to work for medical management and support immidiately after the occurence of a disaster. Therefore, it is possible that the importance of support for infectious control is relatively low for DMAT and the rare script in their reports. But this does not mean that DMAT can not examine patients with infectious diaease. DMAT consists of physicians, nurces and logisticians who genelally work in hospitals all over Japan in peacetime. They examine infectious patients ordinarily. In the meanwhile, infectious control in disaster needs special ability in investigation and support. DMAT will take over their works to disaster medical coordinater in local and national level in sub-acute or chronic phase. To decrease earthquake-related death, DMAT had better manage infectious disease even in acute phase.

21.169 Wild polio virus outbreak in Kebbi State, Nigeria 2011

B. S. Bako¹, P. Nguku², O. Biya³, K. Sabitu⁴, S. Gidado³ ¹Abuja, Nigeria, ²Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ³Nigeria Field Epidemiology and Laboratory Training Programme, Abuja, Nigeria, ⁴Ahmadu Bello University, Zaria, Nigeria

Background: Poliomyelitis caused by Wild Polio Virus (WPV) remains endemic in most parts ofNorthern Nigeria. In 2010, Kebbi State in North-West Nigeria had the highest risk of WPV and Circulating Vaccine-Derived Polio Virus (cVDPV) transmission in the country.

Objectives: To identify reasons for case clustering and institute appropriate preventive and control measures.

Methods and Materials: We Reviewed secondary data from polio virus outbreak and a 30 Thirty household survey between February 1 and April 30, 2011. To obtain information on demographic and household characteristics, vaccination history,reasons for non-vaccination.Data from active case seach was analysed for missed acute flaccid paralysis (AFP) in these communities.We reviewed the State's AFP surveillance indicators.A case was defined as any suspected AFP (Acute flaccid paralysis) case with a positive stool sample for Wild Polio virus or a

Circulationg vaccine derived polio virus.Data were analysed with Epi Info version 7.

Results: The median age was 30.20 (Range19-48) two (40%) had received 1-2 Oral Polio Vaccine (OPV) doses while three (60%) had never received any OPV dose. Families of all the five confirmed cases had no access to pipe borne water and used pit toilet. Parents of all the cases had no formal education. Of the 30 households surveyed 0% of the children under 5years had no OPV at birth (zero dose) through routine immunization,0% of 6-23months had no complete doses of OPV. Among the reasons advanced for lack of immunization among cases and surveyed households was, lack of awareness about routine immunization (86.5%), no consent from husband (5.6%), felt there was no need for immunization (2.8%) and the rest felt clinics and hospitals were only meant for the sick. Two unreported AFP cases were detected during active case seach. Annualized Non-Polio AFP (NPAFP) rate in the state was 12.9/100,000 under-15 and 12.4/100,000 under-15 in 2009 and 2010. while the stool adequacy was 97% and 94% in 2009 and 2010 respectively.

Conclusion: The key reason for clustering of WPV/cVDPV cases appears to be inadequate OPV vaccination and poor living conditions. Government and its stakeholders should strengthen vaccination activities and should scale-up immunization awareness, and surveillance.

21.170

Global migration and tuberculosis trends in non-endemic country

A. M. S. A. AL-Harbie

Ministry of health (Kuwait), Rumaithiya, Kuwait, Kuwait

Background: The World Health Organization considers tuberculosis (TB) to be a global, uncontrolled, fatal, contagious epidemic. Tuberculosis re-emerged (annual incidence 9 million and 3 million deaths) as a public health concern associated with migration. Global migration from TB endemic areas to low incidence areas is considered a major risk factor for the transmission of *Mycobacterium tuberculosis* because 5-10% are latent TB infection unknown dormant carriers, and associated with MTB re-activations post-migration. Misdiagnosis of LTBI cases, due to ineffective diagnostic tools, changes TB epidemiological morbid trends, puts a considerable strain on the health-care system of the host country. A revision of the standard guidelines to identify what is required to better understand the TB status of immigrants.

Objectives: A- Research describes tuberculosis morbid trends in Kuwait over a 26-year-period (1984–2009)

B- Evaluates the accuracy of LTBI diagnosis by comparing the accuracy of standard health policy in detection of latent TB infection using the old TB diagnostic tests with biomarker diagnostic tests; interferon gamma release assays (IGRAs): 1- QuantiFERON Gold In-Tube (QNF-GIT) test, 2- T-SPOT.TB test among the new migrant population.

Methods and Materials: Morbid trends from the authorized Department of Health Information and Medical Records.

Post-entry in Kuwait, 180 individuals newly arrived between February and May 2010 randomly selected at the biggest immigration centre applying two old (CXR, TST) and two new MTB diagnostics (IGRAs) simultaneously. Qualitative variables were tested using the Likelihood ratio (LLR χ 2) and non-normal distribution of quantitative variables using Kruskal-wallis (KW χ 2) at p-value of 0.05.

Results: CXR radiologists 1 and 2: detected between 7.1 and 6.1% LTBI respectively.

CXR Pulmonologists: 0% detection

TST: negative (98%), borderline (0.5%), excluded (3%)

T-SPOT TB positive: 41.1%

QNF-GIT positive: 28.3%

Conclusion: 1) Uncontrolled international migration threatens nonendemic countries; 2) Increased trends of tuberculosis morbidity and mortality rates, due to; 3) Weakness of the current protocol for screening of LTBI/TB within the migrant population to non-endemic country, and with consequent leakage of 'TB suspect' cases.

Poster Presentations I SATURDAY • FEE

SATURDAY • FEBRUARY 16, 2013

International Meeting on Emerging Diseases and Surveillance 2013

21.171 A case of imported dracunculiasis— South Omo, Southern Ethiopia, May 2011

G. E. Yembo Ethiopian Health and Nutrition Research Institute, Addis Ababa, AA, Ethiopia

Background: Ethiopia is one of four remaining Guinea worm endemic countries. 20 cases were reported in 2010. The last indigenous case in South Omo zone was reported in 2001. Treatment of water sources with temaphose to control copepod development was suspended in 2002. In May 2011, the zone reported one Guinea worm case.

Objectives: A response team deployed to confirm the case and determine the source of infection.

Methods and Materials: A case of guinea worm is defined as an individual exhibiting of skin lesions with emergence of one or more worms. We interviewed the patient to obtain information on possible exposures prior to worm emergence. An active search was conducted in surrounding villages. 10 stagnant ponds used as a drinking water source were physically inspected for the presence of infectious copepods using a hand lens.

Results: The identified patient was a 40-year-old female living in Nakorie village within Nyangatom district in southern Ethiopia. Health workers identified her as a suspected case of Guinea worm on 15 April 2011. She presented with swelling and itching on her left leg and was admitted to a health center. The first worm emerged on 17 May 2011 from her left leg and the second emerged on 14 June 2011 from her right buttock. In June 2010, she had traveled to Loteang village, Eastern Equatorial state, South Sudan—within the 10–14 months incubation period. No copepods were identified in stagnant ponds used for drinking water and no additional cases were found. The case was cross-notified to South Sudan. The South Sudan team investigated and identified the possible source of infection in Loteang village.

Conclusion: There was no evidence of dracunculiasis local transmission since 2001 in South Omo, Ethiopia. The history of travel to an endemic area, the 10-year period that had elapsed since the last indigenous case was reported from the area, and the absence of copepods in drinking water sources in the village of the case suggested that exposure had likely occurred in Loteang village, South Sudan and that further localized transmission was unlikely. The case was considered imported. Heighten surveillance and prevention of local transmission is critical.

21.172

The use of diagnostic databases for arbovirus monitoring and surveillance; a feasibility study with a focus on dengue virus

N. Cleton¹, **C. Reusken¹**, M. de Jong², J.-L. Murk³, A. van der Eijk³, M. Koopmans⁴

¹National Institute for Public Health and the Environment, Bilthoven, Netherlands, ²University of Amsterdam, Amsterdam, Netherlands, ³Erasmus University Medical Centre, Rotterdam, Netherlands, ⁴Erasmus Medical Centre, Rotterdam, Netherlands

Background: For arboviruses, limited monitoring and surveillance (MOSS) is performed in a large part of the developing world. Travelers are potential sentinels for real-time monitoring of arbovirus exposure at travel destinations. However, the value of data on travel-related arboviral disease for MOSS would strongly depend on the quality of the diagnostic requests concerning these travelers.

Objectives: The aim of this study is to evaluate the feasibility of using the information in diagnostic databases to monitor trends in arboviral exposure in Dutch travelers, using dengue virus (DENV) as a model.

Methods and Materials: All diagnostic requests for DENV were imported from the laboratory information systems of the three main arboviral diagnostic laboratories in the Netherlands in the period 2000-2011 into an Excel database, along with a minimal dataset (sex, age, travel destination, vaccination history, symptoms). Data formats were reviewed and harmonized, and statistically analyzed for comparability of patient population, and trends of DENV IgM and IgG positive patients using



Results: The completeness of the minimal datasets vaccination history, travel history and clinical were low, stressing the need for reevaluation of data logging methods. Significant differences in patient categories and completeness of data were observed between centers. However, trends in diagnostic results were generally compatible. Additionally, a general correlation could be observed between WHO DENV surveillance data and the number of DENV positive results to the top four travel destinations of Dutch travelers.

Conclusion: When taking these factors into account, data can potentially be used for trend monitoring as part of a DENV MOSS.

21.173 Dengue virus 4 infection with thrombocytopenia and acaclculous cholecystitis in a British traveller

S. Mankad¹, B. Kapadiya²

¹Shalby Hospitals Ltd, Ahmedabad, Gujarat, India, ²Shalby Hospitals Ltd, Ahmedabad, India

Background: Dengue virus infections are a common cause of undifferentiated febrile illness in travellers visiting the Indian Sub continent. This case report of a young female British traveller to India describes the clinical profile and the subsequent clinical course of the traveller. Molecular typing of the virus done by RT- PCR was suggestive of dengue virus 4 infection.

Objectives: The main objective of this case report is to study the clinical profile of the dengue infection in the traveller and to prognosticate subsequent secondary infections after baseline molecular typing of the dengue virus.

Methods and Materials: The clinical profile, laboratory parameters, dengue serology- antigen and antibody detection along with the molecular typing by reverse transcriptase PCR was performed.

Results: The presenting clinical manifestations of this traveller included fever, severe bodyache, retro orbital pain and minimal right upper quadrant abdominal pain. On day 5 of the illness developed a maculopapular rash with severe itching. Laboratory parameters included a thrombocytopenia, leucopenia and increase in transaminase levels with normal serum billirubin. She did not have any signs of leaky capillaries or haemorrhagic manifestations. Ultrasound abdomen was suggestive of peri gall bladder edema and minimal collection suggestive of acalculous cholecystitis secondary to dengue infection. The diagnosis of dengue was confirmed with NS1 antigen positivity. A molecular typing by RT-PCR was done which was suggestive of Dengue virus 4 infection. She recovered well with optimum intravenous fluid and supportive management

Conclusion: Dengue virus infection must be considered as a vital differential in undifferentiated febrile illness in travellers visiting the subcontinent. Identification of the virus by PCR may be a useful tool for prognostication in subsequent secondary infections.

21.174 Understanding causes of death amongst Indonesian Hajj pilgrims: Comparison of verbal autopsy and death certificate data

M. Pane¹, S. Imari¹, K. Alwi¹, N. Kandun¹, G. Samaan²

¹Ministry of Health, Jakarta, Indonesia, ²Australian National University, Canberra, ACT, Australia

Background: Each year, over 200,000 Indonesians undertake Hajj pilgrimage. Mortality rates amongst Indonesian pilgrims are high, ranging between 200 and 380 per 100,000 pilgrims in the last 10 years. Cause of death data are limited in the Indonesian pilgrim mortality surveillance system as variables are based on the generic death certificate issued by a healthcare facility or flight doctor. To address this, a verbal autopsy form was introduced in 2008 to provide more details for each death.

Objectives: Based on 2008 surveillance data, this study compared the death certificate and verbal autopsy categorization of pilgrims' cause of death.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: During Hajj, the doctor and two nurses accompanying each flight group conduct mortality surveillance. Mortality surveillance documents cause of death based on the death certificate. In 2008, the verbal autopsy form introduced was based on WHO standards and adapted for Hajj pilgrimage. The form elucidates medical history, symptoms and other circumstances regarding the death from those who travelled with the deceased. The flight doctors complete and submit the verbal autopsy forms to the Indonesian Hajj public health team for analysis. Percentages for each cause of death category according to the death certificates and verbal autopsy forms were compared using McNemar's test.

Results: In 2008, 206,831 Indonesian undertook Hajj. There were 446 deaths, with an overall mortality rate of 216 per 100,000 pilgrims. Compared to the verbal autopsy method, death certificates attributed significantly more deaths to cardiovascular disease (p<0.001) and neoplasms (p=0.03). The death certificate attributed significantly fewer deaths to respiratory diseases (p=0.007), communicable diseases (p=0.03) and the ill-defined category (p<0.001) compared to the verbal autopsy method.

Conclusion: Understanding cause of death is critical for risk mitigation. The verbal autopsy method may have better categorized cause of death as it reduced the proportion attributed to the allencompassing cardiovascular disease category. The verbal autopsy method may have also reduced misclassification by removing the pressure on clinicians to extrapolate cause of death in situations where it was ill-defined. Indonesian authorities will continue use of the verbal autopsy form for each pilgrim death to improve data quality and evidence-based planning.

21.175 Disseminated histoplasmosis in a domestic cat imported from the USA to Austria

A. Klang¹, I. Loncaric², J. Spergser², S. Eigelsreiter³,

H. Weissenboeck⁴

¹Institute of Pathology and Forensic Veterinary Medicine, Vienna, 1210, Austria, ²Institute of Bacteriology, Mycology and Hygiene, Vienna, Austria, ³Veterinary Clinic Vorgartenstrasse, Vienna, Austria, ⁴Institute of Pathology and Forensic Veterinary Medicine, Vienna, Austria

Background: Histoplasmosis, a fungal disease with worldwide distribution, shows the highest prevalence and incidence in the Midwest and South of the United States and is comparatively rare in Europe. Infections may be subclinical or cause pulmonary disease and dissemination. In Austria, there are only single reports on infections with H. capsulatum in men and animals including one case each in badger and chinchilla. To our knowledge, feline histoplasmosis has never been reported in Austria.

Objectives: We present a case of disseminated histoplasmosis in a domestic cat imported from the USA to Austria. Diagnosis of Histoplasma (H.) capsulatum-infection was proven by histopathological examination, PCR and sequence analysis.

Methods and Materials: A six-year-old female British shorthaircat, was presented with reduced behavior and progressive dyspnoea for one week. Thoracic radiography showed a generalized interstitial pattern of the lung and the cat died within two days after initiation of corticosteroid-therapy.

Subsequently, necropsy was performed and fungi were cultivated from frozen liver samples. PCR amplifications and sequence analysis were performed of a part of the 18S rRNA, and the ITS1-5.8S rRNA-ITS2 region.

Results: Histological examination revealed a systemic mycosis with participation of the lungs, which showed a severe diffuse interstitial to suppurative pneumonia. Hyperplasia of type II pneumocytes and alveolar histiocytosis were prominent findings. Numerous fungal elements suggestive of histoplasma were present within alveolar macrophages. PCR and sequencing confirmed the diagnosis of H. capsulatum.

Conclusion: The animal was originally a stray cat found in Texas, USA, and had been brought to Austria four years later. Since then the animal was kept strictly indoors which strongly suggests that the infection occurred in the USA. Immunosuppression following the administration of corticosteroids might have triggered a reactivation of an until then subclinical infection. This case once againreminds us that imported domestic animals may be the source of zoonotic pathogens which are unknown in the country of destination.

21.176 Learning from a case of imported rabies to establish a rabies control zone

W. Petsophonsakul¹, T. Sripanya², P. Khawplod³, W. Kheuanrat⁴, S. Phornwisedsirikun⁴, M. Srijun⁴, S. Jaisuda⁴, M. Moonpo⁵, A. Noguchi⁶, S. Inoue⁶

¹Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand, ²Faculty of Association Medical Sciences, Chiang Mai, Thailand, ³Queen Saovabha Memorial Institute, Bangkok, Thailand, ⁴Chiang Mai Provincial Livestock Office, Chiang Mai, Thailand, 5Veterinary Research and Development Center (Upper Northern Region), Lampang, Thailand, 6National Institute of Infectious Diseases, Tokyo, Japan

Background: The Chiang Mai Livestock Office, local communities and animal organizations have adopted an intensive national policy to make a rabies free zone by 2020, according to WHO and OIE. The policy has a progressive strategy for controlling rabies in Chiang Mai. Incidentally, many people and animals in Chiang Mai were exposed recently to a rabid puppy that had been imported from a suburban temple in Bangkok. The puppy died after one month after the onset of rabies symptoms. A rapid test to monitor the post exposure rabies vaccination was used in the management of this outbreak.

Objectives: To evaluate the immunity of dogs and humans exposed to a rabid puppy in the Chiang Mai rabies control zone.

Methods and Materials: A brain sample from the dead puppy was found to be rabies positive by the Checkman rabies Ag test kit and mouse inoculating confirmation tests. Sera collected from 12 humans, 13 dogs and 2 cats were tested for an anti-rabies neutralizing antibody by the RAPINA antibody test kit and confirmed by the RFFIT test. The ring rabies vaccination program and constraint for observing symptoms in exposed animals were performed in both in the puppy rescuer's house and shelter according to the rabies prevention guideline.

Results: Several dogs that were kept in the shelter did not have a protective antibody, but they did have a record of rabies vaccination after their rescue from straying. Due to this imported case of rabies, all sectors learned the benefit of a rabies vaccination program and monitoring of the protective antibody for action against a rabies outbreak. A weakness of measures against a sudden imported rabies case in Chiang Mai also was found.

Conclusion: A follow-up rapid test of protective antibody was useful, and it eased the work in managing the outbreak. It was revealed that the care of animal welfare, quality of vaccines used, storage, and skills of vaccinating would solve the problem of immunity in dogs. Therefore, the strategy and remaining issues of a rabies control zone in Chiang Mai are to examine the state of vaccine and provide a protective antirabies neutralizing antibody in dogs.

21.177 Profile of measles confirmed cases notified to National CIEVS from January to June 2011, Brazil

S. Lopes Dias¹, E. T. Masuda¹, M. É. Santos¹, W. A. Oliveira¹, P. Pereira Vasconcelos de Oliveira², G. S. Dimech³

¹Brazilian Ministry of Health, Brasilia, DF, Brazil, ²Ministry of Health, Brasilia, Brazil, ³Ministry of Health Brazil, Brasilia, DF, Brazil

Background: The Center for Strategical Information in Health Surveillance (CIEVS/National), within the practice field of the Secretariat of Health Surveillance of the Brazilian Ministry of Health, continuously monitors events that may constitute public health emergencies classified after a risk assessment. This process is based on the International Health Regulations (IHR, 2005).

Objectives: This study describes the profile of measles confirmed cases in Brazil, during the 1st semester 2011, and their risk classification.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: It is a descriptive study about the measles cases monitored by CIEVS/National from January to June/2011 obtained from the data bank of Events Monitoring Information System (SIME).

Results: In the 1st semester 2011, 17 notifications of measles events were received, including 25 suspect cases, of which 17 (68%) were confirmed, 7 (28%) discarded and one (4%) under investigation. The predominant notifying source was through CIEVS in the Brazilian states_SES (76%). Of the confirmed cases, the mean age and median age were, respectively, 15 and 10 years old (5 months to 43 years); 16 (94%) were not vaccinated or had incomplete scheme, and all of them were considered imported cases. Among the genotypes, 16 cases D4 (Europe) and 1 case G3 (Asia) were isolated. As to risk assessment according to annex 2 adapted from IHR (2005) to be used in Brazil, 14 (82%) were classified as Risk to the National Public Health and 3 (18%) were classified as ESPIN (Public Health Emergency of National Concern). Among the risk assessment groups, group III. A significant risk of national and international propagation determined the classification of the event as ESPIN. Although the infection source of these events was not identified, the international aspect of them is its relation to the importation of measles detected outside the country.

Conclusion: In 2012, Brazil acquired the international certificate on elimination of measles. So the imported measles cases identified highlight the importance of timely detection, risk assessment and communication between health professionals, health authorities, health surveillance teams and CIEVS for the prompt response to the event.

21.178 Risk of latent tuberculosis infection (LTBI) among personnel after conducting humanitarian assistance aboard a United States military hospital ship

N. Adams¹, E. Lederman², J. S. Parrish¹

¹Naval Medical Center San Diego, San Diego, CA, USA, ²San Diego State University, San Diego, CA, USA

Background: It is well documented that military personnel are at risk of acquiring tuberculosis (TB) after deployments. This is particularly true when they are sent to regions with high prevalence of TB. Although there have been reports of personnel developing latent TB (LTBI) after humanitarian assistance, an analysis of data by occupational group and exposure time in the context of humanitarian missions has not yet been systematically evaluated.

Objectives: To assess the risk of new LTBI among personnel providing humanitarian assistance in The Philippines, Vietnam, Micronesia, Timor Leste and Papua New Guinea.

Methods and Materials: We reviewed two electronic medical record systems to record demographic information and to identify new LTBI among military members. In addition we compiled data on civilian participants via correspondence with civilian volunteer coordinators. The ship's manifest for medical civil action projects (MEDCAPS) was utilized to estimate hours of close contact with the civilian population for each member.

Results: Of the 869 active duty medical records reviewed, 98 members were excluded from the analysis because of pre-existing LTBI. Of the remaining 771, four active duty members had developed new LTBI after the mission. In the active duty personnel with new LTBI, all were nonmedical personnel.

Conclusion: The risk of becoming infected with tuberculosis during humanitarian missions is not insignificant; 0.46% of the entire military crew became newly infected with tuberculosis during the course of this mission. This stresses the importance of screening all personnel, medical and support staff, before and after these deployments.

21.179 Intervention strategies for preventing pathogen spread via illegal tiger trade network

N. G. Patel¹, A. Sonricker Hansen², J. Brownstein², D. Joly³ ¹University of Pennsylvania, Philadelphia, PA, USA, ²Childrens Hospital, Boston, MA, USA, ³Wildlife Conservation Society, Nanaimo, BC, Canada

Background: There is a need for better understanding of illegal wildlife trade networks for conservation purposes and—given the increasingly recognized role of wildlife in disease emergence—for public health. Effective interventions have been challenging due to the extent of the trade and limited resources allocated to its control. The application of network analysis could help guide the design of more effective intervention strategies for pathogen spread via illegal wildlife trade networks. Tigers were chosen for this initial study, as it is one of the most heavily illegally traded animals. Furthermore, all tigers fall under one species classification, which facilitates the pathogen literature search.

Objectives: We will examine the illegal tiger trade network and known tiger pathogens using network analysis. The impact of different types of intervention strategies directed at these networks will be evaluated.

Methods and Materials: Methods have been adapted here from examples in the criminology field looking at disrupting drug trafficking networks. Tiger pathogen data was overlaid onto a network constructed of illegal tiger trade data. Location data from illegal tiger trade reports were collected from sources including HealthMap's Wildlife Trade Map and TRAFFIC/WWF's Wildlife Trade Trackers (LEMIS and Tiger Trade). Location data for all known tiger pathogens were collected from sources including HealthMap, PubMed, ENHanCE, and the Global Mammal Parasite databases. The effectiveness of different hypothetical intervention strategies on network disruption was examined. The five strategies tested were (1) targeted interventions based on network properties, (2) targeted interventions based on tiger locations, (3) targeted interventions based on known pathogen locations, (4) interventions based on a combination of the above strategies, and (5) random intervention. Based on repeated simulations of each strategy, the disruption of the network was plotted.

Results: Plots of the disruption of the network allow for a direct comparison of performance of each intervention strategy.

Conclusion: These results provide guidance on how to design potential intervention strategies for the illegal wildlife trade and their pathogens. This approach can be adapted for other taxa involved in the illegal wildlife trade.

21.181 Isolation of the emerging foodborn pathogen *Arcobacter* from human stool

A.-M. Van den Abeele¹, K. Houf²

¹Saint-Lucas Hospital, Ghent, Belgium, ²Ghent University, Merelbeke, Belgium

Background: Arcobacters are Gram-negative slender curved bacteria closely related to campylobacters. In humans, predominantly *A. butzleri* has been associated with enteritis and occasionally septicaemia, but also *A. cryaerophilus* and *A. skirrowii* have been isolated from stool of diarrheic patients. Infection may occur by the consumption of contaminated water and food or by direct contact. At present, for the isolation of arcobacters from human specimens, *Campylobacter or Yersinia* media are used.

Objectives: The aim of this study was to evaluate a specific *Arcobacter* procedure (Houf et al., 2007) for the examination of human stool from patients.

Methods and Materials: From January 2008 till present, all stool samples from out-patients and from in-patients admitted less than 72 hours to a large secondary care hospital are included. Culture for all common bacterial pathogens is performed. *Arcobacter* isolation is carried out inoculating 1g faeces into 9 ml of *Arcobacter* enrichment broth and overnight incubation at 28°C. Subsequently, 50 μ l is streaked onto an *Arcobacter* selective agar plate (Houf et al., 2001). Plates are screened after 72 hours microaerobic incubation at 28°C by dark field

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

microscopy for typical colonies and further identified by a speciesspecific PCR-assay (Douidah et al., 2010). For patients with Arcobacter positive stools, medical records are investigated for the presence of acute or recurrent diarrhoea, abdominal pain and underlying disease.

Results: From the eligible samples cultured for arcobacters, Campylobacter species are on top of the enteric bacterial pathogen list (5.4%) followed by Salmonella (3.0%) and toxigenic C. difficile (2,7%). Arcobacter is the fourth most common isolated genus (1.3%), with almost equally isolation of A. butzleri and A. cryaerophilus. Arcobacter butzleri positives tended to be in-patients with diarrhoea and an underlying disease compared to A. cryaerophilus. Arcobacter thereuis, recently isolated from aborted porcine foetuses (Houf et al., 2009), was isolated for the first time from a human patient.

Conclusion: Arcobacter was significantly more isolated in this study than in studies with other methods applied. Arcobacters were the fourth most common organism isolated from stool in the study population. Using the recently validated veterinary isolation technique, routine recovery of arcobacters in humans becomes feasible.

21.182 Use of saliva and urine for early dengue diagnosis

G. Yap

National Environment Agency, Singapore, Singapore

Background: The necessity of a venous blood collection in all dengue diagnostic assays and the high cost of tests that are available for testing during the viraemic period hinder early detection of dengue cases and thus could delay cluster management. We have developed a saliva based test using antigen capture anti-DENV IgA (ACA) enzyme-linked immunosorbent assay (ELISA) technique. We believe saliva testing can encourage patients to be more receptive towards dengue diagnosis.

Objectives: Following this line of non-invasive methods, and as part of Singapore's STOP DENGUE study, we explored the use of molecular diagnosis on saliva, as well as urine samples collected from dengue confirmed patients.

Methods and Materials: Saliva and urine were collected from Dengue-confirmed patients, alongside blood samples. PCR, NS1 and viral isolation were applied on the samples.

Results: We were able to detect and serotype dengue viruses in both saliva and urine samples, as early as the first three days of fever. Dengue virus in saliva is transient (detection drops drastically after the first three days of fever onset) and in lower titres compared to blood. Conversely, in urine, dengue viruses could be detected (and serotyped) even when the virus has disappeared from the circulatory system. When adapting commercial dengue diagnostics (dengue NS1 rapid tests) on these biofluids, we found that NS1 detection is more sensitive in urine, with positive detection correlating with that in serum samples.

Conclusion: The potential of using non-invasive biofluids for dengue diagnostics is tremendous. This study presents a suite of diagnostic tools to use on saliva and urine samples at different stages of the dengue disease and also offers a possible point-of-care test for dengue.

21.183 Unbiased detection of infectious agents in respiratory syndromes of poultry using a metagenomic approach

E. Liais¹, G. Croville¹, J. Mariette², C. Klopp², C. Donnadieu², J. Lluch², M. Ducatez¹, C. Camus-Bouclainville¹, J.-L. Guérin¹ ¹Ecole Nationale Veterinaire, Toulouse, France, ²INRA, Castanet-Tolosan, France

Background: Respiratory syndromes are of major importance in poultry health. Viruses, bacteria and fungi, act altogether with environment in the pathogenic process of respiratory infections. Unbiased methods of diagnostic are needed to give a comprehensive picture of respiratory pathogens. The development of "next generation sequencing" offers such new opportunities in clinical microbiology.

Objectives: As a proof of concept of application of high-throughput sequencing in veterinary clinical microbiology, we aimed at describing the respiratory viral and bacterial flora of ducks showing respiratory clinical signs and/or egg drop syndromes.

Methods and Materials: A total of 10 flocks of Peking ducks or Muscovy ducks were sampled. Pools of ten swabs were put together to construct libraries. The preparation of specimens for deep sequencing was performed as previously described (Victoria & al., 2009; Phan & al., 2011; Shan & al., 2011). Briefly, clinical specimens were centrifuged, treated with DNase and RNase, then DNA and RNA were extracted and PCR amplified using a random primer (Victoria & al., 2009). PCR products were purified and loaded on a Miseq (Illumina) sequencer. Assembled contigs and singlet sequences were compared to Genbank database using GAAS software with a E-value of 10⁻³ to 10⁻⁵.

Results: More than 2 millions reads were generated and analyzed, 5% of which matching with bacteria and less than 0.5 % with viruses. Regarding viruses, we identified a majority of sequences of (i) bacteriophages (Siphoviridae, Myoviridae, Podoviridae, Microviridae), and (ii) animal viruses (Retroviridae, Reoviridae, Adenoviridae, Poxviridae, Picornaviridae, Orthomyxoviridae, and Paramyxoviridae); as well as few sequences of plant and insect viruses. Altogether, these data resulted in the description of a duck respiratory virome.

In the same way, bacterial reads were identified by 16SRNA analysis: a majority of gram negative (Enterobacteriacaea) was identified.

Conclusion: We have conducted a metagenomic analysis in ducks respiratory syndroms. Deep sequencing is a powerful approach to detect infectious agents in a clinical case. It also detects any opportunistic pathogen flora, unrelated to clinical signs, which will be challenging for the diagnostician. This approach will increase our understanding of microbial diversity in respiratory infections and highlights the complexity of co-infections in poultry respiratory tract.

21.184 SHERPAxMAP: An innovative multiplex microsphere assay platform for the surveillance and rapid serodiagnosis of emerging viral diseases

J. Vanhomwegen¹, S. Paulous¹, J.-C. Manuguerra¹, P. Despres¹, L. I. O. Sawoo²

¹Institut Pasteur, Paris, France, ²pasteur institude, Paris, France

Background: The great majority of emerging or re-emerging infectious diseases that pose a serious public health are caused by arthropodborne viruses (arboviruses). Unfortunately, the highly similar clinical presentation of most arboviral diseases implies that it is virtually impossible to differentiate them without the use of laboratory methods. Additionally, the presence of several genetically close arboviruses within the same geographic regions, poses problems for the diagnostic specificity of serological assays due to the development of crossreactive antibodies during viral infections.

Objectives: The aim was to develop a sensitive and specific multiplex serological assay for the surveillance and differential diagnosis of medically important arboviral diseases such as dengue (DEN), Japanese Encephalitis (JE), West Nile (WN), Yellow Fever (YF), Chikungunya (CHIK), and Rift Valley Fever (RVF).

Methods and Materials: An easy, fast, and low-cost method, designated SHERPADES, was developped for the massive production of recombinant antigens from medically important arboviruses. The viral antigens were fused in frame to SHERPADES protein and produced using the Drosophila Expression System (Invitrogen Inc.) Color-coded MagPlex microspheres (Luminex corp.) were irreversibly conjugated to the recombinant antigens produced through SHERPADES using an optimized coupling protocol, and combined to form a multiplex fluorescent microsphere immunoassay to detect serum antibodies. Specific serum immunoglobulins captured during the assay procedure were revealed by a secondary reporter antibody using a a flow analysis tool (Bio-Plex 200 instrument).

Results: Up to hundreds of milligrams of highly-purified viral antigens, showing a long half-life and thermostability, were obtained using the SHERPADES system. The obtained antigen-conjugated microspheres showed enhanced capture of specific antibodies, and demonstrated a long-term stability (>6 months at 4°C). A multiplex immunoassay associating up to 20 types of antigen-coupled microspheres was successfully used to capture specific IgM and IgG antibodies to

International Meeting on Emerging Diseases and Surveillance 2013

arboviral diseases, greatly reducing the required sample volume and demonstrating enhanced sensitivity and specificity toward target antibodies as compared with classical ELISA.

Conclusion: Together, these technologies allow the rapid and simultaneous detection of antibodies to a wide range of infectious pathogens in biological fluids of infected patients, thereby providing a high throughput, cost-effective, and accurate tool for surveillance and diagnosis of emerging diseases.

21.185 Molecular identification and susceptibility pattern of clinical *Nocardia* species: emergence of *Nocardia crassostreae* as an agent of invasive nocardiosis

S. J. Taj-Aldeen¹, A. Deshmukh¹, S. Doiphode¹, A. Abdul Wahab¹, M. Al lankawi¹, A. AlMuzrkchi¹, C. H. Klaassen², J. Meis²

¹Hamad Medical Corporation, Doha, Qatar, ²Canisius Wilhelmina Hospital, Nijmegen, Netherlands

Background: *Nocardia* are rare opportunistic organisms that cause diseases in immunocompetent and immunocompromised individuals.

Objectives: To investigate the clinical presentations of various *Nocardia* infections based on 16S rRNA gene of the isolate, related risk factors, and susceptibility pattern to antimicrobial agents.

Methods and Materials: A case series of 13 patients with nocardiosis were included in the study. Seven different *Nocardia* species were identified by 16S rRNA. Antimicrobial susceptibility testing was performed against six agents.

Results: Five patients were immunocompromised, and eight were immunocompetent with various predisposing factors such as cystic fibrosis, tuberculosis, and opthalmic infections. *Nocardia* caused pulmonary infections in eight patients (61.5%), invasive systemic infections in three patients (23%), and two local (ophthalmic) infections (15.4%). Pulmonary nocardiosis is caused by the species, *N. cyriacigeorgica*, *N. otitidiscaviarum*, *N. farcinica*, *N. carnea*, *N. testacea*, and *N. asiatica*.

Conclusion: *N. crassostreae* is a multidrug resistant organism was reported as emerging human pathogen causing invasive nocardiosis in a patient with non-Hodgkin's lymphoma. The *N. farcinica*, was isolated from blood in a patient with breast cancer.

None of the *Nocardia* isolates were resistant to linezolid. One *N. otitidiscaviarum* was a multidrug resistant organism. All patients in the present study were treated with the appropriate antibiotics and their condition resolved without further sequelae.

This study is the first report on *N. crassostreae* as a human pathogen. The detection of multidrug resistance species necessitate molecular identification and susceptibility testing be performed for all *Nocardia* infections. Nocardiosis manifests various clinical features depending on the *Nocardia* species and underlying conditions.

21.186

1.180 Bronchoalveolar lavage lateral-flow device test for diagnosing invasive pulmonary aspergillosis

M. Hoenigl¹, W. Duettmann¹, C. Koidl², B. Waitzl², K. Seeber¹, J. Wagner¹, K. Troppan¹, R. Raggam¹, R. Krause¹, C. Thornton³ ¹Medical University of Graz, Graz, Austria, ²Medical university of Graz, Graz, Austria, ³University of Exeter, Exeter, United Kingdom

Background: Due to the crude mortality of 80-90% in absence of adequate treatment, timely diagnosis and early start of antifungal therapy are key factors in the successful treatment of invasive pulmonary aspergillosis (IPA). Diagnosis of IPA, however, remains difficult as clinical signs and symptoms as well as radiological findings are often unspecific and conventional culture methods lack sensitivity. In recent years antigen testing has therefore become one of the cornerstones of IFI diagnostics, even though tests are limited by varying turnaround time and availability. These limitations may be overcome by the Lateral-Flow Device (LFD) test, a single sample point-of-care test that is based on the detection of an *Aspergillus* extracellular glycoprotein antigen by monoclonal antibody JF5.

Objectives: This retrospective study evaluates the LFD test by using bronchoalveolar lavage (BAL) samples.

Methods and Materials: This retrospective study comprises BAL samples from patients that were tested routinely for GM between June 2011 and October 2012 at the Medical University Hospital Graz, Austria. Forty-nine BAL samples from 47 patients were included (35 samples haematological malignancies, 10 samples solid organ transplantation, 2 samples HIV, 8 samples COPD; 14 probable IPA, 12 possible IPA, 23 no IPA). For IPA grading a BAL GM cut-off of 1.0 optical density index (ODI) was used.

Results: Sensitivity and specificity of BAL LFD test for probable IPA were 100% and 80%, respectively. GM levels in cases with negative LFD were significantly lower than in patients with positive LFD (P<0.0001). While no false negatives were observed, LFD resulted positive in a total of seven patients with possible IPA. In four of these cases corresponding GM values were 0.6, 0.61, 0.63 and 0.7 ODI and LFD results were weakly to moderately positive. The LFD also gave positive results in three possible IPA cases with GM values <0.4. All seven patients with divergent results had received mould active antifungal therapy at the time of BAL sampling.

Conclusion: To conclude, the LFD test of BAL specimens is performed easily and provides accurate and rapidly available results. Therefore, this new point-of-care test may be a very promising diagnostic approach for detecting IPA in BAL specimens.

21.187 Acute febrile illness outbreak investigation-Zone1, Afar, Ethiopia, 2011

A. B. Woyessa, A. Ahmed, N. Asamneh

Ethiopian Health and Nutrition Research Institute, Addis Ababa, Addis Ababa, Ethiopia

Background: Acute Febrile Illnesses (AFIs) due to different etiologic agents are the most common causes of morbidity and mortality in developing tropical and subtropical countries. Afar region reported unidentified AFI cases on August 10, 2011.

Objectives: To identify etiologic agent, risk factors and to recommend prevention and control measures.

Methods and Materials: Medical records were reviewed and suspected AFI cases were identified from August 7–September 11, 2011 in Asaita and Dupti districts. Case control study was employed (1:1). Cases were defined as any person with fever \geq 38.3Co, headache, pains in joints, muscles and back, anorexia and weakness. Controls were any person having the same characteristics with case patients except having the history of the above sign and symptoms. Study subjects were identified and interviewed at health facility. Blood-samples and throat-swabs were collected and analyzed for heamoparasites, bacterial-pathogens, hemorrhagic fevers and respiratory viruses. Nucleic acids from serum samples were subjected to high throughput sequencing using the Roche/454 Titanium platform. Odd-Ratio (OR) in 95%Confidence-Interval (CI) was calculated using Epi-Info version-3.5.3.

Results: A total of 12816 suspected AFI cases with no death were identified. All cases were mild and self limited. Of the cases 9107 (71%) were male and 3709 (29%) were female. Attack-Rate (AR) was 8.7% (11.5% in male and 5.4% in female). All age groups were affected, but the AR was relatively high (13.8%) among 15–44 age-groups. On case control, 114 study subjects were employed (57 cases and 57 controls). On bivariate analysis factors associated with illness were: contact with patient (OR: 3.8; 95% CI: 1.5–9.6) and drinking deep-well water (OR: 2.7; 95% CI: 1.2–5.8). However, on multivariate analysis only having contact with patient (OR: 4.1; 95% CI: 1.5–11.3) was associated with illness. Twenty-five specimens were tested negative for malaria parasites, Salmonella species, brucella species, dengue fever, yellow fever and rift valley fever. However, computational analysis of the generated sequences identified 17 (59%) samples positive for Sand fly Sicilian Virus (SFSV).

Conclusion: This study uncovered the occurrence of SFSV in Ethiopia for the first time. Primarily it affected males and older age. Contact history was significantly associated with the illness as a risk factor. Large-scale investigation should be undertaken.

POSTER PRESENTATIONS II

International Meeting on Emerging Diseases and Surveillance 2013

SESSION 22

Poster Presentations II

Sunday, February 17, 2013 Room: Klimt Ballroom I • Upper Level 11:45-14:30

22.001

2009 H1N1 influenza A in Mexico City, second season: Clinical, laboratory and roentgenological characteristics of patients complicated with pneumonia during January and February 2012 at a Mexican General Hospital

J. Reyes Mar¹, R. Valdez Vazquez², P. Rodriguez Zulueta³,

F. Velez Perez⁴, J. A. Garcia Vera⁵

¹Hospital General Manuel Gea Gonzalez, DF, Mexico, ²Hospital General Manuel GEA Gonzalez, DF, Mexico, ³Hospital General Manuel Gea Gonzalez, DF, Mexico, ⁴Hospital Manuel GEA gonzalez, DF, Mexico, 5Hospital General Manuel Gea Gonzalez, Mexico City, Mexico

Background: In the first season, the pneumonia by 2009 H1N1 influenza A virus affected mainly to young adults without comorbidity except obesy. The mortality rate was unexpected high. Here we described the re-emergence cases in 2012 at General Hospital Dr. Manuel Gea Gonzalez in Mexico City.

Objectives: Description of cases of 2009 H1N1 influenza Apneumonia in a General Hospital of Mexico City in January and February 2012.

Methods and Materials: Description of cases.

Results: Characteristics of Cases: After two years from the last case, between January and February 2012, twelve cases with pneumonia by influenza A 2009 H1N1 virus were identified by PCR. The median of age was 44 (range, 26-67) years, male gender in 50%, the median of onset of symptoms was 6.5 (range, 1-30) days, in 66.6% there was a co-morbid mainly smoking and obese, there were no chronical illness in any patient. All patients had fever, malaise and one respiratory symptom at least. Cough and dyspnea were the more common symptom. In 60% of cases the white blood cells counts were normal, and 66% cases had lymphopenia; in 58% there were elevation of some liver enzyme, especially lactic deshydrogenase. The CT scan showed multifocal, bilateral and subpleural opacities and areas of ground-glass in 90% of patients. Two patients (16.6%) died due to respiratory failure.

Conclusion: 2009 H1N1 influenza A re-emerged at beginning of 2012 as a cause of community-acquired pneumonia in Mexico City. Its clinical, laboratory and radiological features were similar than the cases in 2009. A lower mortality was observed, perhaps to early diagnosis.

In conclusion, the clinical and paraclinical characteristics of 2009 H1N1 influenza A pneumonia seem to be a constant profile for the early identification and management.

22.002 Etiological surveillance of influenza like illness in pediatric population at the University Teaching Hospital in Lusaka, Zambia

P. Simusika

virology laboratory, Lusaka, AK, Zambia

Background: Since the global pandemic of H1NI IN 2009, Zambia has locally been actively conducting the surveillance of influenza viruses and other related dieseases resulting from influenza like illness, hence the primary aim of this prospective study is to determine the etiology of influenza like illnesses in the pediatric population.

Objectives: The objective was to determine the etiology of other non influenza respiratory viruses common in children under the age 5.

Methods and Materials: From January 2011 to June 2012, surveillance samples with laboratory confirmed influenza negative results were tested with a panel of other common non influenza respiratory viruses including respiratory syncytial virus (RSV), human adenovirus (HADV), human rhinovirus (HRV), parainfluenza virus type 1, 2 and 3 (HPIV) and human metapneumonia virus using the nucleic acid real-time reverse transcription polymerase chain reaction assay.

Results: Total of 143 specimens were tested, 90 (62%) were positive for other viruses including, 12(8.3%) hMPV, 35 (24.4%) RSV, 27 (18.8%) HADV, 27 (18.8%) HRV, 3 (2%) HPIV-1, 3 (2%) HPIV-2, 4 (2.7%) HPIV-3 and 25 (17%) of the children were found to be infected with more than one virus strain.

Conclusion: In this prospective study, we have identified that RSV is predominant strain. 75.5% of the children were infected with other viruses other than Respiratory Syncytial virus, this outcome calls for routine testing of other viruses so as to help improve diagnosis and treatment, and subsequently reduce disease burden in children.

22.003

Northern or southern hemisphere vaccine composition: Comparison of circulating influenza isolates in Uganda to the WHO recommended vaccine composition, 2007 to 2012

J. T. Kayiwa, T. Byaruhanga, R. Chiiza, B. Namagambo, B. Bakamutumaho, J. J. Lutwama

Uganda Virus Research Institute, Entebbe, Uganda

Background: The World Health Organization (WHO) organizes technical consultations in February and September each year to recommend viruses for inclusion in influenza vaccines for northern and southern hemisphere, respectively. For countries like Uganda, in equatorial regions, epidemiological considerations influence which recommendation individual national and regional authorities consider appropriate.

Objectives: We investigated circulating strains of influenza and related them to WHO recommended vaccine composition for the Northern and Southern Hemisphere from 2007 to 2012.

Methods and Materials: Demographic and clinical data, together with nasal pharyngeal and or throat swabs were collected from enrolled patients using two case definitions; influenza-like illness (ILI) and severe acute respiratory infection (SARI). ILI case was defined as an acute respiratory infection with measured fever of greater than 37°C, and coughing with onset within 3 days; and SARI case was defined as acute respiratory infection with history of fever or measured fever greater than 37°C and cough, onset within the last 7 days and requires hospitalization. Samples were screened at National Influenza Center (NIC) / Uganda Virus Research Institute (UVRI) for influenza A and B using Real Time PCR. All influenza positive specimens were inoculated in Mardin-Darby Canine Kidney (MDCK) cells and observed for cytopathic effect (CPE). The isolates were tested for hemagglutination (HA) and hemagglutination inhibition (HI) using the HA/HI reagent kit from WHO collaborating center, CDC Atlanta, USA.

Results: 473 PCR positive influenza specimens were cultured in MDCK cells. Of 473 samples, 168 (35.5%) isolates were HA positive. 75 were influenza B (B/Brisbane/60/2008), 50 were AH1pdm (A/ California/07/2009), 36 were AH3 (A/Brisbane/10/2007), 4 were AH1 (A/Brisbane/59/2007) and 3 did not characterize antigenically. The median HA titer was 1:32. In 2008 to 2009 season, the circulating B strain in Uganda was B/Brisbane/3/2007 virus-like compared to the WHO recommended B vaccine component of B/Florida/4/2006 viruslike for the same season.

Conclusion: Our results suggest from 2007 to 2012, the vaccine composition for the Northern Hemisphere would be a recommended vaccine for Uganda.

22.004 Analysis of respiratory infectious diseases on a university campus: Application of mathematical models to pandemic influenza and other diseases

H. Kamano¹, T. Mori¹, C. Murakami¹, T. Kugoh², C. Izumi², K. Tomiie², A. Nozaki¹

¹Kagawa University, Takamatsu, Japan, ²Kagawa University, Miki, Japan

POSTER PRESENTATIONS II

International Meeting on Emerging Diseases and Surveillance 2013

Background: We engaged in consultation and surveillance of pandemic influenza and other infectious diseases amongst students and staff at a Japanese university.

Objectives: The aims were to investigate the epidemiological data and clinical characteristics of the pandemic influenza at a university and to develop SIR models in order to simulate the spread of influenza and other diseases on a university campus.

Methods and Materials: Six hundred and seventy one students (368 male, 303 female, average age±SD=20.4±2.0) were diagnosed as testing positive for the pandemic H1N1 2009 influenza by means of a flu test kit. Statistical analysis: students't test and ANOVA were performed. The level of significance was P<0.05. Mathematical models: we used SIR models.

Results: Statistical analysis: It was demonstrated that 11.3% undergraduate tested positive for the virus. For the pandemic influenza cases, 78.7% of patients had a fever of over 38°C; 82.4% had a cough; 67.1% had general fatigue; 59.0% had a sore throat; 58.6% had rhinorrhea; and 58.3% had a headache. The duration until defervescence was 2.0±1.3 days in the oseltamivir-treated patients (N=339) and 2.1±1.0 days in patients treated with zanamivir (N=142). A duration of more than five days until defervescence was observed in 4.5% of the oseltamivir-treated patients, but not observed in the patients treated with zanamivir. Mathematical models: We made SIR models based on the data of the early phase of the pandemic. We used differential equation following, $dS(t)/dt=-\beta S(t)I(t)$, $dI(t)/dt=\beta S(t)$ I(t)-γI(t), dR(t)/dt=γI(t) (S: susceptible, I: infected, R: recovered) to the simulate pandemic. We made an approximate equation from the observed data of the whole pandemic.

Conclusion: There was no significant difference of duration until defervescence between oseltamivir and zanamivir. The prolonged cases in the oseltamivir-treated patients suggested the possibility of the existence of oseltamivir-resistant strain. We analyzed pandemic H1N1 2009 by SIR models based on the observed data. These models were applicable to other types of influenza, pertussis or other infectious diseases on a university campus.

22.005 Severe acute respiratory infections in Nigeria: Analysis of surveillance data 2010–2012

M. S. Balogun¹, A. Adedeji², I. Olorundare², P. Nguku¹

¹Nigeria Field Epidemiology & Laboratory Training Programme, Abuja, FCT, Nigeria, ²National Influenza Sentinel Surveillance, Abuja, FCT, Nigeria

Background: Severe Acute Respiratory Infection (SARI) due to influenza and other respiratory pathogens is a major cause of illness and death worldwide. In 2010, for the first time in Nigeria, a hospitalbased sentinel surveillance system for tracking SARI was set up at four urban centres-Abuja (central), Kano (north), Lagos (south-west) and Nnewi (south-east). Clinical information and respiratory samples were collected from hospitalized patients recruited based on standard casedefinitions. All hospitalizations and mortalities were recorded.

Objectives: After two years of surveillance, we analyzed the data in order to describe the basic epidemiology of SARI in the country.

Methods and Materials: Surveillance data collected from January 2010 to April 2012 was retrieved from the electronic database, cleaned, and analyzed with EpiInfo and Excel software. Frequencies, ratios and proportions were calculated and charted.

Results: Fifty-four percent of the patients were females. Children less than two years of age accounted for 52.9% (684) of all cases. Overall, SARI accounted for 1,293 hospital admissions out of a total of 26,725 (SARI proportion = 4.8%); and 164 (5%) out of 3,284 in-patient deaths. Abuja showed the highest SARI proportion (9.82%). Fifty-eight (4.5%) of the 1,293 SARI patients were influenza-positive by RT-PCR, out of which 52.6% were influenza B subtype and 24.6% pandemic A/H1N1; but were not tested for other pathogens. The overall SARI death-to-case ratio was 12.7 deaths/100 cases, with Lagos showing the highest (26.5/100 cases). Since only aggregate data was collected on the non-SARI admissions and deaths, odds ratios could not be calculated. No seasonality was apparent.

Conclusion: These results show that SARI remains a significant public health problem with very young children bearing the highest disease burden. Lagos appears to have a disproportionately high mortality burden. Testing for other pathogens would give a more complete etiological picture.Surveillance needs to be supplemented with epidemiologic studies to understand the determinants of SARI morbidity and mortality.

22.006 Clinical characteristics and laboratory admission values for differentiation between H1N1 influenza and influenza like illnesses

M. Hoenigl, J. Prattes, M. Drescher, K. Tovilo, H. Kessler, K. Vander, K. Seeber, A. Avian, R. Krause, H. Flick Medical University of Graz, Graz, Austria

Background: Reliable and rapid diagnosis of Influenza A (H1N1) is essential to initiate appropriate antiviral therapy. PCR is the gold standard to confirm H1N1 but time consuming and expensive. The currently available antigen tests are fast but display low sensitivity.

Objectives: Development of a clinical score for H1N1 influenza may faciliate decision making regarding antiviral therapy, improve outcome and reduce mortality. We retrospectively analyzed the differences in clinical presentation and laboratory values between patients with PCR confirmed H1N1 influenza and patients with clinical suspicion but negative PCR for influenza (=influenza like illness (ILI)).

Methods and Materials: During Oct 2009 and Jan 2010 1681 patients with clinical suspicion of influenza were included in the study. 624 patients had pos H1N1 PCR, 1057 patients had negative H1N1 PCR. Complete data sets were available from 199/624 (32%) H1N1 patients and 252/1057 (24%) ILI patients. Univariate and multivariate analysis was performed.

Results: According to univariate analysis patients with H1N1 were significantly younger, and presented significantly more often with rhinitis, fever, cough, wheezing, and fatigue when compared to ILI patients. Also rapid onset was significantly associated with H1N1 infection and initial heart rate was significantly higher. Concerning laboratory findings at presentation total white blood cell count (WBC), thrombocytes, and C-reactive protein (CRP) were significantly lower in patients with confirmed H1N1 infection, while monocytes, eosinophils and creatinin kinase values were significantly higher. In multivariate analysis CRP (p=0,005; OR 0,99; 95%CI 0,99-1,00), WBC (p=0,002; OR 0.89; 95%CI 0.83-0.96), eosinophils (p=0.002; OR 2.93; 95%CI 1,50-5,74), wheezing (p=0,014; OR 3,15; 95% CI 1,27-7,86) and cough (p=0,002; OR 2,89; 95%CI 1,45-5,37) remained significant predictors of H1N1 influenza.

Conclusion: CRP, WBC, eosinophils, wheezing and cough remained significant predictors of H1N1 influenza in multivariate analysis. In contrast to previous publications we did not observe higher rates of gastrointestinal symptoms like diarrhea, nausea or vomiting. Presented data may help to implement a clinical score for H1N1 infection.

22.007 SRSF3 interacts with nucleoprotein of Influenza A virus: Implications on viral mRNA nuclear export?

V. RMT Balasubramaniam¹, B. A. Tejo², T. H. Wai¹, A. R. Omar², I. Othman¹, S. S. Hassan¹

¹Monash University, Bandar Sunway, Malaysia, ²University Putra Malaysia, Serdang, Malaysia

Background: The molecular mechanisms of viral replication leading to the pathophysiologic processes of highly pathogenic Avian Influenza (HPAI) virus infection in lungs of infected chickens are still poorly understood. Preliminary work on protein-protein interactions using yeast-two-hybrid (Y2H) assays to screen for potential host cellular chicken lung proteins that interacts with highly pathogenic avian influenza (HPAI) H5N1 nucleoprotein (NP) lead to the identification of the serine/arginine-rich splicing factor 3 (SRSF3) protein.The investigations undertook to determine the functional biological role of this protein is described.

IMED 2013

Objectives: To determine the biological role and mechanisms of the SRSF3 protein in the pathogenesis of highly pathogenic avian influenza in human and chicken lungs.

POSTER PRESENTATIONS II

Methods and Materials: A chicken (Gallus gallus) lung cDNA library fused inside yeast acting domain vector (pGADT7) was constructed and used in Y2H screening with HPAI H5N1 NP. This assay identified the novel interaction with SRSF3. Further studies to identify the functional role and validation of the interaction was conducted co-immunoprecipitation, mammalian-two-hybrid, indirect using immunofluorescence and siRNA assays. In-silico 3D docking studies using the crystal structure of SRSF3 from PDB with H5N1 NP was also conducted.

Results: Co-Immunoprecipitation and mammalian two hybrid studies indicated that, NP binds strongly to the chicken SRSF3. Immunofluorescence data showed that NP and SRSF3 co-localize in the nucleus of lung cells at 24h post infection. Silencing of SRSF3 in A549 human lung cells resulted in the accumulation of NP in the nucleus in late infection. Although the SRSF3 was isolated from chicken lung, Interestingly, infection of human lung cells with other subtypes of influenza virus such as A/New Jersev/1976/H1N1 and the pandemic A/ Malaysia/854/2009(H1N1) showed that the NP of these viruses also interacted with the SRSF3 of human lung cells. Docking of human SRSF3 and H5N1 NP, showed tight binding of NP with SRSF3.

Conclusion: We hypothesize that this SRSF3 protein facilitates viral mRNA transport from nucleus to the cytoplasm and therefore help to better understand the molecular mechanisms regulating the NPdependent stages of the virus life cycle. The SRSF3 protein may prove to be an attractive target for drug design in the future.

22.008 Clinical features of human H5N1 influenza survival cases in Indonesia

E. Sariwati¹, V. Setiawaty², B. Sutrisna³, S. Giriputro⁴ ¹Ministry of Health, Jakarta, Indonesia, ²Ministry of Health, Centre for Biomedical and Basic Technology of Health, Jakarta, Indonesia, ³University of Indonesia, Jakarta, Indonesia, ⁴Persahabatan Hospital, Jakarta, Indonesia

Background: Avian influenza A (H5N1) occurred in poultry throughout Asia has had major health impact to human. In Indonesia, infections with this virus have been identified in poultry since 2003 and the first human case has been identified on July 2005. The case fatality is still high despite intensive clinical management have been attempted. Epidemiology for survival prediction is complex because of the small number of confirm cases but very high the fatality rate and wide distribution of avian influenza in poultry. A shift in the clinical profile in patients have been observed including the administration of antiviral.

Objectives: To assess the prediction of survival cases based on clinical of human Avian Influenza.

Methods and Materials: Clinical profile and course of the disease, and response to oseltamivir and all available treatment are the tools to assess the survival prediction of avian influenza cases. All of human cases of confirmed avian influenza from July 2005 to December 2010 were analysed for demography, symptoms, clinical laboratory features, hospitalization and fatality. The method of study is retrospective cohort.

Results: A total of 171 cases were confirmed as avian influenza. Distribution of cases were 77 male and 94 female with mean of age 20 years old. Mortality rate was 82.45% of avian influenza cases and around 83,63% of cases were admitted with shortness of breath. Of the remaining 143 cases was administered oseltamivir, while 28 cases were not treated with oseltamivir. 28 out of 143 cases who were treated with oseltamivir with recovery. From the clinical symptoms we found that cases who reported shortness of breath, fever and cough more fatal. As well as the clinical feature of laboratory results from cases who derived trombocytophenia, leucocytophenia and lymfocytophenia more fatal.

Conclusion: Mortality of avian influenza was high and only 19.58% cases who treated with oseltamivir was survive. Only 10.49% cases reported shortness of breath, along with fever and cough was survive. Results of the present study provides evidence that any case of shorthness of breath, fever and cough with laboratory sign as trombocytophenia, leucocytophenia and limfophenia from avian influenza patients were more fatal than other patients who did not develop the symptoms.

22.009 Improving decisions in clinical medicine: Serum antibody titres and specific symptom patterns may classify categories of pandemic H1N1 influenza infection during pregnancy

G. Arteaga¹, A. Cerbulo-Vazquez¹, C. Lopez-Macias²,

G. Cruz-Cureño², I. Bosco-Garate², L. A. Arriaga-Pizano², A. Isibasi², J. Mancilla¹

¹National Institute of Perinatology, Mexico City, Mexico, ²National Medical Centre "Siglo XXI". IMSS, Mexico City, Mexico

Background: The heterogeneous patterns of symptoms among pregnant women exposed to pandemic influenza A (H1N1) virus were analysed.

Objectives: To assess the association between specific symptoms and the serum antibody response to antigens of pandemic influenza virus, and to test the ability of specific symptoms to predict this antibody response during pregnancy.

Methods and Materials: We used cross-sectional survey data to correlate clinical diagnosis of influenza with serological evidence of 2009 pandemic influenza A/H1N1 infection (haemagglutination inhibition titres of \geq 1:40) and to determine what specific symptoms were more likely to be present in different trimester of pregnancy. Serum samples and full symptoms data were collected of a random sample of pregnant women from December 2009 to January 2010, 3 months after the second pandemic wave in Mexico City, Mexico. Using the levels of antibody predictive, a discriminant analysis was performed on the basis of the presence or absence of antibody protective as classes, with the categorical variables as discriminating variables. To verify the discriminant analysis, a hierarchical cluster analysis was carried out.

Results: The strength of association between particular symptoms and antibody showed that general tiredness, fever, sore throat, and hialina rinorrhea were individually significantly associated with the presence and higher titres of antibody at first trimester of pregnancy. Within each pregnant woman's full symptom profile there were significant associations between the description of backache, chest tightness, sore throat, hialina rinorrhea, and shortness of breath at second trimester of pregnancy; and between hialina rinorrhea, and diarrhea at third trimester of pregnancy. Overall seroprevalence against pandemic H1N1 during pregnancy was 15.7% (95% CI 15.6% to 15.8%).

Conclusion: Seroprevalence results following the second wave of pandemic 2009 H1N1 influenza suggest that 15.7% of pregnant women in Mexico City had become infected and developed immunity. In view of the benefit from vaccination or earlier administration of antiviral agents during pregnancy, empirical treatment should be considered, considering specific symtoms of H1N1 influenza. With this the determinants of vaccine refusal can be reduced and alleviate fears by addressing real and historically perceived concerns among pregnant women.

22.010 Enhancing respiratory infection surveillance on the US/Mexico border- Arizona BIDS program sentinel surveillance data

C. Golenko¹, O. McCotter¹, L. M. Erhart², D. M. Wolk³,

F. Vanskike¹, L. Patel³

¹Arizona Department of Health Services, Tucson, AZ, USA, ²Arizona Department of Health Services, Phoenix, AZ, USA, ³University of Arizona, Tucson, AZ, USA

Background: This project was established through the Border Infectious Disease Surveillance (BIDS) program in Arizona (AZ) to monitor infecting respiratory pathogens among hospitalized patients with Severe Acute Respiratory Infections (SARI) in the AZ border region from September 2010 to the present.

Objectives: To present the epidemiology, clinical aspects, and laboratory results of AZ SARI case patients and to describe respiratory viruses in the AZ border region.

Methods and Materials: This SARI surveillance is conducted by BIDS at three acute care hospitals in the AZ border region. Each site

International Meeting on Emerging Diseases and Surveillance 2013

enrolls and collects specimens and clinical data on patients meeting SARI case definition. A SARI case is defined as a patient requiring hospital admission with fever (self-reported or measured \ge 37.8° C) and cough or sore throat. Viral, bacterial, and fungal tests are performed for each enrolled SARI case using extensive laboratory techniques; some case patients may have additional testing such as rapid influenza diagnostic testing (RIDT) and chest x-ray imaging results if they were ordered separately by the physician.

Results: A total of 113 patients meeting SARI case definition have been enrolled in BIDS SARI surveillance from project onset in September 2010 through November 2012. Patients who were 65 years and older comprised the largest age group (42%), Hispanic patients comprised the largest race/ethnicity category (38%), and 52% of cases were male. The most commonly identified pathogens among the positive viral SARI specimens (n=67) were: RSV (24%), influenza (19%), common cold viruses (rhinovirus, coxsackievirus, and echovirus) (16%), parainfluenza (15%), and human metapneumovirus (12%). Among a subset of SARI case patients with additional RIDT data available (n=64), ten patients initially negative by RIDT were later confirmed influenza positive by reverse-transcriptase polymerase chain reaction (RT-PCR) testing.

Conclusion: Enhanced laboratory data from SARI case patients can be used to examine virus distribution, identify novel strains, and aid in the development of public health strategies for infectious disease prevention.

22.011 Integration of syndromic surveillance for monitoring influenza epidemic among children in rural China, 2011–2012

M. Yu¹, Q. Zhao¹, Y. Zhu¹, T. Tao¹, V. K. Diwan², L. Cheng³, L. Palm⁴, G. Zhao¹, B. Xu¹

¹School of Public Health, Fudan University, Shanghai, China, ²Division of Global Health (IHCAR), Karolinska Institutet, Stockholm, Sweden, ³Tongji Medical College of Huazhong University of Science and Technology, Wuhan, China, ⁴Future Position X (FPX), Gävle, Sweden

Background: Children are susceptible to influenza, causing heavy burdens worldwide. As an important approach for early detection of influenza epidemic, syndromic surveillance on influenza-like illness (ILI, fever>38°C, cough and/or sore throat) with different data sources is increasingly being evaluated. However, there is limited information on the integrated effects of ILI reporting in healthcare units and respiratory infection (RI) related medication sales in pharmacies.

Objectives: To explore the relationship between sales of childspecific respiratory infection related medications in retail pharmacies and healthcare visits of children for ILI in rural China.

Methods and Materials: Two rural counties of Jiangxi Province were selected as study fields. Sales volume of 2 antipyretics, 4 cold medicines and 8 cough suppressants specific for children in 2 county and 7 township pharmacies, and healthcare visits of children aged ≤14 years for ILI in 2 county hospitals, 4 township hospitals and 48 village clinics were reported to a web-based system daily in the pilot study. Both data were adjusted for the-day-of-week effect and correlation was examined with spearman correlation coefficient (lag periods from -21 to +21 days).

Results: From September 1, 2011 to August 31, 2012, Sales of 15407 units of medications and 7828 healthcare visits were reported. At the last week of 2011, one pharmacy experienced a promotion, causing dramatic increase of sales. Data on promotion-days were excluded from this analysis.

Figure 1 showed a similar time trend of the two data sources. Sales of RI-related medications was highly correlated with healthcare visits for ILI (r=0.646, 95% CI, 0.563-0.717), and a slightly higher correlation was identified by moving sales data backward by 6 to 13 days in relation to that of healthcare visits (r from 0.651 to 0.675), indicating that the activity of medications purchasing may precede healthcare seeking to hospitals for several days.



Figure 1. Time trends of sales volume of child-specific respiratory infection related medications and healthcare visits of children for ILI in healthcare units in rural China, September 1, 2011–August 31, 2012.

Conclusion: Surveillance of medication sales for ILI among children may have a better timeliness than that of hospital visits. Single data source is subject to limitations; integration of different syndromic surveillance enjoys prospect of synergy for early warning of influenza epidemic among children.

The study is financially supported by a grant under European Union Framework Program 7 (project No: 241900).

22.012 Influenza surveillance in the Pacific island countries and territories during the 2009 pandemic

J. L. Kool¹, B. I. Pavlin², J. Musto³, A. Dawainavesi¹

¹World Health Organization, Suva, Fiji, ²World Health Organization, Boroko, NCD, Papua New Guinea, ³New South Wales Health, North Sydney, Australia

Background: Historically, Pacific island countries and territories (PICTs) have been more severely affected by influenza pandemics than any other part of the world.

Objectives: We herein describe the evolution and characteristics of pandemic influenza H1N1 in PICTs from 2009 to 2010.

Methods and Materials: The World Health Organization gathered reports of influenza-like-illness and laboratory-confirmed pandemic H1N1 cases from all 23 Pacific island countries and territories, from April 2009 through August 2010. Data were gathered through weekly email reports from Pacific island countries and territories and through email or telephone follow-up.

Results: Pacific island countries and territories started detecting pandemic H1N1 cases in June, firstly in French Polynesia, with the last new detection occurring in August 2009 in Tuvalu. Nineteen Pacific island countries and territories reported 1,972 confirmed cases, peaking in August 2009. No confirmed pandemic H1N1 cases were identified in Niue, Pitcairn and Tokelau; the latter instituted strict maritime quarantine. Influenza-like-illness surveillance showed trends similar to surveillance of confirmed cases.

Seven Pacific island countries and territories reported 21 deaths of confirmed pandemic H1N1. Case-patients died of acute respiratory distress syndrome or multi-organ failure, or both. The most reported pre-existing conditions were obesity, lung disease, heart disease, and pregnancy.

Pacific island countries and territories instituted a variety of mitigation measures, including arrival health screening. Multiple partners facilitated influenza preparedness planning and outbreak response.

Conclusion: Pandemic influenza spread rapidly throughout the Pacific despite enormous distances and relative isolation. Tokelau and Pitcairn may be the only jurisdictions to have remained pandemic-free. Despite being well-prepared, Pacific island countries and territories experienced significant morbidity and mortality, consistent with other indigenous and low-resource settings.

For the first time, regional influenza-like-illness surveillance was conducted in the Pacific, allowing health authorities to monitor the pandemic's spread and severity in real-time.

Future regional outbreak responses will likely benefit from the lessons learned during this outbreak.

130 IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

22.013 Influenza mortality in the United States, 2009: Burden and timing

A. M. Nguyen¹, **A. Noymer**²

¹Palomar Health, Escondido, CA, CA, USA, ²University of California, Irvine, CA, USA

Background: In April 2009, the most recent pandemic of influenza A began. We present the first estimates of pandemic mortality based on the newly-released final data on deaths in 2009 and 2010 in the United States.

Objectives: To characterize the mortality buden, by age and sex, of pneumonia and influenza ("P&I") mortality in the United States (nationwide) in 2009, as well as the timing of that mortality.

Methods and Materials: We obtained data on influenza and pneumonia deaths from the National Center for Health Statistics (NCHS). Age- and sex-specific death rates, and age-standardized death rates, were calculated. Using standard Serfling-type methods, excess mortality was calculated separately by age groups.

Results: In the aggregate, 2009 was not an unusual year for pneumonia and influenza mortality. Compared to the typical pattern of seasonal flu deaths, pneumonia and influenza agespecific mortality in 2009, as well as influenza-attributable (excess) mortality, skewed much younger. In many age groups, pneumonia and influenza mortality rates in October and November 2009 broke month-specific records since 1959 when the current series of detail US mortality data began.

Conclusion: Mortality in influenza pandemics skews younger than seasonal influenza. This can be explained in part by a protective effect due to antigenic cycling. When older cohorts have been previously exposed to a similar antigen, immune memory results in lower death rates at older ages. Age-targeted vaccination should be considered in future pandemics.



Time series of age-standardized death rates for P+I.



P+I age-mortality profiles, by month, for calendar year 2009.



Age distributions of excess P+I mortality, 2009 (solid) and 1999-2008 average (hatched).

22.014 Clinical features of infections caused by influenza virus in 2009–2012

K. Herrmannova¹, **M. Trojanek**¹, O. Dzupova², Z. Blechova¹, D. Tomickova³, M. Havlickova⁴, H. Jirincova⁴, J. Kyncl⁴, V. Maresova¹ ¹2nd Medical Faculty, Charles University in Prague, Prague, Czech Republic, ²3rd Medical Faculty, Charles University in Prague, Prague, Czech Republic, ³Hospital Na Bulovce, Prague, Czech Republic, ⁴National Institute of Public Health, Prague, Czech Republic

Background: Influenza is a well-established cause of seasonal illness and represents a significant cause of morbidity and mortality. However, seasonal influenza vaccine-uptake is far from target in the Czech Republic.

Objectives: The aim of our study was to analyze and compare clinical, laboratory markers and complications of influenza virus infection in adult patients in three consecutive seasons.

Methods and Materials: This was a prospective surveillance study evaluating adult patients with RT-PCR confirmed influenza hospitalized at the Department of Infectious Diseases of Hospital Na Bulovce (Prague, Czech Republic) in the years 2009-2012.

Results: There were admitted 217 patients (128 M and 89 F) to Hospital Na Bulovce in the studied seasons: 2009-2010 (143), 2010-2011 (48) and 2011-2012 (26). Age median in the study group was 35 years (IQR 26-48). The length of hospital stay was 4.5 days (IQR 3-7). Infection with influenza A virus was diagnosed in 198 cases (91.2%) and influenza B in 19 cases (8.8%). Pandemic influenza A (H1N1) 2009 virus was detected in 157 cases (72.4 %). The median interval from symptoms onset to hospital admission was 3 days (IQR 1-5). The most common symptoms and signs included: fever and cough (both in 93.2%), pharyngitis (70.2 %), conjunctivitis (43.9%), shortness of breath (38.7%), headache (35.6), muscle pain (34.6%), nasal discharge (28.3%) and diarrhoea (25.7%). Median levels of initial WBC and CRP were 6.3 (IQR 4.8-8.45)×10⁹/L and 41.1 (IQR 16.3-88) mg/L, respectively. CXR signs suggestive of pneumonia were described in 56 patients (25.8%); 45/56 (80.4%) infected with Pandemic A (H1N1) virus. Oseltamivir was administered in 109 patients (50.2%). There were 4 (1.8%) lethal outcomes in our study, 22 patients (10.1%) required clinical management on ICU, 12 (5.5%) required mechanical ventilation support and 10 (4.6%) administration of catecholamines.

Conclusion: The majority of cases included in our study were caused by Pandemic A (H1N1) 2009 virus. However, in 2010/2011 and 2011/2012 significant proportion of infections were caused by seasonal influenza strains. Severe interstitial lung affections were observed more frequently in patients infected with Pandemic A (H1N1) 2009. In contrary the complications of seasonal influenza were detected predominantly in the elderly.

Supported by grant IGA-MZCR-NT/12493-3.

International Meeting on Emerging Diseases and Surveillance 2013

22.015 Influenza sentinel surveillance-Addis Ababa, Ethiopia, 2008–2012

A. B. Woyessa, W. Ayele, E. Zemelak, D. Jima

Ethiopian Health and Nutrition Research Institute, Addis Ababa, Addis Ababa, Ethiopia

Background: Influenza is a contagious acute respiratory disease caused by influenza type A and B viruses. Globally, annual attack rate ranges from 5% to 30% with 250,000 to 500,000 million deaths. In Ethiopia, influenza sentinel surveillance was started in September 2008 with two sentinel sites in Addis Ababa, then expanded to four sentinel sites.

Objectives: The influenza sentinel surveillance was established to describe and characterize trends and types of influenza strains circulating in Ethiopia.

Methods and Materials: Patients those meet case definitions of Influenza Like-Illness (ILI) or Severe Acute Respiratory Infection (SARI) were identified at sentinel sites in Addis Ababa from September 2008 to November 2012. Separate case based reporting formats were filled for all eligible patients. Throat swap samples were collected and transported to national influenza laboratory in viral transport media by trained health personnel. Following RNA extraction samples were analysed using real-time PCR techniques. Data was entered, cleaned and descriptive data analysis was performed using Epi-info version 3.5.3 statistical software.

Results: A total of 1191 samples were analyzed and 204 (17.1%) tested positive for influenza viruses. Among all influenza positive samples 160 (78.4%) were influenza A and 44 (21.6%) were influenza B. Upon further sub-typing of influenza A, 128 (80.1%) were influenza A (H1N1) pdm2009, 24 (15.0%) were seasonal influenza A (H3N2) and 2 (1.2%) were seasonal influenza A(H1N1). The incidence rate was 5.4 (6.1 in male and 4.8 in female) per 100,000 populations letting 15-44 age group more at risk (6.5 per 100,000 population). Monthly influenza virus isolation rate was 4.1-34.6%, which is 62/179 (34.6%) in October, 36/113 (31.9%) in March and 20/87 (23.0%) in November. The sentinel sites were limited in Addis Ababa.

Conclusion: Influenza A (H1N1) pdm 2009 is predominantly circulating in Ethiopia followed by influenza B, seasonal influenza A (H3N2) and A (H1N1). The influenza trend is high in October followed in March and November. Population of age group 15-44 years are relatively more at risk. Since the sentinel sites were limited only in Addis Ababa, the result of the sentinel surveillance could not be generalized for the whole populations. Expanding of sentinel sites to outside of Addis Ababa should be needed so as to increase country representativeness.

22.016 Monitoring of influenza and respiratory syncytial virus activity in children under 5 years of age in Dibrugarh district of Assam, northeast India, 2010–2012

D. Biswas, K. Yadav, P. J. Baruah, B. Borkakoty, J. Mahanta Regional Medical Research Centre for NE Region (ICMR), Dibrugarh, Assam, India

Background: Influenza and other acute viral respiratory infections cause substantial morbidity and mortality among young children, especially in developing countries. Estimating the annual disease burden resulting from respiratory viruses is important for the development and assessment of prevention efforts and for resource planning by health care facilities.

Objectives: The present study aims to highlight incidence, temporal distribution and circulation of genotypes pertaining to influenza and human respiratory syncytial virus (RSV), the two most common respiratory pathogens in children with influenza-like illness (ILI) during 2010–2012.

Methods and Materials: The subjects were selected from regular influenza surveillance in Dibrugarh district (Assam), India. Clinical specimens of throat/nasal swabs collected from children (≤5 years of age) were subjected to nucleic acid extraction using Viral RNA mini kit (Qiagen, Germany). Viral RNA was detected using One Step real time RT-PCR (LC 480, Roche) and genotyping done using two step RT-PCR and sequence analysis. A prior informed consent from parents/guardians and approval from institutional ethics committee was obtained.

Results: A total of 384 (male 207 & female 177) cases were screened for influenza and RSV during April 2010 to March 2012. The overall virus positivity (influenza & RSV) was 19.3% (74/384), where RSV was detected in 8.6% (33/384), seasonal influenza (A & B) 7.8% (30/384) and pandemic *H1N1* 2.9% (11/384). The influenza activity was observed more during May-August (rainy season), whereas RSV was detected more during December-March (cooler months). The pandemic A/H1N1 was the predominant subtype during 2010 which was replaced by seasonal influenza A/H3N2 in 2011 followed by appearance of influenza B from December'11 to March'12.There was a predominance of RSV subtype NA1 (detected recently in Japan) in the present setting which is reported for the first time from India, where circulation of genotypes GA2, GA5 and RSV group B viruses have been documented previously.

Conclusion: A similar rate of detection for both the viruses (influenza 8.6% & RSV 7.8%) further necessitates incorporation of RSV screening during routine influenza surveillance. Thus monitoring the virological and epidemiological activities of influenza and other respiratory viruses will help in understanding the global epidemiology of these viruses as well as selection of appropriate vaccine strains.

22.017 Antiviral susceptibility of influenza A viruses obtained in Kenya 2008–2011

M. Wadegu, W. Bulimo, R. Achilla, J. Majanja, S. Mukunzi, F. Osuna, J. Wangui, B. Opot, E. Wurapa

US Army Medical Research Institute-Kenya, Nairobi, Kenya

Background: Antivirals play an important role in the treatment and prevention of influenza infections. Oseltamivir and Zanamivir are neuraminidase (NA) inhibitors of influenza A and B viruses. H274Y (H275 in N2 numbering) change in the NA protein alters drug binding activity and results in Oseltamivir resistance.

Objectives: Here we characterized the antiviral susceptibility of the 2008-2011 influenza A strains circulating in Kenya, by profiling known molecular markers in neuraminidase protein.

Methods and Materials: Nasopharyngeal specimen from outpatients of ages ≥ 2 months were screened by reverse transcriptase real time PCR (RRT-PCR) using subtype specific primers. Positive specimens were inoculated onto MDCK monolayer. RNA extraction and amplification of neuraminidase gene segment was carried out on influenza positive cultures prior to nucleotide sequencing of the amplified gene segments.

Results: In the 2008–2009, 2009–2010 and 2010–2011 influenza seasons, a total of 836 viruses were isolated. 344 (41%) were influenza A/H3N2, 144 (17%) seasonal influenza A/H1N1 and 348 (42%) belonged to the pandemic influenza A/ H1N1 strain. A total of 108 (13%) isolates were analyzed for susceptibility to NA inhibitors. In the year 2008, 33 influenza A/H3N2 and 11 seasonal influenza A/H1N1 were included in the genotypic characterization assay for neuraminidase

POSTER PRESENTATIONS II

International Meeting on Emerging Diseases and Surveillance 2013

inhibitor resistant mutations. The isolates had H275 which confers sensitivity to oseltamivir. 64% (7) of the 2008 seasonal influenza A/ H1N1 isolates depicted H275Y marker. 4 (36%) of the seasonal A/ H1N1 isolates, lacked the drug resistant marker. Genetic analysis of the 48 pandemic influenza A/ H1N1 strains in 2009 showed that all were sensitive to oseltamivir. All the 2011, 14 isolates of influenza A/H3N2 subtype were sensitive to oseltamivir. Genotypic data obtained in this study demonstrate antiviral resistance in seasonal influenza A/H1N1 viruses isolated in Kenya in 2008-2009 through possession of H275Y (N1 numbering) marker in the neuraminidase protein. All the influenza A/H3N2 isolates analyzed during the entire study period lacked any markers of neuraminidase drug resistance. Our study shows absence of seasonal influenza A/H1N1 in 2010 and 2011 following advent of the 2009 influenza A/H1N1.

Conclusion: Influenza drug resistant strains can emerge, adapt and spread in human population even in the absence of drug selective pressure.

22.019 Full genome analysis of H1N1pdm2009 influenza viruses circulating in italian pig herds

A. Boni¹, A. Moreno², L. Di Trani¹, G. Zaccaria¹, S. Faccini², L. Alborali², M. B. Boniotti², D. Lelli², P. Cordioli², G. Vaccari¹ ¹Istituto Superiore di Sanità, Rome, Italy, ²Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna, Brescia, Italy

Background: Circulation of the influenza H1N1pdm2009 (H1N1pdm) in humans and wide range of animals will continue to pose challenge to public health and scientific community. The main concern is the potential of H1N1pdm viruses to acquire virulence markers through adaptation in susceptible animals, such as pigs. Reverse transmission of H1N1pdm virus from humans to pigs are recognized worldwide thus underlying the continued risk for reassortment with swine influenza viruses (SIVs) and emergence of a new influenza virus strain. Therefore preparedness to identify new or more virulent viral strains would require fast sequencing of the full genome of emerging virus variant in humans and animals.

Objectives: In Italy, swine influenza monitoring programs, based on specific genome detection, virus isolation and molecular characterization of viruses causing respiratory forms, have been applied since the nineties; since april 2009 testing for the H1N1pdm was also performed on swine samples resulting positive to type A influenza. Aim of this study is to perform a surveillance of SIVs in pigs, using an optimised workflow for rapid and complete genome sequencing of H1N1pdm swine isolates.

Methods and Materials: A workflow that allows rapid analysis of the complete viral genomes, from sample collection to sequence analysis was applied. Amplification of the entire genome has been obtained with 46 M13 tail primer pairs, representing overlapped genetic fragments of each influenza virus genes.

Results: Nineteen H1N1pdm isolated in 6 Italian herds from 2009 to 2012 have been fully sequenced. Data analysis revealed a low variability between isolates with the exception of four influenza virus strains. Such isolates derive from the same farm and were collected independently during a four months period; interestingly, a 2 amino acid insertion in the HA gene, at the receptor binding site, that may significantly alter its antigenic phenotype, was detected.

Conclusion: Our data underline the importance of a genetic surveillance activity aimed at evidencing emergence of new influenza strain, from the animal reservoir.

G. Zaccaria¹, A. Boni¹, E. Alm², A. M. Moreno Martin³, P. Cordioli³, L. Di Trani¹, G. Vaccari¹

¹Istituto Superiore di Sanità, Rome, Italy, ²Swedish Institute for Communicable Disease Control, Solna, Sweden, ³Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Brescia, Italy

Background: Next generation sequencing (NGS) technology provides high speed and throughput that can produce an enormous volume of data with increasing applications in several fields of research including virology.

The evolution of influenza A viruses represents a major challenge for both human and animal health. Influenza A viruses may cross species barriers and transmit to humans with the potential to cause pandemics. Swine are susceptible to infection with a subset of both avian and human influenza A viruses subtypes, representing a "mixing vessel" able to generate novel reassortant viruses.

Objectives: To promptly investigate the dynamics of Swine Influenza A viruses (SIV), we are developing a rapid sequencing method using the Ion Torrent PGM sequencing platform.

Methods and Materials: We amplified the 8 genome segments of Influenza A virus by a multiplex RT-PCR (PathAmpTM Flu A Reagents) and submitted to standard sequencing reaction on the Ion Torrent PGM. Base calling, alignment and coverage analysis were carried out with the Torrent Suite Software.

Results: We successfully sequenced 36 SIV isolates belonging to different subtypes (H1N1, H1N2 and H3N2), collected in Northern Italy from 1998 to 2012.

NGS method was compared to the Sanger sequencing method on a single H1N1pdm isolate. The sequence obtained with the two techniques showed 100% nucleotide identity.

We compared the output of two chips with a mean throughput of 10 Mb (314) and 100 Mb (316) using 10 samples per chip. The obtained throughputs were respectively 105 Mb and 450 Mb. The average base coverage depth of the 10 samples ranged between 400x and 800x with a mean uniformity of coverage of 94.4% for the 314 and 1900x and 3500x with a mean uniformity of coverage of 95% for the 316.

Conclusion: Our results show the accuracy of NGS to define the full length sequence of Influenza A genome. The high throughput obtained so far indicates that we can multiplex more than 10 samples in a 316 chip. Additional experiments are needed to define the maximum number of samples loadable in a single chip to obtain a reliable consensus sequence.

22.021

Enterovirus 68 in Cuban Children with Acute Respiratory Tract infections

M. D. L. C. Muné¹, A. Piñon²

¹Institute of Tropical Medicine "Pedro Kourí", La Havana, Cuba, ²National Reference Laboratory of Influenza virus and others resiratory virus Institute of Tropical Medicine 'Pedro Kouri, La Havana, Cuba

Background: Enterovirus 68 (EV 68) is a rare enterovirus associated with respiratory illness that, unlike other enteroviruses, has been identified only from respiratory specimens. The first enterovirus was isolate from hospitalized samples with lower respiratory infection in California in 1962. Since then, EV 68 has been identified sporadically from respiratory specimen

Objectives: Detection of Enterovirus 68 infection (EV 68) from respiratory samples in Cuban children with Acute Respiratory Tract infections.

To perform Partial nucleotide sequencing of VP4/VP2 protein gene capsid coding region to confirm the positive results obtained using molecular diagnosis

POSTER PRESENTATIONS II

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: Molecular diagnosis of respriratory virus was performed using Multiplex RT-PCRs

RNA was extracted using QIA_{amp} Viral RNA Mini Kit (Qiagen) according to the manufacturer's instructions then, Multiplex RT-nested PCR_s assay was used for the detection of viral RNA

Sequence analysis was done by using MEGA3.1software Phylogenetic trees were generated by using the neighbor-joining method, with maximum-composite likelihood as a substitution model. Similarity was calculated for each genome region by using. MEGA3.1 software

Results: We studied 2569 clinical samples received at the National Reference Laboratory of Influenza and other Respiratory Virus during January 2009-September 2011. Results showed 107 positive specimens for (EV68) by RT-PCR, from them 77 samples corresponding to children between 0-4 years old. All patients we identified had severe Illness. The main clinical manifestations were acute respiratory tract infection in lower respiratory tract (bronquiolitis, pneumonia and broncopneumonia), 4 of them were fatal cases. Sequence analysis was done by using MEGA3.1software e High similarity with EV68 (100%) was obtained in 15 clinical samples by sequencing analysis. Phylogenetic tree of VP4/VP2 partial region sequences also confirmed that EV68 detected in the study were located among EV68 clusters with other EV68 strains reported in previous studies.

Conclusion: Our results show the potential role of EV68 infection in infants and children with RTI. Our study suggests that EV68 may be a possible causative agent of severe respiratory illnesses. Clinicians should be aware of EV68 as one of many possible causes of viral respiratory disease. Some diagnostic tests might not detect EV68 or might misidentify it as a human rhinovirus.

22.022 Severe acute respiratory infection surveillance on the US/Mexico border, 2010-2011 influenza season data from Arizona and California

P. Kriner¹, M. Fierro¹, O. McCotter², C. Golenko², J. Smith³, L. Fajardo³, M. Fonseca-Ford⁴, R. M. Philen⁵, S. H. Waterman⁴, A. Phippard⁴

¹Imperial County Public Health Department, El Centro, CA, USA, ²Arizona Department of Health Services, Tucson, AZ, USA, ³California Department of Health Services, San Diego, CA, USA, 4CDC, San Diego, CA, USA, 5CDC, Atlanta, GA, USA

Background: This project has been established through the Border Infectious Disease Surveillance (BIDS) program in Arizona (AZ) and California (CA) to monitor respiratory pathogens among hospitalized patients with Severe Acute Respiratory Infections (SARI) in the US/MX border region.

Objectives: To present the epidemiology, clinical characteristics, and laboratory results of SARI case patients presenting to sentinel sites in AZ and CA counties bordering Mexico during the 2010-2011 influenza season.

Methods and Materials: Enhanced SARI surveillance through the BIDS program is conducted year round at two sentinel hospitals in Imperial County, CA; one sentinel hospital in San Diego County, CA; and at three sentinel hospitals in Pima County, AZ. All persons presenting with clinical signs and symptoms of severe respiratory disease that meet the case definition for SARI are enrolled in the surveillance project. A SARI case is defined as a patient requiring hospital admission with fever (reported or ≥ 37.8° C) and cough or sore throat. Clinical data are collected on all identified case-patients using a standardized form. Nasopharyngeal swabs and throat swabs or lower respiratory samples are sent to the Naval Health Research Center (NHRC) Laboratory in San Diego, CA, for virologic and bacteriologic testing.

Results: Among all SARI patients in the 2010-2011 influenza season (N=255), the majority tested negative for any viral or bacterial etiology (62%). The most common etiologies in both Arizona and California were viral pathogens: respiratory syncytial virus (14.0%), influenza (8.5%), and adenovirus (3.0%). Relatively few SARI cases tested positive for bacterial pathogens (4.4%). In California, 35% of SARI cases were 0-4 years of age, while in Arizona, 39% of SARI cases were 65 years and older. SARI patients were predominantly Latino/ Hispanic (61%). Cough, shortness of breath, and pneumonia were the most frequently reported respiratory symptoms. The most commonly identified preexisting medical conditions were cardiac disease, chronic lung disease, and metabolic disorder. Antibiotics were prescribed more frequently than antivirals at all border sites.

Conclusion: SARI surveillance in the US-Mexico border region facilitates the detection of circulating influenza strains and other causes of morbidity and mortality among inpatients with acute respiratory disease.

22.023 **Clinical and Epidemiological Picture of Respiratory Infections Causing Viruses** Among Hospitalized Children in a Rural **Community in India**

B. Pandey¹, S. Broor¹, S. Rai¹, V. Gupta¹, R. Wigh¹, A. Krishnan¹, W. Sullender², D. Erdman³, R. Lal³

¹all India Institute of medical Sciences, Delhi, India, ²University of Alabama, Alabama, AB, USA, 3Influenza Division, Atlanta, GA, USA

Background: The burden of disease due to respiratory viruses among children in India is not well defined, but is likely to be substantial as India accounts for 20% of global childhood deaths due to acute respiratory infections.

Objectives: The aim of this study was to determine the prevalence of respiratory viruses in rural Indian among children <5 years old hospitalized for medical illness.

Methods and Materials: 262 children (<5 years) were enrolled from August 2009 to September 2011 from a rural community of Ballabgarh Health and Demographic Surveillance System (HDSS).Clinical and epidemiologic information and nasopharyngeal swabs were collected from hospitalized children for any acute medical condition. Real-time reverse transcription-polymerase chain reaction (RT-PCR) assays for influenza A and B viruses (Flu), respiratory syncytial virus (RSV), parainfluenza viruses 1-3 (PIV), human metapneumovirus (hMPV), rhinovirus (RV), coronaviruses 229E, OC43, NL63 and HKU1 (CoV) and adenovirus (AdV) were carried out using CDC protocols.

Results: Respiratory viruses were detected in 141 of 262 (54%) specimens, with a high prevalence of RSV (55; 21%), followed by RV (44; 17%) and influenza (17; 6%). All other viruses, including AdV, PIV, hMPV and CoV collectively accounted for <5% of detections. Most virus detections were from infants <1 yr of age (116; 64%) as compared with children >1-5 yr (41; 49%). RSV was the most common virus detected in infants (43/179; 24%), followed by RV (35/179; 17%) as compared with children >1-5 yr (14% and 10%, respectively). In contrast, influenza positivity was greater in children >1 yr of age (11%) than infants (4%). Twenty-six of 262 (10%) specimens had more than one virus detected. Significant difference was observed in ARI : non ARI cases like for (RSV;30.4:2.5),but some other pathogen were not differentiable in ARI and Non ARI category

Conclusion: This study provides evidence that respiratory viruses singly or in mixed infections are detected in >50% of medically attended hospitalized children from a rural community in India using sensitive detection methods like RT-PCR. These findings will help guide efforts to reduce the disease burden due to viral ARIs in developing countries.

22.024

Assessing the mortality link between respiratory infections and heart disease: A time-series approach

A. M. Nguyen¹, C. Li², A. Noymer² Palomar Health, Escondido, CA, CA, USA, ²University of California, Irvine, CA, USA

Background: It has long been known that the seasonal mortality patterns of respiratory infections and heart disease are similar. One hypothesis is

IMED 2013

that the link is causal not coincidental. The causal connection is plausible, since heart disease is a chronic disease and thus there is no reason to expect, a priori, that mortality should be seasonal. The question is of major public health importance since heart disease is the leading cause of death in many fully-industrialized countries.

POSTER PRESENTATIONS II

Objectives: To measure the statistical association between respiratory disease mortality and heart disease mortality, in an age-specific and time series perspective.

Methods and Materials: We obtained all available cause-specific data on monthly mortality by age and sex for the United States. This spans the years 1959–2010. We conducted Goodman-Grunfeld co-movement analysis on the resulting time series of mortality rates by age groups and separately by sex. We performed two pairwise comparisons, noninfluenza pneumonia ("P") with influenza ("I"), and pneumonia-andinfluenza ("P+I") with heart disease. The logic is that comparing P to I is a benchmark, since these two causes of death are known to be associated. We also performed a canonical correlations analysis, which is a way of combining data on all the age groups as a single vector, and then making the comparisons.

Results: We find strong links between P+I mortality and heart disease mortality, for both the Goodman-Grunfeld co-movement analysis and the canonical correlations analysis. In both cases, P+I is more closely associated with heart disease than P and I are, when considered separately. This is in spite of the well-established links between P and I.

Conclusion: Using two modes of analysis that have not been applied to this question before, we find that the empirical connection between heart disease mortality and respiratory disease mortality to be very robust. Given the magnitude of heart disease mortality, the connection with respiratory diseases should be explored further.



Canonical correlation analysis; males (blue) females (red), heart disease and respiratory disease mortality

22.025 Respiratory virus mortality in the Southwest of England during the winter of 2010/2011

K. Sithamparanathan, J. Lagan, P. Muir, R. Brindle Health Protection Agency, Bristol, United Kingdom

Background: The UK 2010/2011 winter influenza activity was the highest since the winter of 1999/2000. This was however lower than that was seen during the pandemic in the summer of 2009. Health Protection Agency (HPA) data reported that > 90% of those who had died were positive for Swine influenza A (pH1N1).

Objectives: The aim of this data analysis was to look at the differences in 30 day mortality between various different respiratory virus groups.

Methods and Materials: All samples submitted for respiratory viruses PCR testing to the regional Southwest HPA laboratory between December 2010 and May 2011 were divided into Swine influenza A (pH1N1) (Swine A), influenza B (flu B), respiratory syncytial virus (RSV), others (positive for parainfluenza viruses, adenovirus or human metapneumovirus) and those tested negative for all respiratory viruses (negative). Each group was then divided into those < 10 or \geq 10 years of age. NHS batch tracing system was used to identify those who had died and their date of death.

Results: There were a total of 5264 patients, with 1679 aged < 10 years and 3585 patients aged \ge 10 years of age.

There were 133 Swine A, 114 flu B, 543 RSV, 191 others and 698 negative patients within the < 10 age group. Within the \ge 10 age group, there were 688 Swine A, 347 flu B, 135 RSV, 123 others and 2292 negative patients.

In the < 10 age group, the 30 day mortality was 0% (0/1679) for Swine A, 0.06% (1/1679) for others, 0.18% (3/1679) for flu B, 0.30% (5/1679) for RSV and 1.13% (19/1679) for the negative group.

In the \ge 10 age group, the 30 day mortality was 0.11% (4/3585) for others, 0.28% (10/3585) for flu B, 0.36% (13/3585) for RSV, 0.92% (33/3585) for Swine A and 5.52% (198/3585) for the negative group.

Conclusion: Surprisingly, in both age groups, those who tested negative for all respiratory viruses had the highest 30 day mortality.

22.026 Application of nanofluid technology to multiple detection of respiratory viruses in pediatric respiratory diseases during 2011–2012 winter season in Mexico City

C. O. Orozco-Sanchez, V. A. Hernandez-Hernandez,

Y. Moreno-Valencia, J. A. Vazquez-Perez

Instituto Nacional de Enfermedades Respiratorias, Mexico City, Mexico

Background: Respiratory viruses are one of the most important etiological agents causing diseases in children. The predominant viruses detected in acute respiratory infections (ARI) are influenza, parainfluenza, sintitial respiratory virus, adenovirus, metapneumovirus, coronavirus and novel viruses like bocavirus. Molecular diagnostic of all possible viruses by a single test with high sensivity and specificity still need to develop.

Objectives: The aim of this study was employ a real-time qPCR methodology based on a nanofluids technology that allows amplify and identify 48 possible agents on 48 samples in only one amplification assay, diminishing the cost, time and materials needed for the obtainment of a diagnose. Also we describe the frequency of predominant respiratory viruses in pediatric ARI.

Methods and Materials: Primers for seven different respiratory virus families were designed in order to typing and subtyping each viruses. We standarized a real time qPCR on the Biomark (Fluidigm) platform. We analyzed nasopharyngeal swabs using this assay and clinical data were obtained. All specimens were collected from pediatric patients with different ARI, principally Community-adquired pneumonia (CAP), Influenza-like Illness (ILI) and asthma exacerbations at the National Institute of Respiratory Diseases, Mexico city, in the period from October 2011 to august 2012.

Results: Specificity and sensibility our assay were similar when compared with Seeplex RV15 assay detection. Viruses were detected in 94 (54%) of the 175 children admitted at the Institute. Rhinoviruses were the most common virus detected (47%), followed by respiratory syncitial virus A (RSV-A) (15%) and Influenza A virus (12%), other viruses detected were Human metapneumovirus (7%), Human parainfluenza 3 (7%), coronavirus (2%) Human parainfluenza 1 (1%) and Coxsackie virus (1%), 10% of the samples were co-infected.

Conclusion: This molecular diagnostic technique allowed identifying viral respiratory pathogens, and determining co-infections among children admitted at the National Institute of Respiratory Diseases. Nanofluid technology could be an option for multiple detection of several microorganism in different clinical samples.

22.027 European surveillance network for influenza in pigs 3 (ESNIP 3)—Expanding our knowledge of the epidemiology and evolution of swine influenza viruses

G. Simon¹, S. Reid², L. E. Larsen³, P. Kellam⁴, **L. Kaartinen⁵**, K. Van Reeth⁶, I. Markowska-Daniel⁷, E. Foni⁸, Á. Dan⁹, W. Loeffen¹⁰ ¹Anses, Ploufragan, France, ²AHVLA, Surrey, United Kingdom, ³DTU, Copenhagen V, Denmark, ⁴Wellcome Trust Sanger Institute, Cambridge, United Kingdom, ⁵Evira, Helsinki, Finland, ⁶Ghent University, Ghent, Belgium, ⁷National Veterinary Research Institute, Puławy, Poland, ⁸IZSLER, Brescia, Italy, ⁹Central Agricultural Office, Budapest, Hungary, ¹⁰CVI, RA Lelystad, Netherlands

SUNDAY • FEBRUARY 17, 2013

POSTER PRESENTATIONS II

International Meeting on Emerging Diseases and Surveillance 2013

Background: Running from 2010 to 2013, the ESNIP 3 (http://www.esnip3.eu/index.html) represents the only organised surveillance network for influenza in pigs in Europe.

Objectives: ESNIP 3 aims to expand the knowledge on the epidemiology and evolution of SI virus (SIV) in European pigs and to strengthen interactions with human and avian surveillance networks.

Methods and Materials: Of 24 participants, 16 are actively involved in swine influenza surveillance. Activities have focused on the exchange of information on surveillance systems and standardisation of methods.

To confirm that laboratories were capable of detecting relevant SIV subtypes, a PCR ring trial was arranged. Also in order to confirm the performance of the selected HI protocol to be used for preliminary antigenic subtyping, a standard panel of five sera and antigens was prepared for four testing laboratories.

Results: Passive surveillance is used in most countries. Selected virus isolates have been collected and curated in a central virus bank at AHVLA, UK. These isolates are subjected to detailed antigenic (HI assay characterisation using swine hyperimmune monospecific sera and antigenic cartography) and genomic (full genome sequencing) characterisation.

The results of the PCR ring trial showed that all 12 laboratories employed diagnostic tests capable of detecting all relevant circulating SIV subtypes, including the 2009 pandemic variant H1N1 (H1N1pdm09), although some differences in sensitivity and specificity were seen.

Reference panel testing by HI assay in four laboratories revealed small differences in obtained titres, but in general the consistency was good.

In most countries, the European subtypes avian-like (av)H1N1, H1N1pdm09, H1N2 and H3N2 constituted the dominating subtypes since November 2010.

H1N1pdm09 viruses have been isolated at an increasing prevalence in some countries, likely indicating that this subtype has become established in the swine population. In contrast, the H3N2 subtype has not been isolated in some geographic areas whereas it was prevalent in other parts of Europe.

Conclusion: The ESNIP 3 project will improve SI diagnostics and aid pandemic preparedness and planning for human influenza whilst providing an evidence base for decisions relating to animal health. This work was supported by the ESNIP3 project (Grant #259949, headed by Prof. IH Brown; AHVLA, UK).

22.028 Adaptive-based system development association for early awareness-based dengue area in the city of Padang, West Sumatra Province

Provincial Health Office West Sumatra Province Indonesia, Padang, West Sumatra, Indonesia

Background: The spread of dengue is very dependent on the behavior, climate and the movement of the virus and the human, where the temporal and spatial differences do not show a linear pattern. So far, existing research has not seen the factors that influence the overall DHF in a non-linear relationship.

Objectives: Look at environmental factors that may affect the DHF, which can be measured routinely and other specific factors, to be used as indicators to predict dengue cases. Based on that created an Environmental Information System for the Early Alert System DBD with the approach Adaptive System Based on Associations (SABA).

Methods and Materials: To obtain information about the factors that are likely associated with dengue cases used cross-sectional design. For the development of SABA, in addition to cross-sectional study, also conducted by analytical epidemiological ecological studies. Unit of analysis is a sub district.

Results: The results showed that climatic factors related to variable monthly case is the humidity and wind speed, with regression equation of Cases Monthly was 0.421 + 0.001* humidity - 0.004* wind speed. From the results of Chi-Square test showed that there were no environmental variables and behavioral characteristics of respondents

were statistically significant. With the Mann-Whitney test concluded that there was no significant difference between CI and the PP group of cases and non cases, CI significance scored 0.249 and PP significance scored 0.823.



I. Irene

SUNDAY • February 17, 2013

POSTER PRESENTATIONS II





Conclusion: The model consists of a server and client module Server module to process data processing on the server computer. Processing method used is called SABA, is a processing technique which is adaptive with the input design is obtained through the mechanism of change of the points input into the input association levels. This module uses a single interface and run automatically through scheduling system based on various variables are processed.

Client module is a module for data input and viewing of the process, that is integrated in the SABA to automate data processing and spaciotemporal sequential dengue in order early warning system of dengue fever. In this module we will see the warning in accordance with data already entered.

22.029 SAGES update: Open-source electronic disease surveillance software for use in resource-limited settings

B. Feighner, T. Campbell, J. Coberly, R. Wojcik, S. Patel, S. Lewis Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Background: The WHO International Health Regulations 2005 (IHR) significantly expanded each member nation's responsibility to detect and report health events of international concern. The Suite for Automated Global Electronic bioSurveillance (SAGES) aims to improve local public health surveillance and IHR compliance, with particular emphasis on resource-limited settings.

Objectives: The presentation will describe the SAGES collection of tools, update attendees on new SAGES functionality, and describe lessons learned from collaborations with international SAGES users.

Methods and Materials: SAGES tools are organized into four categories: 1) data collection, 2) analysis and visualization, 3) information sharing, and 4) modeling and evaluation. Within each category, SAGES offers a variety of tools compatible with surveillance needs and the existing technology infrastructure. SAGES tools are modular in nature, which allows the user to select one or more tools to enhance an existing system or use the tools en masse for an end-toend electronic disease surveillance system.

Although the primary data analysis tool, OpenESSENCE, is webbased and completely web-enabled, emphasis is placed upon the collection of health data by cell phone technology, especially the use of forms on smart Android phones transmitted by SMS technology. The ability to concatenate SMS messages allows for SMS encryption and also extensive data collection if desired.

Results: SAGES tools are now in use in six countries on three continents, with several more installations planned. Lessons learned from our collaborations include: 1) all organizations wish to control access to their data, 2) open-source software is much desired, 3) new systems must place minimal burden on those providing data, 4) acceptance results from enabling users to easily tailor the system, and 5) sustainability results from local ownership and working within existing technological capabilities.

Conclusion: The SAGES project is intended to enhance electronic disease surveillance capacity in resource-limited settings around the world. We have combined tools developed at JHU/APL with other freely-available, interoperative tools to create SAGES. We believe this this suite of tools will facilitate local and regional disease surveillance, regional public health collaborations, and IHR compliance.

22.030

Reporting to international health and veterinary organizations using national electronic integrated disease surveillance system T. Wahl¹, A. Burdakov¹, A. Oukharov¹, S. Schillinger²

¹BLACK & VEATCH, Overland Park, KS, USA, ²WHO Regional Office for Europe, Copenhagen, Denmark

Background: Timely and accurate reporting of epidemiological and veterinary in-country situation to WHO, OIE and FAO according to international regulations contributes to global public health security.

Objectives: Facilitate national disease surveillance system improvement by providing an integrated approach to disease surveillance that corresponds to a country's surveillance needs as well as helps to comply with IHR reporting requirements.

Methods and Materials: The Electronic Integrated Disease Surveillance System (EIDSS) is a disease surveillance system developed to improve national disease surveillance by providing a secure way to collect, share and analyze human, veterinary, vector and laboratory data in one integrated database with capabilities to electronically transfer required information to global data repositories of international entities. EIDSS is customized for each country to collect case-by-case data for diseases of priority using approved case definitions as well as aggregate data for other diseases. Data is collected from district level and rapidly transferred to the national level. This capability allows the country focal point to have all information required for international reporting in a near real-time manner. Manual data entry can be eliminated by an electronic bridge between EIDSS and international organization's database (e.g. WHO) improving transparency, timeliness and accuracy,

Results: EIDSS is currently operated at 470+ sites in Kazakhstan, Georgia, Azerbaijan, Ukraine and Armenia as a part of the Cooperative Biological Engagement Program sponsored by the U.S. Defense Threat Reduction Agency. Tens of thousands of cases are entered into the EIDSS systems across these countries. Data transfer to the WHO Europe CISID (communicable diseases) database was implemented first time for WHO Europe in a test mode in Azerbaijan. Development of an improved version of a data transfer module is currently being performed in collaboration with WHO Regional Office for Europe.

Conclusion: Electronic reporting to global data repositories of international organizations can be implemented from electronic disease surveillance systems (in particular EIDSS) improving transparency, timeliness and accuracy of health data. This allows making a next step in global disease surveillance by rapidly detecting and disseminating information on events of regional and international concern.

POSTER PRESENTATIONS II

International Meeting on Emerging Diseases and Surveillance 2013

22.031 **Timeliness of syndromic surveillance** system in the early warning of influenza epidemics in rural China

T. Tao¹, Q. Zhao¹, M. Yu¹, F. Yang², H. Yuan², L. Palm³, W. Yan⁴, W. Yan⁵, B. Xu¹

¹School of Public Health, Fudan University, Shanghai, China, ²Jiangxi Provincial CDC, Nanchang, China, ³Future Position X (FPX), Gävle, Sweden, ⁴Karolinska Institutet, Stockholm, Sweden, ⁵Tongji Medical College of Huazhong University of Science and Technology, Wuhan, China

Background: Timeliness is the core advantage of syndromic surveillance towards traditional surveillance methods in the detection of infectious disease epidemics.

Objectives: To understand the timeliness of different syndromic data sources in the early warning of influenza epidemics.

Methods and Materials: From August 1, 2011-September 30, 2012, a web-based pilot syndromic surveillance system (ISSC) has been implemented in two rural counties of Jiangxi Province, China, which covered 53 health care facilities and 9 pharmacies. Weekly counts of influenza-like illness (ILI) patients and the weekly sale volumes of 4 different categories of drugs (cold medicine, antibiotics, antipyretics and cough suppressant) were extracted from ISSC database. We used the weekly influenza virus positive rate (VPR) collected from sentinel surveillance hospitals of Jiangxi Province (PCR using clinical specimen) to indicate the trend of influenza epidemic in our study sites, and Pearson cross correlation tests were introduced among different data sources.

Results: Positive correlations were observed between VPR and ILI counts with different lags (-5 to +2 weeks), and the correlation coefficient peaked at 0 week's lag (r=0.794, p<0.001). After dividing ILI data by age groups, we found the 5~14y and 25~59y groups with -1 week's lag reached the maximum correlations with VPR (r=0.672 and 0.694, p<0.001). For drug sale data, cold medicine, antibiotics and cough suppressant correlated most with VPR at -3 weeks' lag (r=0.759, 0.753 and 0.741 respectively, p<0.001), whereas antipyretics with -2 weeks' lag had a low correlation with VPR (r=0.36, p<0.001).We introduced 6 control bar algorithms to simulate the real-time detection for influenza epidemics among cold medicine time series data, and found the Exponentially Weighted Moving Average (baseline: 7 weeks, lambda: 0.2, threshold: 2.1) had the best performance in detecting the starts of winter and summer influenza epidemic seasons (defined as the week when VPR exceeded 30%).

Data source	Sub-group	Time lag with VPR (week)							
		+2	-11	0	-1	-1	-3	4	-5
Weekly ILI Court	All	0.729	0.767	0.794	0.729	0.681	0.582	0.45	0.237
	5-14y	0.457	0.587	0.64	0.671	0.671	0.577	0.552	0.471
	25°29y	0,614	0.657	0.684	0.554	0.665	0.584	6.471	NS
Weikly Drug Sole Volume	Gold medicine	0.358	0.548	0.618	0.618	0.791	0.759	0.733	0.724
	Antibiotics	NS	0.433	0.526	Q.659	0.752	ñ.753	9.704	0.715
	Antipyretics	NS	NS	0.885	0.335	9.35	0.334	15	15
	Cough suppressant	0,497	0.619	0,651	0.736	0,736	0.741	0.683	0.647

NS: p >0.05, for other cells p < 0.05; Maximum correlation coefficient highlighted

Table 1. Cross correlation coefficients between VPR and sub-groups of syndromic data.



X: Alarm generated by control bars

Table 2. Simulation of real-time outbreak detection using weekly sale volume of cold medicine.

Conclusion: Sale volumes of cold medicine, antibiotics, cough suppressant, and ILI counts in 5~14y, 25~29y age groups had potential timeliness of 3 to 1 weeks in the early warning of influenza epidemics. It is necessary to further dig timely sub-groups of syndromic data for other disease epidemics, and test them in the real-time surveillance circumstances using aberration detection models in ISSC.

22.032

Digital disease surveillance: The global safety net

C. Wenham

Aberystwyth University, Aberystwyth, United Kingdom

Background: In recent years, infectious disease has come to be seen by many Western governments as a security threat. As a result of this discourse there has been a gradual paradigm shift to early detection, rapid response in reacting to an outbreak. Consequently, effective surveillance has become increasingly important as a key tool for alerting the international community to any potential health threats. With traditional surveillance infrastructure suffering from bureaucratic lag-times, leading to a delay in disease containment, many states and the WHO have turned to non-state digital disease surveillance systems (ProMed, HealthMap, Biocaster etc) to monitor outbreaks.

Objectives: Whilst some consider this shift as evidence of the decreasing role of state sovereignty in global surveillance, this paper seeks to argue that the use of digital disease surveillance systems is not replacing the state. Such technology merely provides a more effective apparatus for data collection for the governments concerned, and simultaneously offers a safety net for global health security at large.

Methods and Materials: Primary and secondary source analysis: government policy documents, semi structured interviews, media reports etc. triangulated with a conceptual 'health security' framework.

Results: This paper shall show how digital disease surveillance is used to 'fast-track' reporting at the National Focal Point level: the state still retains authority over this function and crucially the reporting decision and mechanisms of the International Health Regulations (IHR). Moreover, enhancing international health security depends on all countries' commitment to surveillance and using the examples of the UK, US and Canadian governments it shall show that they are encouraging developing states to engage with digital disease surveillance in order to meet their core requirements of IHR (2005). This act reconfirms their commitment to global health security, but also their leading role within such a global agenda.

Conclusion: The paper shall conclude that whilst states remain core to global outbreak response, digital disease surveillance provides further means to the global community to protect against those states which may have cause to conceal such an outbreak. Furthermore this transparent technology has lead to increased cooperation between governments and the WHO in the monitoring of infectious disease.

22.033 Are informal digital surveillance systems currently capable of detection disease outbreaks in real-time?

A. Magid, A. Gesser-Edelsburg, M. S. Green University of Haifa, Haifa, Israel

Background: The digital resources for the detection of infection disease outbreaks are increasing dramatically. A new generation of informal digital surveillance systems (i.e. not solely based on formal data) collects information from multiple sources, and then mines, categorizes, filters and disseminates it. Whether such systems are currently capable of early detection of disease outbreak remains unclear.

Objectives: To compare some existing informal digital systems for disease outbreak detection, and to evaluate their capability of early detection of disease outbreaks.

Methods and Materials: A systematic literature review was carried out to compare some informal digital systems, including ProMED-mail, Healthmap, Biocaster and Google flu trends with regards to their source of information, the manner in which they process and disseminate the information, and whether and to what extent these systems are capable of early detection of disease outbreaks.

Results: Most of the reviewed systems use the same type of information sources. However they complement each other with respect to their geographic coverage. Some of the systems perform purely automatically, whereas others incorporate experts decisions before information is disseminated. There is a "communication" between some of the systems (i.e. some of the systems use other systems reports as input). All reviewed systems disseminate reports regarding disease cases, and there is evidence in the literature regarding their usefulness in communicating the information during previous outbreaks, however, none of them use the reports for real-time syndrome based analysis, which may early detect outbreaks. So far, evaluation of the systems' ability to early detect outbreaks was based solely on offline collection and analysis of similar reports.

Conclusion: Currently, there is no evidence that existing informal digital systems are capable of real-time early detection of disease outbreaks. A more general informal system, which provides syndromic-based analysis of reports disseminated by all currently existing systems, may be the next step toward disease outbreak detection based on informal systems.

22.034 Are developed countries missing polio cases?

B. J. Paterson¹, D. Durrheim²

¹University of Newcastle, Newcastle, Australia, ²University of Newcastle and Hunter New England Population Health, Wallsend, Australia

Background: The occurrence of polio is at its lowest level, yet the goal of eradication remains elusive with the last cases proving incredibly difficult to eradicate. With the focus of polio eradication on endemic and re-established countries, developed countries have a low index of suspicion for polio—relying on astute clinicians to detect imported cases and high immunisation rates to prevent community outbreaks. Weaknesses in routine immunisation coupled with weaknesses in surveillance may put developed countries at risk of high impact polio outbreaks. Few developed countries have tested the sensitivity of their polio surveillance systems or questioned whether existing polio surveillance are the optimal surveillance at this stage of the global eradication initiative.

Objectives: Australia recently reviewed its polio surveillance to answer the question "Is Australia able to detect an imported case of poliomyelitis?" The review considered whether current strategies were optimal for a high income country, with a long history of freedom from endemic polio circulation.

Methods and Materials: Document review and semi-structured key informant interviews were used during the review. Interviews were recorded, transcribed and thematically analysed. The review was an iterative process and feedback on the findings was sought from interviewees.

Results: Since Western Pacific regional verification, one adult polio case was detected in Australia in 2007 and no paediatric cases have been identified. Respondents reported that it was not possible to prevent importations, that paediatric cases would be more likely to be identified

due to current surveillance than adult cases, and that there may be a low level of suspicion among clinicians. The risk for further community transmission is considered low because of high immunisation rates. Case detection and outbreak mitigation are key reasons to undertake polio surveillance.

Identified issues included: importance of supplemental environmental and enterovirus surveillance systems; potential high costs resulting from an importation; continued importation risks; low stool sample collection rates; possible biosecurity inadequacy for imported samples; and opportunities for improved legislative controls around polio.

Conclusion: The importance of surveillance in all countries increases as a disease approaches eradication; ensuring that every case is identified and appropriate public health responses implemented.

22.035

Using influenza-like illness (ILI) data for early warning of respiratory disease outbreaks in rural China

L. Tian¹, L. Tan¹, L. Liu¹, J. Zhang¹, S. Wei¹, W. Yan¹, W. Yan², L. Cheng¹, Y. Ding³, S. Nie¹

¹Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China, ²Karolinska Institutet, Stockholm, Sweden, ³University of Heidelberg, Heideberg, Germany

Background: Syndromic surveillance is increasingly used as a tool to detect disease outbreaks. Most illness will first manifest with nonspecific symptoms (e.g. fever) before diagnosis, and a possible correlation between influenza-like illness (ILI, fever >38°C, plus cough and/or sore throat) and respiratory infectious diseases exists. Theoretically, ILI syndromic surveillance should have the ability for early detection of respiratory infectious diseases' outbreaks.

Objectives: To explore the possibility of using ILI data for early warning of respiratory disease outbreaks in rural China.

Methods and Materials: An integrated surveillance system (ISSC) was implemented in rural Hubei Province of China since April 1, 2012. Daily information of patients with at least one targeted symptoms related to infectious diseases was collected by doctors from health facilities. The ILI data reported by 74 health facilities in Shayang County from April 1 to September 30, 2012 were extracted from ISSC database. Accordingly, respiratory cases in the same period and same region were exported from China Information System for Diseases Control and Prevention (CISDCP). The correlation between two data sources was explored by comparing weekly cases number, time sequence trend was represented.

Results: 4283 reported records from ISSC were ILI, and 264 cases from CISDCP were respiratory cases. The male-female ratio was higher in respiratory cases than in ILI (2.2:1 vs. 1.2:1). Both data were concentrated on people between 18 to 64 years, which accounted for 59.1% and 42.1% of the total records respectively. 99.4% of the ILI cases visited doctors within 7 days after symptom onset, while just 21.2% of respiratory cases were diagnosed within 7 days after symptom onset. There was an peak in middle July of ILI data, and it was about 5–6 weeks earlier than the peak of respiratory cases in early September (Figure 1), but no significant correlation (rs=0.075, P>0.05) was found between the two data sources.



Figure 1. Weekly trend of ILI count and case of respiratory infectious diseases from Apr.1 to Sep.30 in Shayang county, Hubei, China.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: Although the peak observed in present study was not a real outbreak, it still shows a potential capacity to early detection of respiratory disease outbreaks by ILI syndrome surveillance. Further study such as simulated outbreak evaluation and intensive study of specific infectious disease (e.g. influenza) are needed.

22.036 Applicability of different data sources in syndromic surveillance system for detecting infectious disease outbreaks in China

J. Zhang¹, L. Tan¹, L. Liu¹, L. Cheng¹, W. Yan¹, W. Yan², S. Wei¹, V. K. Diwan², H. Dong³, S. Nie¹

¹Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China, ²Karolinska Institutet, Stockholm, Sweden, ³Heidelberg University, Heidelberg, Germany

Background: Syndromic surveillance has been an important approach for early detection of infectious disease outbreaks. While it may provide valuable information that might be missed by conventional systems, there is still a need to figure out what data sources are optimal for what kind of outbreaks.

Objectives: To evaluate the applicability of different data sources in syndromic surveillance system for detection of infectious disease outbreaks.

Methods and Materials: A syndromic surveillance system (ISSC) has been implemented in Shayang County, Hubei Province, China. Outpatients with at least one specified symptom from one county hospital, sales volume of 98 medications related to infectious diseases from four county pharmacies, and absentees with syndrome-specific information from one county primary school were reported daily to a webbased system. Daily supervisions were performed by researchers. If any aberration was detected, timely verifications would be carried out. Data from April 1 to June 30, 2012 were extracted for an exploratory study.

Results: 998 specified outpatients, 20410 units of medications, and 429 absentees were reported during the three months. Of the outpatients, fever (45.2%) and cough (38.6%) were the most common symptoms. Compound cold medicines (41.6%), cough suppressants (27.7%), and antibiotics (26.0%) accounted for 95.3% of the medications sales. 85.1% of the absentees were on illness. There was an obvious aberration in June in absenteeism data which was finally confirmed to be a varicella outbreak, while no corresponding increase was found in outpatients or medications sales data during the same period. As for outpatients data, the time trend was at a low level until an increase since late May, which was mainly ascribed to a quality control symposium conducted on May 31. Medications sales trend was relatively steady with some abnormal sales volume at the beginning of implementation due to promotion. No other outbreaks were detected by these data sources.



Figure 1. Time trend of three data sources from April 1 to June 30, 2012.

Conclusion: School absenteeism data may be more sensitive to detect localized outbreaks, but that is limited by lack of data on weekends and holidays. The specified outpatients data or medications sales data might be more applicable for detecting respiratory disease outbreaks in general population. Longer observation and further exploration are needed for more valid findings.

22.037 Open source health intelligence (OSHINT) for biological event characterization

J. Blake¹, **C. Ordun**², S. Aslam³, A. Gentilcore³, V. Grigoryan³, C. Reffett⁴, N. Rosidi³, M. Shelton⁴, J. Klenk⁴ ¹Booz Allen Hamilton, Washington, DC, USA, ²Booz Allen Hamilton,

Atlanta, GA, USA, $^3\text{Booz}$ Allen Hamilton, Rockville, MD, USA, $^4\text{Booz}$ Allen Hamilton, McLean, VA, USA

Background: Social media data presents a publicly available and highly accessible view into real-time activity that can be leveraged to detect, monitor, and respond to biological events; however, responders require confidence in data to make operational decisions. Open Source Health Intelligence (OSHINT) can leverage social media using customized algorithms to structure data into meaningful, actionable information.

Objectives: OSHINT is a cloud-based analytic system that uses open source social media outlets, primarily Twitter, to automatically characterize foodborne illness use cases: #sick; #dead; and, #hospitalized. OSHINT aims to provide near real-time situational awareness for more efficient use of resources and personnel countermeasures.

Methods and Materials: We collected social media data related to Salmonella and Escherichia Coli events during 2006–2012 due to the emergence of Twitter and the magnitude of multistate outbreaks reported to the Centers for Disease Control (CDC) [1]. We determined that # sick, #hospitalized, or #dead were valuable use cases for characterization. Analytical methods, such as term-frequency-inverse document frequency (TF-IDF) and natural language processing (NLP), were used to automatically characterize events. Lexicon development, during NLP implementation, was generated from Twitter posts describing events.

[1] CDC. Retrieved 9/7/2012 from http://www.cdc.gov/outbreaknet/ investigations/

Results: We evaluated two factors: precision of the NLP algorithm and accuracy of OSHINT compared to CDC epidemiologic curve and situation reports. For the 2012 multistate tuna Salmonella event [2], preliminary results indicate that the NLP algorithm effectively identifies tweets associated with foodborne illness for #sick, #hospitalized, and #dead, at 100%, 100%, and 88% respectively. Furthermore, OSHINT algorithms identify #sick, #hospitalized, and #dead with relative accuracy compared to CDC reports, primarily because CDC reports are tweeted; however, there remains a gap between OSHINT and the CDC epidemiologic curve.

[2] CDC. Retrieved 11/29/2012 from http://www.cdc.gov/salmonella/ bareilly-04-12/index.html

Conclusion: While OSHINT shows promise for characterization, forecasting and detection, it contains only one grammar rule (number, actor, qualifier) and does not yet contain algorithms to combine individual tweet case counts, which would narrow the gap between OSHINT and CDC epidemiological curves. Additional NLP algorithms are required to increase specificity, so that we can identify emerging events, pinpoint location and demographics of affected individuals, and forecast response requirements.
International Meeting on Emerging Diseases and Surveillance 2013



22.038 Intravenous Immunoglobulin-

A serological sentinel C. Planitzer, J. Modrof, T. R. Kreil Baxter BioScience, Vienna, Austria

Background: Intravenous immunoglobulin (IVIG) is a therapeutic preparation containing the pooled antibodies from thousands of

healthy plasma donors, thus representing the immune status of a large donor population. Individual lots of IVIG are therefore a valuable tool to conduct epidemiological serology studies in order to monitor and newly detect the spread of infectious diseases. Objectives: The suitability to use IVIG as a serological investigation tool has been already shown through the demonstration of declining antibody levels against Hepatitis A virus (Farcet MR et al., 2010) and Measles virus (Audet S et al., 2006) during the last years, which can be explained with increasing vaccination against these viruses. Proof of concept to use IVIG for monitoring the spread of emerging infectious diseases has been shown by the gradual US seroconversion after the introduction of West Nile virus (WNV) in 1999 (Planitzer CB et al., 2009).

Methods and Materials: Neutralizing antibody titers against WNV were determined for IVIG preparations produced from plasma collected in central Europe. In total, 55 IVIG preparations produced between 2006 and 2010 were analyzed.

Results: Virus neutralization assay was used to newly detect emerging pathogens such as WNV in central Europe: while clinically overt human cases were reported from Southern Europe, e.g. Greece and Italy, serological evidence obtained from IVIG preparations indicated a geographically extended subclinical circulation of the virus: WNV seropositivity was shown in asymptomatic plasma donors from Austria, Germany and the Czech Republic (Rabel P et al., 2011).

Conclusion: The presented work demonstrates the feasibility of using IVIG to investigate the serostatus of an entire plasma donor population, by analyzing comparably few samples.

22.039

Establishing a web-based application for respiratory pathogen biosurveillance within a diverse global partner network

J. A. Cockrill¹, A. Y. Tsai¹, T. Campbell², M. J. Cooper¹ ¹AFHSC, Silver Spring, MD, USA, ²Johns Hopkins University, Laurel, MD, USA

Background: Lessons learned from the 2009 influenza pandemic have driven many changes in the standards and practices of respiratory disease surveillance worldwide. The U.S. Department of Defense (DoD) Armed Forces Health Surveillance Center (AFHSC) and the Johns Hopkins University Applied Physics Lab (JHU/APL) have partnered to develop an Internet-based data management system known as the Respiratory Disease Dashboard (RDD). The goal of the RDD is to provide AFHSC partners with a centralized system for the monitoring and tracking of lab-confirmed respiratory pathogens.

Objectives: The objective of this abstract is to communicate the development of a DoD respiratory pathogen surveillance system used in a multitude of settings worldwide.

Methods and Materials: The RDD is based on the OpenESSENCE platform and developed as a web-based application. It is highly flexible and can be modified by a public health administrator. Currently eight DoD partner laboratories are actively entering respiratory pathogen data into the RDD, encompassing specimens from sentinel sites in 11 countries: Cambodia, Colombia, Kenya, Ecuador, Egypt, Honduras, Nicaragua, Paraguay, Peru, Uganda, and the United States. Users have been individually trained on data entry and visualization within the application. Most laboratories currently only test respiratory specimens for influenza, but select laboratories have the ability to routinely test for an expanded respiratory panel, to include RSV, adenovirus, coronavirus, Haemophilus influenzae, and other pathogens.

Results: To date, 11,644 respiratory pathogens have been isolated from 44,527 specimens and input into the RDD. Of the isolated pathogens, 10,365 were influenza, 272 were Haemophilus influenzae, 341 were Rhinovirus, 134 were Streptococcus pneumonia, and the remaining 532 were other respiratory pathogens.

Conclusion: The RDD is an effective platform for data entry and visualization, and provides a central database from which to pull global DoD respiratory information. Six additional DoD partner laboratories will be contributing to the RDD in the first quarter of 2013. The RDD application is being explored for use in enteric pathogen data reporting and visualization.

22.040

Implementation of modern approaches to surveillance and outbreak investigation in Kazakhstan: Evaluation of the long-term success of an epidemiology training course, 2011

Y. Bumburidi¹, A. Zholshorinov ², C. Pitenko¹ ¹CDC/CAR, Almaty, Kazakhstan, ²Ministry of Health of Kazakhstan, Astana, Kazakhstan

Background: National, oblast, and rayon level epidemiologists and antiplague service specialists are involved in surveillance for extremely dangerous pathogens (EDPs) in Kazakhstan. The current professional education of epidemiologists does not include the concept of standardized case definitions nor training in analytic epidemiology. Based on these needs, and to enhance EDP surveillance in Kazakhstan, a five-week epidemiology training course for practicing epidemiologists was designed and started in 2008.

Objectives: We evaluated the trainees' satisfaction with the course content and influence on practice subsequent to the training.

Methods and Materials: The training objectives and follow-on assessments from trainings were used to construct a survey instrument. A combination of ordinal and nominal measurements was utilized. The instrument included a verification component designed to confirm some responses based on supervisory opinion on-site. We evaluated trainees with more than one year since completion of training.

Results: Out of 33 trainees, 30 (91%) were interviewed. Each part of the training was relevant for 83-93% of trainees. Most used in practice were the following skills: the "Presentation of Surveillance Data " by 26 trainees (86,7%, 95% CI 69,3%-96,2%), "Standardized Case Definitions" and "Analysis of Surveillance Data" by 17 trainees (56,7%, 95% CI 37,4%-74,5%). Least used in practice were the following skills: "Elements of Analytic Epidemiology" 8 trainees (26,7%, 95% CI 12,3%-45,9%), and "Biostatistics" 10 trainees (33,3%, 95% Cl 17,3%-52,8%). The main reasons for not applying them were "not relevant to the current duties" 10 trainees (33%), and "lack of time" 3 trainees (10%).

Five trainees out of 20 (25,0%) using skills taught indicated they would like assistance in their daily work to implement new knowledge and skills gained from the training. According to trainee's supervisor, 21 out of 27 trainees (77,8%, 95% CI 57,7%-91,4%) had positive changes in their skills and knowledge.

Conclusion: The training program was successfully used in practice. For better implementation of analytic and biostatistics skills, there is a need to continue training in the field (on-the-job training); this could be through the implementation of projects, outbreak investigations, or data analysis that involve trainees and trainers.



⁽⁴¹⁾ Geographic information systems in epidemiological monitoring of malaria in Uzbekistan

F. Saipov

Research Institute of Epidemiology, Microbiology and Infectious diseases, Tashkent, Uzbekistan

Background: The use of geographic information systems (GIS) is increasingly finding applications in various sectors of the economy. In malaria monitoring, GIS is a relatively new and promising methodology.

Objectives: In this study we created territory maps in the Surkhandarya and Kashkadarya regions of Uzbekistan to show the location of tertian *Vivax* outbreaks of malaria and *Anopheles* mosquito reservoirs.

Methods and Materials: HealthMap was used to construct a map of the Surkhandarya region, with layers of data on: population with reported cases of malaria, landscape, climate, water reservoirs, and vectors. Changes of this data measured in real time will allow forecasting of malaria outbreaks.

Results: Currently in the Surkhandarya and Kashkadarya region, there are recorded up to 7 types of mosquitoes: Anopheles (An.) maculipennis, An. martinius, An. superpictus, An. pulcherrimus, An. hyrcanus, An. claviger, and An. algerensis. The most common are An. superpictus and An. pulcherrimus-the overall density of Anopheles larvae in the season from April to November is 160 larvae of pulcherrimus and 284 larvae of superpictus per 1m² water surface. The main places for mosquitoes breeding/hatching are ponds, floodplains and river mouths. Malaria is most distributed in the following districts: Baisun, Sariasijsky, Oltynsaysky, Sherabad, Kumkurgan and Jarkurgan. In Kashkadarya oblast, the regions are Karshi City, and Karshi, Dehkanabad, Kitab, Shakhrisabz, Karshi, and Nishan districts. In the Surkhandarya oblast, the Baisun, Sariasijsky and Oltynsaysky districts are located in the mountain river area, which is a high-risk zone for malaria. Sherabad, Kumkurgan and Jarkurgan areas are located in an irrigated valley delta, which is a zone with a moderate risk of recurrence of malaria. In Kashkadarya, foci of malaria are recorded in the floodplain of the Kashka River, in a foothill river delta and irrigated valley.

Conclusion: We are creating an electronic version of the landscape (malaria map) of the Surkhandarya region. Development of an electronic version of the map will enable real-time changes to reflect the epidemiological situation for malaria

22.042 Development of systems to detect hospital outbreaks from automated laboratory surveillance

R. Freeman¹, S. Hopkins², N. Andrews², J. Freed², A. Holmes¹, A. Charlett², M. Catchpole²

¹Imperial College London, London, United Kingdom, ²Health Protection Agency, London, United Kingdom

Background: Automated analysis of laboratory surveillance reports of infectious diseases has been undertaken at the Health Protection Agency (HPA) for over two decades. The development of automated methods for outbreak detection at the hospital level was required following recent cases of delayed detection of hospital outbreaks. Our aim is to create algorithms capable of detecting outbreaks and rising trends in reported infection to enable early identification of emerging problems, with minimal false positive detection rates.

Objectives: Evaluate data available from the voluntary reporting system, investigate issues associated with hospital level analysis and describe the data processing necessary to enable the development and application of outbreak detection methods.

Methods and Materials: Electronic surveillance data from microbiology laboratories (LabBase2) was evaluated prior to developing algorithms capable of functioning effectively across a range of infections and variations in reporting practices of hospital laboratories. Additionally, a specimen hierarchy was developed to ensure that specific specimen sites were prioritised before data deduplication.

Results: Over a five-year period, 167 hospital laboratories have reported to the HPA. 1,921,559 reports of interest were made between March 2007 and May 2012. After the application of the specimen hierarchy and removal of duplicates, 1,705,126 reports remained. There is large variation in how laboratories report to the system. Across hospitals with annual KH03 bed-days between 300,000 and 350,000 the total number of reports ranged from 370 to 84,510. Just under half (48.5%) report in a timely manner with >90% of infections reported within three weeks of the specimen date. Overall, there was a significant increase of 17.5% in reporting after October 2010, when new statutory reporting regulations were introduced (95% CI 13.8-21.4%, p<0.001). However, significant decreases in reporting were also observed within some hospital trusts.

Conclusion: The currently applied algorithm requires further modification to optimise outbreak detection for individual hospitals. Development of outbreak detection methods for hospital-level data requires a multi-disciplinary approach, including input from specialists in process management, epidemiology, statistics, microbiology and infectious diseases. To provide useful information to hospitals, it is imperative that surveillance systems and processes ensure complete, regular and consistent reporting.



43 Health care seeking initiation of symptomatic patients in an integrated syndromic surveillance system in Jiangxi Province, China

Q. Zhao¹, T. Tao², X. Li³, Z. Pu⁴, H. Cheng⁵, V. K. Diwan⁶, G. Zhao¹, B. Xu¹

¹Fudan University, Shanghai, China, ²School of Public Health, Fudan University, Shanghai, China, ³Future Position X, Gävle/SE, Sweden, ⁴Department of Health of Jiangxi province, Nanchang, China, ⁵Jiangxi Provincial Center for Disease Control and Prevention, Nanchang, China, ⁶Karolinska Institutet, Stockholm, Sweden

Background: Syndromic surveillance system set in health facilities has great advantages in early detection of infectious disease epidemics. The health facilities for symptomatic patients' first visit might be influenced by demographics and social economic status of patients and the severities of disease.

Objectives: To understand where patients initiated their health care seeking for infection-related symptoms, and how these symptoms distributed in different health facility in rural China.

Methods and Materials: The study of integrated syndromic surveillance system was carried out in two counties of Jingxi Province. Ten infection-related symptoms including cough, fever, sore throat, diarrhea, headache, rash, nausea and vomit, mucocutaneous hemorrhage, convulsion and disturbance of consciousness were reported daily to a web-based information system by health workers in village health stations (VHS), township hospitals and county hospitals. Facility-stratified symptom distribution was described and logistic regression was applied to understand the association between symptoms and health facility preference.

Results: From April 1-October 31, 2012, 116425 records of first health care visit for the studied symptoms were reported to the system; of which 10.8%, 14.9% and 74.3% were reported by data collectors in county hospitals, Township hospitals and VHS respectively. The first three symptoms reported in VHS and TM were fever, cough, and headache, while the top three in county hospitals were fever, cough and nausea and vomiting. Age and gender adjusted regression analysis showed that patients with cough (aOR=1.252, 95%CI: 1.219-1.286), or sore throat (aOR=1.850, 95%CI: 1.791-1.912), or diarrhea (aOR=1.391, 95%CI: 1.323-1.462) had a higher possibility to visit VHS first, while patients with fever (aOR=1.195, 95%CI: 1.160-1.230), or nausea and vomiting (OR=1.494, 95%CI: 1.424-1.527), were more likely to visit high level hospitals like township and county hospitals directly. Children (<14 years) and adult patients younger than 60 years old with fever, or cough, or diarrhea were more likely to visit high level hospitals than the elderly patients with same symptom.

Conclusion: Patients' preference to healthcare units could be a result of individual factors and disease performance. Identifying the pattern of symptom distribution in different levels of health facility would improve the timeliness and effectiveness of the syndromic surveillance system.

22.044 Automated learning of naive medical language to support syndromic surveillance via blog mining

A. E. Tozzi¹, M. De Vincenzi², P. Velardi², F. Gesualdo¹,

M. Gonfiantini¹, E. Pandolfi¹, E. Agricola¹

¹Bambino Gesù Pediatric Hospital, Rome, Italy, ²Sapienza University, Rome, Italy

Background: Analyzing how people discuss about health-related topics on dedicated blogs and social networks such as Twitter, can provide valuable insight for syndromic surveillance and to predict disease outbreaks. Since people refer to their health status and diseases using everyday language more often than medical jargon, a prerequisite for blog mining implies being able to associate the medical terminology with the correspondent common terms (e.g. h1n1 and swine flu, erythematous rash and red spots).

Objectives: We present a minimally trained graph-based algorithm to learn associations between technical and everyday language terms.

Methods and Materials: Patterns that relate technical and everyday terms are automatically extracted from Wikipedia, Freebase, on-line glossaries and other web resources. Starting from few examples of technical term/naïf term pairs (TT-NT), our algorithm learn clusters of patterns relating a TT and a NT. Clusters are weighted according to their precision and relevance, that eventually allows it to produce, for each TT, a list of NT in order of importance. We apply our technique to learn hundreds of TT/NT pairs.

Results: Tracing the frequency of TT/NT terms on a corpus of Twitter messages and medical blogs, we have observed that a knowledge of naïve medical language allows to collect a considerably larger corpus of evidence to support an effective monitoring of health-related behaviors, increasing sensitivity. Furthermore, being able to trace patient's discussions on their perceived symptoms (described most often with a naïve language, like red spots, bone pain, etc.) could provide valuable support for medical diagnosis, e.g. by identifying frequently and unexpected co-occurring symptoms.

Conclusion: Syndromic surveillance may benefit of natural language processing techniques that are useful to mine social networks and health blogs. The increase in sensitivity obtained with this apprach must be balanced with a potential decrease in specificity. Coherence between different information sources should be verified for a correct interpretation of signals.

22.045 Timeliness of data reporting in a web-based syndromic surveillance system in rural China

T. Tao¹, Q. Zhao¹, J. Yang², J. Zhou³, K. Engstrom⁴, Y. Zhu¹,

H. Cheng⁵, B. Xu¹

¹School of Public Health, Fudan University, Shanghai, China, ²Yongxiu County CDC, Yongxiu, Jiangxi Province, China, ³Fengxin County CDC, Fengxin, Jiangxi Province, China, ⁴Invotech Solutions, Gävle, Sweden, ⁵Jiangxi Provincial CDC, Nanchang, China

Background: Timely data reporting is crucial to the overall timeliness of syndromic surveillance system in the early warning of infectious disease epidemics.

Objectives: To explore the data reporting timeliness and potential influencing factors in a web-based syndromic surveillance system in rural China.

Methods and Materials: From August 1, 2011-September 30, 2012, a pilot syndromic surveillance project (ISSC) has been implemented in two rural counties (Yongxiu and Fengxin) of Jiangxi Province, China, which involved 2 county hospitals (CH), 4 township hospitals (TH) and 47 village health stations (VHS). In each surveillance unit, doctors used paper-based clinic logs to record 10 infectious related main complaints as well as the demographic information of daily outpatients. Then, these data were reported to a web-based surveillance system via computer by lay worker (CH), public health staff (TH) or village doctor (VHS) on a daily basis. We calculated the mean reporting timeliness of all data records in ISSC database for each surveillance date. A "delayed reporting" was occurred if the timeliness of any data record reported by one surveillance unit on a given date exceeded 36 hours.

Results: During the 427 surveillance days, 263 days (61.6%) had a reporting timeliness of <=24 hours, with the mean at 24.5 hours (Figure 1). The four obvious drops of timeliness occurred in the start period of ISSC, the Spring Festival, the extension of surveillance areas (massive increase of data traffic) and one prolonged shutdown of ISSC web server caused by unknown errors. Delayed reporting occurred in 2,906 out of 22,267 Unit-Days (13.1%). The delayed reporting rate (DRR) was much lower in Yongxiu County than in Fengxin County (7.8% vs 17.7%, p<0.001). VHS had the lowest DRR (10.2%) in contrast to TH (31.4%) and CH (41.2%). Village doctors aged above 40 years had a higher DRR than others (17.9% vs. 10.4%, p<0.001).



Figure1. Time trend of reporting timeliness in ISSC project.

Conclusion: Web-based system greatly improved the timeliness of data reporting. However, more efforts should be made to strengthen the stability of web server and resolve the reporting difficulty in national holidays. The superior timeliness in Yongxiu County was probably attributed to the internet-based supervision through Instant Messenger, carried out by local CDC staffs.

22.046

Holistic assessment of country surveillance, early detection and response systems: Towards a European approach

G. Fraser¹, F. Hruba², T. Mollet³, P. Penttinen¹, P. Rosin¹ ¹European Centre for Communicabled Disease prevention and Control, Stockhokm, Sweden, ²ECDC, Solna, Sweden, ³European Centre for Disease Prevention and Control, Stockholm, Sweden

Background: The need for systematic appraisal of country surveillance, early detection and response (SEDR) systems has been highlighted by international public health emergencies over recent years, in addition to the continuing burden of less high profile international outbreaks. Single disease surveillance system evaluations are reported increasing frequently, but the identified improvements usually require generic rather than 'single disease' system changes. The European Centre for Communicable Disease Control (ECDC) has been developing an holistic approach to the appraisal of country SEDR systems, for use in conjunction with country leaders, for both member states and EU candidate countries.

Objectives: To develop and test an holistic approach to the appraisal of country SEDR systems, for use in conjunction with country leaders, for both member states and EU candidate countries.

Methods and Materials: Multidisciplinary expert teams at ECDC defined items appropriate for a country system assessment, their rationale and logical taxonomy, and method of obtaining evidence relating to them. Instruments for systematic information provision by country system leaders were developed. The instrument also covers key supporting infrastructure, including regulatory framework, human resource capacity, and public health microbiology infrastructure. Part of the instrument was pre-tested by field interviews in two countries.

Results: The assessment instruments and procedures have been deployed, with country support, in three European countries, including two candidate countries. The assessment outcomes were subject to detailed response from country system leaders. In each country the process identified both specific and generic system strengths, and areas

International Meeting on Emerging Diseases and Surveillance 2013

for development, with substantive country agreement. The assessment provided an overall synthesis within which individual potential system improvements could be evaluated for priority and likely effectiveness, in context of the state and needs of the overall system.

Conclusion: Systems for evaluation of country surveillance and response systems are increasingly available, but mostly not applied systematically, or limited to single disease reviews. There is increasing need for assurance of system responsiveness and reliability. ECDC is developing, in collaboration with countries, an approach to system appraisal which has potential to provide countries with an holistic assessment of their systems to support review of options for development in a whole system context.

22.047

Identifying unobserved heterogeneity of influenza-like illness trajectories within health care units

X. Song¹, Q. Zhao¹, C. Zhou¹, H. Yuan², X. Lu³, V. K. Diwan³, B. Xu¹ ¹Fudan University, Shanghai, China, ²Jiangxi Province CDC, Nanchang, China, ³Karolinska Institutet, Stockholm, Sweden

Background: From two counties of Jiangxi province, China, symptoms of influenza-like illness (ILI) were reported daily via a web-based system by health workers in county, township and village health care units.

Objectives: To assess the ability of early detection of influenza epidemic at different levels of health facilities in an integrated syndromic surveillance system in rural China (ISSC).

Methods and Materials: Group-based trajectory modeling (GBTM) is applied to describe the trajectory of ILI over time and to identify distinct subgroups within 170 healthcare units. Based on Bayesian Information Criterion (BIC) and local experiences and knowledge, the "best" model was determined in terms of the number of subgroups and the trajectory fitness shape.

Results: In total, 14616 ILI related outpatient visits were reported to ISSC during May 1–August 31, 2012, by 170 healthcare units including 2 county hospitals, 15 town hospitals and 153 village clinics. Findings from GBTM show that group 4 is composed by 2 town hospitals and 9 village clinics, and group 5 consists of 2 county hospitals and 1 village clinic. With only 1.8% of health care units involved, group 4 presents 2423 (16.58%) of all ILI reports. Combining group 4 with group 5, the healthcare units involved increases to 8.6% and the coverage of reported records rises to 39.4%. Group 4 and 5 show better ability on the description of the fluctuation of ILI (Figure 1).



Figure 1. Five-Group-Trajectory Model with 95% CI.

Conclusion: GBTM using real-time ILI data suggests that county hospitals and low level healthcare units with condensed patients should play important roles in early detection of influenza epidemic.

22.048 Syndromic surveillance systems in Albania, from a humanitarian emergency to an integrated surveillance system

S. Bino, A. Simaku, E. Tomini, A. Vasili, D. Ulqinaku Institute of Public Health, Tirana, Albania

Background: Syndromic surveillance of infectious diseases was set up since 1999, during a humanitarian crisis. The system uses a specific software package known as "Albanian Epidemiological Reporting Tool" (ALERT). It is a nationwide system, based on nine syndromes and on daily primary care and hospital emergency departments reporting with a primary aim to early warn about potential outbreaks and be more sensitive than the diagnosis based routine surveillance.

Objectives: The aim is to demonstrate the value of syndromic surveillance system in signaling infectious disease dynamics and outbreaks and its role to prevent and control epidemics

Methods and Materials: We undertook a retrospective analysis of ALERT data from the National Surveillance Unit at the Institute of Public Health. Data records of aggregated cases of notifiable syndromes examined during the week, including zero reporting, from all primary health care facilities and emergency departments in the country forwarded weekly to the Institute of Public Health were analysed. An alert was defined as an increased number of cases of syndromes. Moving epidemic method (MEM) is used to generate thresholds and intensity levels of acute respiratory infections (ARI). For all other syndromes the threshold is the sum of the mean number for the 5 previous weeks and 1.96 times the standard deviation. In the "Hemorrhage with fever" item, a single case constitutes an alert

Results: ALERT detected three large hepatitis A outbreaks. The large increase in 'jaundice" cases in 1999, in 2003 and 2006 was related to a hepatitis A. ALERT notified a total of 57 signals, 5 of which turned out to be current epidemics. The system produced 1067 alerts across all syndromes monitored. There was a remarkable increase in weekly counts ARI during the influenza pandemic period with hundreds of signals. Last year the system detected a large outbreak of ARI which target the influenza.

Conclusion: The ALERT system was successful in detecting several outbreaks of various causes between 1999 and 2011 and allowed data analysis in real time. Subsequent optimization of the system by public health professionals and engagement of primary and emergency care doctors combined with field investigation prompted early control measures.



.049 Developing a common approach to monitor and evaluate completeness of public health surveillance in European Union Member States

K. Mellou¹, I. Devaux², S. Mc Nabb³, G. Priotto⁴, L. Ferland⁵, J. Brazil⁶, J. Freed⁷, J. Kerlic⁸, S. van der Plas⁹, B. Ciancio² ¹Hellenic Center for Disease Control and Prevention, Athens, Greece, ²ECDC, Solna, Sweden, ³Emory University, Atlanta, GA, USA, ⁴WHO, Lyons, France, ⁵Public Health Practice, Atlanta, GA, USA, ⁶Institute of Public Health, Dublin, Ireland, ⁷Health Protection Agency, London, United Kingdom, ⁸Institut of Public Health, Bratislava, Slovakia, ⁸RIVM, Blthoven, Netherlands

Background: Data quality of public health case reporting can be improved by assessing both external completeness (the capacity to capture all cases of a health outcome in a population) and internal completeness (a complete set of data for each notified case). To assess whether public health surveillance meets its objectives, it is essential to monitor and evaluate completeness regularly. However, there is no standard approach to monitor and evaluate this surveillance attribute across European Union (EU) Member States which could benefit in data comparability across countries.

Objectives: To design, pilot, and publish a common approach to monitor and evaluate completeness of public health surveillance to provide comparability of reportable communicable diseases among EU Member States.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: A step-by-step approach was conceived to monitor (continuous) and evaluate (points in time) data quality, including completeness, in both individual and group meetings of the working group for surveillance system quality of the European Centre for Disease Prevention and Control (ECDC). This approach was supported by literature documents, including guidelines, published articles, collected through a systematic process.

Results: A conceptual framework to monitor internal completeness of reporting included: 1. description of the surveillance system; 2. planning of monitoring (targets to be reached, diseases and variables to be monitored, checks to be performed) ; 3. measure of internal completeness ; 4. display and interpretation of results (gap analysis) and 5. interventions for improvement. The same framework also applies to evaluation of external completeness, except that the evaluation process (opposed to monitoring) is not continuous and methods consist in comparison of several data sources in step 3. Practical guidance were given on methodological issues. Examples of approaches in different settings were also included, as well as directions to supporting material.

Conclusion: Completeness is an important attribute of surveillance systems. Yet, different completeness levels do not allow an accurate comparison of data reported by different European countries. Having a common tool to guide monitoring of internal completeness and evaluating external completeness, will strengthen public health surveillance activities inside countries and enhance data comparability among them.

22.050

Developing national syndromic epidemic intelligence for early detection of health threats linked to a mass gathering event: The Olympic Games London 2012

A. Backx¹, L. Vaillant¹, J. Linge², V. Bousquet¹,

C. Caserio-Schönemann¹, P. Barboza¹

¹French Institute for Public Health Surveillance (InVS), Saint Maurice, France, ²Joint Research Centre, Ispra, Italy

Background: During the Olympic Games London 2012 (OG), France hosted some of the participants, and expected an increase in tourism, in the regions IIe de France (Greater Paris), West, Normandy and North. Hence, the French Institute for Public Health Surveillance (InVS) implemented enhanced syndromic surveillance in these regions. The International Department (ID) of InVS performs epidemic intelligence (EI) work that focuses on international public health threats to the French population. For the OG, the ID participated by developing and performing syndromic EI dedicated to these regions. To detect public health events as real-time as possible, EI primarily uses internet public health intelligence systems. For one, the Medical Information System (MedISys), the ID created and tested syndromic categories.

Objectives: The objective was to develop syndromic EI focused on a specific mass gathering event. A second objective was to see if EI applied to French regions would increase the timeliness of event detection in comparison to enhanced syndromic surveillance.

Methods and Materials: In MedISys syndromic categories were created from the list of syndromes defined for the enhanced syndromic surveillance. To add the national component, together with the InVS inter-regional epidemiological units in the regions of interest, the ID added an exhaustive list of media sources to MedISys. Two operators then screened the retrieved articles daily in the period from early July to mid-September 2012.

Results: On average, MedISys retrieved 76 articles per day of which the operators selected 5 that fell into the list of syndromes and regions of interest. They did not detect any event that could potentially affect people linked to the Games in France and the United Kingdom.

Conclusion: The OG allowed testing EI adapted to regional media analysis in a specific context. The developed national and syndromic EI functioned. However, no event in France related to the OG was detected during the enhanced surveillance period, neither by EI nor by syndromic surveillance. Therefore, the EI could not be evaluated for increased timeliness of event detection against conventional detection methods. Nevertheless, the ID learned valuable lessons on how to develop categories for different syndromes that will serve further focused EI development in the future.

A. Ziemann¹, T. Krafft¹, M. Sala Soler², A. Fouillet², A. Hulth³, L. Müller⁴, S. Conti⁵, M. Kanieff⁵, C. Dupuy⁶, S. Medina²
¹Maastricht University, Faculty of Health, Medicine and Life Sciences, CAPHRI School of Public Health and Primary Care, Maastricht, Netherlands, ²Institut de Veille Sanitaire, Saint Maurice, France,
³Smittskyddsinstitutet, Solna, Sweden, ⁴Statens Serum Institut, Copenhagen, Denmark, ⁵Istituto Superiore di Sanità, Rome, Italy,
⁶Agence nationale de sécurité sanitaire de L'alimentation, de L'environnement et du travail, Lyons, France

Background: Syndromic surveillance (SyS) based on clinical signs and symptoms or proxies (e.g. drug sales), as opposed to confirmed diagnoses, is being increasingly used as supplementary information to attain timely detection and monitoring of communicable and noncommunicable public health threats but no general compilation of good practices is available. The European Commission co-funded Triple-S Project develops practical guidelines for implementing SyS systems in Europe based on a review of SyS activities and lessons learnt with one focus on data sources.

Objectives: The objective was to assess different SyS data sources for their use in detecting and monitoring different health threats.

Methods and Materials: The assessment was based on a structured review of PubMed indexed literature and on study visits to SyS systems in Europe. The literature review included 173 articles published between 2002 and June 2012 describing SyS systems in high-income countries. The study visits were conducted between June 2011 and June 2012 and covered existing, planned, pilot or expired SyS systems in 11 countries. The utility of the data sources was assessed based on the criteria for evaluating SyS systems of the U.S. Centers for Disease Control and Prevention.

Results: A variety of data sources are used for SyS (n=11 presented in literature, n=14 presented in visits) depending on the system's objectives (e.g., monitoring communicable diseases or environmental events), data availability (e.g., costs, legal access) and target population (e.g., persons with mild or severe symptoms). Many SyS systems follow a trend to use multiple data sources to increase validity and representativeness. Health services are the most common type of data source used, which can be explained by the fact that they exist in every country and have a relatively high specificity compared to e.g., web search logs. Emergency department patient records are by far the most common data source (31% of reviewed articles, 63% of countries covered by visits), and they are most often used for influenza surveillance.

Conclusion: This assessment resulted in an evidence-based directory on data sources currently used for SyS in order to guide public health authorities in choosing data sources for future SyS systems in Europe.

22.052 Open-intelligence analysis for disease and pest surveillance

A. Lyon¹, G. Grossel²

¹University of Maryland, College Park, MD, USA, ²Australian Department of Agriculture, Fisheries and Forestry, Canberra, Australian Capital Territory, Australia

Background: AquaticHealth.net is an open-source aquatic biosecurity intelligence gathering and analysis application. The system collects information in much the same way as other similar systems (e.g., HealthMap, BioCaster). However, the information collected undergoes minimal automated analysis, and analysis is largely left to AquaticHealth. net's users. The result is an automated system of intelligence gathering, combined with a manual system of intelligence analysis. This approach relies on a large number of users, and so AquaticHealth.net relies on an *open-intelligence analysis* method: any user can publish their own analyses for all to see and analyse, AquaticHealth.net will provide fast and accurate forecasts, accompanied with nuanced explanations.

International Meeting on Emerging Diseases and Surveillance 2013

These methods can be applied to other areas of biosecurity and disease surveillance.

Objectives: To forecast aquatic biosecurity events using an openintelligence platform.

Methods and Materials: Automated: AquaticHealth.net performs hourly scans of an array of RSS feeds, blogs, social networks, and news sites. It analyses this information and removes redundancies, applies taxonomy and geospatial tags. The information is then pushed to the Daily Scan, where users then analyse it further. Manual: Users asses the information for inaccuracies and its importance. They decide whether an article should be a disease alert, which is emailed to all users. Users can change tags, edit reports, add commentary, apply rankings, change searchterms, and summarise issues in the Emerging Issues blog (formerly a wiki).

Results: AquaticHealth.net publishes 7 daily reports and 2 weekly disease alerts (on average). 90% of CEFAS's (www.cefas.defra.gov.uk) Emerging Disease Updates cite AquaticHealth.net. The Australian Sub-Committee for Aquatic Animal Health (SCAAH) have used the system to compile their quarterly reports for 1.5 years. The Australian Department of Agriculture, Fisheries and Forestry (DAFF) have use AquaticHealth. net to make forecasts-e.g., used aquaculture equipment would be a high-risk pathway for OsHV. AquaticHealth.net's users are currently forecasting an increase of emerging marine finfish disease outbeaks in South East Asia, and are actively watching this issue.

Conclusion: AquaticHealth.net's open-intelligence approach has proven to be an effective and flexible biosecurity forecasting method.

22.053 Epidemiology of sudden unexplained death in young persons, at an acute care hospital in Singapore

R. Sridhar, I. Venkatachalam, H. C. Chan, G. K. Goh, P. A. Tambyah

National University Health System, Singapore, Singapore

Background: Mortality surveillance at our hospital is done to detect emerging infectious diseases and as part of the emergency preparedness for SARS affected countries recommended by the World Health Organization (WHO). WHO anticipates that pandemics will commence in developing countries due to rapid unplanned urbanization and population growth.

Objectives: To describe characteristics of young patients with sudden unexplained death of possible infectious etiology.

Methods and Materials: National University Hospital, Singapore, is a 1000-bed tertiary hospital. Mortality data is downloaded from the hospital information systems daily. Demographic, clinical and laboratory data are obtained from electronic case records. Cause of death is ascertained from case records and coroner's reports.

Patients aged one to fifty years, without pre-existing chronic medical illness, who died from possible infectious causes between July 2004 and June 2011 were included in this study. Death due to possible infectious etiology was defined by the presence of fever or organ specific symptoms in the week preceding death, where no cause was identified by preliminary investigations. Data was analysed using STATA version 10.1.

Results: Of 1247 patients in the study, 177 (14.2%) died from possible infectious causes. The mean mortality rate was 0.42 per 100,000 population. 129 (72.9%) were male. The most susceptible age was between 10 and 35 years with a median age of 29 years.

Between 13 to 17% of deaths each year were of possible infectious etiology. An increased number of young patients died of unknown cause, in the age groups of 1 to 10 and 11 to 20, with symptoms related to infectious causes. Many young persons also died due to Myocardial Infarction.

Biological samples identified organisms for 49 (27.7%) patients. 24 cases had viral infections, including Influenza A, Epstein-Barr virus, Rhino virus and Dengue virus. Bacterial organisms identified were Streptococcus pneumonia, tuberculosis, and Mycoplasma pneumonia.

Conclusion: 14% of unexplained deaths, each year, are due to infectious causes. A search for an infectious etiology revealed unidentified viruses caused a significant number of them. Myocardial infarction (MI) in young persons was identified as the cause of death in some cases and warrant further investigation to determine if an infection precipitated the MI.

22.054 INDICATOR: One Health surveillance using primary and secondary data

I. Brooks, W. Edwards, S. Rao, M. Vaughan, B. A'cs, M. Felarca University of Illinois, Urbana, IL, USA

Background: Traditional approaches to biosurveillance monitor a limited number of sources such as emergency departments, reportable diseases, or school attendance, often with different systems for each data source. There are, however, many more data sources that contain information about the health of a community, some, like social media, now being considered for biosurveillance, but others like weather, airborne allergens, animal control, and veterinary diagnoses that are usually omitted.

Objectives: The goal of the INDICATOR project is to develop an open-source cyberinfrastructure for One Health biosurveillance, modeling, and response that can handle data from any source, human, animal, or environmental. By combining all of these sources and applying modern machine learning approaches we expect to obtain a timely and accurate picture of the health of the community.

Methods and Materials: INDICATOR has been developed using a combination of readily available open-source tools, including MySQL, SpagoBI, Talend, and Drupal. We have developed a single high-level data format that can be used by all healthcare data providers, human and veterinary.

Results: We have been successful in getting community partners to contribute to INDICATOR and are receiving human data from emergency departments, ambulatory clinics, nurse call centers, reportable disease databases, and school attendance; animal data from private veterinary clinics, university diagnostic labs, animal shelters, and animal control; and pollen and weather data.

During the 2009 H1N1 pandemic the standard vaccination strategy in Illinois was to hold vaccination clinics open to the public followed by school-based clinics. As a result of following the relative effect of H1N1 on school attendance, nurse calls, and ED visits public health decided to alter this approach to vaccinate the harder hit school-age population first, leading to the best results in Illinois.

Preliminary modeling of the relationship between veterinary, human and climate data has shown that there is a significant correlation between growing degree days and Lyme disease cases, both human and veterinary.

Conclusion: We have developed an open-source cyberinfrastructure for One Health biosurveillance, are gathering routine surveillance data from many different sources, have caused change in public health policy, and are starting to discover relationships between the different types of data source.

22.055 Epizootic monitoring of classical swine fever (CSF), Aujeszky's disease, Teschen Disease, Circovirus infection in wild boars population in Ukraine

A. Golovko¹, S. Nychyk², M. Sytyuk² ¹NAAS, Kiev, Ukraine, ²IVM, Kiev, Ukraine

Background: Viral infections as classical swine fever (CSF), Aujeszky's disease, Teschen disease, circovirus infection are spread and registered in majority of contries. Today in industrial and traditional pig farming the diseases including CSF, Aujeszky's disease and Teschen disease have received considerable attention from scientists around the world. However the wild boar population in Ukraine continues to grow annually, less attention is paid to an area of infectious and parasite diseases studies. The wild boars circulate and distribute infections; increasing number of wild boars is one of preconditions for the distribution of various infectious diseases.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: To identify dominant number of wild boars for CSF, Aujeszky's disease, Teschen disease and circovirus infection.

Methods and Materials: During research have been used 3462 blood sera, 3919 of which were researched for CSF, 3462 for Aujeszky's disease, 3441 for Teschen disease and 78 organ samples (spleen, lymph glands) from sampled shot wild boars in hunting seasons of 2001-2010 within Ukraine. Blood sera were tested for available specific antibodies to CSF by ELISA using IDEXX test-systems, for Aujeszky's disease and Teschen disease by neutralization test at revaccinated cell cultures of PTP and SNEB. 78 swine samples were tested for available DNA circovirus of type II by PCR.

Results: Monitoring research was effected in CSF research diagnostic center at IVM. Over the last 10 years population of wild boars within Ukraine is increased in 1.8 times, and number of wild boars at the end of 2010 made 61800 animals. Upon results of the laboratory monitoring research have been revealed serological dominance of antibodies to CSF at a level of 10,2 %, to Aujeszky's disease at a level of 13,46 %, Teschen disease at a level of 17,99 %. Prevalence of circovirus of type II made 83.3 %.

Conclusion: Obtained results from monitoring research confirm availability and circulation of abovementioned viral agents of swine diseases in population of wild boars within Ukraine, which may serve as a reservoir of an infection agent. Perspective for further researches is to isolate and characterize isolates of the viruses and definite role of wild boars in infectious pathology of domestic swine.

22.056 Biosecurity evaluation of Poultry Production Cluster (PPCs) in Thailand

W. Aengwanich

Mahasarakham University, Maha Sarakham, Thailand

Objectives: The objective of this study was to evaluate the biosecurity levels of Poultry Production Clusters (PPCs) in Thailand.

Methods and Materials: Biosecurity levels of poultry farms in the PPCs were determined with criteria specified in biosecurity score form in 3 provinces i.e., Mahasarakham (contract farm with company), Nakhon Phanom (cooperative farm) and Nong Khai (individual farm) in the Northeast region of Thailand. In each province, biosecurity levels were evaluated both in the controlled group and in the cluster (15 farms each). Biosecurity scores were compared between farms in the controlled group and the cluster and among 3 provinces.

Results: From the results, it was found that scores of attractiveness to wild bird, measures for visitors and traders, measures for equipments and vehicles of poultry farm, local environment, measures taken at the entrances to poultry sheds in poultry farms and biosecurity plans of poultry farmers in Mahasarakham were significantly higher than in Nakhon Phanom and Nong Khai (p<0.05). The score of measures related to staffs of the poultry farms in Nakhon Phanom was significantly higher than those in Nong Khai (p<0.05). The score of feed quality in Mahasarakham and Nong Khai was significantly higher than that in Nakhon Phanom (p<0.05). In Mahasarakham, scores of local environment and biosecurity plans of poultry farmers of the controlled group were significantly higher than those of the cluster (p<0.05). In Nakhon Phanom, scores of attractiveness to wild bird, measures for incoming poultry, measures for visitors, measures taken at the entrances to poultry sheds and biosecurity plans of poultry farmers in controlled group were significantly higher than in the cluster (p<0.05).

Conclusion: This demonstrated that biosecurity levels of contract farm with company were better than cooperative and individual ones. The difference of biosecurity levels was due to the farming pattern, farm's ecology, the compliance to governmental measures and policies and the ability to invest in biosecurity system of each group. As a result, the scores of biosecurity differed.

22.057

Exploring disease indicators: An interdisciplinary approach to surveillance. detection, and modeling of Chagas Disease in southwestern United States

M. McConnell

University of New Mexico, Albuquerque, NM, USA

Background: Discipline-specific disease indicators often do not transcend to other disciplinary concepts often resulting in a "monoculture" approach to disease research. This presents challenges to investigating re-emerging infectious diseases because while the rate of research information produced by the discipline-specific research is expanding, it also exceeds time available for scientists of all disciplines to remain updated on the latest scientific results. The New Mexico Geo-Epidemiology Research Network (NM GERN), represents 13 disciplines with a common interest of infectious disease. The main goals are to integrate old concepts of "mono-culture" infectious disease research into new, effective collaborations on disease surveillance and identify a regional problem that would benefit from these new approaches.

Objectives: NM GERN identified Chagas Disease as a potential challenge to the public health of residents of New Mexico. Challenges included effective disease surveillance among human populations, species distributions of Trypanosoma cruzi (the parasite that causes Chagas Disease), Triatoma (the primary vector of T. cruzi), and the sylvatic environment. New surveillance strategies include tracking Chagas reservoir movement associated with long-term research on climate change as drivers, GIS vector and sentinel mapping, as well as mathematical modeling and information management. By combining research methods as a planned surveillance strategy rather than waiting for disease emergence, resources are effectively managed.

Methods and Materials: Based upon work performed in 1959 by Wood and Wood (1961), a north-south transect in New Mexico was sampled for T. cruzi during the summer of 2011.

Results: Of the 12 specimens collected in southwest New Mexico, 7 Triatoma bugs tested positive for T. cruzi by PCR analysis, demonstrating the persistence of T. cruzi. Now that T. cruzi has been reestablished in the sylvatic enviroment, NM GERN may now proceed with more complex modeling of T. cruzi and Triatoma.

Conclusion: Because parasite species distributions are closely matched to southern Texas and Arizona, NM GERN is now poised to expand research into GIS modeling, along with climate change and human population changes over time. By examining these parameters from different disciplines, effective public health outreach programs may be created for changes in disease surveillance.

22.058

Sixty years of Indonesian Hajj demographic and health surveillance

M. Pane¹, G. Samaan²

¹Ministry of Health Rep of Indonesia, Jakarta, Indonesia, ²Australian National University, Canberra, ACT, Australia

Background: Every year, 2-3 million moslems undertake pilgrimage. Of these, 10% are from Indonesia. Collection of surveillance data commerced in 1950 and forms the basis of Hajj health policy.

Objectives: Using the health surveillance data for management and policy.

Methods and Materials: Demographic data are collected regularly by the religious affair and immigration, health data are collected by Ministry of Health. Descriptive analysis were conducted to assess demographic, health status and diseases activity data.

Results: Since 1950, the number of Indonesian pilgrims has increased consistently from 7000 to 221,000 pilgrims. This is per the allocation made by the Islamic Conference Organization which allows for 1 per 1000 moslem population. However, in 1998 the number decreased by 30% due to the global financial crisis. A similar fall was not seen following the 2008 global financial crisis. Women comprise 55.6% (standard deviation,sd 9.4) of Indonesian pilgrims. The largest age cohort is 50-59 years old (24.9%, sd 3.5) and the education level is

SUNDAY • FEBRUARY 17, 2013

Poster Presentations II

International Meeting on Emerging Diseases and Surveillance 2013

elementary school education(42.5%, sd 8.0). pilgrims considered high risk (>60 years old or with chronic diseases) ranged from 28.4-43.5% per year (sd 10.9). the majority had hypertension (35-40%) or Diabetic (10-18%). One in three patients visited the Indonesian health posts in Saudi Arabia with more than 50% having respiratory complaints every year. Between 2500 to 3000 pilgrims are admitted to hospital with 25-30% due to cardiovasculair diseases and 18-22% respiratory diseases.

Conclusion: the yearly number of Indonesian pilgrims highlights the potensial for diseases spread. To minimize health problems such as cardiovasculair and respiratory diseases, screening was introduce in 2002 to identify pilgrims with chronic health conditions or of older age. Similarly, policy was introduced so that doctors accompany pilgrims to triage and provide support. This shows that the surveillance program has influenced the hajj health policy.

22.059

A mobile phone application for pertussis classification based on machine learning

M. Adamczyk¹, D. Parker², J. Cremer³, J. Picone⁴, A. Harati⁴, P. Polareen³

¹University of Iowa, Iowa City, IA, USA, ²GTD Unlimited, Oxford, MS, USA, ³The University of Iowa, Iowa City, IA, USA, ⁴Temple University, Philadelphia, PA, USA

Background: Early identification of pertussis cases is essential to control outbreaks. Although early stages of the disease resemble other infections, the cough often becomes more severe, and a paraoxysmal phase begins. This stage is characterized by bursts of coughs followed by gasps and a "whooping" sound. Experienced clinicians can easily identify these classic coughs. However, many clinicians have never seen a case, and thus may misdiagnose cases, especially early in an outbreak

Objectives: The purpose of this project was to use mobile phone technology to expand our ability to collect and analyze cough files.

Methods and Materials: Previously, we developed a way to classify pertussis cases based on sound files. We collected a series of sound files representing pertussis and non-pertussis coughs and manually categorized them and extracted features for each category. The underlying machine learning algorithms approaches employ neural networks, k-nearest neighbor (KNN), and a 200 tree random forest (RF). Now, in addition, we have developed a mobile software application (app) for iOS (iPhone/iPad) that enables convenient anytime, anyplace collection and analysis of coughs. To collect cough data, a person simply holds the phone in front of his or her mouth when coughing.

Results: Using a variety of machine learning algorithms, over 90% of all pertussis coughs were properly classified, suggesting that we can build a robust classifier and identify pertussis cases with typical paroxysmal symptoms. In addition, our app can record sound files in a convenient fashion for users. These files can then be analyzed on the phone using our previously reported machine-learning based algorithms or on a remote server. The app can also transmit sound data, assessment results, and any user-supplied annotations, enabling development of a more substantial body of cough data.

Conclusion: The development of a simple mobile app combined with our cough classification algorithm represents a powerful tool for collection of pertussis (and non-pertussis) cough data. It enables data collection anywhere, anytime, and should improve our ability to classify coughs for pertussis and other disorders.



22.060 Enhancement of existing infectious disease early warning system using a novel modeling approach in a resource poor setting: Pakistan

K. Ahmed¹, M. Rahim², R. Kakar³, G. Sabatinelli¹ ¹World Health Organization, Islamabad, Pakistan, ²World Health Orgnization, Islamabad, Pakistan, ³World Health Organization, Islamabad, Pakistan

Background: Infectious disease threats in developing countries are common due to lack of many public health resources and infrastructure, particularly in countries with poor disease surveillance mechanisms.

Effective preventive and control measures through early detection and rapid identification of infectious diseases are necessary to save lives, prevent diseases, and contribute to rationalizing resources and fulfilling global responsibilities significantly.

Objectives: The intended objective was to develop cost-effective online disease surveillance programme that prvoides ease in data transmission using technologies, possibilities for replicability of the system in other humanitarian settings and expanding the system into a more robust electronic system for public health surveillance in the longer future.

Methods and Materials: The existing surveillance system was enhanced with the development of online platform using both internet based on-line application and mobile phone based cellular technology for increasing efficiency of surveillance system in line with international health regulation recommendations. This electronic platform facilitates automatic compilation and analysis of data at district, provincial and national levels with automatic generation of SMS alert notifications for immediate response, based on defined criteria of surpassing median endemic index. Only verified SMS alert notifications are considered as true alerts.



Figure 1. Flow diagram showing functionality of electronic disease early warning system (eDEWS) in Pakistan.

Results: Overall percent reporting rates of eDEWS notifiable diseases remained >70% with steady increase to >80% in few months. eDEWS central database generated 25811 SMS alerts, of which 8540 SMS alerts were verified as true alerts and more than 80% of true alerts were investigated and responded within 24hours. Of these 8540 true alerts (positive predictive value [PPV] 33.1%), or about 31 true alerts per day, 1060 were confirmed as outbreaks. Prompt public response proved to be effective and efficient with early containment of detected outbreaks.

Conclusion: Despite the many challenges, the results of pilot project indicate that the online reporting system has helped in improving the disease surveillance capacity and capabilities in Pakistan through reducing the latency in data collection and collation using a novel modeling approach that involves transformation of complete and validated data from simple presentation to computer-based analysis, and mainly it facilitates the transformation of data into actionable information.

22.061 Serological and cultural detection of Brucella infection in cameland its public health significance in selected districts of Afar region, Ethiopia

S. W. Zeweld

Mekelle University College of Veterinary Medicine, Mekelle, Ti, Ethiopia

Background: Brucellosis is a widespread zoonotic diseases mainly transmitted from food animals through consumption of contaminated raw animal products. In Ethiopia, the status of animal brucellosis and its public health consequences is unknown especially in the pastoral and agro-pastoral residential districts of the country.

Objectives: This study was delineated to investigate the prevalence of camel and human brucellosis in Afar region, Ethiopia, to assess the geographical distribution and the associated risk factors and to attempt the isolation of Brucella organism from raw camel milk.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: A cross-sectional study design was carried out in selected pastoral and agro-pastoral districts of Afar region, Ethiopia, in the period from October 2010 to May 2011. A total of 768 camel blood sera were randomly collected from eight pastoral and agro-pastoral residences and human sera were collected from 200 purposely selected clinical patients from two health centres of the districts. Sera were screened using Rose Bengal Plate Test (RBPT) and positive samples were then confirmed by Complement Fixation Test (CFT).

Results: The overall prevalence of camel brucellosis in the districts investigated was 11.9% by RBPT and 7.6% by CFT and the overall prevalence of human brucellosis was 16% by RBPT and 15% by CFT. The logistic regression on animal level including age, herd size, contact or rearing with ruminants and parity of the camels were showed statistically significant different and were the potential risk factors associated with camel brucellosis (P=0.026, P=0.004, P=0.0001 and P=0.004) respectively. The ownership of milking camels, living within the pastoral and agro-pastoral communities, keeping of livestock in close contact, consumption of raw camel milk and milk products, assisting animals during parturition and grooming livestock were potential risk factors associated with human brucellosis.

Conclusion: The results of the present investigation indicate that human and camel brucellosis is widely distributed in the study districts of Afar. Hence, controlling the risk measures, proper hygienic practices and team work between veterinary and health personnel should improve the efforts to mitigate the economic losses and public health hazard caused by the disease.

22.062 Vector transmission of human cutaneous anthrax during an animal outbreak

A. Fasanella¹, R. Adone², M. Galella³, L. Pace¹, A. Aceti¹, L. Serrecchia¹

¹Istituto Zooprofilattico of Puglia and Basilicata, Foggia, Italy, ²Istituto Superiore di Sanità, Rome, Italy, ³Istituto Zooprofilattico Sperimentale of Puglia and Basilicata, Foggia, Italy

Background: Human cutaneous anthrax is often associated with the slaughter of infected animals.

Objectives: We reported a case of probable vector transmission of human cutaneous anthrax during an anthrax outbreak in animals.

Methods and Materials: Between the 22nd and the 26th of August 2012, two sheep died on a 422-head farm near Melfi (Basilicata, Italy). On August 28th, a young man presented at the San Carlo Hospital of Potenza with five papular nodular lesions on his right arm. Although he had had no contact with infected or dead animals, he had been bitten on the arm by a gadfly three days before hospitalization while present in a pasture frequented by the affected flock. The patient added that only after scratching the first lesion, which was very itchy, did he notice the other four. Two scabs were removed from the patient's arm. Each scab was divided into two aliquots and were used for bacteriological and biomolecular testing, respectively. Blood samples were collected from the two dead sheep during the autopsy. DNAeasy Blood and Tissue kits (Qiagen) were used to extract both microbial DNA and DNA from human scabs.

Results: The bacterial cultures performed on human scabs remained negative, while those on sheep blood produced white, non-hemolytic colonies. PCR on DNAs extracted from both suspect colonies and human scabs were positive for B. anthracis, with matching MLVA and SNR patterns.

Conclusion: The negative bacteriological result obtained from the human scabs could be attributed to the difficulty to isolate B. anthracis from skin lesions once the patient has started antibiotic therapy. It is, however, possible to make a diagnosis by PCR on DNA extracted from scabs up to the second day of antibiotic treatment. This case study supports the hypothesis that human cutaneous anthrax may be transmitted by tabanid vectors. Although we are unable to prove beyond doubt that the tabanid transmitted the disease after sucking blood from one of the dead sheep, this seems very likely since the sheep's blood and the patient's scabs yielded the same subgenotype, in a geographical context in which many subgenotypes of B. anthracis are known to be present.

22.063

Fatal case of Crimean-Congo haemorrhagic fever imported into the UK: Laboratory diagnostics, genomic sequencing and phylogenetic characterisation

R. Hewson

Health Protection Agency, Salisbury, United Kingdom

Background: On 2nd October 2012, a 38-year-old male UK-resident returned to Glasgow after visiting Afghanistan where he had been involved in the slaughter of an animal. He arrived in Glasgow from Kabul, Afghanistan via Dubai and was symptomatic from around 28th September with fever, diarrhoea, abdominal pain, haemoptysis and haematemesis. He attended the Emergency Department of Southern General Hospital, Glasgow within three hours of his arrival and was transferred to a negative pressure room in the Brownlee Unit on the Gartnavel site. On 3rd a serum sample couriered to the Health Protection Agencies Microbiology Service Division at Porton Down and was confirmed as PCR positive for CCHF. This is the first confirmed case of CCHF in the UK. Rapid PCR diagnosis is dependent on a broad understanding of circulating strains of CCHF virus which can subsequently be used to validate such assays.

Objectives: Laboratory work to demonstrate the utility of approaches which employ circulating strains to test and validate a newly devised RT-PCR assay for the rapid diagnosis of CCHF.

Methods and Materials: A simple real time PCR approach was devised to detect a wide selection of CCHF strains. This was tested against reference strains and fine tuned with circulating strains.

Results: The devised assay performed well with a wide range of test samples. Importantly it was able to detect in imported case of CCHF in the UK and provided rapid information to physicians.

Conclusion: Access to circulating strains of CCHF through international collaboration provides important information on the utility and confidence of specialist assays. Such validation work ultimately feeds back to patient and hospital management of highly infectious haemorrhagic fever.

22.064 An interesting case of cutaneous melioidosis D. Madi, B. Achappa

Kasturba Medical College (affiliated to Manipal University), Mangalore, Karnataka, India

Background: Melioidosis is an emerging infection in Southern India. It usually present as sepsis, pneumonia and multiple abscesses. Skin and soft-tissue infection comprise 13%-24% of clinical presentations of melioidosis. Cutaneous melioidosis can present as an ulcer, pustule or as crusted ervthematous lesions. Cutaneous melioidosis may be primary (patients in whom the major presenting symptom is skin infection) or secondary (melioidosis at other sites in the body who have incidental skin manifestations).

Objectives: To report a case of cutaneous melioidosis.

Methods and Materials: Case report: A 22 year-old gentleman was admitted in our hospital with complaints of an ulcer over the left thigh of 7 days duration. Our patient initially noticed a nodule on the left thigh which eventually progressed to form a ulcer. He was a known case of diabetes mellitus (type 1) on insulin. Clinical examination revealed a 5× 5 cm ulcer on the left thigh with purulent discharge.

Results: Discharge from the ulcer grew Burkholderia pseudomallei which was sensitive to ceftazidime. He was treated with injection ceftazidime for 3 weeks followed by oral Trimethoprim-sulfamethoxazole and he responded to the treatment.

Conclusion: Melioidosis is also called as the remarkable imitator because it can mimic many diseases. Melioidosis must be considered in the differential diagnosis of a ulcerative cutaneous lesion in a diabetic patient. A delay in diagnosis can be fatal, since empirical antibiotics used for suspected bacterial infections in diabetics do not provide adequate coverage for meliodosis. Such a case report would serve to sensitize the clinicians about cutaneous meliodosis so that they can provide aggressive treatment to patients thereby decreasing morbidity and mortality.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

22.065 Toxocariasis: Underdiagnosed in Europe due to broad range of presenting features?

M. Hoenigl¹, K. Seeber¹, T. Valentin¹, I. Zollner-Schwetz¹, J. Wagner¹, W. Duettmann¹, N. Wutte¹, M. Palfner¹, H. Auer², R. Krause¹ ¹Medical University of Graz, Graz, Austria, ²Meduni Wien, Vienna, Austria

Background: Toxocariasis is caused by Toxocara canis or Toxocara cati. Their definitive hosts are the domestic dog and cat, in which they live as adults within the lumen of the small intestine. In contrast, the human host is aberrant with respect to the completion of the life cycle. Infective larvae wander throughout the body for months or up to several years, causing damage to whatever tissue they happen to enter.

Objectives: The global impact as well as indirect and direct costs of human toxocariasis are poorly understood. Main reason is insufficient clinical awareness due to the broad range of presenting features with the majority being non pathognomonic. The objective was to report two cases of human toxocariasis occuring in Austria.

Methods and Materials: Toxocariasis may be keenly underestimated especially in the developed world where cases are considered rare. Diagnosis is established by combination of clinical and laboratory investigations, including serodiagnosis. We report two cases of human toxocariasis occuring in Austria.

Details of the patients are are depicted in the Table below.

Results:	Pt 1	Pt 2
Age (years) / Sex	45/m	47/m
Underlying condition	Colo-rectal carcinoma	SOT (pancreas-kidney; 7 years earlier)
Symptoms at presentation	Fever up to 40° Celsius, Exanthema (disseminated on the patients trunk)	Nausea Vomiting Massive ascites
Additional symptoms during course of disease	Cough Fatigue Myalgia	Recurrent aszites
Eosinophilia	62%	12%
Travel History	unremarkable	Rumania, Croatia, Hungary, Turkey, Netherlands, France
Animal contacts	Multiple cats (including cats living in the wild)	Multiple dogs
Diagnosis established before presenting to the I.D. clinics	DRESS (Drug Rash with Eosinophilia and Systemic Symptoms) Syndrome	No diagnosis established despite extensive diagnostic workup for >1 year
Toxocara Serology TES ELISA (IgG)	70 U	25 U
Treatment	Albendazole 400mg bid, 5 days	Albendazole 400mg bid, 2x 5 days
Outcome	Rash, pulmonary symptoms and eosinophilia resolved	Aszites stabilized, eosinophilia vanished

Conclusion: In both cases of human toxocariasis presented diagnosis was established after disease was ongoing for several weeks to months. Our understanding of the global impact and cost of human toxocariasis is poor because there is insufficient clinical awareness. Rates of toxocariasis may be keenly underestimated worldwide.

22.066 First results from the Hanta Hunting study: "Hantavirus infection in leptospirosis suspected patients in the Netherlands."

M. Goeijenbier¹, C. Reusken², M. Goris³, A. Osterhaus¹, R. Hartskeerl³, J. Wagenaar¹, J. Reimerink⁴, B. Martina¹, M. Koopmans⁵, E. van Gorp⁶

¹ErasmusMC, Rotterdam, Netherlands, ²RIVM, Bilthoven, Netherlands, ³Kit, Amsterdam, Netherlands, ⁴National Institute for Public Health and the Environment RIVM, Bilthoven, Netherlands, ⁵Erasmus Medical Centre, Rotterdam, Netherlands, ⁶Erasmus Medical Center, Rotterdam, Netherlands

Background: With hallmark symptoms as: "fever, renal failure and hemorrhage" in both leptospirosis and hemorrhagic fever with renal syndrome (HFRS), these two diseases are hard to distinguish. Both are important rodent-borne zoonoses. Leptospirosis is caused by a spirochete while HFRS is the result of an infection with certain hantaviruses. In the Netherlands both diseases are relatively rare. In recent years an increase in hantavirus infections has been observed in countries neighboring the Netherlands. Since this rise in incidence has not been registered in the Netherlands, we hypothesize that due to overlapping clinical manifestations, hantavirus infections may be confused with leptospirosis.

Objectives: To gain insight into the potential under-diagnosis of hantavirus infections in patients suspected for leptospirosis.

Methods and Materials: We selected 360 serum samples from the period 2010-2011 of non-travelling Dutch patients with symptoms suggestive for leptospirosis but with a negative diagnosis after both MAT and ELISA. Additionally 40 sera from confirmed leptospirosis patients were selected. All sera were tested in an IgG and IgM panhanta ELISA (Focus diagnostics). Sera showing equivocal and unequivocal IgM reactivity were selected for immunofluorescent assay (IFA) testing using slides with Puumala and Hantaan virus infected cells (PROGEN Biotechnik) to confirm the ELISA results and gain insight in type of serogroup. Hantavirus under-diagnosis will be quantified by omitting sera for which hantavirus diagnostics were requested in one of the three diagnostic laboratories in the Netherlands.

Results: Forty-six samples responded in the IgG and/or IgM ELISA (13 IgG & IgM, 15 IgM and 18 IgG). 9/13 IgG/IgM ELISA positive sera were confirmed by IFA as well as 7/15 IgM ELISA positives. Three sera showed reactivity in the hantaanvirus serogroup only (1x IgM; 2x IgM and IgG).

Conclusion: We found a substantial seroprevalence (7.8%) of antibodies indicative for an acute hantavirus infection in a cohort with specific clinical symptoms. Furthermore, we have indications that hantaan serogroup vriuses are circulating in the Netherlands although this still needs to be confirmed by virus neutralisation. Our results should raise awareness for hantavirus infections in the Netherlands and indicate a need for combined hantavirus and leptospirosis testing in the Netherlands.

22.067 The status and challenges for the control of rabies in Nepal

G. R. Pant

Rabies Vaccine Production Laboratory, Directorate of Animal Health, Kathmandu, Nepal

Background: Rabies is a disease of priority in Nepal. It is an endemic in different parts of country. The estimated human and animal death due to rabies is about 100 and 200 respectively per year. Limited study has been done on status, epidemiology and control strategy of this disease in Nepal. Dogs play a major role for the transmission of rabies in human and animal. About 35,000 people get post exposure treatment in Nepal after getting dogbite. Health authority of Nepal spends 10 million rupees every year to purchage rabies vaccine form other country. Control of rabies in Nepal is a big challange.

Objectives: The purpose of this study is to know the status and to discuss the challenges of rabies in Nepal.

Methods and Materials: A study was conducted in Nepal to know the status of rabies. Five years data (from 2005 to 2009) on human rabies information recorded at Epidemiology and Disease Control Division under the Department of Health Service and animal rabies information recorded at Veterinary Epidemiology Centre as well as Central Veterinary Laboratory under the Department of Livestock services were analyzed to know the status of rabies in Nepal. Five rabies positive clinical samples collected from Nepal were also analyzed by performing molecular characterization and phylogenetic analysis at Australian Animal Health Laboratory in Australia to know the clades of circulating rabies virus in Nepal.

International Meeting on Emerging Diseases and Surveillance 2013

Results: There were 411 outbreaks and 700 animal deaths in 45 districts of country from 2005 to 2009. A total number of 48,760 animals were given post exposure treatment after bitten by suspected rabid animals. The total number of animal samples submitted for laboratory confirmation from 2005- 2009 were 149 out of which 99 (66%) was positive. Rabies has been confirmed on laboratory test on dog, cattle, goat, sheep, buffalo and human. The total numbers of rabid human (hydrophobia) cases admitted to hospital from 2005 to 2009 were 163 however all of these cases were diagnosed on the basis of clinical symptoms and history of dog bite.

Conclusion: It is needed to adopt suitable and effective control strategy to control rabies in Nepal.

22.068 Clinical features of Helicobacter cinaedi

bacteremia Y. Uwamino¹, K. Muranaka¹, H. Kitazono², N. Hosokawa¹ ¹Kameda Medical Center, Chiba, Japan, ²Tokyo-Bay Urayasu lchikawa Medical Center, Chiba, Japan

Background: *Helicobacter cinaedi* is a Gram negative spiral-shaped bacillus that inhabits the intestinal tracts of mammals. There is growing number of case reports in human recently. But there are few case series with large number, and clinical features of *H. cinaedi* bacteremia are still unclear.

Objectives: To identify the major clinical features of *H. cinaedi* bacteremia.

Methods and Materials: We searched all patients with *H. cinaedi* bacteremia at Kameda Medical Center from January 2009 to September 2012, using microbiology database. Then we retrospectively reviewed their medical records. We checked all the documented symptoms they had during the course of illness when the patient had the positive blood culture for *H. cinaedi*. We also checked their clinical backgrounds and treatment, prognosis at 30 days after the positive blood culture.

Results: 19 patients with *H. cinaedi* bacteremia were identified. Median age was 59-year-old. 15 patients (79%) were male. 13 patients (68%) had no significant prior medical condition. Six patients had healthcare exposure including hospitalization, outpatient dialysis, and chemotherapy.

Common symptoms include fever greater than 37 degrees (15/19; 79%) and painful skin erythema (13/19; 68%). Chills and rigors were relatively uncommon for bacteremia; 42% and 16% respectively. Most community-acquired cases had skin erythema (12/13; 92%) whereas none of the healthcare-associated cases had it (0/6; 0%).

Most patients were treated with cefazolin initially. After the positive blood culture, most patients were treated with ceftriaxone. Only one patient relapsed. No patient died within 30 days.

Conclusion: Major clinical features of *H. cinaedi* bacteremia were fever and erythema. The prognosis of *H. cinaedi* bacteremia is generally good, even with frequently inappropriate initial antimicrobial treatment.

22.069 Diagnosis of a suspected Rift Valley Fever outbreak using IgM captured ELISA in Sudan.

T. M. A. A. Elhassan, A. M. Elhassan, M. B. Abdelrahman, M. E. A. Mansour, A. M. Elhussein, N. A. Ibrahim veterinary research institute, Khartoum, Khartoum, Sudan

Background: Rift Valley Fever (RVF) is an arthropods born, viral

zoontic disease that threatens the African continent as well as the rest of the world, (FAO, 2007). Human acquired infection by RVFV from infected animal tissues or mosquito bites, (Flick, 2005).

RVF virus, is a member of the Bunyaviridae family, genus Phlebovirus (McIntosh et al., 1980), the disease is characterized by storm of abortion in all pregnant animals and high mortality rate in their offspring.

Objectives: To detect anti RVF IgM antibodies in suspected samples. To assess the situation of Rift Valley Fever infection in Central Sudan. **Methods and Materials:** Study was carried out in White Nile,

Algizera, Blue Nile, Sinnar states, these states are the mostly affected. Blood samples were collected from caprine, ovine, and bovine. Sera were prepared, preserved at 4°C and transported to, Department of Virology, Rift Valley Fever Unit, Veterinary Research Institute, and kept at -20°C till used. Commercial IgM ELISA kit for determination of RVF IgM antibodies were purchased from the National Institute of Communicable Diseases (NICD), Johannesburg, South Africa.

Results: A total of 323 serum samples from caprine, ovine and bovine in Algezira, the White Nile, Sinnar and the Blue Nile states were examined for anti-rift valley fever virus IgM antibodies. The results showed that 63 (61%) caprine, 38 (51%) ovine and 10 (23%) bovine were positive in Algezira State. However, 4 (18%) caprine, 6 (50%) ovine and 5 (17%) bovine were positive in the White Nile State. In Sinnar and the Blue Nile State no caprine sample were tested, but 1 (14%) ovine, 7 (22%) bovine were positive.

Conclusion: The presence of anti-RVF IgM antibodies is indicative for active and circulating virus in the investigated area. The nature of these states (water, abundance of canals and rich grasslands) lead to the transmission of the virus to a wide area. The incidence of Rift Valley Fever Virus in the studied states has to be controlled by using different strategies like vector control, strict animal movement and vaccination of all animal population.

22.070 Farming system affects seroprevalence of hepatitis E virus in pigs

S. Rutjes, M. Bouwknegt, J. van der Giessen, A. M. De Roda Husman, **C. Reusken**

National Institute for Public Health and the Environment, Bilthoven, Netherlands

Background: Sporadic non-travel related hepatitis E virus (HEV) infections have been reported in industrialized countries. These infections are caused by genotypes 3 and 4 which are zoonotic and also circulate in swine.

Objectives: To investigate the HEV seroprevalence in pigs raised in conventional, free-range and organic farming systems in the Netherlands. Differences in seroprevalences may give indications on the exposure of pigs to HEV due to for instance contact with the environment or the consumption of different feed.

Methods and Materials: Blood samples were taken at the slaughter house in 2004. 5–20 serum samples were taken per flock. Serum samples of 846 fattening pigs were obtained from farms that applied conventional 265 pigs at 24 farms), organic (417 pigs at 42 farms) and free-range (164 pigs at 12 farms) farming. HEV-specific antibodies were detected by a species independent double sandwich ELISA (MP Biomedicals). Pig specific cut-off values were applied making the test very accurate in distinguishing between HEV-positive and negative pig populations.

Results: HEV specific antibodies were detected in one or more pigs from all conventional and free-range pig farms and in 41 of 42 organic pig farms. The estimated average seroprevalence was significantly higher for pigs raised on organic farms (89%) than for pigs raised on conventional farms (72%; (p=0.04). The difference with free-range farms (seroprevalence of 76%) tended to significance (p=0.06). The average seroprevalences at the latter two types of farms was not significantly different (p=0.8). Six out of ten organic pig farms were estimated to have a within-herd seroprevalence of >95%, compared to one in ten and four in ten of the free-range and conventional pig farms.

Conclusion: The probability of HEV introduction at a farm seemed equal for the different farming types as all but one farms had one or more seropositive pigs. The higher within-herd seroprevalence of pigs reared on organic farms suggests a higher force of infection for those pigs as compared to pigs reared on conventional or free-range farms, maybe due to repetitive exposure through feed (which should originate for at least 80% from organic agriculture) or increased contact between pigs that facilitate within farms epidemics.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

22.071 Seroprevalence of brucellosis among high-risk individuals in suburban Khartoum, Sudan

N. Osman¹, A. A. A. I. Ismail², A. H. Elduma³, E. S. Saeed⁴, M. E. Hamid ⁵

¹National Health Laboratory, Khartoum, Sudan, ²University ofBahri, Khartoum, Sudan, ³National Public Health Laboratory, Khartoum, Sudan, ⁴University of Khartoum, Sudan, Khartoum, Sudan, ⁵College of Medicine, King Khalid University, Abha, Saudi Arabia

Background: Brucellosis is an important zoonotic disease, which affect a variety of domestic and non-domestic animals and humans, causing high economic loss and public health burden especially in countries with no effective control programs.

Objectives: The objectives of the present study were to survey brucellosis and to determine risk factors among humans in occupational contacts with dairy cattle in suburban and peri-urban regions in Khartoum State, Sudan.

Methods and Materials: Using a serological method. Three hundred sixty two (n = 362) serum samples were collected from people in association with 11 farms in Khartoum State between August 2009 and February 2010. These farms have history of bovine brucellosis. Competitive ELISA (cELISA) was used to test serum samples as per standard criteria. A questionnaire was designed for data collection; collected data were analyzed using EPI Info statistical software.

Results: Out of the 362 serum samples 14 (3.9%) were positive for brucella infection using ELISA. Of the positive cases 13 (92.9%) were apparently healthy, but one (7.1%) was under treatment for brucellosis from a previous screening. Risk of brucella infection was noticed among the study group notably age group between 21 and 40 years (p = 0.02), males (p = 0.04), illiterate (p = 0.002), milkers (p = 0.03) and among those consumes milk and milk products (p = 0.04). A significant association was observed between the seropositivity and community living in association with brucella-infected livestock notably: illiterate males, middle age group (21–40 years) and consumers of raw milk and milk products are at risk of infection.

Conclusion: The threat of pathogen spillover and interactions between livestock and man are the potential hazards. The study identified males; middle age (21–40) and consumers of unpasteurized dairy products especially in endemic areas are at a significant risk of food-borne brucellosis.

22.072 Prevalence and presence of virulence associated gene profiles of *Streptococcus suis* in pigs and humans in upper northeast Thailand **T. C. Nutravong**¹, S. Angkititrakul², N. Panomai¹

¹Faculty of Public Health, Khon Kaen University, Khon Kaen, Thailand, ²Khon Kaen University, Khon Kaen, Thailand

Background: *Streptococcus suis* is a zoonotic agent that important causes severe infections in pigs and humans, for example meningitis, septicemia, septic shock, infective endocarditis and arthritis. *Streptococcus suis* serotype 2 is a frequent cause of diseades in pigs and humans worldwide including Thailand. In Thailand a lack of studies concerning epidemilogical serotype and virulence associated gene profiles in pig and huaman isolates in the same period of time was not reported. So our study collected data from pigs and humans during 2007 to 2012 and examined prevalence of capsular serotype and virulence associated gene by PCR method.

Objectives: To know the serotype and presence of virulence factors in disease strains from pigs and human being and compare to healthy pig isolates.

Methods and Materials: Our group gathered data by collecting of eleven diseased pig isolaes from the veterinary research and development center (uppermost northeast region) and thrity human isolates from the hospital of upper northeast Thailand including healthy pig isolates from slaughterhouse in upper northeast Thailand, then isolated and identified using biochemical test by Gottaschalk method, confirmed *S. suis* by PCR amplification of 16sRNA gene and detected virulence associated gene profiles by PCR method.

Results: This study found that three of *S. suis* serotype 2 which is from one septic arthritis, one meningitis and one brain infection, three of *S. suis* serotype 9 had brain infection and the less nontype (not serotype 1, 2, 7, 9) had heart, lung or brain infection was shown in diseased pig isolates. One *S. suis* serotype 2 and three *S. suis* serotype 7 presented in healthy pigs from slautherhouse of upper northeast Thailand. It showed that thrity of *S. suis* serotype 2 from 26 septilicemia and 4 meningitis was presented in all human isolates from upper northeast Thailand. Every *S. suis* serotype 2 in humans carried epf (87%), mrp (90%), and sly (90%) those more than in diseased or healthy pigs, 30% and 0% respectively.





Conclusion: These indicated that people may have a risk of infection with *S. suis* serotype 2 from diseased pigs.

SUNDAY • February 17, 2013

IMED 2013

22.073 Virulence determinants in clinical and non-clinical human and animal Arcobacter butzleri strains

K. Houf, L. Douidah Ghent University, Merelbeke, Belgium

Background: Interest for arcobacters in veterinary and human public health enhanced since the first report of the isolation of arcobacters from food of animal origin. Since then, studies worldwide have reported the occurrence of arcobacters on food and have highlighted the possible transmission of especially A. butzleri to the human population. To assess their clinical relevance for humans and animals, evaluation of potential virulence factors is required. However, up to now, little is known about the mechanisms of pathogenicity.

Objectives: Since their close affiliation to the foodborn pathogen Campylobacter and their similar clinical manifestation, the presence of nine putative genes (CadF, CiaB, Ci1349, HecA, HecB, IrgA, MviN, PldA, TlyA) previously described in Campylobacter and in the genome of the recently sequenced Arcobacter butzleri reference strain, was determined in a set of clinical and non-clinical Arcobacter butzleri strains.

Methods and Materials: Primers were designed for the detection of the different genes, and their specificity was verified by sequencing the amplicons and using dot-blot hybridization. In total, 108 A. butzleri isolates from humans and farm animals, previously identified and characterized at strain level, were examined.

Results: PCR analyses revealed that the genes CadF, CiaB, Cjl1349, MviN, PldA and TlyA were commonly present in all strains. The genes HecB, HecA and IrgA were present in respectively in 60,99%, 25.82%, 29,67% of the strains. An origin dependent pattern between human and animal strains or among animal strains was not detected.

Conclusion: Examination of A. butzleri strains by gene-specific PCR assays confirmed the potential pathogenicity of this species. As no origin relation in the gene distribution was observed, a specific animal reservoir for human infection was not identified.

22.074 Investigating the role of forages in acquired equine polyneuropathy

H. K. Telama, A.-M. Virtala, R.-M. Tulamo University of Helsinki, Helsinki, Finland

Background: Acquired Equine Polyneuropathy (AEP) is an emerging equine neurological disease, so far only documented in the Nordic countries. The main clinical feature is bilateral paresis of the hind limb extensor muscles, which in nearly 50% of the cases proceeds to recumbency and death. The etiology of AEP is still unknown. Our hypothesis isthat AEP is acquired through the ingestion of toxins in baled haylage or (unique to Finnish outbreaks) fresh cut grass.

Objectives: The objective of this study was to design and pilot an epidemiologic questionnaire that will enable us to collect data from outbreaks of AEP in Finland.

Methods and Materials: Two causal diagrams for AEP were constructed to model how AEP may be acquired from baled haylage and fresh cut grass. The causal diagrams were used to construct an epidemiologic questionnaire with 85 questions. Data were collected from ten outbreaks, involving nine farms with a total of 156 horses. The primary results were used to redesign an improved final questionnaire, using the University of Helsinki's online application E-lomake. Preliminary association between AEP and feeding haylage vs. fresh cut grass was studied using univariable logistic regression without accounting for farms as random effect.

Results: Of the ten studied outbreaks, seven occurred while feeding baled haylage and three outbreaks occurred while feeding fresh cut grass. The results support our hypothesis that AEP is associated with feeding baled haylage. Horses fed on baled haylage had five times higher odds of developing AEP than those fed fresh cut grass.

Conclusion: Feeding horses with baled haylage has become increasingly popular in Scandinavia in the past decade. It is thus important to better understand the relationship between baled haylage and AEP. This pilot study produced an epidemiologic questionnaire we can use to further study the role of forages in the etiology of AEP.



Sero-epidemiology of Coxiella burnetii in companion animals

S. Anastacio¹, K. Sidi-Boumedine², G. J. da Silva³ ¹University School of Vasco da Gama, Coimbra, Coimbra, Portugal, ²ANSES-Sophia-Antipolis Laboratory, Sophia Antipolis, France, ³Center of Pharmaceutical Studies, Faculty of Pharmacy, Coimbra, Portugal

Background: Q fever is a zoonotic infection that regained interest from health authorities during the recent large-scale human Q fever in The Netherlands. In a scientific opinion, EFSA highlighted some uncertainties that still exist about Q fever epidemiology, namely the scarce knowledge about the role played by domestic animals beyond ruminants

Objectives: This study aimed to investigate the seroprevalence of Coxiella burnetii, the causative agent of Q fever, in companion animals from the center region of Portugal.

Methods and Materials: A cross-sectional study was developed during the 2nd semester 2011. Blood samples were collected from pets attending veterinary clinics for routine procedures. Sera or plasma were tested for the presence of specific antibodies anti-C. burnetii using a commercial ELISA adapted for multi-species detection, using a multi-antispecies conjugate (LSIVET Ruminant Milk/Serum Q Fever®, LSI). Laboratory results were expressed in S/P values. Samples with an S/P% <50% were considered to be negative.

Results: A total of 97animals were sampled (dogs n=69; cats n=28). The infection rate was estimated in 1% (95% CI: 0-3%). Only one positive result was obtained (1/97) with an S/P of 97%, corresponding to a one-year-old female cat living in a rural area.

Conclusion: To our knowledge, this is the first study on C. burnetii infection among companion animals in Portugal. The rate of infection was very low, and inexistent in dogs' population, suggesting that household animals are not so exposed to the pathogen. However, hospitals treat (accept or receive) animals from different origins (rural areas, contact with livestock), and the potential zoonotic implications for owners and veterinarians is highlighted.

22.076 First report and molecular characterization of hepatitis E virus in renal transplant recipients in Brazil

A. M. Passos, T. P. Heringer, J. Medina-Pestana,

M. L. G. Ferraz, C. H. Granato

Federal University of Sao Paulo, Sao Paulo, SP, Brazil

Background: Hepatitis E virus (HEV) can cause acute and chronic hepatitis in organ transplant recipients. Serological evidence for HEV infection has been found among different population groups in Brazil and a single acute case has been confirmed. However, no cases of HEV infection in immunocompromised patients have been reported to date in Brazil.

Objectives: This study aimed at conducting a molecular identification and characterization of hepatitis E cases among renal transplant recipients in Brazil.

Methods and Materials: A retrospective study was carried out with 96 serum samples from renal transplant recipients with unexplained liver enzyme elevation from 1998 to 2007. HEV RNA was tested by RT-nested PCR and positive samples were submitted to direct sequencing. Human and swine HEV strains sequences for the same fragment were collected from public databases, and a phylogenetic tree was reconstructed by the neighbor-joining method, with Kimura 2-parameter model of nucleotide substitution, with MEGA v. 5.0.

Results: Three confirmed cases of HEV infection in the absence of seroconversion to HEV IgG antibodies were identified. The prevalence of HEV in this population was 3.1%. The analysis of the sequence of a 304-nucleotide fragment from the ORF2 genome region classified the HEV strains Brazilh2 (JX173928) and Brazilh3 (JX173929) within genotype 3. The HEV strains isolated in this study shared less than 88% homology to each other, to sequences of swine HEV previously

International Meeting on Emerging Diseases and Surveillance 2013

characterized in Brazil and other countries in Latin America, and to 3a-i sequences from databases; except from Brazilh3 strain, which shared 90% homology to Bolivian 3i sequences.

Conclusion: This first report of hepatitis E infection in renal transplant recipients in Brazil indicates that there may be a novel genotype 3 subvariant circulating in Brazil and that further investigation is needed to characterize the HEV circulating in this region. HEV infection should be considered as cause of abnormal liver tests of unknown origin in this setting.

22.077 Use of wild birds surveillance and GIS spatial analysis for determining predictive epidemiological patterns of future spatial dispersion of West Nile virus: The example of Greece

G. Valiakos¹, A. Giannakopoulos¹, K. Papaspyropoulos²,

P. Birtsas³, A. Touloudi¹, L. Athanasiou¹, C. Chadjichristodoulou⁴, V. Spyrou⁵, L. Petrovska⁶, C. Billinis¹

¹University of Thessaly, Karditsa, Greece, ²Hunting Federation of Macedonia and Thrace, Thessaloniki, Greece, ³Technological Education Institute of Larissa, Karditsa, Greece, ⁴University of Thessaly, Larissa, Greece, ⁵Technological Education Institute of Larissa, Larissa, Greece, ⁶Veterinary Laboratories Agency, New Haw, Addlestone, Surrey, United Kingdom

Background: From 2010 until nowadays, the largest European West Nile virus (WNV) disease outbreak takes place in Greece with more than 524 laboratory confirmed cases and 60 deaths.

Objectives: Our team has performed a study to evaluate exposure of wild birds to WNV, correlate results with human cases and discover environmental factors associated with the disease spread, creating possible spatial patterns of future dispersion. The results of the 2012 surveillance and analysis are presented.

Methods and Materials: A serological and molecular surveillance has been performed in serum and tissue samples from wild birds hunter-harvested, found dead and trapped in 2012 in various areas of mainland Greece. Results were correlated with human cases in 2012. Spatial analysis of previous years human cases and wild birds serosurveillance results was performed using GIS spatial data and multivariate statistics (2 step cluster analysis, logistic regression etc.) to correlate spatial distribution with various environmental factors.

Results: Seropositive sedentary wild birds were detected in areas that human cases were reported in 2012 (Attica, central Macedonia). No positive results were obtained in samples collected in Thessaly indicating a recession of viral circulation in an area of major incidence of WNV human cases in 2010 and 2011. Positive samples were obtained in the area of Thebes (no reported human cases) in 2012 indicating an active circulation of WNV in the area.

Multivariate statistical analysis showed that distance from permanent water and altitude are important attributes with a high positive correlation to WNV exposure in 2010 and 2011. Appliance of these attributes to unaffected areas of Greece revealed possible high risk areas of potential dispersion for 2012. This analysis was verified by 2012 results, as most human cases were reported in these referred areas.

Conclusion: Epidemiological analysis using GIS spatial data and wildlife surveillance results proves to be an invaluable tool for epidemiologic monitoring of a disease outbreak allowing even the prediction of possible dispersion patterns. An active surveillance program undertaken on sedentary wild birds could be added to active and passive surveillance focused on humans and horses greatly helping in evaluating and dealing with future outbreaks linked to flaviviruses.

22.078 An Interesting Case Of Eosinophilic Meningitis D. Madi¹, B. Achappa¹, S. Pai²

¹Kasturba Medical College (affiliated to Manipal University),

Mangalore, Karnataka, India, ²manipal university, Mangalore, India

Background: Eosinophilic meningitis is defined as the presence of ≥ 10 eosinophils/mL in CSF or at least 10% eosinophils in the total CSF leukocyte count. Angiostrongyliasis, Gnathostomiasis, Toxoplasmosis, Neurocysticercosis, lymphoma and medications can produce eosinophils in the CSF.

Angiostrongylus cantonensis is one of the causative agents of eosinophilic meningitis. Humans get infected when they ingest raw or partially cooked snails or monitor lizard (Varanus bengalensis). Monitor lizards are eaten in parts of southern India where their meat is considered an aphrodisiac.

Objectives: We describe a case of eosinophilic meningitis due to Angiostrongylus cantonensis (rat lungworm) following ingestion of monitor lizard.

Methods and Materials: Case report—A 16-year-old boy presented to us with altered sensorium of one day duration. He had fever, headache and vomiting for 7 days prior to hospital admission. History of diplopia was present. There was no history of seizures. On examination he was febrile. Central nervous examination showed bilateral lateral rectus palsy, left third nerve palsy, and neck stiffness.

Results: MRI brain showed multiple cortical and subcortical hyperintensities. CSF analysis showed cell count—620 (per μ L), DC–(of 100 cells counted); Eosinophils–70%, Lymphocytes–30%. CSF protein–62 (mg%),CSF glucose–92 (mg%). Gram stain, Ziehl Neilsen stain, and culture of CSF were negative. CSF wet mount showed larval form of Angiostrongylus cantonensis (Figure 1).

He gave history of consumption of raw meat of monitor lizard 10 days before the onset of symptoms. An immunologic study was not done as it is not available in our state. He was treated with oral Albendazole and Prednisolone for 2 weeks. His symptoms improved gradually within two weeks from his admission.



Figure 1. Larval form of Angiostrongylus cantonensis.

Conclusion: Eosinophilic meningitis due to Angiostrongylus cantonensis should be suspected in all patients who present with headache and vomiting after eating monitor lizard.





9 Coxiella burnetii in small ruminants: Assessing the public health risk

T. Dewé¹, A. Nigsch², K. Stärk³

¹Royal Veterinary College, London, United Kingdom, ²Amt der Vorarlberger Landesregierung, Bregenz, Austria, ³Royal Veterinary College, North Mymms, United Kingdom

Background: *Coxiella burnetii* causes Q fever, a zoonosis that can have serious consequences. Most human cases are associated with small ruminant parturition, as was the case in the large Netherlands outbreak of 2007-2010. This outbreak prompted assessment of the Q fever risk in Switzerland, where small ruminants live in close proximity to people.

Objectives: To assess the risk of acute Q fever attributable to small ruminant-associated *C. burnetii* in Switzerland.

Methods and Materials: Risk pathways were defined (Figure 1) according to the OIE framework, and the model was developed using Palisade @RISK Version 5.7. The most influential input parameters were determined by sensitivity analysis and significant uncertainties were identified.



Figure 1. Pathways for assessment of the public health risk of small ruminantassociated Coxiella burnetii (Cb).

Results: Goat flocks were shown to represent a greater risk of *C. burnetii* shedding than sheep flocks: mean annual probability of shedding was 0.083 [95% confidence intervals: 0.002-0.182] and 0.031 [0-0.094], respectively. The number of *C. burnetii* released by an infected sheep or goat flock was estimated to be up to 13 \log_{10} organisms, resulting in a very large exposure dose if direct contact occurred.

The mean probability of symptomatic Q fever resulting from close contact with sheep was 0.006 [0-0.029]; with goats, 0.016 [0-0.057]. This translated to 79 [0-384] and 139 [0-491] acute cases in sheep and goat farmers annually. The mean annual probability of airborne infection ranged from 0.007 [0-0.030] for people within 100 metres of a goat flock, to essentially zero at 5 kilometres away.

The model was most sensitive to the *C. burnetii* concentration in small ruminant placental tissue. Other influential inputs were the within-flock shedding prevalence, flock infection prevalence, and flock size.

Conclusion: To our knowledge, a quantitative assessment of the public health risk of livestock-associated *C. burnetii* has not previously been performed. Q fever has rarely been reported in Switzerland, however, this study indicated that the risk of acute symptomatic infection is non-negligible. Differences may be due to under-reporting, or model over-estimation because of parameter uncertainty. The identification of key parameters allows prioritisation of future research that would reduce uncertainties, thereby allowing more accurate quantification of the public health risk, and ultimately, investigation of control measures.

22.080

Study of *Giardia duodenalis* in rodents from the Canary Islands (Spain) and the possible role in the transmission of zoonotic genotypes

A. Fernandez-Alvarez¹, A. Martín-Alonso¹, N. Abreu-Acosta²,

C. Feliu³, B. Valladares¹, P. Foronda¹

¹University Institute of Tropical Diseases and Public Health of the Canary Islands, University of La Laguna, Santa Cruz de Tenerife, Spain, ²Analytical Biotech, Santa Cruz de Tenerife, Spain, ³Laboratory of Parasitology, Faculty of Pharmacy, University of Barcelona, Barcelona, Spain

Background: *Giardia duodenalis* is a flagellated parasite, considered one of the most common causes of protozoal diarrhea in both humans and animals worldwide. Molecular analysis of isolates from the different host species has revealed the presence of eight different *G. duodenalis* assemblages (A–H) of which only assemblages A and B are of zoonotic importance. These genotypes have been detected in a wide range of mammalian hosts, including humans. At present, there is no information about the occurrence of *Giardia* in rodents on the Canary Islands (Spain).

Objectives: The present study aimed to obtain data on the infection occurrence and the potential zoonotic role of rodent isolates of *G. duodenalis* in the seven islands and two small islets of the Canary Islands.

Methods and Materials: For this study, stool samples were collected from 284 wild rodents (116 *Rattus rattus*, 3 *Rattus norvegicus* and 165 *Mus musculus domesticus*) and *Giardia* cysts were detected by light microscopy after sedimentation. Positive samples were further characterised based on an assemblage-specific PCR targeting the triose phosphate isomerase (tpi) gene and sequenced.

Results: The overall prevalence of giardiasis was 25.4% and ranged from 19.4% in El Hierro island to 34% in Gran Canaria island, highlighting the high infection rate of *G. duodenalis* in rodents in the Canary Islands. The nucleotide sequences obtained showed the presence of two assemblages of *G. duodenalis* in the Archipelago, being one of them a zoonotic assemblage. Furthermore, the assemblage G was found in all the islands, and the sequencing revealed a new subgenotype both in *R. rattus* and *M. m. domesticus*, showed consistent mutations at specific positions, some of which were not characterized previously.

Conclusion: This finding is of relevance from the public health point of view, considering the health risk that implies the presence of a zoonotic assemblage in rodents from a rural area in La Palma island. On the other hand, a new haplotype widely distributed in the Archipelago is described.

22.081 Key determinants of vulnerability to Zoonotic Cutaneous Leishmaniasis in central Tunisia

H. Bellali¹, A. Mrabet², S. Ennigrou¹, N. Ben Alaya³, S. Dridi⁴, N. Achour⁵, **M. K. Chahed¹**

¹Medical university of Tunis, Tunisia, ²Health Military Direction, Tunis, Tunisia, Tunis, Tunisia, ³ Ministry of Public Health, Tunisia, Tunis, Tunisia, ⁴Ministry of Public Health, Tunisia, Tunisi, Tunisia, ⁵National Observatory of New and Emerging Diseases, Tunis, Tunisia

Background: In Tunisia, Zoonotic Cutaneous Leishmaniasis (ZCL) is an emerging vector born disease since 1982. This scarring disease, caused when *L. major* parasite is transmitted by sandfly bites.

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: The aim of this study was to identify the population at risk for ZCL in order to seek and discuss possible solutions to reduce the incidence in the vulnerable population and diminish the importance of its social impact.

Methods and Materials: An exhaustive cross-sectional survey was carried out in July-August 2009 in Sidi Bouzid, collecting informations about families living in the endemic area such as irrigation activities, animal's shelters, and the number of years living in the area. An active epidemiological surveillance of new human cases has been in place since July 2009. To determine the population at risk for ZCL, we compared those who contracted the disease during the study period (July 2009-June 2012) with people living in the same area and who have never presented ZCL lesions.

Analyzes were performed with SPSS 11.5. Chi2 and Fisher's exact tests were used to compare proportions and Student's T test was used to compare means. Multivariate analysis was conducted using backward logistic regression. All variables with significance level less than or equal to 20% in univariate analysis were included in the multivariate model. The significance level was fixed at 5%.

Results: A total of 7837 individuals were included in the study, the median age was 28 years, and females were 50%. Three hundred and sixty one new cases were notified between July 2009 and June 2012, the median age was 12 years, 64% were children (<20 years) and 52% were females. Children were most vulnerable to ZCL. Low education level seems to be associated with high risk of ZCL. Families who have irrigation wells and live near animal shelters were at risk of the disease more than others. The risk of contracting ZCL decreases with the number of years living in the endemic area.

Conclusion: Risk factors of ZCL are demographic, professional and socio-economic as education level, rural residential area, agricultural activities. Eradication of the disease or at least the prevention of epidemics should be based on the participation of the local population and involvement and accountability of all institutions.

22.082 Characterization of genetic diversity of *Brucella* isolates from South East Asia

K. K. Tan, L.-Y. Chang, S. S. Nor'e, F. L. Jafar, S. AbuBakar University of Malaya, Kuala Lumpur, Malaysia

Background: Brucellosis is a zoonotic bacterial disease of a wide range of animals. It is caused by a number of Brucella species. Humans can acquire infection either through direct (occupational activities) or indirect (ingestion of unpasteurized dairy product) exposure to the infected animals. Though brucellosis occurs widely in South East Asia, currently, there is very limited information on the specific Brucella strains that caused the infections. Two Brucella isolates, BM200501 and BM201201, were recovered at the University Malaya Medical Center in 2005 and 2012. The later isolate was from a patient who acquired the infection from a dairy farm in Philippines (BM201201).

Objectives: The aim of our study is to infer the phylogenetic relationships of the Brucella species isolated from South East Asia (Malaysia and Philippines) with other Brucella strains available in the Genbank.

Methods and Materials: Brucella isolates were cultured on Brucella broth and DNA was extracted for genome sequencing. All sample handling was done in a BSL-3 biocontainment laboratory of the Tropical Infectious Disease Research and Educational Center (TIDREC), University of Malaya. The whole genome of the Brucella isolates was sequenced using the Ion Torrent PGM[™] sequencer. The genomes were assembled against the reference genome sequence obtained from the Genbank. The phylogenetic relationship of the Brucella species was established using the complete sequence of the OMP2a, OMP2b and OMP25 genes.

Results: Phylogenetic analysis performed using concatenated sequence of complete OMP2a, OMP2b and OMP25 genes showed that the Brucella species formed well-separated clusters similar to that previously described using other genes. Using these genes, the BM200501 and BM201201 isolates examined in this study showed high sequence similarities and phylogenetically clustered in a distinctive clade with B.melitensis isolated from China (M28 and M5-90) and Turkey (ATCC23457).

Conclusion: Finding from the study suggests that the *B.melitensis* isolated from Malaysia and Philippines shared high sequence similarity at the OMP2a, OMP2b and OMP25 genes to those previously isolated from China and Turkey. This suggests the possibility that the B.melitensis species from the different endemic regions may share a common ancestral lineage.

22.083

Risk factors associated with cutaneous leishmaniasis en Chontalpa, Tabasco, México

G. Carrada¹, B. Cadena¹, V. Leal², B. Sanchez³, A. Jimenez⁴, I. Becker⁵

¹Universidad Juárez Autónoma de Tabasco, Villahermosa, Tabasco, Mexico, ²Secretaría de Salud del Estado de Tabasco, Villahermosa, Mexico, ³Universidad Juarez Autonoma de Tabasco, Villahermosa, Mexico, ⁴Universidad Juárez Autónoma de Tabasco, Villahermosa, Mexico. 5Universidad Nacional Autónoma de México. México DF. Mexico

Background: During the period 1990-2011, 18 547 cases of leishmaniasis were reported in Mexico, of which 6 944 (37.4%)were in Tabasco State, in the southeast of Mexico. Most cases occurred in the Chontalpa Region, that was inhabited by the Olmec Culture, one of the most important pre-Columbian cultures of Mesoamerica. The Chontalpa Region comprises five municipalities: Cunduacán, Cárdenas, Comalcalco, Huimanguillo and Paraíso. In this region there are many cacao and other tropical plantations. We believe that in this region the cacao plantations are a risk for transmission therefore we decided to study this risk factor and other environmental factors, as well as those related to human behavior.

Objectives: identify risk factors associated То with cutaneous leishmaniasis in Chontalpa, Tabasco

Methods and Materials: We performed a survey of case-control studies in Cunduacán, Tabasco. The sample size was 41 patients with cutaneous leishmaniasis and 82 healthy controls. We conducted a survey to identify environmental and human behavioral risk factors. OR, 95%CI were calculated for these factors.

Results: Environmental risk factors associated were: previous cases in the house (OR 3.76, 95%CI 1.59-8.87), cats inside (OR 4.64, 95%CI 1.58-13.69) or outside (OR 3.44, 95%CI 1.35-8.73) the house, banana plantations (OR 5.87, 95%CI 2.59-13.33) gardens (OR 3.61, 95%CI 1.15-11.26) and rodent (OR 2.59, 95%CI 1.19-5.65) around the house. Human behavioral risk factors associated were: working in cacao plantation (OR 3.35, 95%Cl 1.35-8.28), there remain more than four hours (OR 2.52, CI95% 1.06-5.98), outdoor bathroom (OR 2.21, 95%CI 1.03-4.73) and take a shower after 18 hours (OR 2.35, 95%CI 1.05-5.26). Protective factor found is: presence of poultry (OR 0.44, 95%CI 0.20-0.95).

Conclusion: This study determined risk factors that had not been reported before, these allow to analyze the transmission mechanisms that exist in this area. It will develop strategies for the control of leishmaniasis in the area. Risk factors will be known to the people of rural communities to take protective measures to prevent the transmission of leishmaniasis

22.084 Disseminated cutaneous leishmaniasis in Tabasco, México

G. Carrada

Universidad Juárez Autónoma de Tabasco, Villahermosa, Tabasco, Mexico

Background: Disseminated cutaneous leishmaniasis is a chronic form of leishmaniasis caused by Leishmania mexicana in México, characterized by multiple, slowly progressive nodules or plaques without ulceration, involving almost the entire body.

Objectives: To describe the clinical characteristics of four cases of disseminated cutaneous leishmaniasis in the Chontalpa Region, Tabasco, Mexico.

SUNDAY • FEBRUARY 17, 2013

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: We report four cases of disseminated cutaneous leishmaniasis from Chontalpa Region, México. Clinical features of disseminated cutaneous leishmaniasis were studied. The lesions were photographed and described

POSTER PRESENTATIONS II

Results: We present four cases of disseminated cutaneous leishmaniasis due to Leishmania mexicana: 1.A 58-year-old man with an evolution time of 21 years, DCL characterized by multiple nodular nonulcerated lesions, diffuse infiltration and hyperpigmentation in some areas of the trunk and face, absence of mucosal involvement. He had some ulcerated nodules on dorsal surface of fingers with impaired function. 2. A 64-year-old man with an evolution time of 20 years, with diffuse infiltration on the face, trunk and extremities, multiple nodules of up to 3 cm, ulcerated in the face, fingers and feet. He had a squamous cell carcinoma in a chronic lesion located in his right nasal ala, with metastasis to the neck. 3. A 65-year-old man with an evolution time of 2 years, characterized by multiple nodules on the nose and malar region, the right elbow and few on the trunk. 4. A 25-year-old woman with an evolution time of 18 years, with multiple hyperpigmented and infiltrated plaques, and with irregular diffuse edema in body. Multiple scattered 1-2 cm sized nodular lesions, some of them secondarily ulcerated, but more closely clustered over the dorsa of the hands, lesions with residual fibrosis, causing functional disability of the fingers and wrist (inward-curling fingers). All patients have had some degree of nasal obstruction and were refractory to treatment, so that the chemotherapy produced only transient improvement of clinical disease.

Conclusion: DCL occurring in Tabasco is incurable and can be incapacitating and disfiguring, and can cause functional disability in the hands and feet. The disease affects face and limbs more often in the early stages, but in later stages can involve all skin.

22.085 Human rabies confirmed cases reported to Brazil National IHR Focal Point from March 2006 to June 2012

S. Lopes Dias¹, E. T. Masuda¹, M. É. Santos¹, W. A. Oliveira¹, P. Pereira Vasconcelos de Oliveira², G. S. Dimech³

¹Brazilian Ministry of Health, Brasilia, DF, Brazil, ²Brazilian Ministry of Health, Brasilia, Brazil, ³Brazilian Ministry of Health, Brasilia, DF, Brazil

Background: The Center for Strategical Information and Response in Health Surveillance (CIEVS/National) of Secretariat of Health Surveillance (SHS) of Brazilian Ministry of Health (MH) represents Brazil National IHR Focal Point and continuously monitors events that may constitute public health emergencies based on International Health Regulations (IHR, 2005) risk assessment.

Objectives: To describe the human rabies confirmed cases in Brazil from March/2006 to June/2012 and their risk classification.

Methods and Materials: A descriptive study about human rabies confirmed cases reported to CIEVS/National using the database of Events Monitoring System (SIME).

Results: In the study period, CIEVS/National received 40 notifications of human rabies events, of which 15 (37,5%) were confirmed, 24 (60%) discarded and one (2,5%) inconclusive. The mean number of events reported to CIEVS/National was 7 cases/year, ranging from 3 to 9 cases/year, of these, 65% the source of notification was the technical area of the SHS/MH, 23% CIEVS/State, 5% the technical area of State and 7% others. Of the confirmed cases, 14 (93%) progressed to death and 1 (7%) to healing; as to gender, 8 (53%) were male, 4 (27%) female and 3 (20%) had no information; the mean age and median age were, respectively, 20 and 15 years old, ranging from 9 to 58 years old; for 9 (60%) cases, the aggressor animal was the dog, 4 (26%) the bat, 1 (7%) the cat and 1 (7%) the marmoset; 12 (80%) of cases occurred in the northeast region of the country. Although endemic in Brazil, at a differentiated degree according to the geopolitical region, human rabies is of immediate compulsory notification and requires integration between medical assistance and epidemiological surveillance for its control. However, the human rabies events notified to CIEVS/National were classified as National Public Health Risk.

Conclusion: It is essential to continuously improve the processes of integrated work between CIEVS and the competent technical units to ensure the timely notification in the three Brazilian Public Health Unified System (SUS) management spheres and their investigation within 72 hours to allow the adoption of control measures.

22.086 How does Rhodesian sleeping sickness affect rural households? Results from a qualitative study in Uganda

K. L. Bardosh

University of Edinburgh, UK, Edinburgh, United Kingdom

Background: Rhodesian sleeping sickness is a deadly parasitic zoonosis. The disease is responsible for a large estimated DALY burden in East Africa among poor, rural households.

Objectives: Despite the interconnections between neglected diseases and poverty, few burden assessments go beyond an econometric DALY estimate to elucidate the multiplier effects of illness on patients and their households as situated within its social context. This study provides an analysis of the multiplier effects of Rhodesian sleeping sickness infection in Uganda and explores the relevance of such qualitative studies in complementing DALY approaches.

Methods and Materials: The study combined structured interviews with previously diagnosed patients (n=98) and participatory techniques in 6 endemic villages carried out in late 2010.

Results: Acquiring trypanosome infection, delayed health-seeking behaviour and the variety of observed coping strategies were found to be mediated by the high poverty rate in the area. The study observed that the most dramatic multiplier effects of illness were on agricultural productivity, food security, income generation activities, the education of children and long-term mental and physical health. On average sleeping sickness infection was found to cost the equivalent of 70% of a household's annual income in terms of treatment costs and losses in revenue. A high rate of permanent disability was also associated with sleeping sickness: out of the 98 selected patients, 29 suffered from various physical disorders, 7 suffered major mental disability and 4 suffered from severe paralysis of a leg or arm. For the 15 death cases involved in patient interviews, medical costs, loss of income during illness and burial expenses were equivalent to 150% of the household's annual income. The burden of the disease, however, extended beyond these financial costs to include a number of less quantifiable, livelihoodrelated consequences.

Conclusion: Qualitative studies on patient experiences of neglected diseases offers an avenue to explore facets of burden that are unexplored in DALY studies. This study shows that Rhodesian sleeping sickness is a major factor perpetuating a cycle of poverty among effected rural, resource-poor households in endemic areas. As a poverty reduction strategy, policymakers, donors and local government in Uganda should remain committed to sleeping sickness elimination.



Austria's role in the Europe-wide outbreak of the emerging Salmonella Stanley strain since 2011

E. Kanitz¹, S.-W. Jian¹, S. Maritschnik¹, E. J. Simons¹, C. Kornschober², F. Allerberger¹, D. Schmid¹

¹AGES, Vienna, Austria, ²Austrian Agency for Health and Food Safety, Graz. Austria

Background: Until mid-2011, few Salmonella (S.) Stanley cases occurred in Europe related to travel mainly from Asia. In Europe, no regulations for S. Stanley contaminated productive livestock or animal products exist to date.

Objectives: In July/2012 ECDC launched an investigation following an increase of autochthonous S. Stanley cases in seven EU countries including Austria, to describe the outbreak and to identify the animal reservoir(s) in the EU.

Methods and Materials: A confirmed outbreak case was defined as a person with Nx-monoresistant S. Stanley infection since begin of 2011 without travel history outside Europe, and with a PFGE-profile identical to the "Belgian strain". A probable case fulfilled the above criteria without PFGE-profile available. Data on S. Stanley positive human and non-human samples were provided by the Austrian National reference center. AGES investigated a local 2011-outbreak by microbiological investigation and a local 2012-outbreak by a case-cohort study.

Results: Between July/2011 to mid-October/2012 178 outbreak cases (107 confirmed) were identified in 8/9 Austrian provinces;

International Meeting on Emerging Diseases and Surveillance 2013

59 in 2011 and 119 in 2012. The only Austrian turkey hatchery tested positive for the Belgian strain between June/2011 to June/2012. The eggs originated from a Hungarian parental flock farm, which also tested positive for the Belgian strain. Hatchlings were distributed to 104 fattening farms in Austria-in eight the Belgian strain was detected at least once since July/2011-and to other ten European countries. The local 2011 outbreak (32 cases) was associated with turkey kebab and traced back to a S. Stanley positive turkey fattening farm. The local 2012 outbreak (54 cases) was associated with grilled chicken (OR= 37.54; 95%CI 8.77-329.29) and potato salad (OR=17.47; 95%CI 6.06-60.39) offered at a village party.

Conclusion: We hypothesize that the potatoes salad was contaminated with S. Stanley during concurrent preparation of turkey meat by the village party caterer, and the grilled chicken was contaminated during serving. The Austrian turkey hatchery tested S. Stanley negative after June 2012, therefore no contaminated turkey flocks are expected to be alive after November 2012. A decline in human cases has been observed since October 2012. We conclude that the majority of the Austrian S. Stanley cases are due to the turkey food chain.

22.088 Changing patterns of Puumala hantavirus outbreaks in Baden-Württemberg 2007–2012

C. Wagner-Wiening, I. Boone, G. Pfaff

Baden-Wuerttemberg State Health Office, Stuttgart, Germany

Background: In 2012, an outbreak of Puumalavirus (PUUV) infections occurred in Baden-Wuerttemberg (BW). The reservoir of PUUV is the bank vole (Myodes glareolus). Climate factors and fructification intensities of decidious trees in previous years correlate with bank vole population density and with the occurrence of PUUV outbreaks in endemic regions.

Objectives: We compared epidemic characteristics and concurrent environmental factors observed in the 2012 PUUV outbreak with earlier outbreaks in 2007 and 2010 in order to explore potential predictors for PUUV outbreaks in Southwest Germany.

Methods and Materials: PUUV infections meeting the national case definition and notified in BW in the years 2006-2012 were extracted from the State database of reportable diseases. The outbreak periods were defined as PUUV cases notified from October of the preceding year to November of the following year (2006/2007; 2009/2010; 2011/2012) in BW. Climate und beech mast data were obtained from the Forest Health Monitoring Report for BW.

Results: A total of 1072 PUUV cases were reported 2006/2007, 1035 cases 2009/2010 and 1849 cases 2011/2012.

Cases were predominantly male (range 71-77%) and between 20 and 60 years old (80%). The epidemic curve of the 2011/2012 PUUV outbreak showed an early increase of cases as of October 2011, followed by a continuous rise, and a peak in April. Outbreaks in 2007 and 2010 started slower and peaked one month later in May/ June. The hospitalisation rate increased from 48% in 2006/2007 and 61% in 2009/2010 to 65% in 2011/2012. Five counties with 19% of the population of BW located in a hantavirus-endemic area lining the Swabian Alb mountain range contributed 50% of all cases. Autumnal beech mast events preceded all outbreaks.

Conclusion: Repeated PUUV outbreaks indicate high endemicitiy of this zoonosis in parts of BW. The rising case burden underlines the public health importance of PUUV infections in endemic areas. The influence of climatic and biological factors on the dynamics of human PUUV outbreaks remains poorly understood and warrants further interdisciplinary research. Beech mast events in conjunction with an autumnal increase in human PUUV cases are candidate predictors for PUUV outbreaks in the subsequent year, and may help to guide decisions on public health communication.

I. Mendez¹, A. Rodriguez², D. Pachón³, L. Cabrera⁴ ¹Universidad Militar, Bogota D.C., Cundinamarca, Colombia, ¹Universidad Militar, Bogotá D.C., Colombia, ¹Universidad Militar, Bogota D.C., Colombia, ¹Universidad de la Salle, Bogota D.C., Colombia

Background: Leptospirosis is a zoonotic infection caused by serovars of the genus Leptospira, present mainly in the renal tubules of reservoirs such as rodents, dogs, cattle, pigs, among others. Transmission occurs by direct or indirect contact with secretions, or material contaminated with the urine of these reservoirs. The clinical presentation in humans is asymptomatic, mild (90%) and severe or Weil syndrome (5-10%).

The spread in tropical areas is favored by environmental conditions such as humidity, temperature and rainfall. The incidence of this disease is related to occupational risk activities in contact with animals (veterinarians, farmers, slaughterhouse workers, rural workers and farmers)

Objectives: This study aimed to determine the seroprevalence of Leptospira in students of a Faculty of Veterinary Medicine in Bogotá.

Methods and Materials: Descriptive and observational study for establishing the seroprevalence against Leptospira by the IgM ELISA and microagglutination in 455 veterinary students.

Sera were tested using an ELISA kit IgM, positive samples were subjected to microagglutination against six serovars (hardjo, pomona, canicola, tarassovi, bratislavae, icterohaemorrahagiae)

Results: 7.7% (35/445) were positivity by ELISA, of 42 samples that were subjected to agglutination, positivity was obtained in 34 of them at least for one serovar.

Demographics: 16-45 years with a mean of 21.3 years, by gender: 224 (50.3%) men, 221 (49.7%) women, 72.6% from Bogota. 441 students (99.1%) reported contact with animal secretions, 78 rodents (17.5%), 429 (96.4%) with dogs, 355 (79.8%) with cattle, 312 (70.1 %) with horses, and less than 15% with other species such as pigs, poultry, sheep and goats, and 89.4% of subjects had contact during his training.

Symptoms: fever (25.1%), joint pain (20.4%), muscular pain (30.8%), headache (59.6%), jaundice (3.8%), retroauricular pain (5%), suffusion (11.3%) and burning urination (7%).

Conclusion: This study demonstrates the usefulness of serological diagnosis in individuals with occupational risk for leptospirosis.

Seropositive subjects reported having had any contact with animals or secretions; highlight exposure for one or more than one serovar.

We suggest that serological test have good correlation and can be used in screening populations at risk (35 by ELISA versus 34 positive confirmed by MAT).

Finally, stand out the importance of use of protective barriers by veterinary students.

22.090 Ecohealth assessment on poultry production cluster (PPC) in West Java Indonesia-Focus on biosecurity

E. Basuno¹, N. Ilham¹, E. Martindah², Y. Yusdja¹

¹Indonesian Center Agriculture Socio Economic and Policy Studies (ICASEPS), Bogor, West Java, Indonesia, ²Indonesian Research Center for Veterinary Sciences (IVETRI), Bogor, Indonesia, Bogor, West Java, Indonesia

Background: Study on eco-health assessment on Poultry Production Clusters (PPCs) is on-going and qualitative survey was carried out to better understanding of PPC. PPC was established by partnership between company and farmers with no risk involve on farmers' side. A good economic return experienced by farmers partly from selling products in the form of chickens and manure. Manure application for fertilizer without composting, which could have impacts on public health, especially food-borne disease such as salmonella. In such partnership, company facilitates bio-security application to control infectious

IMED 2013

diseases. Bio-security is the product of all actions undertaken by an entity to reduce the risk of transmission of infectious diseases and to prevent introduction of disease agents into a specific area. Chickens are vaccinated against Newcastle Disease, Infectious bronchitis (IB), Avian Influenza (AI) and Infectious Bursal Disease (IBD). ND is the most alarming disease and become the priority to manage.

Objectives: Assessment on bio-security in the cages has been conducted in the study sites to determine the practice of farmers in implementing bio-security and to assess the level of bio-security.

Methods and Materials: For this purpose, 14 standard parameters previously used by IDRC's control measures study was applied and 20% randomly selected cages were observed.

Results: Results showed that farmers did not apply biosecurity standard operational procedures (SOP) as required. This was reflected in the bio-security level which only 19 in Subang, while in Ciamis, 9,97 and 7,40 in Sukadana and Baregbeg sub-districts respectively, out of 42 point. Company provides disease preventions through vaccination program and provides feed supplements and antibiotic. PPC has negative impacts on environment as unpleasant odor and flies are a direct interference perceived by villagers. Such negative impacts, should become the concern of both company and farmers.

Conclusion: Chicken business in PPCs will continue if company and farmers manage both flies and odors better and vice versa. It is recommended that farmers have to follow some basic principles of biosecurity, at least to keep poultry in good condition, and to keep poultry in a protected environment. In addition, government should give more attention to PPCs that basically provide income for rural communities.

22.091 Detection of imported case of tick-borne encephalitis in the UK (ex Sweden)

R. Hewson

Centre for Emergency Preparedness & Response, Salisbury, United Kingdom

Background: The Rare and Imported Pathogens Laboratory (RIPL) at HPA-Porton is a national and international reference centre for viral haemorrhagic fevers and arboviral zoonoses.

In August 2012, a 29-year-old UK resident returned from a two week trekking holiday to Southern Sweden, where they received numerous tick bites. The patient developed a fever and severe headache, and presented at the local Accident and Emergency (A&E) department. They were treated empirically with doxycycline for suspected Lyme disease and discharged.

Although symptoms of disease subsided initially, they returned approximately one week later along with severe confusion and dysphasia. The patient again sought medical attention, and samples were sent to RIPL for analysis with a suspect diagnosis of Lyme disease

Objectives: To ascertain whether samples were PCR positive for TBR virus.

Methods and Materials: Patient samples were tested against a panel of published and in-house molecular and serological assays to identify the causative agent of disease. Based on patient information provided, samples were tested for Lyme disease, West Nile, Sindbis, sandfly fever and Tick-Borne Encephalitis (TBE).

Results: Samples tested negative for Lyme disease, West Nile, Sindbis and sandfly fever via serological techniques. TBE serology was positive in serum and CSF indicating generation of reactive antibodies; however these data alone are not indicative of TBE infection due to the cross-reactive nature of anti-flavivirus antibodies. TBE RNA was detectable in a patient serum sample using both primary (published) and secondary (in-house) TBE specific real-time PCR assays.

Conclusion: A combination of serological techniques and specific real-time PCR confirmed that the patient had acquired TBE. Sequence analysis of viral RNA indicated that a European subtype of Tick-Borne Encephalitis was the causative agent of disease. This represents the first confirmed report of TBE imported into the UK this millennium, although it is likely that this is an underrepresentation of the true incidence of disease.



Serologic evidence of Crimean-Congo hemorrhagic fever virus infection in Hungary

V. Németh¹, M. Oldal¹, G. Kemenesi², M. Gyuranecz³, K. Kvell², N. Kalvatchev⁴, H. Zeller⁵, K. Bányai⁶, F. Jakab⁷

¹University of Pécs, Pécs, Hungary, ²University of Pecs, Pecs, Hungary, ³Hungarian Academy of Sciences, Budapest, Hungary, Budapest, Hungary, ⁴National Centre of Infectious and Parasitic Diseases, Sofia, Bulgaria, ⁵Institut Pasteur, Unité de Biologie des Infections Virales Emergentes, Lyons, France, ⁶Veterinary Medical Research Institute, Budapest, Hungary, 7University of Pécs, Pécs, Baranya, Hungary

Background: Crimean-Congo hemorrhagic fever virus (CCHFV) is a typical tick-borne pathogen that causes an increasing number of severe infections in many parts of Africa, Asia, the Middle East, the Balkans as well as in some other parts of Europe. The virus is transmitted primarily by Hyalomma spp, and the spectrum of natural hosts for CCHFV is broad including wild and domestic animals.

Objectives: Although, the presence of CCHFV was hypothesized in Hungary, no significant research activity has been carried out in the past thirty years.

Methods and Materials: In the present study we have developed two validated antibody detection assays, an enzyme-linked immunosorbent assay (ELISA) and an immunofluorescence assay (IFA), both using recombinant CCHFV nucleoprotein (rNP) as antigen.

Results: A total of 198 serum samples collected from European brown hares (Lepus europeus) in the surrounding area of Dévaványa village between 2008 and 2009 were tested parallelly with ELISA and IFA. Out of the 198 samples 12 (6%) were positive for IgG antibody against CCHF virus by both methods. Four samples were positive with IFA and one serum was positive with ELISA only. 181 samples were negative, therefore, the homology was 71% between the two tests. Our findings nicely complement historic observations that endemic foci of CCHFV are present in the country.

Conclusion: The antibody detection methods we developed will enable us to perform large-scale surveillance that should help us to gain a clearer picture of the epidemiology, ecology and public health risk of CCHFV infections in Hungary.

22.093 Human and canine dirofilariasis in Greece: An emerging second main focus

E. Vassalou, C. Vassalos, G. Spanakos, A. Mpimpa, V. Kontos, N. Vakalis

National School of Public Health, Athens, Greece

Background: Human dirofilariasis due to Dirofilaria repens is a rare infection considered to be an emerging neglected zoonosis. In Greece, only 27 human D. repens infection cases had been reported in the literature up to the year 2000. Greece's northern part has been described as a canine D. repens-affected area (Vakalis NC, Himonas CA. Human and canine dirofilariasis in Greece. Parassitologia 1987; 39:389-391)

Objectives: This study presents a look at the locations of origin of human *D. repens* infections detected in Greece over the recent 10-year period and the canine D. repens-affected areas in the country.

Methods and Materials: We studied the areas of origin of human D. repens infection cases diagnosed in the Department of Parasitology, National School of Public Health, Greece from mid-2002 to mid-2012. Further, we reviewed the locations of origin of published human dirofilariasis (D. repens) cases reported in the country over the same period. Results from the first phase of an ongoing canine health survey, conducted in different Greek regions in 2002-2007, were also available.

Results: Most (9/15; 60%) cases of human D. repens dirofilariasis, recorded in Greece during the study period, originated from the country's western part (Figure 1). The main canine D. repens-affected areas were North Greece and West Greece, with D. repens-infected dog population ranging from 0% to 16.3% and 13.1% to 14.3%, respectively (Figure 2). In Greece's east and south regions of zero prevalence of canine infection by D. repens, no human D. repens infection took place.

International Meeting on Emerging Diseases and Surveillance 2013



White pattern filled pins; cases detected in the Department of Parastology, National School of Public Health, Greece, where surgically removed worms were identified by their murphology and histology; hiernatoxylin-cosin-stained human biopsy specimens were investigated for parastes; PCR with specific D. repens-primers was performed in all cases.

Black-and-white pattern filled pins; published case reports: [1] Gorezis 5, Psilla M, Asproudis I, Peschos D, Papadopoulou C, Stefaniotou M, intravitreal diroflamasis: a rare ocular infection. Orbit. 2006; 25:57-59. [2] Malteros ES, Sivridis EL, Giatromanolalu AN, Simopoulos CE, Humain subcutaneous dirofiliariasis: a report of three cases manifesting as breast or axillary nodules. Scott Med J. 2002; 47:86-88. [3] Mela EK, Blatsion G, Marangos MN. Subconjunctival Dirofiloria repens infection. Arrib Hel Med. 2011; 28:706-708. [4] Tennetou K, Gasteratos S, Pantacoposinu A, Gogou C, Konidaris D, Fragia K. Subcutaneous dirofiliariasis caused by Dirofileria repens in Greece: a case report. J. Curan Pathol. 2009; 36:892-895. [5]. Tranetou K, Gogou C, Sionnovidopulora A, Patraavis C, Fragia K. Sibrous subcutaneous nodule caused by Dirofileria repens. Travel Med Infect Dia, 2009; 7:318-322.

Sorarouf A, Petkolis P, <u>Vastalou E</u>, Vakaks N. (Ocular dirofilanasis: a new case). 6th Hellenic Congress of Public Health and Health Services, Athens, Greese, 2006. [in Greek].

Figure 1. Human *D. repens* dirofilariasis cases recorded in Greece from mid-2002 to mid-2012 and their localities.



Results from a still-running canine health survey; dog blood samples were examined by Knott's test, histochemical staining and PCR with specific D. repens- and D. immitis-primers.

Figure 2. Presence of *D. repens* among canine population in different Greek regions in 2002–2007.

Conclusion: This work reports that in recent years human *D. repens* infection cases mostly appeared in Western Greece. Interestingly, in addition to the described canine *D. repens*-affected region of North Greece, our as-yet-obtained results also argued for the presence of canine infection by *D. repens* in West Greece. Perhaps the recent emergence of human *D. repens* dirofilariasis in Greece's *D. repens*-affected west region that is characterized by a high pluviometry might correspond to increasing presence of sunrise/sunset-biting mosquito vector species in the area. Further entomological research should be encouraged.



Modeling ST-246, vaccination, and the effect of contagiousness in a smallpox outbreak

E. Graeden

Gryphon Scientific, Takoma Park, MD, USA

Background: Despite eradication of the naturally-occurring disease, smallpox has re-emerged as a major public health concern due to the threat of a bioterror attack or unintentional laboratory release. In 2011, a new antiviral, ST-246, was purchased by the US Department of Health and Human Services Strategic National Stockpile for use in the event of a national emergency.

Objectives: In this study, we address the comparative efficacy of vaccination and ST-246 for the prophylaxis and treatment of smallpox. To identify conditions under which ST-246 is required to curtail the epidemic, we explore how the interaction between contagiousness and prophylaxis coverage of the affected population affects the ability of the public health response to control the outbreak.

Methods and Materials: We built a system dynamics model to characterize conditions under which ST-246 is required to curtail a smallpox epidemic. Each parameter value in the model is based on meta-analysis of published empirical data.

Results: Our results indicate that the addition of antiviral treatment against smallpox reduces fatalities by 91% in a large-scale outbreak. In addition, post-event co-administration of ST-246 and vaccines as prophylaxis reduces the caseload by 55% compared to vaccination alone. When vaccination coverage of the population decreases below 70%, even when the outbreak is caused by a virus with an R₀ less than 4, ST-246 treatment is required to control the outbreak. These results are independent of initial outbreak size and are consistent across a range of public health response assumptions.

Conclusion: The addition of an effective antiviral such as ST-246 would significantly reduce morbidity and mortality in a smallpox outbreak when co-administered with vaccine prophylaxis post-event. This study is the first to explore highly uncertain epidemiological parameters to identify the relative importance of prophylaxis and treatment as part of a public health response to a large-scale smallpox outbreak.

22.095 Modelling reporting chain delays and their impact on outbreak control: Room for improvement

A. A. Bonacic Marinovic, C. Swaan, J. Van Steenbergen, M. Kretzschmar

RIVM, Bilthoven, Netherlands

Background: Timeliness of notification is crucial for effective control of infectious disease outbreaks. Early notification results in more timely and therefore probably more effective interventions. There are few quantitative assessments of how disease notification speed impacts on outbreak control and potential case reduction.

Objectives: We aim to gain quantitative insight into the timeliness of notification by mathematical modelling of notification and transmission dynamics.

Methods and Materials: For 6 notifiable infectious diseases we developed a model that computes expected proportion of new infections caused by index cases and their secondary cases at notification time. We characterized the distribution of notification times by its median and standard deviation. We took into account knowledge on distributions of latent periods and serial intervals. We informed the model using data

about time between symptom onset and notification ('notification delay') from the Dutch notification system to evaluate current notification speed of mandatory notifiable diseases Hepatitis A, Hepatitis B, Measles, Mumps, Pertussis and Shigellosis. We studied quantitatively how decreasing notification delays can reduce the expected attack rate during an outbreak, considering outbreak control as ultimate goal.

Results: Applying case-based interventions only on index cases has almost no effect on outbreak size, as for all studied diseases more than 90% of expected secondary infections already have taken place at notification. However, considering the proportion of infections caused by secondary cases that can be prevented, the current notification speed of Hepatitis A and Hepatitis B is sufficient for controlling outbreaks if effective interventions targeting secondary cases are applied. For Measles and Mumps, the proportion of infections caused by secondary cases can be reduced in 30-40% with notification delay reductions of 3 days. For Shigellosis and Pertussis, however, notification delays have to be reduced substantially (10 and 20 days, respectively) to achieve a similar reduction on infections caused by secondary cases, suggesting that current surveillance for these disease needs to be reconsidered.

Conclusion: Our method provides insight in how notification delay affects the expected attack rate for various transmissible diseases. It proves as a tool for quantitatively evaluating current timeliness of notification and for prompting required notification delay reductions to achieve attack rate reduction and outbreak control.

22.096 The analysis of the factor to affect to outbreak of resistant type malaria: Application of Mathematical Epidemiology to the control of the drug-resistant type

K. Shirakawa¹, M. Nishibuchi²

¹Graduate School of Medicine, Kyoto University, Kyoto, Japan, ²Center for Southeast Asian Studies, Kyoto University, Kyoto, Kyoto, Japan

Background: The spread of drug resistance is making malaria control increasingly difficult. Mathematical models for the transmission dynamics of drug sensitive and resistant strains can be a useful tool to help to understand the factors that influence the spread of drug resistance, and they can therefore help in the design of rational strategies for the control of drug resistance.

Objectives: The anti-malaria drug is effective for treatment of malaria, but the outbreak of the resistant type is a medical problem. We control outbreak of resistant type malaria and devise a method to decrease a malarial patient efficiently.

Methods and Materials: We present an epidemiological framework to investigate the spread of anti-malarial resistance. Several mathematical models, based on the familiar Macdonald-Ross model of malaria transmission, enable us to examine the processes and parameters that are critical in determining the spread of resistance. We used Mathemacica and R to find some parameters.

Results: In our simplest model, resistance does not spread if the fraction of infected individuals treated is less than a threshold value; if drug treatment exceeds this threshold, resistance will eventually become fixed in the population. The threshold value is determined only by the rates ofnfection and the infectious periods of resistant and sensitive parasites in untreated and treated hosts, whereas the intensity of transmission has no influence on the threshold value. In more complex models, where hosts can be infected by multiple parasite strains or where treatment varies spatially, resistance is generally not fixed, but rather some level of sensitivity is often maintained in the population.

Conclusion: The models developed in this paper are a first step in understanding theepidemiology of anti-malarial resistance and evaluating strategies to reduce the spread of resistance. However, specific recommendations for the management of resistance need to wait until we have more data on the critical parameters underlying the spread of resistance: drug use, spatial variability of treatment and parasite migration among areas, and perhaps most importantly, cost of resistance.

22.097 The H index as a measure of disease impact-When and why it works

K. M. McIntyre¹, I. Hawkes¹, S. Morand², M. Baylis¹

Institute of Infection & Global Health, University of Liverpool, Chester, United Kingdom, ²CIRAD, Montpellier cedex 05, France

Background: The H-index for diseases is a rapidly obtained, userobjective measure which correlates with the Disability Adjusted Life Year (DALY), which quantifies human disease burden. It has been proposed, therefore, as a convenient tool for prioritising diseases or the pathogens that cause them.

Objectives: Within this work, we explore two aspects of the H index's relation to pathogens or disease. First, we examine whether H indices for pathogens are correlated with the results of previously published disease prioritisation exercises, to corroborate when it works, and its usefulness as an indicator of impact. Second, we investigate epidemiological variables or combinations of variables which explain variation in the H index to establish why it works.

Methods and Materials: Other pathogen or disease prioritisation exercises were identified using literature searches; their scores or rank results were compiled and statistical comparison was made against H-index scores for the relevant pathogen or disease.

For a short-list of diseases, data was gathered on other potential variables likely to influence when and whether scientific papers are published, and therefore the H index scores of diseases or pathogens. In addition, a number of epidemiological indicators of disease impact were included where available. Uni-variable and multi-variable regression analyses were used to examine potential explanatory variables affecting the H-index scores for diseases.

Results: Significant correlations were found between previous prioritisation exercises and the H-index in 9 out of 12 (75.0%) comparisons. Higher H-index scores were associated with larger numbers of human deaths and annual disease incidence, as well as economic input into research and development. The best multivariable model explained 72% of variation between H-indices, suggesting that a high H index is a result of greater research spend and a greater incidence of disease.

Conclusion: We propose that the H-index for diseases works best when users need an objective, rapid method of distinguishing the relative impacts of pathogens or diseases; when examining a large number of pathogens or diseases; and when examining pathogens for which estimations of other impact measures (such as DALYs, incidence, prevalence and the number of deaths arising as a result of disease) are not readily available.

22.098 Strategy to prevent *Clostridium difficile* infection outbreak in municipal hospital

H. Ishikawa¹, K. Kojima¹, T. Watanabe¹, S. Maruyama², S. Matsuo² ¹Tokai Central Hospiotal of Japan Mutual Aid Association of Public School Teachers, Gifu, Japan, ²Nagoya University Graduate School of Medicine., Aichi, Japan

Background: Clostridium difficile infection is one of the common hospital-aquired infection, and is sometimes a cause of morbidity and mortality among elderly hospitalized patients. We experienced an out break of Clostridium difficile associated diarrhea (CDAD) in one floor of our municipal hospital.

Objectives: We attempted to clarify the cause for CDAD and assessed a suitable strategy to prevent the spread of CDAD.

Methods and Materials: As the surveillance, we performed the isolation of CDAD patients and prescribed vancomycin orally for 14 days, and monitored fecal CD toxin as a disease marker for CDAD. We verified our procedure of disinfection during that period. We investigated risk factors associated with CDAD during the 64-day study period, and discussed how to treat CDAD patients and others.

Results: Characteristics of patients (n=75) were as follows. Age = 70.4±12.6, M/F = 43/32. Diarrhea was observed in 18.7% of patients, and half of them were CDAD. The surveillance of CDAD commenced at 47th day of the study when we recognized the situation as an outbreak.

International Meeting on Emerging Diseases and Surveillance 2013

Using univariate analysis, #every one week prolonged in duration of hospitalization (odds ratio: 10.1 [95% CI: 1.01-1.06] p = 0.003), #tube-feeding (odds ratio: 16.4 [95% CI: 2.75-97.54] p = 0.002), #use of diaper (odds ratio: 31.0 [95% CI: 1.69-567.17] p = 0.0008), which were associated with an increased risk of CDAD. Every 1g/dl increase in #alb (odds ratio: 0.16 [95% CI: 0.04-0.73] p = 0.0008), which was associated with a decreased risk of CDAD.

Conclusion: Our results suggest that patients who require long term care have a potential risk for CDAD. Greater attention and improved methods of disinfection were required for use of the feeding tube. Responsible patient management requires improved surveillance for CDAD and rapid response possibly including patient isolation. Maintaining nutritional status may further serve to avoid CDAD. In the case of outbreak, we should immediately assemble the infection control committee and institute measures to avoid further spread of the disease.

22.099

Even Series 2.099 Foodborne outbreak in Ugljevik municipality, North-east Bosnia, August 2012

Z. Dakić, Z. Maksimović

Health Center Bijeljina, Bijeljina, Bosnia and Herzegovina

Background: Foodborne diseases caused by microorganisms is a large and growing public health problem. Most countries with systems for reporting cases of foodborne illness have documented a significant increase in recent decades in the incidence of diseases caused by microorganisms in food, including pathogens such as *Salmonella, Campylobacter jejuni* and enterohaemorrhagic *Escherichia coli*. Foodborne disease outbreaks are relatively common in developing countries. What is the situation in Bosnia and Herzegovina (B&H)?

Objectives: The aim of this paper was to determine what is the current practice of foodborne outbreak response in B&H? The most recent example is an outbreak in the Ugljevik coal mine worker's canteen (North-East Bosnia, August 2012).

Methods and Materials: Descriptive, retrospective study. The data used in this paper came from field epidemiological investigation performed in Ugljevik and reports of microbiology laboratories: Public Health Institute of Republika Srpska and General Hospital Bijeljina. Epidemiological surveillance of communicable diseases in the Republic of Srpska (B&H governing entity) is regulated by the Law on Protection of Population from Infectious Diseases but there is no specific guidelines for foodborne disease outbreak detection and response.

Results: On August 18, 2012 at 11pm, patients with a fever, vomiting, diarrhea and abdominal pain came to the to the local health center. In the next 48 hours, a total of 75 patients had same symptoms. All of them are mine workers who had lunch that day in the local worker's canteen. They all received antibiotics cotrimoxazole without stool cultures. Due to administrative reasons, epidemiological survey was carried out after 5 days and only 30 stool samples were taken for analysis. *Salmonella enteritidis* isolates were obtained from 5 stool samples. Microbiological Laboratory of Public Health Institute detected *Escherichia coli* in vanilla pudding sample and *Proteus vulgaris* in grilled chicken liver. Contaminated pudding was found as a source of the outbreak.

Conclusion: Most recent outbreak response show that the situation requires need for improving practice. Legislation for public health surveillance of communicable diseases exists, but is not sufficiently accurate and efficient. It is necessary to strengthen the role of epidemiology services, to educate inspection bodies and through appropriate guidelines and training clarify the role of the family doctors in the surveillance system.

22.100 Outbreak of salmonellosis in pastoral setting-Borena Zone, Ethiopia, 2012

G. B. B. B. Defi

Oromia Regional Health Bureau, Addis Ababa, Oromia, Ethiopia

Background: Salmonellosis is an infection with bacteria called *Salmonella*, and *Salmonella* germs are common in uncooked food products from animals. In August 2012 suspected cases of Salmonellosis were reported from the Utallo kebele in Yabello woreda of Borena zone.

Objectives: We investigated to confirm the etiology, identify risk factors, and establish control measures.

Methods and Materials: We defined a suspected case of salmonellosis as any person with cramps, foamy diarrhea, fever, nausea, and sometimes vomiting. We conducted an active case search in the locality, reviewed clinical manifestation, and compiled line lists. We compared cases with matched controls using a questionnaire. We also collected laboratory specimens for stool and conducted an environmental inspection to propose source of infection. Data were analyzed using Epi Info version 3.5.1.

Results: Laboratory investigation of stool specimen found motile bacteria but no any parasites including protozoa's. We identified 36 suspected salmonellosis cases and no death. The overall attack rate was 923/1000. We found both eating sick camel and un-cooked meat was associated with higher rates of disease [OR: undefined, 95% Confidence Interval (CI): undefined].

Conclusion: We confirmed an outbreak of Salmonellosis with a high attack rate in a pastoral setting. Eating of raw or uncooked meat and using of sick animal for food purpose may have contributed to the outbreak. The outbreak was contained due to early detection and prompt treatment.



Count

Knowledge, attitudes and occupational exposure to needle stick injury among health care workers in Tripoli Central Hospital

A. M. Elbahi¹, H. Zeglam²

¹Tripoli central hospital, Tripoli, Libya, ²Tripoli Central Hospital, Tripoli, Libya

Background: This study was the first conducted in TCH, to describe the prevalence of NSI & to assess the awareness of management to prevent it. The questionnaire were distributed to all HCW (152) which 47% (72) had NSI. It was found that the majority of HCW were lacking the awareness of management required following NSI. There is a high rate of NSI in TCH. effort should be made to prevent NSI, and constant education is recommended.

Objectives: To describe the prevalence and to assess the awareness and the knowledge of precautions and management required following NSI.

Methods and Materials: The two-page questionnaire was divided into three sections. The first consisted of personal data. The second included questions consisted of Yes/No answers. The third section consisted of self-answered questions. The data was analyzed by SPSS.

Results: 152 participants responded to the questionnaire. 47% (72) had NSI, according to the questionnaires, 35% of the samples had had one NSI, 6% had two, and 57% had more than twice, the highest incidence among HCW was found to be in Surgery 29%, followed by Medicine 19%, (Table 1).

Count				
		Had sha	Had sharp injury?	
		yes	no	
Place of work	medicine	14	18	32
	surgery	21	8	29
	infectious department	8	23	31
	dermatological department	4	7	11
	trauma	7	7	14
	ER	3	5	8
	pathological department	7	4	11
	other	7	7	14
Total		71	79	150

 Table 1. Frequency of NSI according to specialty.

The most common causative devices were needle for blood drawing (24.8%), suture needle (24.8%), and needle for IV line (11%). (Table 2).

Type of s	harp object		
		Frequency	Percent
Valid	needle for blood drawing	18	11.8
	glass slide	5	3.3
	needle for IV line	8	5.3
	suture needle	18	11.8
	scalpel blade	3	2.0
	others	2	1.3
	more than one object	19	12.5
	Total	73	48.0
Missing	System	79	52.0
Total		152	100.0

Table 2. The most causative device.

A major finding was that the majority of HCWs were lack the awareness of management required following NSI, (43.7%) were not aware, (39.7%) were 50% aware, and few (16.6%) were 100% aware.

Conclusion: We conclude that the frequency of NSI in our hospital is high, there-fore, preventive measures should be taken into consideration. Settings up an NSI management center in every department in TCH is recommended.

Each HCW should be encouraged for constant education and for improvement and maintained of acquired knowledge, therefore we recommend that should have a lecture in community medicine for forth year about the occupational hazards of NSI. Of course, this multifaceted approach will definitely improve the attitudes, knowledge and practice towards NSI.

22.102 Meningococcal meningitis outbreak investigation-Harenabuluk District, Southeastern Ethiopia, 2011

G. E. Yembo, D. J. Wayessa

Ethiopian Health and Nutrition Research Institute, Addis Ababa, AA, Ethiopia

Background: Ethiopia is one of the Sub-Saharan meningitis belt countries. Localized outbreak occurs almost yearly with >3000 cases/ year and case fatality (CFR) 1.4-8.5% primary caused by Neisseria meningtidis serogroup A. In February 2011, Harenabuluk District detected an increasing numbers of meningitis cases, which is outside the meningitis belt areas of Ethiopia. Ministry of Health deployed a team for investigation.

Objectives: To confirm outbreak, identify etiologic agent, determine risk factors, and establish appropriate control measures.

Methods and Materials: We conducted frequency matched (for age and sex) case-control study in Mekanagobale locality of Harenabuluk. Cases were individuals who resided in Mekenagobele from February 2-March 17, 2011. The controls were the neighbor of each case who did not suffer from meningitis. A structured questionnaire was used to collect information from cases and controls through direct interview. Using bivariate and multivariate analysis, we compared exposures for meningitis. We collected five samples of cerebrospinal fluid for laboratory analysis to confirm the responsible serogroup.

Results: We enrolled 49 cases (with six deaths) and 49 controls; median age of the cases was 14 year (1-56 years) and controls were 16 year (1-54 years). There were overall attack rate (AR) of 61/10,000 and 8 /1000 CFR. The highest (115 / 10,000) AR was observed among children

Conclusion: We confirmed the occurrence of meningitis outbreak in Harenabuluk which is not a usually a locality for this type of outbreak. The occurrence of the outbreak and the risk factors for becoming a case, which this study has identified, demonstrate that meningitis outbreaks are possible in all situations once the meningococcal meningitis has been introduced. Thus, the Harenabuluku District Health Authority should consider annual vaccination with monthly community health education on meningitis and its risk factors.

G. E. Yembo, G. A. Estayew, D. J. Wayessa

Ethiopian Health and Nutrition Research Institute, Addis Ababa, AA, Ethiopia,

Background: In Ethiopia, 6-10 million malaria cases occur annually and transmission is seasonal and unstable characterized by frequent focal and cyclic epidemics. On November 25, 2011, Gambella Region notified Ministry of Health (MoH) that malaria cases exceeded epidemic threshold in Abobo Town. On December 2, 2011, MoH deployed a response team.

Objectives: To confirm the outbreak and determine risk factors.

Methods and Materials: Used third quartile epidemic threshold to confirm the epidemic; conducted frequency matched case-control study (with 1:1 ratio). Cases were slide-confirmed malaria cases who resided in Abobo Town from December 1-31, 2011. The controls were the neighbor of each patient, but did not suffer from malaria. Collected information by interviewing the patients and controls. Using bivariate and multivariate analysis, we compared exposures for malaria infection. Mosquitoes breading sites and larvae identification, and inspected indoor resting adult mosquitoes.

Results: Identified 463 cases with no death. Epidemic threshold was crossed and attack rate was highest (6.7/100) among children.

Observed indoor resting mosquitoes, breeding sites and larvae. This entomologic information was not used.

Conclusion: The risk of developing malaria was multi-factorial with a risk factor profile similar to in highland of Ethiopia. Households within close proximity to Alwero River and those not using bed nets were at higher risk of malaria. Health education on the use of bed nets, annual indoor residual spraying, environmental controls and entomologic surveillance recommended.

22.104 Outbreak of mumps at village jumma khan lund, Tando Allahyar, Sindh Pakistan 2011

M. Nadeem Shah Syed¹, D. R. Muhammad Safdar²,

D Jawed Juneio³

¹Government of Sindh, Hyderabad, Sindh, Pakistan, ²NIH, Islamabad, Pakistan, ³NHO, Hyderabad, Pakistan

Background: Mumps is generally a mild disease but complications do result in overall mortality of 1/10,000. Incidence is higher in countries such as Pakistan where mass vaccination has not been introduced. On March 2, 2011, five suspected cases were reported in a small village of Sindh. We report findings of the investigations and response carried out during March 3-6, 2011.

Objectives: To determine risk factors for mumps infection during outbreak and control the outbreak

Methods and Materials: We planned a case control study. Using WHO standard case definition; cases were identified through active household search covering entire village population. One sample was sent to central laboratory for analysis. Equal number of age and sex matched community controls were selected. Clinical and epidemiological information was collected through a pre-tested questionnaire. Frequencies and Odds ratio were calculated using Epi Info 7.0

Results: 42 cases were identified among 850 village dwellers (AR 4.9%). Mean age of cases was 9.6 years with range of 4-33. Thirty (71.4%) were males. Main clinical features included parotitis100% (n=42), fever 64.2% (n=27), Jaw Pain 57% (n=24), sore throat 45.2% (n=19), Headache 42.8% (n=18) and cough 28.6% (n=12). Laboratory sample was confirmed for Mumps. Appearing on 17th February 2011, index case had exposure to mumps patient during travel. Cases were more likely to have visited local school (OR=3.1, p< 0.01). Low routine immunization coverage was eminent; only 45.2% cases and 57% controls had received DPT-III. One case (2.4%) and 03 controls (7.1%) were vaccinated against Mumps. All cases were treated symptomatically and none requiredhospital admission.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: Infection acquired during travelling initiated outbreak in the village. Interaction at a local school facilitated spread of infection. Health education and simple hygiene and isolation measures helped in early control.Further disease burden and economic analysis studies were recommended to decide introducing Mumps vaccination in Pakistan.

22.105 Investigation of post-flood dengue cases in Hyderabad city, Sindh, Pakistan 2010 M. Nadeem Shah Syed¹, D. R. Muhammad Safdar²

¹Government of Sindh, Hyderabad, Sindh, Pakistan, ²NIH, Islamabad, Pakistan

Background: Two-fifth of world population is at risk for Dengue in over 100 endemic countries. About 100 million get infected each year. Dengue Hemorrhagic Fever is its potentially lethal complication with case fatality of 2.5%. The disease is rising in Pakistan since first cases in 1994. Hyderabad city reported 50 cases of dengue during 2009. Expecting outbreaks after 2010 floods and on receipt of alert from a local hospital, we conducted field investigations.

Objectives: To identify risk factors for dengue upsurge during postflood period in Hyderabad.

Methods and Materials: Based on standard case definitions, we conducted active case detection in all major public and private sector hospitals during October-December 2010. Household contacts were looked for additional case finding. Rapid immuno-chromatography was used for laboratory confirmation. Standard pretested questionnaire was used to collect epidemiological information and data analysis done in Epi Info version 6.

Results: Of total 567 identified suspects, 407 (71.7%) were lab. confirmed. Mean age of confirmed cases was 28.7 years (range 1-70); 307 (75.4%) being males. Major sign and symptoms included fever (n=407,100%), headache (n= 398,97.7%), muscle pain (n= 303,74.4%), joint pain (n=233,57.2%), retro-bulbar pain (n=202,49.6%), skin rash (n=71,17.4%), Haemorhagic manifestations (n=25,6.1%). 209 (51.3%) cases were hospitalized with no mortality. 366(89.9%) cases lived in houses with no protective nets, 321 (78.8%) stored water in open utensils, 233 (57.2%) used half sleeve shirts whereas 21 (5.1%) reported use of mosquito repellents.

Conclusion: Eight times rise over preceding year indicated an outbreak. Besides establishing Infectious Diseases Task Force and dengue surveillance cell, a mass health education campaign was undertaken. Isolation wards were established in major hospitals with case management trainings. Facilities of lab. investigation and mega platelets were provided free of charge. The said interventions along with fumigation in the affected areas brought the outbreak under control.

22.106 Is hospital-based sentinel pneumonia surveillance system useful for pandemic preparedness and response? Lessons learned from the Indonesian surveillance system

Y. Praptiningsih¹, A. Bratasena², M. Sitorus², M. Amalya¹, G. Samaan¹

¹US Centers for Disease Control and Prevention, Jakarta, Jakarta, Indonesia, ²Ministry of Health, Jakarta, Indonesia

Background: In 2007, the Indonesian Ministry of Health established a syndromic pneumonia surveillance system to support pandemic preparedness and response. The sentinel system operates in 40 district hospitals in 20 provinces. Aggregated data on cases and clusters are reported monthly from the hospitals to the Ministry of Health. Data on contact with H5N1-infected poultry are collected to detect pandemic epicenter clusters and hospital denominator data are collected to calculate disease rates and detect changes indicative of outbreaks.

Objectives: This study describes the utility of the system for pandemic preparedness and response based on an evaluation conducted in September 2012.

Methods and Materials: The evaluation was conducted using the standard tool from the United States Centers for Disease Control and Prevention (CDC). Surveillance data were reviewed to assess disease trends and outbreaks detected, and stakeholders were consulted using a semi-structured questionnaire to assess utilization of system outputs. Stakeholders consulted included hospitals, data managers at district, provincial and central level, and data users at national level.

Results: Many sentinel sites were located in provinces affected by avian influenza outbreaks in poultry where epicenter clusters may have occurred. The system did not detect increases in pneumonia activity during the 2009 pandemic. One sentinel site detected a cluster of pneumonia cases that was later found to be associated with a bushfire. The pneumonia case definitions were not well understood by district authorities, and there was no laboratory testing to assess etiologies. Since data were aggregated, analyses were limited. Risk factor and patient outcome data could not be analyzed due to poor completion rates.

Conclusion: The monthly syndromic sentinel system had limited utility for pandemic preparedness due to limited hospital coverage, no laboratory-testing and difficult-to-analyze aggregated data. Surveillance objectives have been updated and the case definition changed to severe acute respiratory infection (SARI) that is broader and easier to apply. Laboratory testing was added to enable viral pathogen monitoring, and reporting was changed to a case-based system. These changes are aligned with the World Health Organization's latest recommendations for influenza surveillance to monitor disease trends, risk factors as well as disease severity during a future pandemic.

22.107 European Union "Yellow Pages" for **Microbiology Laboratory Services to** support outbreak response and control-A needs analysis

A. J. Ozin-Hofsaess¹, J. I. M. Vaz¹, A. Pierson², F. Guedez², M. Struelens¹

¹European Centre for Disease Control and Prevention, Solna, Sweden, ²Integrated Quality Laboratory Services (IQLS), Lyons, France

Background: Timely and reliable surveillance of infectious agents which may threaten public health is an essential component of effective disease prevention and control. Studies of the EU public health microbiology system and structures have revealed some gaps in provision of, or access to, reference level microbiology services needed for surveillance and epidemic preparedness. Particularly for rare and emerging pathogens and those requiring specialised facilities (e.g. biosafety level 4 containment laboratories). The European Centre for Disease Prevention and Control (ECDC) has a mandate to foster collaborations between experts and expert reference laboratories.

Objectives: In 2012, ECDC set-up a needs analysis study to answer the question of whether EU Member States partners can adequately access information about available microbiology laboratory services and how this could be improved.

Methods and Materials: The methods used to collect perspectives from EU stakeholders included both bi-lateral interviews (22 persons from 15 countries) and broader on-line survey (140 respondents from 31 countries), divided into 3 groups: "Service provider" (labs), "Service customer" or "Both" from the EU/EEA National Microbiology Focal Points and other relevant experts leading EU disease specific laboratory networks.

Results: The results confirmed that such a directory of services would be a useful tool and would formalise what is happening (mostly ad hoc) through professional connections. It was confirmed that the directory should be simple, easy to search, and the basic-level information (e.g. pathogen and name of institution offering service) should be open to the public and offer better information that a simple Google search. More detailed information including contact details and diagnostic methods used would require a registration process as well as some information being restricted to the responsible Member State authorities.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: Considering the current economic crisis and the need to strengthen laboratory capabilities in the EU, this study supports that ECDC go forward in its "information broker" role and develop, jointly with the MS stakeholders, an EU directory of microbiology laboratory services. This would not only have added value for the ECDC and its expert partners in the disease networks but would contribute to global access to this laboratory capacity in a more efficient way.

22.108 Visit delay and report delay of patients and health facilities in a syndromic surveillance system for infectious diseases in rural China

C. Zhou¹, Q. Zhao¹, X. Li², B. Xu¹, X. Song¹, H. Yuan³ ¹Fudan University, Shanghai, China, ²Future Position X, Gävle/SE, Sweden, ³Jiangxi Province CDC, Nanchang, China

Background: Syndromic surveillance has been widely used for early detection of infectious disease epidemic. Although an internetbased case report system for notifiable infectious diseases has been established in China, the validity and timeliness of this system are constrained by the weak capacity in diagnosis in the resource-scarcity rural areas. Symptom-based syndromic surveillance might be a good supplement to the case report system.

Objectives: To evaluate the delay of outpatient visit and delay of report in a syndromic surveillance system in rural China (ISSC).

Methods and Materials: The ISSC was carried out in two rural counties of Jiangxi Province, China. Health providers from 2 county hospitals, 15 township hospitals and 152 village health stations (VHS) worked as data collectors. Information collected in the ISSC included target symptoms (fever, cough, sore throat, nausea/vomiting, diarrhea, rash, headache, convulsions, mucosal hemorrhage, disorders of consciousness), date of symptom onset and healthcare visit, gender, age and village of patients. Daily data should be reported before 9:00am next day through the website: isscproject.com.

Results: From April 1, to October 31, 2012, 116393 records of symptomatic patients' first outpatient visit were reported. The time intervals from onset of symptoms to health care visit vary among different levels of health facilities. In county hospitals, of the 12551 visits, 25.27% had a 1-day delay. In township hospitals, 1-day delay accounted for 43.02% of the 17377 visits. In VHS, 47.94% of the 86465 visits happened right on the symptom onset. The over 3-day delay in county, township and VHS were 41.68%, 14.08% and 5.24% respectively. Regarding report delay, about 55.2% of the reports from county hospital were in time. For VHS and township hospitals, the in time report rate were > 83%. If the report time was set at 12:00 next day noon, the in time report in county hospital would have a significant rise to 79.6%.

The time interval from onset date to visit date (d)	County hospital		Township hospital		VSH		Total	
	No	461	No.	54	No.	15.1	No.	194
	1943	15.48	4764	27,42	41409	47.94	48156	11.17
1	3372	25.27	7475	43.02	33722	39	44369	38.12
ź	2264	17.56	2691	15.49	6766	7.83	11668	10.61
3-7	3666	28.68	2216	\$2,75	4159	-4.81	9975	8.57
17	3632	13	231	1.57	349	0.43	2252	1.30
Total	12551	100	\$7577	100	86465	100	116353	100

 $\ensuremath{\text{Table 1.}}$ The time interval from onset date to visit date of patients in different level units.

Conclusion: VHS plays an important role in the symptomatic surveillance in rural China for its wide population coverage and easy access. It also has a better performance of "In time report." The time set for report should be adjusted to 12:00 noon for fitting the local work schedule.

22.109

2.109 Yellow Fever outbreak investigation and response, Darfur State, Sudan, September–November 2012

M. Nogoudalla¹, D. Bashir², M. Nogoudalla³

¹Federal Ministry of Health Khartoum, Sudan, Khartoum, Khartoum, Sudan, ²Penn state hershey childrens hospital, Hershey, pa, USA, ³Federal ministry of health,Sudan, Khartoum, SU, Sudan

Background: Sudan is in the yellow fever (YF) belt of Africa. In 2005 Sudan experienced the last outbreak in South Kordofan. In September 2012 Darfur states started to report YF cases. An ongoing field investigation and management of YF outbreak was conducted.

Objectives: Establish existence of outbreak; describe epidemiology of disease. To provide feedback for prevention and control.

Methods and Materials: A Field based assessment was conducted by, interviews, lab test, questionnaires and standard lab forms. Interviews conducted with key informants, patients, health personnel, family of deceased and nomads in the city and market. Blood samples taken. Quantitative and qualitative data analyzed using SPSS for interpretation of results.

Results: From September 1, up to November 28, 2012 a total of 578 cases reported to Federal Ministry of health(FMOH) and resulted in 129 deaths, with CFR=29%, AR 22.3. Common symptoms include; fever (98%), headache (71%), bleeding manifestation (50%), jaundice (39%). The most affected age group was 15-29.9 years (51%). All cases were notified from Darfur states, (Central 62%), East (0.5%), West (17%), North (11.5%) and South (9%), where 30 localities out of 57 were included. Male to female ratio 2:1. Similar sex and age distribution of exposure found among nomads and residents. Risk factors include; nomadic lifestyle, refugee camps, mountainous areas, presence of monkeys and vectors. Two samples out of first five were confirmed by IgM ELISA test and RT-PCR by the WHO reference laboratory for YF in Dakar, Senegal. Total of 67 samples from outbreak processed locally in National Public Health lab revealed 11 positive, 11 negative for YF, 2 negative 2 positive for flavivirus.

Conclusion: FMOH detected YF outbreak in Darfur states and the causes of the disease are declining after measures were taken to control and prevent further outbreak which include cases management and isolation. Mass vaccination Parallel direct control measures: environmental-vector control, health education and community mobilization. Lack of infrastructure and the poor security situation in the area certainly complicate situation. Recent report received about the circulation of the mosquito to several parts of the country risking further spread of the disease.



2.110 Cholera outbreak in Akinyele local government area, Oyo State, Nigeria, August, 2012—Effect of multi-sectoral intervention

A. O. Gbolahan¹, P. B. Adewuyi², O. Iyiola¹, V. Fapohunda³ ¹Ministry of Health, Ibadan, Nigeria, ²Nigeria Field Epidemiology and Laboratory Training Programme, Abuja, Nigeria, ³Babcork University, Remo, Nigeria

Background: Cholera is a highly infectious disease which is usually transmitted through infected persons or from environmental reservoirs. In August, 2012 we received a report of Cholera outbreak in Akinyele LGA and carried out multi-sectoral intervention. There was a similar outbreak in Oyo State which started in June, 2011 and spread to 24 LGAs in the State.

Objectives: We carried out this analysis to determine the effect of multi-sectoral intervention in outbreak management.

Methods and Materials: We compared the multi-sectoral intervention with that of last year's unilateral intervention and identified key strategies that affected a favorable outcome this year.

Results: In 2011 outbreak, of 974 patients from 24 LGAs in the State, there were 28 deaths. Case Fatality Rate of 2.9%. In 2012, Outbreak started in Akinyele LGA, 23 patients were affected with no mortality. Case Fatality Rate was 0%. No further spread. This favorable

International Meeting on Emerging Diseases and Surveillance 2013

intervention was due to rapid response from the Epidemiology unit of the Ministry of Health, within twenty four hours of notification involving ministries of Environment, Agriculture, Information and Akinyele LGA. There was evidence of epidemic preparedness as drugs were readily available to the patients and the local authority mobilized resources to contain the spread by chlorinating the wells and providing relief materials.

Conclusion: Epidemic Preparedness and Rapid Response involving all related sectors can reduce the spread, avoid fatalities and ensure favorable outcome as the case was in this cholera outbreak in a developing country.

22.111 Case control investigation of an outbreak of acute jaundice in a refugee population in Dadaab, Kenya, 2012

L. Chepkurui

Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

Background: Every year there are 20 million hepatitis E virus (HEV) infection, over three million acute cases, and 70,000 HEV related deaths. An outbreak of acute jaundice was reported in a section of Dadaab refugee camp in Kenya from july 2012 that was laboratory confirmed as HEV.

Objectives: To characterize the outbreak and to support control measures.

Methods and Materials: Acase control study was used: cases were randomly selected from an acute jaundice linelist obtained from health facilities serving the affected sections of the camp from july to september 2012. Cases were defined as PCR confrmed HEV, controls were randomly selected from patients presenting to any of the three health centres and were reported not having signs or symptoms of jaundice in the last 30 days.

Results: We enrolled 50 cases of which 38% (19),were laboratory confirmed and 100 controls. Median age of cases was 26 years(range 4–55 years) and majority of the cases were females 66% (33). Most of the controls were females 52% (52), with median age among controls being 28 years (range 6–63 years). Being pregnant (Odds ratio (OR), 2.6208, 95% Confidence Interval (CI), 1.0562-6.5035), having no formal education (OR 2.1, CI=1.0176-4.4222), having a latrine (OR 2.4, CI=1.2219-4.8796), and always using latrine for defecation (OR 5.7, CI=1.9615-17.0839) was significantly associated with the disease.

Conclusion: Acute HEV infection is higherr among persons aged 15 to 45 years. Pregnant women are at greater risk of severe outcome. Public health education on personal, household and environmental hygiene should be scaled up in the camp.

22.112 Aedes albopictus as vector in Dengue Hemorhagic Fever (DHF) outbreak in Kaimana District, West Papua Province: An entomological investigation

T. N. Kridaningsih¹, H. Krismawati¹, M. Rahardjo¹, E. Natalia¹, Y. Y. R. Mirino²

¹Institute of Research and Development for Biomedicine, Papua, Jayapura, Indonesia, ²Institute of Research and Development for Biomedicine Papua, Jayapura, Indonesia

Background: Dengue outbreak first case had been occured in May-July in Kaimana District West Papua. This Dengue was the first case in Kaimana in last 50 years base on records of West Papua Health Department, presumptively caused by transmission of Dengue virus from infected temporer visitor that participating one of religious event, held by local goverment.

Objectives: Entomological survey was intended to study the species of suspected mosquito vectors, distribution and abundance of mosquito larva and detect the dengue virus in mosquito using RT-PCR. Epidemiology survey was to study the distribution of the DHF cases related to patient household

Methods and Materials: Interview on positives patients and an entomology investigation were overtaken on June 2012. Mosquitoes sample were collected on resting habitat as well as human landing collection. Larvae were collected from water container at 25 sampling site consist of patient household, school, and hospital. Larvae collection was rearranged in Entomology Laboratory of Institute of Research and Development for Biomedicine, Papua. Dengue virus was detected in mosquitoes that had been collected from research area as well as from rearranged mosquitoes using RT-PCR method Lancioti primer

Results: Case report show that the age majority of DHF cases is 6-12 (48,1%) and dominan patients were woman (63%). The study found one dead (3,7%) cases and 26 (96,3%) sick cases. Result of entomology survey indicated that *Aedes agyepti* had been known as dengue main vector in most area in Indonesia were absent, while the second vector *Aedes albopictus* was present abundantly in adult stage as well as in larvae stage. The mosquitoes were found more in their resting habitat than in patient's houses. The study from 25 sampling location indicated that 40% *Aedes albopictus* breteau with *House Index* 26,6% and *Container Index* 21,2%. The house index was more than 10% mean that this area has high susceptibility in DHF outbreak according to Ministry of Health criteria. Dengue virus detection using RT-PCR indicated that the dengue virus were present in sample specimen.

Conclusion: We found *Aedes albopictus* as vector in first DHF outbreak in Kaimana District, West Papua Province

22.113 A food handler-associated Norovirus outbreak following a wedding, Austria, 2012

S. Maritschnik¹, E. J. Simons¹, I. Lederer², M. Höhne³,

E. Kanitz¹, D. Schmid¹

¹AGES, Vienna, Austria, ²Austrian Agency for Health and Food Safety, Graz, Austria, ³Robert Koch Institute, Berlin, Germany

Background: On October 12, 2012, the local public health officer informed AGES about a cluster of cases of gastroenteritis among guests following the attendance of a wedding reception at a hotel in Salzburg.

Objectives: To identify the source(s) of infection in order to implement the appropriate measures to prevent future outbreaks

Methods and Materials: A probable case was a guest who consumed food at a wedding dinner prepared by a hotel in Salzburg on October 6, 2012 and who became ill with diarrhoea or vomiting between October 7 and 8, 2012. A confirmed case was a probable case with a NV-positive stool specimen. We conducted a retrospective cohort-study with the wedding guests; information on food consumption was collected via a self-administered questionnaire. Attack-rates were compared between food exposed and unexposed guests. Food inspectors examined the kitchen and took 3 food samples. Stool specimens were tested using a real-time RT-PCR and the detected NV was characterized by genogroup and sequence-based genotype.

Results: Twenty-six cases fulfilled the case definitions including two (8%) confirmed cases. The outbreak lasted from October 7 until October 8. Stool specimens from six (43%) out of 14 tested kitchen workers were positive for NV. Out of these six, one was sick with gastroenteritis during work on October 5 and 6. The outbreak strain identified was genogroup II.4/2012 and found in 2 food handlers and 2 wedding guests. Food samples tested negative for NV. The attack rate among the wedding guests was 25% (26/103). The food-specific cohort-analyses revealed that consumption of the wedding cake (RR: 2.21; 95%CI: 0.92-5.28; p-value=0.0529) and a mushroom dish were associated with illness (RR: 2.33; 95%CI: 1.25-4.35; p-value=0.0083). 85% (22/26) of cases can be explained by consumption of the mushroom dish or the wedding cake.

Conclusion: This foodborne NV outbreak can be explained by a NV-excreting kitchen worker with diarrhoea during work. Foods identified as the outbreak source may have been contaminated during preparation or plating. Despite numerous national guidelines to ensure food safety and hygiene standards, there was probably not enough awareness in this kitchen worker to stay away from work until 48 hours after resolution of gastrointestinal symptoms.

166 IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

22.114 Characterization of cholera outbreaks, preparedness and response in Niger State, Nigeria 2012: Transition to best practice

A. T. Bashorun¹, A. Ahumibe¹, S. Olugbon¹, P. Nguku², K. Sabitu³ ¹Nigeria Field Epidemiology and Laboratory Training Program, Abuja, Nigeria, ²Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ³Ahmadu Bello University, Zaria, Nigeria

Background: In 2011, 23,366 cases (case fatality rate [CFR]: 3.2%) of cholera cases were reported in Nigeria and Niger state was one of the affected states. To halt the cholera epidemics in Nigeria, steps at promoting best practices in preparedness and response were developed. Despite this,309 cholera cases (CFR: 1.29%) were reported in 6 states in Nigeria by week 26, 2012, hence we conducted study in July, 2012 in Niger.

Objectives: To characterize Niger's cholera outbreaks, determine trends, assess preparedness and response, and functionality of cholera control action plans and multi-sectoral approach to inform best practices.

Methods and Materials: We used a descriptive study design and secondary analysis of cholera surveillance data over from 2005-2007. We conducted key informant interviews with using i guides, appraised cholera action plans, outbreak preparedness/response, and laboratory using WHO checklists. Data was analyzed using Epi-Info version 3.5.5. and thematic analysis.

Results: In 2005, 4 cholera cases were reported, while 2006 reported 23 cholera cases. In 2011, 2,472 cholera cases (CFR: 2%) was recorded in 13(52%) local districts. The outbreak peaked at 827 cases in August (correlation Coefficient=0.02, P value=0.45). Kontagora had highest=1,306 (52.8%) while Agwara=highest CFR:20%. 522 (21.1%) of cases were younger than 5 years. Age specific CFR was greater than 2.0% for age groups above 10 years and below 1.8% for those less than 10 years; Age below 10 years tend to be protective from death at OR=0.66 (0.34-1.25, 95%CI).

Attack rate in state= 5.3/10,000 persons.

Antibiotic prophylaxis practiced in the state. Cary Blaire not available. No multi-sectoral committee for Cholera outbreak, no formal emergency plan, no water chlorination, no routine/periodic food inspection.

Surveillance system is simple, flexible, sensitive, poor data quality (55%), low Positive predictive (63%), and timeliness (68.7%). lincorporated into Integrated Disease and Surveillance Response (IDSR). Captures age only and no gender. It takes 24-96 hours between outbreak onset and laboratory confirmation.

Conclusion: Previous years' outbreaks have increased awareness/ preparedness in Niger but there is still need to provide the basic social amenities. Health education should be intensified and usage of prophylactic antibiotics discouraged. We provided guides on development and implementation of a cholera control action plan.

22.115

2.115 Epidemiological analysis of a large restaurantassociated outbreak of hemolytic uremic syndrome and encephalopathy caused by *Escherichia coli* O111 in Japan

Y. Yahata¹, T. Misaki¹, M. Nagira¹, Y. Tada¹, K. Taniguchi¹, K. Oishi¹, N. Okabe²

¹National Institute of Infectious Diseases, Tokyo, Japan, ²Kawasaki

City Institute for Public Health, Kawasaki, Japan

Background: Enterohemorrhagic Escherichia coli infection and related food borne disease is one of the major international public health concerns. On April 26, 2011, suspected *E. coli* infection case has reported from a general hospital to a local public health center in Toyama prefecture. And then, Toyama prefecture reported *E. coli* cases, some of whom developed sever complication and 2 of whom were fatal outcome.

Objectives: The objective of this investigation was to identify the cause of outbreak and response and to estimate the risk factor for the severe complications.

Methods and Materials: This outbreak investigation conducted a case-control study and trace-back investigation. Case defined as a person presenting with at least one gastroenteritis symptom (diarrhea, blood stool, abdominal pain, etc.) or diagnosed HUS by physician and isolate the *E. coli* O111 or detection of anti-lipopolysaccharide (LPS) antibody to the *E. coli* O111. Data collected from 26 local public health centers and 27 medical institutions. Pulsed-field gel electrophoresis (PFGE) analysis was performed clustering analysis. The exact logistic regression analysis used to estimate the identification of source of infection and the risk factors for severe complications.

Results: A total of 86 persons met the case definition in this outbreak as the case, 34 of which (40%) involved hemolytic-uremic syndrome (HUS) and 21 of which (24%) involved acute encephalopathy. This outbreak peaked on April 25 and 26, 2011. Based on the logistic regression analysis, gastrointestinal illness was significantly associated with consumption of the Yuhoke (OR=19.6, 95%CI: 7.0-54.8). The isolate from the fecal and raw meat material had a closely-related PFGE pattern to the outbreak strain with two bands difference. Comparison with 30–39 years of age, the development of HUS was significantly associated with 5–9 years of age (OR=16.5, 95%CI: 1.3->999.9) and 15–19 years of age (OR=13.4, 95%CI: 1.5-673.8). The development of encephalopathy was associated with 5-9 years of age (OR=13.9, 95%CI: 1.6- ∞).

Conclusion: In this outbreak, the prevalence rate of sever complication such as HUS and encephalopathy was higher than previous *E. coli* related reports. Outbreak investigation identified the Yuhoke consumption as the most likely outbreak vehicle of *E. coli* O111.

22.116 Epidemiological characterization of Chikungunya outbreak in Lahj Governorate, Southern Yemen, March–April 2012

A. A. Q. Thabet¹, S. M. A. M. Al-Eryani², N. AbdulAziz³, M. Obadi⁴,

M. Saleh⁵, A. AlKohlani⁶, A. Al-Samei⁴

¹Thamar University; Faculty of Medicine, Dhamar, nil, Yemen, ²Sna'a University, Sana'a, Yemen, ³Minstry of Public Health and Population, Sana'a, Yemen, ⁴Ministry of Public Health and Population, Sana'a, Yemen, ⁵Ministry of Public Health and Population, Sana'a, Yemen, ⁶Ministry of Public Health and Surveillance, Sana'a, Yemen

Background: An outbreak of Chikungunya fever is poorly documented in the twenty three countries of the Eastern Mediterranean Region of the World Health Organization. The first case of Chikungunya fever has been reported in Northern Yemen in the beginning of January 2011. **Objectives:**

This paper documents the first outbreak of CHIKV fever in Southern Yemen and highlights the activities and findings of the epidemiology and laboratory team during the outbreak

Methods and Materials: This was a case-series investigation in which the response teams conducted epidemiological and laboratory investigations on suspect cases. The cases identified were line-listed and a data analysis was undertaken regularly to guide the outbreak response.

Results: Overall, 234 cases meeting the Chikungunya fever suspected case definition, were reported between March 21 May 8, 2012, from 19 areas in Al-Hawtah district, Lahj Governorate, Southern Yemen. Only 30 (12.8%) of the suspected Chikungunya cases underwent laboratory testing and only 13 (43.33%) of them were laboratory confirmed as Chikungunya. Suspected Chikungunya cases had fever (100%) and arthralgia and joint swelling were reported in 95% and 64% of the cases, respectively. The overall attack rate was 7.52 cases/1000 populations. All age group and gender were affected.

Conclusion: This is the first time that Chikungunya virus has been isolated in Al-Hawtah district of Lahj governorate, Southern Yemen. The risk of expansion of Chikungunya fever to other governorates in Yemen and also to neighboring countries remains considerably high, as many of these governorates and countries are dengue prone, host large number of travelers from abroad and competent vectors for indigenous transmission of both dengue and Chikungunya exist in these countries. The location of this outbreak in a coastal area of the country makes the spread of the disease a further possibility.

International Meeting on Emerging Diseases and Surveillance 2013

22.117 Assessment of the compliance of poultry farmers and live poultry sellers to preventive measures against bird flu in Benin City, Nigeria

A. M. M. Qasim¹, V. Y. Adam², M. O. Kazeem³ ¹National Veterinary Research Institute, Vom, PLATEAU, Nigeria, ²University of Benin, Benin City, Edo, Nigeria, ³University of Ilorin, Ilorin, Kwara, Nigeria

Background: Bird flu epidemic in Nigeria caused socioeconomic dislocation that caused anxiety, depression in farmers and live poultry sellers; and near collapse of the poultry industry.

Benin City serves as major route for distribution of poultry of all ages to the southsouth and southeast zones of Nigeria from commercial hatcheries in southwest particularly and indigenous domesticated and wild birds northern zones of Nigeria.

Objectives: To avert future Bird flu epiemic, the compliance of poultry farmers, live poultry sellers and veterinarian to preventive and control measures adopted during the 2006-2007 to combat the epidemic was investiated.

Methods and Materials: Cross sectional study was utilized using structured questionnaire to collect data. Respondents included 236 poultry farmers, live poultry sellers and veterinarian aged 12-70 years in contact with birds through husbandary and sales of live poultry. The study duration was from October 2010–May 2011. Poultry farms and live poultry markets were viisited. Verbal informed consent was obtained from participants. The study objective was explained to them clearly and assured the research has no harm to participants. Their confidentiality was assured.

Results: The research found poor compliance to: disease reporting to appropriate veterinary authority 37.2%; training of workers on prevention 31.9%; wearing of face mask while handling sick birds 21.6%; raring of birds at home 69.4%; while 88.4% beleive public health information communication awareness program was helpful in preventing bird flu. Sale 6.6% and consumption of dead and moribund birds 0.9% were discovered in this study

Conclusion: Governmental incentives and repackaged educational information are neccessary for the compliance to be effective. Education of these occupational groups is a desideratum, which must involve active participation by veterinarian.

This study is exceptionally useful in strengthening bird flu prevention and control programs.

22.118 Knowledge of HIV/AIDS and attitude towards HIV patients among the educated youth of Pokhara valley: A Cross-sectional study from Western Nepal

R. P. Adhikari¹, B. Sathian²

¹Prithvi narayan college, Pokhara, Kaski, Nepal, ²Manipal College of Medical Sciences, Pokhara, Kaski, Nepal

Background: Adolescence is a period of great physical, mental and emotional confusion with teenagers in search of their identity, very often start experiencing with intravenous drugs or sex, both making them vulnerable to contracting HIV.

Objectives: Objective of the study was to assess the awareness of HIV among the youths of the Pokhara valley

Methods and Materials: A cross sectional study carried out in 2000 educated youths of Pokhara, Nepal between 01 January 2011 and June 2011 using a structured questionnaire containing details of HIV aetiology, risk factors, attitude towards HIV patients, Source of information. Descriptive statistics and testing of hypothesis were used for the analysis using EPI INFO and SPSS 16 software.

Results: All of the respondents were aware about HIV. 97.5% had correct knowledge about the risk factors. 60 % of the respondents attitude towards the AIDS patients was positive. Among them 70% had no objection in treating AIDS patients in the general hospital and working with them. The main sources of their information were from TV and Mass media.

Conclusion: These findings have implications for those who are responsible for providing care to the increasing numbers of people with HIV/AIDS. Whether it is their religious beliefs, their educational level, or effect of both that has led to the positive attitudes of educated youth towards people with HIV/AIDS. It will have a divine effect as they are the professionals of the future.

22.119 Refugees, reforms and drug resistance: Political transition and artemisinin resistant malaria in Myanmar

I. M. P. Ghinai¹, **T. T. W. Hla²**, T. Hesketh²

¹London School of Hygiene and Tropical Medicine, London, United Kingdom, ²University College London (UCL), London, United Kingdom

Background: Malaria control has been one of the public health successes of the last decade with a reduction in global mortality from 1.8 million deaths in 2004 to 1.2 million in 2010. Therapies based on artemisinin have been an essential part of this.

But progress is fragile: resistance to artemisinin-based drugs emerged in Cambodia in 2004 and has spread through Thailand to the eastern border of Myanmar. Refugees and migrants living on the Myanmar-Thailand border have long experienced excess mortality from *Falciparum* malaria due primarily to poor access to healthcare. These mobile populations may provide the conduit for artemisinin resistance to enter Myanmar.

In the 1970s, Myanmar was of international importance in the dispersal of chloroquine-resistant malaria and later provided a path for sulfadoxine-pyrimethamine resistance to spread to the Indian subcontinent and Africa, with immense public health consequence. The Myanmar-Thailand border is therefore a crucial battleground for the containment of artemisinin resistant malaria.

Objectives: WHO believes there is a "finite window of opportunity to contain artemisinin resistance." We argue that this window coincides with the time-limited opportunity to maximise the public health benefits from recent political reforms in Myanmar. We scrutinise prospects for the international effort to contain artemisinin resistance in the context of political change in Myanmar.

Methods and Materials: We reviewed the published and grey literature around artemisinin resistance and the political reform process and interviewed key political and public health stakeholders.

Results: We elucidate 5 key areas which provide opportunities and challenges for artemisinin resistance containment within Myanmar. 1) Improved national regulation of malaria diagnoses and antimalarial treatment. 2) Strengthened surveillance through increased engagement with the international scientific community. 3) Increased funding for malaria control—internationally and domestically. 4) Improved relations with neighbours enabling harmonised cross-border programmes to target migrants. 5) Improved health-and-safety regulation of high-risk industries such as forestry.

Conclusion: We are at a critical juncture—containing artemisinin resistance is a global public good and Myanmar is of central importance to this. The political reforms in Myanmar provide a unique opportunity for improving malaria control. Current artemisinin resistance control strategies could make more of the opportunities presented.

22.120 Influence sociopolitical factors to human leptospirosis in Crimea (Ukraine)

O. L. Pavlenko, O. B. Khaytovych

Public Institution "Ukrainian Anti-Plague Station" Ministry of Health of Ukraine, Crimean State Medical University named after S.I. Georgievsky, Simferopol, AR Crimea, Ukraine

Background: Epidemic process can vary quantitatively and qualitatively under the influence of social and environmental conditions. **Objectives:** Determine the value of the socio-political changes in the

incidence of human leptospirosis in the Crimea (Ukraine).

Methods and Materials: The incidence rate of leptospirosis in the period from 1946 to 2011 was analyzed on base of archival materials and on base of 197 cards epidemiological survey (1981–2011).

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

Results: There are three periods, which have distinctive epidemiological features in the dynamics of the epidemic process of leptospirosis in the Crimea. The 1st period (1946-1961): leptospirosis was associated with farm animals; disease was manifested by anicteric form and the formation of risk groups-agricultural workers and children who use contaminated water for swimming leptospirosis. The 2nd period (1962-1979) (no any human cases of leptospirosis) was determined by the stability of social and economic conditions, and good health activities on the prevention of animals and people diseases in the risk groups (vaccination). The beginning of 3rd period (1980-2011) coincided with the improvement of laboratory and clinical diagnosis. During this period there have been significant social and political changes in Ukraine. In the beginning of period, the morbidity dominated in group of farmers and slaughterhouses, but late the disease has become the most frequently occur among the officially unemployed and pensioners, because farms were restructured and due to the change of ownership, downsizing and bankruptcy of industrial complexes. Decrease in social standards of living contributed to the change of human activity (fishing became a means of livelihood and subsistence), so people were more likely to be in the natural foci. Active urbanization led to the growth of cities, but the low hygienic level recent decades (poor housing, untimely garbage collection, etc.) contributed to the increased incidence of leptospirosis in urban population.

Conclusion: Changes in the characteristics of the leptospirosis in Crimea were promoted by social and political conditions. This was manifested in the intensity of the epidemic process; seasonal change; change of risk group; expanded area of infection spread; change the prevailing source of infection and prevailing Leptospira serogroups.

22.121

Understanding risky behaviours among those slaughtering, selling and buying poultry in live bird markets in Indonesia

S. Naysmith

London School of Economics and Political Science, London, United Kingdom

Background: Live bird markets (LBMs) in Indonesia, and around the world, pose a health risk to both workers and customers. The many surfaces where birds are kept, killed and sold in LBMs provide myriad opportunities for potential zoonotic transmission of avian influenza A (H5N1) virus. While there are ample data on epidemiological conditions in these markets, there is a dearth of social research exploring risk behaviour in these environments.

Objectives: This paper examines the rationale for LBM workers and customers to undertake risky behaviours, such as touching poultry, not wearing personal protective equipment, inadequate cleaning and hygiene, and not reporting sick or dead poultry arriving in the market.

Methods and Materials: This paper draws from in-depth interviews (N~240) and participant observation conducted in three LBMs in three provinces in Indonesia over three years (2009-2012).

Results: Findings suggest that LBM workers' and customers' behaviours are shaped largely by economic and social incentives. People touch poultry to determine the quality and freshness of the meat and in order to determine the health of live birds. Recent scandals involving sellers injecting meat with water and the use of formaldehyde to preserve meat makes this tactile contact imperative. Workers opt not to employ Personal Protective Equipment (PPE) because to use PPE may mark them as the source of disease and render their products undesirable, jeopardizing sales. Washing hands routinely between slaughter and sale in LBMs is difficult because water is a paid-for commodity that is not always readily available until the end of the workday. Sellers hesitate to report sick and dead birds because they do not want to attract unwanted attention from government officials and prefer to kill and sell sick birds before they die so as not to lose profit.

Conclusion: LBMs are the source of multiple human infections with H5N1. Controlling the spread and impact of avian influenza (H5N1) requires a greater understanding of high-risk behaviours at the animal-human interface. This research helps explain human behaviours linked to disease emergence and spread and concludes in arguing for greater consideration of the social and economic incentives of at-risk communities in the worst affected countries.

.122 The 1994 Outbreak of Pneumonic Plague in Surat, India: A Retrospective Analysis

J. Varco

Georgetown University, Washington, DC, USA

Background: In the fall of 1994, pneumonic plague ravaged Surat, India, a city located in the western Indian state of Gujarat. This occurred prior to the robust electronic surveillance systems of the post-SARS arena, and organizational response was characterized by chaos and inefficiency, as well as a notable lack of publically available data and collaboration. To this day, events that transpired remain enigmatic. It is imperative that the global community understands these events in a retrospective manner, so as to better prepare communities for future zoonotic events.

Objectives: To better understand the events of the 1994 outbreak of pneumonic plague in Surat, India.

Methods and Materials: A retrospective analysis was conducted of publically available data and literature. A special emphasis was placed on examining data provided by the scientific community, public health sector, industrial institutions, and governmental offices.

Results: A poster is presented elucidating a retrospective analysis of the pneumonic plage outbreak in Surat, India at the close of the 20th century. We provide a holistic analysis of the confluent events leading up to the outbreak, as well as how it was addressed on both a local and global level. We also provide a comprehensive graphical timeline by which one can better understand these events in their contextual settings. Sociopolitical issues, as well as confluent events and cultural viewpoints are explored in depth.

Conclusion: A color poster, in a readily accessible format with graphical representations of the events that transpired is presented. This enables readers to understand the outbreak of pneumonic plague that struck Surat in a holistic manner. Using the data presented, decision-makers will be better able to generate frameworks by which to address future outbreaks.

22.123 The use of compulsory powers to control the spread of HIV in New Zealand: The case of a man detained without trial for eleven years; a challenge for legislators, public health practitioners and community alike.

A. R. G. Humphrey

Canterbury District Health Board PO Box 1475, Christchurch, New Zealand

A conviction of criminal nuisance on an HIV positivie male prostitute was quashed on appeal in the District Court of Christchurch, New Zealand in 1999. The judge asked that a more appropriate approach to incarceration would be for public health authorities to invoke section section 79 of the Health Act 1956, which provides the Medical Officer of Health with compulsory powers to isolate and detain any person suspected of spreading an infectious disease.

The use of such powers in some form goes back to the nineteenth century in New Zealand and many other countries, and the ability to confine people at short notice in the light of SARS, Pandemic influenza and other emerging diseases has been reviewed and retianed in some form in many countries.

Unfortunately, the legal provisions provided for under the New Zealand Health Act 1956 are woefully inadequate in the 21st century for a disease which was perceived as lifelong and incurable.

This poster describes the difficult legal, medical, sociological and virological issues with which the health authorities were confronted, how they addressed these problems and contained a public health threat without breaching human rights ethics, principals and laws, and how the problem of reconciling human rights and public safety was eventually resolved in the face of extreme media pressure and community interest.

This case provides valuable lessons for those considering the issue of public health powers to contain public health threats, particularly from new and emerging diseases.

International Meeting on Emerging Diseases and Surveillance 2013

22.124 Disclosure of HIV status by HIV positive patients attending adult anti-retrovival therapy (ART) clinic at Gombe State Specialist Hospital, Gombe, Nigeria 2011

R. Dankoli¹, A. A. Aliyu², P. Nguku³, T. Dahiru², O. Ossai⁴ ¹State Specialist Hospital, Gombe, Gombe, Nigeria, ²Ahmadu Bello University, Zaria, Nigeria, ³Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ⁴Nigerian Field Epidemiology and Laboratory Training Programme(NFELTP), Abuja, FCT, Abuja, Nigeria

Background: Disclosure of HIV status especially to sexual partners is an important prevention goal. Many international organizations including UNAIDS, WHO and CDC are emphasizing the importance of HIV status disclosure.

Objectives: This study was undertaken to determine the prevalence of HIV status disclosure and the factors that are associated with disclosure of HIV status by HIV positive patients attending the adult ART clinic in Gombe State Specialist Hospital (GSSH)

Methods and Materials: We conducted a cross sectional descriptive study among adult HIV positive patients at GSSH. Study participant were sample using a systematic random sampling technique with a sampling interval of 5. An interviewer administered structured questionnaire was used to collect data. Data was analyzed using Epi info version 3.5.1.

Results: A total of 198 out of 200 respondents were interviewed yielding a response rate of 99%. There were more female (80.3%) respondents compared to male (19.7%). Majority (76.8%) of the respondents were between 20 and 39years old with a mean age of 32.9years (SD ±9.5). Sixty percent of the respondents were married with majority (78%) of them in a monogamous family setting. The vast majority (97.5%) had disclosed their HIV status and majority (36.8%) of them disclosed to their spouses. Sixty four percent of the respondents had treatment supporter and spouses (42.9%) were their choice of a treatment supporter. Disclosure of HIV status was found to be associated only with young age (<40years) [AOR 38.16; 95% CI 2.42-602.61]. Female gender [AOR 1.53; 95% CI 0.14-17.02] being employed [AOR 9.76; 95% CI 0.64-148.65] are more likely to disclose HIV status. While being educated [AOR 0.69; 95% CI 0.07-6.74], short duration of infection (<1year) [AOR 0.18; 95% CI 0.01-3.17] and being married [AOR 0.31; 95% CI 0.02-4.23] are less likely to disclose HIV status.

Conclusion: Disclosure of HIV status was high in the study population. Spouses were the most preferential choice of persons HIV statuses were disclosed to and also the most adopted as treatment supporter. HIV status disclosure should be made soon after diagnosis because of its importance especially to couples. This may encourages family support and lessens stigmatization.

22.125 Quantification of factors influencing pig farmers' intention to apply On-Farm Biosecurity measures based on theory of planned behavior T. Wilke, B. Petersen

University of Bonn, Bonn, Germany

Background: The term On-Farm-Biosecurity measures covers actions and facilities that fall under the responsibility of the farmer and are intended to shield the farm from biological risks. Pig farmers in Germany are confronted with increasing requirements from slaughter companies, private food standards, veterinary authorities and societal stakeholders to comply with strict On-Farm-Biosecurity (e.g. as part of risk-based surveillance systems). On-Farm-Biosecurity measures are mostly well-known but are frequently not consequently applied, because effectiveness, costs, benefits and other parameters are highly uncertain, making it difficult to integrate them into animal health-management concepts.

Objectives: Although a number of potential influencing factors could be found in scientific literature, little seems known about what are the main drivers for German pig farmers to consequently apply On-Farm-Biosecurity measures. Goal of this study was to explore the main factors for farmers' intention using quantitative methods.

Methods and Materials: Potential influencing factors were collected from literature review and expert consultation. Based on Ajzen's theory of planned behavior a conceptual model was constructed how these factors interrelate. Data collection was done through a web-based survey among members of three pig producer associations in Germany (fattening farms and piglet producers). Statistical analysis was done by structural equation modeling based on the Partial Least Squares (PLS) approach.

Results: The structural model consists of three latent exogenous variables (Attitude, Subjective Norms and Perceived Behavioral Control) and one latent endogenous variable (Behavioral Intention). All latent variables have reflective imeasurement variables. Quality criteria for the measurement model indicate that it is reliable and valid: Indicator loadings above 0.7, *Average Variance Explained (AVE)* all above 0.69, *Construct Reliablities* above 0.81. Assessment of structural model was also successful: R^2 of the endogenous variable "Behavioral Intention" is >0.6, path coefficients are all meaningful have values >0.3 and bootstrapping proved them to be significant at least at the 5%-level. *Redundancy* is >0, showing that the chosen model has prognostic power.

Conclusion: Theory of planned behavior proved to be a valid approach to explain pig farmer's intention to apply On-Farm Biosecurity measures consequently. This forms the basis to support pig farmers in On-Farm Biosecurity Management concepts.

22.126 Epidemiological pattern of measles infection in children under five in Oyo State, Nigeria, 2007–2011

L. A. Okeke¹, P. B. Adewuyi¹, O. Ajumobi², S. Gidado¹, P. Nguku³, O. Fawole⁴, H. Akpan⁵

¹Nigeria Field Epidemiology and Laboratory Training Programme, Abuja, Nigeria, ²Nigerian Field Epidemiology and Laboratory Training Programme, Abuja, FCT Abuja, Nigeria, ³Nigeria Field Epidemiology & Laboratory Training Program, Abuja, Nigeria, ⁴University of Ibadan, Ibadan, Nigeria, ⁵Epidemiology & Health Emergency Response Division, Abuja, Nigeria

Background: Measles is one of the leading causes of death among young children in spite of the routine childhood immunization program. The burden in Nigeria is not well documented and this varies from state to state. Worldwide measles vaccination campaign focuses on children under 5 (U5) years of age in order to reduce mortality and morbidity among them. In Nigeria, the National Policy recommends vaccination campaign. We conducted this study to describe the epidemiological pattern of measles infection among the U5 children in Oyo State.

Objectives: To describe the epidemiological pattern of measles infection among under five in Oyo State.

Methods and Materials: We reviewed surveillance record from 2007-2011 in Oyo State Ministry of Health. A descriptive analysis of socio- demographic data and vaccination status using Epi info 3.5.3 and Microsoft excel 2007 to determine mean, standard deviation, proportions and odd ratios was performed.

Results: Of 928 under 5 suspected measles cases, 483 (52.0%) were males. Overall mean age was 2 years (SD1.4). Of the suspected measles cases, 628 (68.0%) live in urban areas while 554 (59.7%) had at least one dose of measles vaccine. Of the 554 vaccinated children, 382 (69.7%) live in urban area. Of the suspected measles cases, 194 (20.9%) were measles IgM positive. The incidence rate among the U5 is 14/100,000. Vaccinated U5 children are less likely to have measles infection (Odds ratio=0.3, 95% CI: 0.22-0.44).

Conclusion: In the study vaccination proffered protection to U5 children against measles. However, fewer than expected children were vaccinated. We recommend intensified measles campaign and improvement of routine immunization.

22.127 Production of tissue culture rabies vaccine for human in Nepal

G. R. Pant

Rabies Vaccine Production Laboratory, Directorate of Animal Health, Kathmandu, Nepal

Background: Rabies is an endemic zoonotic disease and causes 200 human death anually in Nepal.

Objectives: Production of safe, pure and potent vaccine to control rabies in Nepal

Methods and Materials: A trail batch of tissue culture inactivated anti rabies vaccine was produced at Rabies Vaccine production Laboratory in Kathmandu in 2012. Vero working cell line (164P) was used for propagation of cell that was infected with PV/RV at 100 MOI working rabies virus strain at 169 serial passages of cells. Virus cultures fluid was harvested and pooled sample of fluid was tested by using Anigen Rapid Test Kit for the detection of rabies virus. Pooled sample was found positive for rabies virus antigen where as the fluid collected from control cell was negative for rabies virus. The harvested virus was then centrifuged at 10,000 rpm into angle rotor and condensed for purification in pellicon machine (milli pore) under Pump Master flex speed 0.5, feed pressure 0.2 Kg/cm² and pellicon filter membrane 0.02 um pore size.

Results: The titer of virus before inactivation was 10^{8.5} TCID 50/0.1ml. Finally this virus fluid was inactivated with beta propiolactone. The ED 50 of the titer of vaccine was 1:72 when challenged with CVS 500 LD50 /0.03 ml in NIH test. The titer of vaccine was 2.2 IU when tested at Changchun Veterinary Research Institute, China. The result of other quality test such as inactivation, toxicity, safety, specificity, sterility and pH test were found satisfactory.

Conclusion: This is remarkable development toward the production of rabies vaccine inNepal.

22.128

Evaluation of the immune response during experimental infection of vaccinated and unvaccinated pigs with Classical Swine Fever Virus (CSFV) using Fluorescent Activate Cell Scanning (FACS)

G. Curina, M. Bazzucchi, G. M. De Mia, M. Mari, L. Molinari,

K. Forti, G. Rizzo, M. Cagiola, G. Severi

Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche, Perugia, EU, Italy

Background: Few studies have investigated the mechanisms of interaction between Classical Swine Fever Virus (CSFV), a disease characterized by initial leukocytosis followed by severe leukopenia affecting both peripheral-blood B and T lymphocytes, and immune response. Little is known about the role played in the humoral immune response by the cell populations remaining after lymphocyte destruction.

Objectives: The aim of this work was to study the immunological mechanisms associated with the humoral immune response of unvaccinated and vaccinated pigs with a live attenuated vaccines (obtained from spleen of rabbits inoculated with Chinese strain of Classical Swine Fever Virus). Full knowledge of the humoral immune response to CSF virus is essential to a better understanding of host defence mechanisms and to develop a new generation of CSFV vaccines.

Methods and Materials: For five weeks, two groups of pigs were involved, six vaccinated and six unvaccinated. Two weeks after vaccination both groups were infected with ISS 60 CSFV strain. At interval time of 72 hours, blood samples were collected to detect antibody production, virus replication, cytokines expression and finally to analyse four lymphocytes subpopulation using BD FACSCalibur. Specific monoclonal antibody mouse anti pig CD3, CD21, CD4, and CD8 were used.

Results: During the experiment we studied the immune response of

porcine leukocytes populations in the acute infection of pigs vaccinated and unvaccinated caused by virulent strain of classical swine fever virus (ISS 60 strain). Unvaccinated pigs showed initial leukocytosis followed by severe leukopenia that lead to death the animals. In the other group of vaccinated animal we observed an important protective immune response and the animals survive.

Conclusion: Home made live attenuated vaccine demonstrated high protection and safety. Further information will be acquired expanding the number of fluorescent monoclonal antibody directly to other lymphocytes subpopulations with the aim of deepen the knowledge regarding intimate aspects of porcine immune response in classical swine fever infection and vaccination. Then, a better understanding of the immune response in case of different viral strains will be achieved using fluorescence activated cell scanning (FACS) technique.

22.129

Cytokines expression in vaccinated and unvaccinated pigs infected with Classical Swine Fever Virus strain ISS 60: Preliminary results.

M. Bazzucchi, G. Curina, G. M. De Mia, F. Feliziani,

M. Giammarioli, A. De Giuseppe, G. Rizzo, K. Forti,

M. Cagiola, G. Severi

Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche, Perugia, EU, Italy

Background: Classical swine fever virus (CSFV) is the ethiological agent of a devastating disease that poses one of the greatest risks to the swine industry worldwide. CSF has been controlled in the EU through a stamping-out slaughter policy. The presence of CSFV in European wild-boar populations, together with increasing public opposition against stamping-out strategy, have now led to an increased likelihood that vaccination may be deployed as a last resort component of a control policy.

Objectives: During the experiment we have explored the kinetics of the cytokine responses from peripheral blood cells of pigs unvaccinated and vaccinated with a live attenuated vaccine and subsequently infected with CSFV–ISS 60 strain. With a view to providing additional information on cellular mechanisms that may contribute to protection, which in turn may aid the development of the next generation of CSFV vaccines.

Methods and Materials: For five weeks, twelve pigs were involved. Two weeks after vaccination of six pigs all the animals were infected with ISS 60 CSFV strain. At interval time of 72 hours, blood samples were collected to detect antibody production, virus replication, lymphocytes subpopulation analysis and finally cytokines expression. The presence of IFN- γ and other cytokines was analysed using different ELISA tests which measures porcine IL-1b, IL-6, IL-8, IL-10, IL-12, and TNF- α .

Results: The results observed during the experimental infections of pigs with ISS 60 strain of CSFV showed that immunological mechanisms underlining the rapid protection afforded by live attenuate vaccines were not well defined, however prevention may precede the appearance of neutralising antibody but not IFN- γ secreting cells in peripheral blood, suggesting that cellular immunity was involved. Also CSFV vaccines provide a rapid onset of complete protection but pose problems in discriminating infected amongst vaccinated animals.

Conclusion: Comparing and correlating the value and the role of the different citokynes we find additional information concerning the cytokine mediated mechanisms that may contribute to protection or pathology, and therefore aid the development of the next generation of CSFV vaccines. Further information will be acquired comparing citokyne results with fluoscence activated cell scanning (FACS) analyses to better identify different responses between vaccinated and infected animals.

International Meeting on Emerging Diseases and Surveillance 2013

22.130 Outbreak Investigation of Measles among fully vaccinated children in Village Khair Muhammad (KM) Dasti, District Naushahro Feroze, Sindh, April 2012.

M. P. Jokhio

FELTP Pakistan, Naushahro Feroze., Pakistan

Background: On April 24, 2012, eight patients of suspected measles were reported by the Experimental dispensary of village KM Dasti to EDO (health). A 4-member team was deployed to confirm the outbreak and formulate recommendations for control.

Objectives: To confirm the outbreak and formulate recommendations for control.

Methods and Materials: Investigation was carried out from April 24–27, 2012. Case was defined as a child ≤ 15 years of age residing in village KM Dasti with: a generalized rash for three or more days, a fever at or above 101°F, and one or more of the associated symptoms, including cough, or coryza (runny nose), or conjunctivitis (red eyes) from April 14-27, 2012. Active case finding was done from a population of 340 who are less than 15 years of age (37% of a total population of 919). Two blood samples were collected and sent to NIH Islamabad for Laboratory diagnosis.

Results: Eight cases were identified, out of which 75% (n=.06) were females. Median age was 10 years (range: 4.7 to 14 years). The prevalence of measles was 2.4%. Fever with rashes & itching (100%, n=8), cough with throat pain (75%, n=6) and nasal discharge (60%, n=5) were common complaints. All cases belonged to 2 closely related families. All cases were fully immunized against measles, according to EPI records. No death was reported. All the cases visited OPD of local Dispensary. Laboratory results are still awaited.

Conclusion: Cases appeared in vaccinated children which implicates that either there is some problem with the quality of vaccine, cold chain maintenance or vaccination techniques. Two Mopping-up activities were conducted in the village and surroundings 2 villages, Five Health Education sessions were conducted by LHWs on hygiene and disease prevention.

22.131 The ocular conjunctiva as a possible mucosal immunization route

A. Inic-Kanada¹, M. Stojanovic², S. Belij¹, E. Marinkovic²,

I. Stojicevic², J. Montanaro¹, E. Stein¹, N. Bintner¹,

T. Barisani-Asenbauer¹

¹Medical University of Vienna, Vienna, Austria, ²Institut of Virology, Vaccines and Sera-Torlak, Belgrade, Serbia

Background: Ocular surface infections include several blinding disorders that affect the cornea and conjunctiva at the front surface of the eye. Since antimicrobial therapy has shown its limitation to protect from reinfection and vision threating sequels, also partially protective vaccines against ocular surface pathogens would impact ocular morbidity. As mucosal immune responses are most efficiently induced by the administration of vaccines onto mucosal surfaces, we wanted to assess the ocular mucosa with the conjunctiva-associated lymphoid tissue (CALT) as a mucosal route of immunization.

Objectives: The aim of the present study was to elucidate local and systemic immune responses after CALT immunization using a tetanus toxoid (TTd) as a model antigen.

Methods and Materials: BALB/c and C57BL/6 mice were immunized via conjunctiva with TTd, either alone or mixed with 2% glycerol and whole-cell B. pertussis (wBP) as adjuvants. Mice were immunized on days 0, 7 and 14 via either conjunctival or s.c. route, and the evaluation of local and systemic immune response were done two weeks after the last immunization. Four weeks after the course of conjunctival and s.c. immunization, anesthetized mice were challenged with lethal dose (2 LD₅₀) of tetanus toxin (TTn).

Results: The conjunctival application of TTd in BALB/c mice induced skewing of TTd-specific immune responses toward a Th1/Th17 profile, as determined by the stimulation of IFNy and IL-17A secretion and/or the concurrent pronounced reduction of IL-4 secretion, irrespective of the applied adjuvant. In conjunctively immunized C57BL/6 mice, only TTd administered with wBP promoted the establishment of a mixed Th1/Th17 TTd-specific immune response, while TTd alone or with a glycerol adjuvant initiated a dominant Th1 response against TTd. In all cases, this response was accompanied by an intense rise in IL-10 secretion. Immunization via the conjunctiva with TTd plus wBP adjuvant resulted in a 33% survival rate of challenged as compared to a 0 % survival rate in non-immunized animals.

Conclusion: Immunization via conjunctiva with TTd in different contexts induced TTd-specific local and systemic immune responses, predominantly of Th1 type. The strongest immune responses developed in mice that received TTd together with wBP.

22.132 Detection of rabies antibodies in dog sera

A. Ondrejková, E. Slepecká, J. Süli, R. Ondrejka, Ľ. Korytár, M. Prokeš, P. Čechvala

University of Veterinary Medicine and Pharmacy in Košice, Kosice, Slovakia

Background: Vaccination is irreplacable and very important when it comes to the prevention of rabies in animals and humans. For the detection of specific antibodies, two neutralizing tests are being used RFFIT and FAVN tests; they are the current reference methods, which are recognized and intended by WHO and OIE. In recent years, several ELISA tests have been developed, which have been used to determine rabies antibodies in sera from vaccinated carnivores in combination with the neutralization test

Objectives: The aim of our study was to compare the results of detection of rabies antibodies by in vitro methods as is rapid fluorescent focus inhibition test (RFFIT), fluorescent antibody virus neutralisation test (FAVNT) and the immunoenzymatic assay ELISA.

Methods and Materials: For comparison of detection rabies antibodies, by individual serological methods we used 339 sera obtained from dogs vaccinated with commercial rabies vaccines as well as from 23 unvaccinated dogs. The blood of vaccinated dogs was collected on the thirtieth day from vaccination. Sera obtained from vaccinated and unvaccinated dogs, were heated before the testing (30 minutes at 56°C) and stored at -20 °C. The serum from dogs was tested by three serological methods: RFFIT (Smith a kol. 1996), FAVNT (Cliquet et al., 1998) and ELISA test (Bio RadPlatelia Rabies II Kit).

Results: In 312 sera (92.04%) coming from vaccinated dogs was detected requiring levels of antibodies, ie. antibody titer greater than 0.5 at IU/cm3 RFFIT and FAVN test. The titer of anti-rabies antibody less than the desired value was detected by RAFT and FAVN tests in 27 sera, which represents 7.96%. The titers of rabies antibodies were obtained by ELISA test, and they are in correlation with the results obtained with RFFUT and FAVN tests.

Conclusion: 362 dog seras were examined with FAVNT, RFFIT methods and the ELISA test. Sera with low and sufficiently high titre of antibodies has a similar result in determining by those methods. A critical level was seen in rabies antibodies close to the required protected level (0.5 IU/cm3) in sera of 27 dogs (7.96%); these were the sera obtained after primary vaccination of dogs.

22.133 Sublingual immunization as an alternative route for vaccine delivery

H. M. Amuguni¹, S. Lee¹, X. Sun¹, S. Tzipori²

¹Tufts University, North Grafton, MA, USA, ²Tufts University Cummings School of Veterinary Medicine, North Grafton, MA, USA

Background: Mucosal delivery of vaccines has the potential to eliminate the requirement for needles and induce strong immunity against pathogens. However, most protein antigens are poor immunogens when delivered orally, because of the degradation in gastric secretions during gastrointestinal transit, and the induction of tolerance.

Sublingual (SL) immunization is currently receiving attention as a novel delivery site for therapeutic drugs and vaccines. As opposed to oral administration, SL administration of proteins and peptides

is a convenient way to deliver them to the bloodstream. This route avoids the enterohepatic circulation and immediate destruction of ingested molecules by gastric acid or partial first pass effects of hepatic metabolism.

Objectives: Previously, we have evaluated the efficacy of SL immunization with Bacillus. subtilis engineered to express tetanus toxin fragment C in mice and piglets. Animals developed protective IgG antibodies against tetanus. Immunized mice survived challenge with tetanus toxin. The objective of this study was to evaluate the efficacy of SL immunization using other immunogens. Cholera toxin, measles (rubeola) virus and a chimera of *clostridium difficile* toxin A and B (C. diff Wi-ar) were used as antigens in mice.

Methods and Materials: Groups of 5-7 mice, aged 6-8 weeks, received 3-5 immunizations via SL route with ten ul of measles (Rubeola) virus antigen, cholera toxin and C. diff Wi-ar. A non-toxic mutant of E. coli heat labile enterotoxin (mLT) was included as adjuvant in some of the studies. Measles vaccine was used as a positive control. All animal samples were tested for the presence of IgG antibodies against cholera toxin, measles, and C. difficile antibodies by a standard ELISA test.

Results: Robust anti-Cholera toxin titers were detectable after two immunizations. Rubeola antigen with mLT induced higher antibody response in comparison to the non mLT group. C. diff Wi-ar toxin A (rTcdA) animals developed higher antibody titers than the ones given toxin B (rTcdB) and addition of adjuvant improved antibody response.

Conclusion: SL immunization is a promising effective non-invasive route for delivery of immunogens. The robust antibody response to multiple antigens confirms that effectiveness of SL immunization is not unique to one imunogen.

22.134 Implementation of rotavirus surveillance in Albania

A. Simaku, M. Kota, I. Preza, A. Ahmeti, S. Bino Institute of Public Health, Tirana, Albania

Background: Rotavirus infections are common in infants and young children causing a significant morbidity burden and ≈527000 deaths in the world, predominantly in the developingcountries. Ahospital based surveillance system was established in Albania to estimate the burden of diarrheal disease caused by rotaviruses in children <5 years, its geographical distribution, seasonality and strains.

Objectives: Evaluate the rol of surveillance of vaccine preventable diseases and the burden of disease such as rotavirus infections for introduction of new vaccines

Methods and Materials: Five regional hospitals participated in the surveillance. Stool specimens were collected from children with diarrhea based on specific case definition over the period January 2011-May 2012.Epidemiological and clinical information was obtained through parental interview and medical chart review, and stool specimens were tested for rotavirus with enzyme immunoassays

Results: In total, 836 children with diarrhea were tested.Rotavirus detection rate varied according to surveillance site, from 24.5% in Tirana district to 48.5% in the districts of Lezha and Fier respectively. Overall, 256 (31.7%) specimens tested positive for rotavirus. The mea hospitalization duration was 3 days. The mean duration of illness among inpatients from the sentinel surveillance (rotavirus diarrhea severe) was 7 days. 40% of acute rotavirus gastroenteritis cases occurred during the first year of life, 31 during the second year of life. These episodes tended to decrease as children grew older and occurred with a frequency of 14%, 8%, and 6% during the third, fourth and fifth year of life, respectively. The rotavirus detection rate was highest during the months of January (60.9%) and November (60.3%). Rotavirus annual incidence is 5,146 cases per 100,000 population <5 years. The cumulative risk for hospitalization due to rotavirus disease is 70 per 1,000 or 7 children in every 100 being hospitalized by age <5 years.

Conclusion: The hospital-based rotavirus surveillance in Albania indicated a considerable burden of disease on the health care system and suggests the importance of introduction of vaccination

22.135 Clinical and host genetic characteristics of the patients with BCG osteomvelitis

T. Hoshina¹, H. Takada¹, Y. Mihara¹, K. Kusuhara², T. Hara¹ ¹Kyushu university, Fukuoka, Japan, ²University of Occupational and Environmental Health, Japan, Kitakyushu, Japan

Background: A small number of children develop osteomyelitis as a complication of the BCG vaccination. There have been no precise reports on the clinical characteristics and genetic backgrounds of the patients with BCG osteomyelitis.

Objectives: The aim of this study is to investigate clinical characteristics and genetic backgrounds of the patients with BCG osteomyelitis in Japan.

Methods and Materials: Twenty-seven patients diagnosed as having BCG osteomyelitis were enrolled in this study. We analyzed the clinical characteristics and the genetic backgrounds of all patients.

Results: The median interval of time between BCG vaccination and the development of osteomyelitis was 11 months (5-46 months). The long bones such as femur and humerus were commonly affected. Although many patients had a single lesion, 5 patients developed multiple ostepmyelitis. All patients were treated with anti-tuberculosis drugs for an average of 12 months (6-72 months) with the curettage of the bone. We performed the genetic analysis on these patients for the IFNGR1, IFNGR2, IL12B, IL12RB1, STAT1 and NEMO which have been known to be associated with the development of infections caused by weakly virulent mycobacteria. Four patients had mutations in the IFNGR1 gene. All of the patients diagnosed with interferon-g receptor 1 deficiency had multiple osteomyelitis, and 3 of the patients had recurrent mycobacterial infection. Among 23 patients without genetic mutations, only 1 patient had multiple osteomyelitis, and 2 had recurrent mycobacterial infection.

Conclusion: BCG should be considered as one of the causative pathogens in infants having osteomyelitis, if they had received BCG vaccination. Furthermore, the analysis of IFNGR1 gene should be performed in the patients with multiple BCG osteomyelitis and recurrent mycobacterial infection.

22.136 A mobile phone application for recording vaccine refusals

D. Murphy, J. Cremer, P. Polgreen The University of Iowa, Iowa City, IA, USA

Background: Although vaccines are a safe and effective approach for preventing morbidity and mortality, many people in developed countries are refusing vaccination for themselves and their children. Low vaccination rates are contributing to the re-emergence of vaccine preventable diseases around the world. More information is needed regarding when, where, and why vaccines are refused.

Objectives: Create a mobile app for health professionals to report vaccine refusals guickly and easily, so that refusal data can be collected and reported on a large scale.

Methods and Materials: A vaccine-refusal app (Vaccine Refused) for iOS was created using Objective-C and Apple's Cocoa Touch framework. The server component uses an app written in Python, using the open-source Django-Tastypie API framework to communicate app data via JSON feeds. Health professionals submit anonymized refusal reports by inputting patient sex and age range, hospital location, the vaccines refused, and reason for refusal. The app also offers a map of all reported refusals, filterable by date and vaccine, built using Apple's MapKit framework and open source pin visualization libraries.

Results: Vaccine Refused has already been deployed to doctors and health professionals in the United States. Over 20 different versions of the app were tested over a three month period, allowing maximal refinement of the application design to allow for quick and simple data logging. The server component provides secure data storage and fault-tolerant geocoding using the Google Geocoding API. First-time app users try a test submission using a demo mode that geocodes data locally but does not report to the server. Once the demo mode is switched off, submission reports are sent to the server and the submitter is asked to identify themselves during their first submission.

International Meeting on Emerging Diseases and Surveillance 2013

Conclusion: Vaccine Refused provides health professionals with a fast, secure, and anonymized way of reporting vaccine refusals. The data collected by Vaccine Refused will give computational epidemiology researchers an invaluable look at the numerous vaccine refusals occurring worldwide. The application will be available in the iTunes App Store and a link will be available at http://compepi.cs.uiowa. edu/vacref/ before the end of 2012.



22.137 Immunogenicity and safety of a Vero cell culture-derived whole-virus H5N1 influenza vaccine in immunocompromised and chronically ill patients

G. Aichinger¹, M. van der Velden¹, D. Portsmouth², W. Herr³, E. Distler³, E. M. Wagner³, M. Zeitlinger⁴, R. Sauermann⁴, C. Stephan⁵, N. Barrett²

¹Baxter Bioscience, Vienna, Austria, ²Baxter Bioscience, Orth/Donau, Austria, ³University Medical Center of Johannes Gutenberg-University, Mainz, Germany, ⁴Medical University of Vienna, Vienna General Hospital, Vienna, Austria, 5 Johann Wolfgang Goethe-University Hospital, Frankfurt am Main, Germany

Background: The development of vaccines against H5N1 influenza viruses is a cornerstone of pandemic preparedness. Clinical trials of H5N1 vaccines have been undertaken in healthy subjects but studies in risk groups are lacking. For that reason, the immunogenicity and safety of a non-adjuvanted cell culture-derived whole-virus H5N1 vaccine was investigated in specified risk groups.

Objectives: Assess the immunogenicity and safety of a non-adjuvanted cell culture-derived whole-virus H5N1 vaccine in immunocompromised and chronically ill adults.

Methods and Materials: Subjects received two priming immunizations with a clade 1 A/Vietnam H5N1 vaccine and a booster immunization with a clade 2.1 A/Indonesia H5N1 vaccine 12-24 months later. Antibody responses in both populations were assessed by microneutralization (MN) and Single radial hemolysis (SRH) assay and T-cell responses in a subset of immunocompromised patients were assessed by ELISPOT. Vaccine safety was assessed throughout.

Results: Two priming immunizations induced neutralizing antibody titers ≥1:20 against the A/Vietnam strain in 41.5% of immunocompromised and 64.2% of chronically ill subjects. After the booster vaccination, 71.6% and 67.5% of immunocompromised subjects and 77.5% and 70.8% of chronically ill subjects achieved neutralizing antibody titers ≥1:20 against the A/Vietnam and A/Indonesia strains, respectively. The MN data were broadly supported by the SRH data. T-cell responses against both H5N1 strains increased significantly (p<0.0001) compared to baseline. Substantial heterosubtypic T-cell responses were also elicited against the 2009 pandemic H1N1 virus and against seasonal H1N1, H3N2 and B subtypes. There was a statistically significant correlation between T-cell responses and antibody titers. Priming and booster vaccinations were safe and well-tolerated in both risk populations and adverse reactions were predominantly mild and transient.

Conclusion: A Vero cell culture-derived whole-virus H5N1 influenza vaccine is immunogenic, safe and well-tolerated in immunocompromised and chronically ill patients and induces antibody and T-cell memory responses which can be effectively boosted by a heterologous vaccine up to two years after priming. These data support use of the nonadjuvanted whole-virus cell culture-derived H5N1 influenza vaccine in both pre-pandemic and pandemic vaccination programs for these highly vulnerable risk groups.

22.138 Evaluation of polio supplementary immunization activity (SIA) in Bungoma Kenya, 2012

N. M. Muriu¹, Y. Ajack², S. Amwayi³, Z. Gura¹, I. Njeru², D. Langat² ¹Field Epidemiology and Laboratory Training Programme, Nairobi, Kenya, ²Division of Disease Surveillance and Response, Nairobi, Kenya, ³Field Epidemiology and Laboratory Training Programme, Centers for Disease Control, Nairobi, Kenya

Background: Poliomyelitis is a highly infectious viral infection often recognized by acute onset of flaccid paralysis. On August 2011, a case of wild poliovirus type-1 was confirmed in Kenya. The Division of Immunization conducted a Polio Supplementary Immunization Activity (SIA) targeting all children <5 years in 86 districts in July 2012. A hybrid strategy of door to door vaccination and static centers in strategic sites was implemented. We conducted an evaluation to assess vaccine coverage and effectiveness of social mobilization strategies in Bungoma West District.

Objectives: 1) To assess vaccination status of target children. 2) To determine the most effective strategies of passing immunization messages to community. 3) To identify main reasons for missed children. 4) To validate administrative data.

Methods and Materials: We conducted a cross-sectional survey using simple random sampling. A minimum of 2% of the target population was sampled both at household level and public places. Vaccination status was ascertained by corroboration of finger mark after vaccine administration. Data collection was done using a standardized questionnaire capturing vaccination status, reasons for non-vaccination and exposure to social mobilization.

Results: Results: Independent monitoring coverage was at 94 % (577) and the reported administrative coverage was 101 %(28,450) with a zero dose of 0.3 %(101). Among households with nonvaccinated children 27(75%) of the caregivers reported households not visited, 6(16%) reported absence of children and parents. Eighty-five percent (275) of caregivers were aware of the campaign; 24 %(123) reported learning about the campaign from health workers, 19% (96) through radio and 17.5 %(90) through public address system (PAS). Sixty-nine percent were aware of the disease being vaccinated against.

Conclusion: Conclusion: Health workers, radio and public address system were identified as the most effective strategies for social mobilization. This informed the consecutive rounds on the most effective strategies for socio-mobilization. The high administrative coverage of >100% was attributed to vaccination outside the target age-group.

22.139 Betraying the redox system for leishmania parasite

V. K. Dubey

Indian Institute of Technology Guwahati, Guwahati, Assam, India

Background: According to the World Health Organization report, over 12 million cases of leishmaniasis exist worldwide with 1.5 to 2 million new infections annually. Leishmaniasis evokes a major public health problem among 88 developing countries predominantly affecting the poor living in remote regions of Africa, Asia and Latin America. Leishmania donovani is most common Indian species of the parasite.

Objectives: Three enzymes of redox metabolism, ornithine decarboxylase, spermidine synthase and trypanothione reductase, are validated drug target of Leishmaniai and inhibition of these enzymes likely to be a strategy to develop novel drugs.

Methods and Materials: We have cloned these Leishmania donovani enzymes, expressed and purified. We have carried out extensive studies on trypanothione reductase (TryR), a drug target enzyme of Leishmania parasite. Using integrated computational and biochemical approaches, our group has identified few antitumor agents as competitive inhibitors as well as subversive substrates of TryR enzyme which subvert biological function of enzyme making it pro-oxidant from anti-oxidant. This mechanism leads to subversive substrate was investigated using various methods like FT-IR analysis and enzyme activity. Further, these candidate drugs were further screened for their mode of action (inhibition studies, ROS generation, cytotoxicity studies on parasite and human cell lines etc.).

Likewise, we have identified potential inhibitors of other enzymes of redox metabolism of the parasite and effect on parasite survival and parasite cellular biochemistry was investigated. We have also identified novel drug target proteins of the pathogen.

Results: The results so far indicate inhibition of redox enzymes of the pathogen results in apoptotic death of the pathogen by redox homeostasis imbalance.

Conclusion: We have indentified inhibitors of these enzymes that may be further developed as potential drug. Moreover, our study provides important insights into redox metabolism of the pathogen.

IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

22.140 Malaria outbreak investigation in a rain relief camp of internally displaced persons at village Bhimani, Kandiaro district Naushahro Feroze, Sind, Pakistan, August–September 2012

A. A. Ghanghro

FELTP, Government of Sind, Naushahroferoze, SIND, Pakistan

Background: Unpredicted monsoon rains started in late August 2012 in Sind province resulted in water surrounding populated areas added risk for mosquito breeding sites. On August 28, 2012 a local NGO doctor reported to Epidemic Investigation cell Naushahroferoze regarding malaria outbreak in rain relief camp of internally displaced persons (n=190) located at village Bhimani, Kandiaro district Naushahro Feroze.

Objectives: A three members committee was constituted to investigate the outbreak and recommend control measures.

Methods and Materials: A descriptive study (August 28-September 6, 2012) was conducted to select any person having fever with chills within period of August 23-September 6, regardless of age, sex and was registered in same rain relief camp. Every tent house was surveyed while blood slides were taken from each case for malaria microscopy.

Results: We investigated 45 cases with mean age 19.3 (1-55) years. 32 (71%) of 45 blood slides remained positive manifested by Plasmodium falciparum 18 (40%) while rest were Plasmodium vivax. 13 (29%) of 45 patients reported vomiting besides fever and chills. Malaria attack rate was 24%. Onset of more cases (n=9) showed in Epi curve on dated September 2, 2012 while spot map indicated cluster of more cases in two adherent tent houses which were close to a stagnant water pond.

Conclusion: Stagnant water pond (major mosquito breeding site) was likely the source of this outbreak. Residual sprays, treatment of ponds by larvicidals, supply of mosquito repels and bed nets followed to prophylactic treatment with chloroguin were able to control the outbreak. No new cases were reported after September 5, 2012. Improving sanitation and promoting methods to ensure expulsion of stagnant water from residential areas are likely to be effective measures in moderating future malaria outbreaks in this setting.

22.141 Understanding the effects of the Chagas disease control program in Venezuela after 50 years using eco-epidemiological modelling

E. Sulbaran Romero¹, M. Lange¹, J. L. Concepcion², H.-H. Thulke¹ ¹Helmholtz Center for Environmental Research, Leipzig, Saxony, Germany, ²Universidad de Los Andes, Merida, Merida, Venezuela

Background: The most important path to fight Chagas disease is the interruption of vector transmission by controlling vector populations. Nevertheless, after 50 years of the Chagas disease control program (CDCP) in Venezuela, the infection persists, and the processes leading to such persistence are not fully understood.

Objectives: The aim of this work is to broaden the understanding on the effect of the CDCP on the seroprevalence trend of anti-Trypanosoma cruzi antibodies within the Venezuelan population.

Methods and Materials: We developed and parameterized an epidemiological model applying pattern oriented modelling paradigms, which allowed us to identify relevant parameters but also overcome incomplete knowledge of given processes in the system. Moreover, a comprehensive analysis of the seroprevalence trend as well as of the infection persistence is provided.

Results: We quantify the probability of vector infection for the period 1958-1968 in two ways; constant and age-dependent. We show how the observed diminishing on age-dependent seroprevalence is related to the decreasing on such probability and we also quantified the time horizon for the extinction of seroprevalence from the system without any way of transmission or when the only possible path of transmission is the congenital. This study represents one of the first attempts to quantify probability of infection, as well as a deeper understanding on the effects of the CDCP on age-dependent seroprevalence in terms of the reduction of the infection probability. Conclusion: We conclude that the CDCP, as it was conceived, constitutes a robust starting point above which new strategies should be built since it allowed such a dramatic decrease in seroprevalence. However, improved control measurements are still necessary to avoid a new increasing on Chagas disease seroprevalence in Venezuela.

22.142

Epidemiology of vector-borne zoonotic and livestock viral diseases in central Thailand, 2012: A pilot study

N. Ketusing¹, P. Opaschaitat¹, C. Sirisukeepradit¹,

P. Boonpornprasert¹, M. Tattiyapong¹, J. Wattanamethanont¹,

J. Ratthanophart¹, H. Shirafuji², T. Yanase²

¹National Institute of Animal Health, Bangkok, Thailand,

²Kyushu Research Station, Kagoshima, Japan

Background: This study was initiated as part of a project under a collaboration between Thailand and Japan with the aim to understand the epidemiology of arthropod-borne viral diseases of livestock in central Thailand as a model for tropical and subtropical Asia.

Objectives: The ultimate goal of the project is to establish a system for surveillance and diagnosis of arbovirus infection in South East Asia.

Methods and Materials: Serological tests, detection of arboviral genes, and investigation on vector biology were initiated as part of this study. Livestock's serum samples were tested for Japanese encephalitis virus (JEV), Akabane virus (AKAV) and bluetongue virus (BTV) by HI and ELISA, respectively. The real-time RT-PCR was used to detect AKAV and BTV gene.

Results: The tests were positive with anti-JEV (11/20) and anti-AKAV (139/325), however, there were no positive results from detection of AKAV and BTV genes. Additionally, Culicoides spp. was collected in Ayutthaya and Saraburi provinces by using light traps. These were included C. oxystoma, C. imicola and C. brevitarsis. A part of Culicoides biting midges were used for RNA extraction and tested for AKAV and BTV genes by real-time RT-PCR, but all of the samples tested negative.



Wing patterns of Culicoides biting midges collected in Thailand during this study. Species are identified mainly by the wing patterns. Bar = 1 mm.

Conclusion: This study provided the evidence of arboviral infection in livestock and presence of vectors in central Thailand, however, this study was not considered epidemiology factors such as host species, location, farm management, and the link between entomology and serology. Further study is required for understanding arthropod-borne viral diseases in Thailand and other countries of Southeast Asia.

22.143 Determination of the association of nTreg (natural regulatory T cells) and its produced cytokines IL-10, TGFB with Kala azar disease and detection of its variations with treatment

M. Keshavarz¹, M. Rasouli², A. Alborzi³

¹Prof. Alborzi clinical microbiology research center, shiraz university of medical sciences, Shiraz, Iran, Islamic Republic of, ²Clinical microbiology research center, shiraz university of medical sciences, Shiraz, Iran, Islamic Republic of, ³Shiraz University of Medical Sciences, Shiraz, Iran, Islamic Republic of

Background: Kala azar currently among the most life-threatening diseases if it is not cured. The pattern of the immune response to *L. infantum* is believed to determine disease progression and clinical outcome. However, Kala azar patients, particularly those with the most severe forms of the disease, show an impaired cellular immune response characterized by the production of large amounts of suppressive cytokines such as interleukin-10 (IL-10) and transforming growth factor β (TGF β).

Objectives: The aim of this study was to investigate whether natural regulatory T cells (Treg cells) are involved in kala azar immunosuppression by analyzing the number, phenotype of these cells in patients with kala azar before and after the treatment.

Methods and Materials: PBMCs of kala azar patiens before, during and after treatment were isolated by using Ficoll-Hypaque density gradient, counted, and used to isolate T-cell subpopulations. CD4+ CD25+ (Treg cells) T cells were isolated by using the isolation kit and MACs column. All cells were grown in RPMI 1640. ELISA used to measure the production of IL-10 and TGFβ in the cultures, CD4+ CD25+ T cells were cultured. Culture supernatants were removed after 72 h and assayed for cytokine production. After this period, the cells were harvested and further labeled with anti-FOXp3 antibodies (FITC) and anti-TGFβ antibodies (PE) and fixed. The cells were acquired with a FACScalibur flow cytometer, and the analysis was performed by using FCS Express software.

Results: Our results showed that the VL patients had more natural Treg cells before the treatment and also had elevated levels of expression of regulatory markers.

In conclusion, the elevated numbers of these cells with an increased regulatory phenotype and strong suppressive activity suggest a potential role for them in the immunosuppression characteristic of kala azar before treatment and we have a decrease after treatment. In addition, our results indicate that Treg cells act by cytokine production.

Conclusion: Our results suggest that the activation of regulatory T cells (CD4+ CD25+) contributes to immune suppression during kala azar infection and that the mechanism by which these cells exert their suppressive effect is mediated, at least partially, by the production of IL-10 and TGF β .

22.144 Schmallenberg virus RNA detected in *Culicoides* biting midges in the Netherlands in 2011

A. R. W. Elbers¹, R. Meiswinkel², E. van Weezep³,

M. Sloet van Oldruitenborgh-Oosterbaan⁴, B. Kooi⁵ ¹Central Veterinary Institute, part of Wageningen University, Lelystad, Netherlands, ² Rome, Italy, ³Central Veterinary Institute, part of Wageningen UR, Lelystad, Netherlands, ⁴Faculty of Vetwrinary Medicine, University of Utrecht, Utrecht, Netherlands, ⁵Central Veterinary Institure, part of Wageningen UR, Lelystad, Netherlands

Background: Commencing in early summer 2011, a novel Orthobunyavirus of the Simbu serogroup, named Schmallenberg virus (SBV), spread silently across much of northern Europe, infecting ruminants. Simbu serogroup viruses are known for their teratologic effects in ruminants and are arthropod-borne, the majority having been isolated from mosquitoes and *Culicoides* biting midges. **Objectives:** Do *Culicoides* act as field vectors for SBV? and if so, what *Culicoides* species act as vector? What is the proportion of SBV-infected *Culicoides* ?

Methods and Materials: *Culicoides* were collected at two sheep flocks and one dairy herd situated in the central and (north)-eastern part of the Netherlands in the autumn of 2011 in the framework of research projects unrelated to SBV. *Culicoides* were stored for 6 months in 70% ethanol prior to assay. A total of 610 pools of heads (10 *Culicoides/* pool) from female *Culicoides*, subdivided by species, were analyzed. To identify the SBV-positive *Culicoides* molecularly, the 18S-ITS1-5.8S region was amplified.

Results: Twelve pools of the Obsoletus Complex and two pools of *C.chiopterus* tested positive, the majority with C_t-values of between 20 and 30. Molecular sequencing of positive Obsoletus Complex midges revealed eleven to be *C.scoticus* and one *C.obsoletus sensu stricto*. C_t-values found in the heads of midges matched closely those obtained from their associated abdomens. Proportion of SBV-infected midges of the ObsoletusComplex was 0.56%, and 0.14% in *C.chiopterus*. This is 10-times and 5-times higher when compared to bluetongue virus detected in the same midge species in Europe during 2002-2008, respectively.

Conclusion: The low C₁ values obtained indicate that high concentrations of the virus were present in the majority of SBV-positive *Culicoides.* The close match in C₁ values found in the heads of midges and their associated abdomens renders it certain that SBV had replicated to transmissible levels in these midges. The high proportion of SBV-infected midges is the result of the interplay between vector, host and environment. Climatic circumstances in 2011 (above-normal temperatures in autumn; dry spring, wet summer and dry autumn) have probably contributed to a prolonged vector season, a higher vector survival rate and increased vector abundance, resulting in a high prevalence of infection.



45 Oxabicyclo derivatives as a new class of antileishmanial agents: Target identification and understanding molecular mechanism of parasite death

P. Saudagar, V. K. Dubey

Indian Institute of Technology Guwahati, Guwahati, Assam, India

Background: Visceral leishmaniasis (VL) which is mainly caused by *L. donovani* (most common Indian species), *L. infantum* and *L. chagasi* is an emerging public health problem in different parts of the world. The current scenarios of chemotherapeutics against leishmaniasis pose a huge fall due to their high toxicity, high cost, tiresome to administer, and the emergence of drug resistance. To overcome the current issues there is a pressing need to discover novel, safe and economically affordable chemotherapeutic agents.

Objectives: Target identification of oxabicyclo derivatives, a new class of antileishmanial agents and to trace the molecular mechanism of parasite death.

Methods and Materials: Docking studies with redox enzymes of the parasite were performed. Based on the docking statistic and antileishmanial activity, inhibition studies with trypanothione synthetase (TryS) from *L. donovani* and trypanothione reductase (TryR) from *L. infantum* were chemically validated using oxabicyclo derivative compound PS-203. Individual thiols, trypanothione [T(SH)₂] and glutathione (GSH) were measured using HPLC method. Further the molecular mechanism of action was traced by performing series of apoptosis assays like double staning with Annexin V-FITC and PI, measuring ROS, measuring mitochondrial membrane potential, caspase like protease activity and DNA fragmentation. The effect on intracellular amastigotes and infectivity index was also studied.

Results: Oxabicyclo derivatives showed good docking statistics with trypanothione synthetase (TryS) and trypanothione reductase (TryR) from *L. donovani* and *L. infantum* respectively. Oxabicyclo derivatives compound PS-203 inhibited TryS ($K_{\rm I}$ = 12.83 μ M) and TryR ($K_{\rm I}$ = 25.83 μ M), destabilized the redox homeostasis by drastically reduced T(SH)₂ levels and ROS generation in the cell. PS-203 caused mitochondrial
International Meeting on Emerging Diseases and Surveillance 2013

membrane depolarization which elicited cascade of apoptotic processes resulting in death of the parasite. The dose dependent effect was observed with PS-203 on amastigote and promastigote forms of L. donovani. There was a decrease in infectivity index observed with PS-203 treated cells, compared to untreated control.

Conclusion: Inhibition of redox enzymes by oxabicyclo derivative consequence in variation of T(SH), levels, which elicited apoptotic stimuli by ROS generation that finally lead to the apoptotic death of the parasite. These compounds can be a possible lead for the development of novel drug against leishmaniasis.



22.146 Schmallenberg Virus pathogenesis, tropism and interaction with the innate immune system of the host

M. Varela¹, E. Schnettler², M. Caporale³, C. Murgia⁴, G. Barry⁴, A. Shaw⁴, M. Beer⁵, W. Baumgärtner⁶, A. Kohl⁴, M. Palmarini⁴ ¹Centre for Virus Research, University of Glasgow, Glasgow, United Kingdom, ²CVR-University of Glasgow, Glasgow, United Kingdom, ³Istituto G. Caporale, Teramo, Italy, ⁴MRC Centre for Virus Research, Glasgow, United Kingdom, 5Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany, 6University of Veterinary Medicine, Hanover, Germany

Background: Schmallenberg virus (SBV) is an emerging orthobunyavirus of ruminants associated with outbreaks of congenital malformations in aborted and stillborn animals. Since its discovery in 2011, SBV has spread rapidly to many European countries. Here, we developed molecular and serological tools, and an experimental in vivo model to study SBV pathogenesis, tropism and virus-host cell interactions.

- Objectives: 1) Characterize SBV in vitro tropism and growth.
- 2) Develop a reverse genetic system to rescue SBV in vitro.
- 3) Develop an experimental animal model of infection.
- 4) Characterize SBV tropism in naturally infected animals.

5) Investigate SBV determinants of virulence.

Methods and Materials: Three antigenome plasmids were commercially synthesized and used for transfections in 293T or BSR-T7 cells for virus rescue. Newborn Swiss mice were injected intracerebrally and samples collected at different time post-infection.

Results: We successfully rescued SBV using two different protocols. We show that SBV has a wide tropism in cell culture and rescued SBV replicates in vitro as efficiently as wild type virus (wtSBV). In newborn Swiss mice SBV replicates abundantly in neurons causing cerebral malacia and vacuolation of the cerebral cortex. These virusinduced acute lesions are useful in understanding the progression from vacuolation to porencephaly and extensive tissue destruction, often observed in aborted lambs and calves. Indeed, we detected high levels of SBV antigens in the neurons of the gray matter of brain and spinal cord of naturally affected lambs and calves, suggesting that muscular hypoplasia observed in SBV-infected lambs are mostly secondary to central nervous system damage.

Finally, we investigated the molecular determinants of SBV virulence. We found a biological SBV clone that after passage in cell culture displays increased virulence in mice. We also found that a SBV deletion mutant of the non-structural NSs protein (SBVDNSs) is less virulent in mice than wtSBV. Attenuation of SBV virulence depends on the inability of SBVDNSs to block IFN synthesis in infected cells.

Conclusion: This work provides the experimental tools to understand how this newly emerged virus causes disease in ruminants. In addition, it will now be possible to manipulate the SBV genome in order to develop effective vaccines.



Discovery of novel mosquito-dengue viral protein interactions: Construction of whole adult Aedes aegypti cDNA library for use in yeast-two-hybrid system

H. W. Tham¹, V. Balasubramaniam¹, H. Ahmad², I. Othman¹, S. S. Hassan¹

¹Monash University, Sunway Campus., Kuala Lumpur, Malaysia, ²Universiti Sains Malaysia, Pulau Pinang, Malaysia

Background: Protein-protein interactions may lead in the elucidation of biological functions. To initiate a comprehensive study on protein interactions using the yeast-two-hybrid (Y2H) system, between Dengue virus 2 (DENV2) NS1 protein and DENV main vector, Aedes aegypti, necessitates the generation of a yeast cDNA library of whole adult mosquito of A. aegypti. Here, we described the construction of this library and the putative interacting proteins identified in Y2H system assavs.

Objectives: To create a Y2H cDNA library of whole adult A. aegypti mosquito for interaction with DENV2 NS1 protein in a Y2H system.

Methods and Materials: Total RNA was extracted from whole adult mosquito A. aegypti using Trizol® (Invitrogen, US). First- and secondstrand cDNA was synthesized using SMART™ cDNA synthesis technology (Clontech Laboratories Inc), and co-transfected with linearized pGADT7-rec vector into yeast Saccharomyces cerevisiae Y187 strain using polyethylene glycol (PEG)/LiAc-based method (Clontech Laboratories Inc). The cDNA library was tested with DENV2 NS1 protein. In brief, bait and prey were mated and plated on low stringency agars (-Leu/-Trp), followed by high stringency agars (-Leu/-Trp/-His/-Ade). Surviving colonies were screened for cDNA insert, sequenced, and blast using online tools (BLAST, NCBI).

Results: Mosquito DNA topoisomerase, checkpoint kinase 1 (CHK1), proacrosin protein, acyl-coA dehydrogenase, and ribosomal protein S15p/S13e, which seemed to play a role in DNA replication, mitotic progression, proteolysis, fatty-acid metabolism, and protein expressions and modifications, respectively were among the genes identified. Other hypothetical genes identified were similar to those found in bacteria, such as type 4 prepilin-like and signal transduction histidine kinase (LytS) proteins. The vast variety of proteins detected indicated the complexity of the cDNA library created, and its capacity in discovering novel protein interaction partners in A. aegypti with Dengue virus.

Conclusion: A whole adult A. aegypti yeast cDNA library used in Y2H system is capable of revealing novel protein interactomes with DENV2 NS1 protein. This library can be used to discover novel protein interactions with other arboviruses such as yellow fever virus and Chikungunya virus, where A.aegypti is the main vector.

22.148 Detection of Usutu virus and a novel mosquito-borne virus in mosquitoes in north-western Italy

F. Rizzo¹, M. Ballardini¹, S. Peletto¹, M. Calzolari², C. Boin¹, P. L. Acutis¹, C. Casalone¹, L. Chiavacci¹, M. Prearo¹, M. L. Mandola¹ ¹IZS PLV, Turin, Italy, ²IZSLER, Reggio Emilia, Italy

Background: Many arboviruses, transmitted by mosquitoes, belong to the Flavivirus Genus and are classified in the antigenic group defined Mosquito Borne viruses (MBV), which comprises several human pathogens. Evidence of MBV circulation, as West Nile virus (WNV) and Usutu virus (USUV) in animals and humans occurred in Italy since 1998. The Piedmont region, in North-western Italy, represents a high risk area, due to the abundance of migratory/resident birds and mosquitoes species with competence for several zoonotic arboviral pathogens transmission and spreading.

Objectives: Here we present the preliminary results of an arboviral surveillance program on mosquitoes, performed in Piedmont since 2011.

Poster Presentations II

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: Virological surveillance was performed from June to September 2011 on 16 CO_2 -baited traps and from August to October 2012 on 30 traps. Mosquitoes were tested with a PCR assays for: Flavivirus genus (Scaramozzino, 2001), WNV (Tang, 2006) and USUV (Manarolla, 2004). Amplicons were sequenced and homology with sequences available in the Genbank database was calculated and expressed as nucleotide identity percentage.

Results: A total of 7833 mosquitoes in 2011 and 8533 in 2012 underwent biomolecular analyses. One *Culex pipiens* pool in 2011 and four pools in 2012 resulted positive for USUV-E protein gene, showing sequence identities with an italian 2010 strain ranging from 97% to 99%. Moreover, 2 pools of *Ochlerotatus caspius* and one of *C. pipiens* in 2011, as well as 4 pools of *O.caspius* in 2012, all collected from the same trap, resulted positive for a *Flavivirus* that revealed a 97% nucleotide identity with an italian sequence from *Aedes caspius* (Calzolari, 2010) and 93% nucleotide identity with a novel *MBV* recently isolated from *O. caspius* in Spain, named *Marisma Mosquito virus* (MMV) (Vázquez, 2012).

Flavivirus identified	2011	2012	Location
Novel MBV	- 1 pool of <i>C.pipiens</i> - 2 pool of <i>O.caspius</i>	2 pool of O.caspius	Alessandria province
USUV	1 pool of <i>C.pipiens</i>	4 pool of <i>C.pipiens</i>	Novara province

Table 1. PCR positive pools for novel Mosquito Borne virus and Usutu virus in 2011 and 2012

Conclusion: The Piedmont USUV strains show a high homology with austrian ones from blackbirds, thus supporting the hypothesis of a possible role of some migrating bird species in the natural transmission cycle of this pathogen. The occurrence of the other MBV strain in the same trap in both years is remarkable; its affinity for the new MMV could indicate a zoonotic potential for this virus. Investigations are currently ongoing to confirm this hypothesis.

22.149 The West Nile-induced encephalitis with respiratory distress mimicking Guillain-Barre syndrome

A. Ndreu¹, S. Bino², E. Ramosaco³, E. Mingomataj⁴ ¹Service of Infective Diseases, University Hospital Center, Tirana, Albania, 1007, Albania, ²Institute of Public Health, Tirane, Albania, ³Nursing Faculty, University of Tirana, Tirana, Albania, ⁴Service of Immunology, University Hospital Center, Tirana, Albania., 1007, Albania

Background: The West Nile virus (WNV) is a pathogenic flavivirus. Every five persons with WNV experience fever that lasts from 3 to 6 days, while meningoencefalitis has been reported in every 150 infected people. Fever, diarrhea, headache, muscle pain and cutaneous rash are the commonest symptoms. Usually, WNV-related meningoencefalitis is evidenced in patients older than 50 years. Temporary muscular paralyzemay mimic the clinical pattern of Guillain–Barre syndrome (GBS).

Objectives: In this presentation we aimed to describe 3 cases of WNV infection showing GBS-like muscular paralysis and respiratory distress.

Methods and Materials: Three cases of WNV infection admitted at the ICU (Infective Service–Tirana UHC) were diagnosed with meningoencefalitis and distress respiratory during august 2011. All patients were men older than 50 years. The etiological agent of infection was confirmed due to serological methods.

Results: Regarding clinical symptoms, fever ranged from 39 to 40°C, consciousness was altered at the level of 7–8 GSC, and weakness was evidenced in all subjects. Additional symptoms were psychomotor agitation, dyspnea, hypoxia, tachypnea, hemodynamic lability, and neck rigidity. Any neurologic deficiencies were observed. Regarding

laboratory findings, patients showed leukocytosis, cellular presence in the cerebrospinal liquid (predominantly lymphocytes), while CT examination of the head was normal. The gasometrical blood analysis revealed a decreased O_2 -saturation under 90%, while radiological examination of thoracic region revealed bilateral reticular infiltration in both lungs. Two of three cases were treated noninvasive ventilation (NIV-facial mask, CPAP-PSV), while the third subject was treated with O_2 -therapy via nasal ways. Additionally, these subjects were treated with ceftriaxone, mannitol, dexamethasone and antiviral agents. The clinical outcome was favorable.

Conclusion: A typical WNV infection of central nervous system may mimic GBS, which shows muscular paralyze and respiratory distress. The etiologic therapy combined with NIV one is helpful in the treatment of these complications.

22.150 Emergence control of mosquito vectors and surveillance of mosquito and water borne viruses in natural disaster areas

R. E. Morales Vargas¹, T. Okabayashi¹, N. Komalaminsra¹,

R. Srisawat¹, N. Phumala-Morales², S. Lee³, N. Orii⁴

¹Faculty of Tropical Medicine, Mahidol University, Bangkok, Bangkok, Thailand, ²Faculty of Science, Mahidol University, Bangkok, Thailand, ³Thailand Pest Manegement Association, Bangkok, Thailand, ⁴Nippon International Cooperation for Community Development, Kyoto, Japan

Background: Due to un-precedent Monsoon rain activity in Thailand in 2011, vast areas on the central plain were flooded and remained flood for periods up to 3 months in certain areas. Natural disasters, for instance flooding, can affect vector-breeding sites and vector borne disease transmission; and water related diseases.

Objectives: To obtain information about the abundance and control of mosquito vectors and the prevalence of arbovirus and water-borne virus in the area affected by the heavy rains and flooding.

Methods and Materials: Chemical control, environmental management and social measurements approaches was carried out. As chemical control, insecticide space spraying (Deltamethrin 2.5%EC) and larvicide (Pyriproxifen) was applied in/out the houses, and the natural water bodies, respectively, was done. As environmental management, cleaning of the drain system and removal of natural and artificial breading sites; while as social measurements an educative programs, was carry out. Whereas the prevalence of arbovirus and water-borne virus, were assessed by molecular based methodologies in the mosquitoes and polluted water, respectively, collected at flooded areas.

Results: The light-trap collections yielded mosquitoes representing 14 species. The most abundant species was *Culex quinquefasciatus, Cx. vishnui* and *Cx. gellidus,* vectors of Japanese Encephalitis in Thailand. Other species were collected also (in decreasing order): *Mansonia annulifera, Ma. uniformis, Anopheles barbirostris, An. vagus.* By the control methodologies used, overall, 20–97% reduction of the adult mosquito fauna was achieved up to 2–3 weeks post operations, while 70–98 % reduction of the mosquito larvae up to 3 weeks post operations. No arboviruses were detected in any of the mosquitoes tested for Flavivirus and Alphavirus in this survey. Whereas, among the 30 water samples tested the following enteric virus, Norovirus (6.6%), Hepatitis A virus (6.6%) and Rotovirus (3.3) were detected.

Conclusion: Our findings did not support the assertion that human risk for arboviral infection was increased in the flooding areas, however the presence of the enteric viruses in the water samples, represented a risk factor for enteric virus infections by contact with flood water. A taxonomic description of the mosquito species were determined which it would be useful as baseline data of the mosquito fauna of Ayuthaya and Nontaburi provinces of Thailand.

International Meeting on Emerging Diseases and Surveillance 2013

22.151 Development of a TaqMan assay for detection of arboviruses belonging to the genus Orthobunyavirus: Universal detection of Japanese strains of orthobunyaviruses and specific detection of Akabane, Aino and Peaton viruses

H. Shirafuji¹, R. Yazaki², Y. Shuto³, T. Yanase¹, T. Kato¹, M. Yamakawa4

¹National Institute of Animal Health, NARO, Kagoshima, Japan, ²Oita Prefectural Government, Kusu, Japan, ³Oita Prefectural Government, Oita, Japan, ⁴National Institute of Animal Health, NARO, Tsukuba, Japan

Background: Various arthropod-borne viruses (arboviruses) have been isolated repeatedly since 1970s in Japan and are recognized as major obstacles to the production of beef and dairy cattle. In this decade, there have been more frequent epidemics/sporadic outbreaks of arboviral diseases of cattle than ever, including abortion, stillbirth, premature birth and congenital abnormalities caused by Akabane and Aino viruses (AKAV and AINOV) that belong to the genus Orthobunyavirus. Furthermore, Peaton, Shamonda, and Sathuperi viruses (PEAV, SHAV and SATV), which belong to the same genus as AKAV and AINOV, have been newly detected in Japan since 1999.

Objectives: Due to the changing situation regarding arbovirus infections in cattle, it is essential to improve diagnostic techniques for more effective monitoring systems against the arboviruses in Japan. In this study, we developed a TaqMan assay for rapid, sensitive and specific detection of arboviruses belonging to the genus Orthobunyavirus.

Methods and Materials: We designed a primer/probe set for universal detection of Japanese strains of orthobunyaviruses and three other primer/probe sets for specific detection of AKAV, AINOV and PEAV, respectively. These primer/probe sets were tested for the detection by using AgPath-ID One-Step RT-PCR Kit (Ambion, Life Technologies) and a real-time PCR system, MyiQ2 (BIO-RAD). Specificity of the assay was evaluated by using viral RNA extracted from supernatant of virus-infected cells, and sensitivity was evaluated by using synthesized RNA containing a target sequence of each virus prepared by in vitro transcription.

Results: The assay detected AKAV, AINOV, PEAV, SHAV and SATV with the primer/probe set for universal detection in about 2 hours, and its detection limit was 1-100 copies/tube. Also, the assay detected each of the target viruses with the specific primer/probe sets for AKAV, AINOV and PEAV, and their detection limits were 10-1,000 copies/tube.

Conclusion: A TaqMan assay was developed for rapid, sensitive and specific detection of bovine arboviruses belonging to the genus Orthobunyavirus. Our next step will be detection of the viruses in clinical and field samples including bovine blood and tissues and Culicoides biting midges for assessing the assay's suitability for practical use at veterinary diagnostic laboratories.

22.152 Organ distribution of Schmallenberg virus **RNA** in malformed calves

W.-I. Bock¹, F. Hühn¹, C. Schulze², A. Hlinak², S. Bilk² ¹Thuringian State Authority for Food Safety and Consumer Protection (TLLV), Bad Langensalza, Germany, ²State Laboratory Berlin-Brandenburg (LLBB), Frankfurt (Oder), Germany

Background: Schmallenberg virus, a novel Orthobunyavirus, emerged in Germany and other parts of Europe in 2011/2012. In March 2012 and onwards, malformed calves were submitted to the federal veterinary state laboratories of Thuringia and Brandenburg. At the beginning of the epidemic, no data were available concerning the distribution of the virus in the organs of malformed calves. First details about the distribution of the virus were received from own investigations in typically malformed and SBV-RT-qPCR-positive lambs.

Objectives: The aim of this study was, to define the most suitable organs for reliable, accurate diagnosis of SBV in calves with typical malformations under routine diagnostic conditions.

Methods and Materials: From March to June 2012 154 calves (71 at TLLV and 93 at LLBB) with and without typical malformations (arthrogryposis, malformations of the brain, cerebellum and/or vertebral column) were tested for the presence of SBV RNA using RT-qPCR. The following organs and body fluids were investigated: cerebrum, cerebellum, spleen, spinal cord, bone marrow, skeletal muscle, thymus, lung, heart, thyroid, meconium, umbilical cord, rib cartilage and placental fluid.

Results: Out of the 154 calves investigated, 55 were SBV positive (34 at TLLV and 21 at LLBB). For most of the foetuses with typical malformations SBV genome sequences could be detected in placental fluid, umbilical cord, lung, spinal cord and meconium. Cerebrum, cerebellum and spleen, which were recommended for SBV-detection, as well as bone marrow and skeletal muscle, resulted positive in a far smaller number of cases. However, none of the examined organs have had a positive result in every single SBV infected calf. For 5 calves SBV-RNA couldn't be detected in any of the analysed organs, although the malformations looked like SBVinduced

Conclusion: To our opinion, most suitable materials for reliable detection of SBV RNA in malformed calves are the placental fluid, umbilical- and spinal cord, lung and meconium. However in some cases the range of investigated organs must be extended to detect SBV genome sequences in calves with typical malformations. Additionally, calves with typical malformations without the confirmation of SBV-RNA do occur.

22.153 Opisthorchiasis in the basin of the lower Don in Russia

N. Pshenichnaya¹, L. Ermakova², T. Tverdokhlebova², O. Dumbadze²

¹Rostov State Medical University, Rostov-on-Don, Russian Federation, ²Rostov Research Institute of Microbiology and Parasitology, Rostov-on-Don, Russian Federation

Background: Opisthorchiasis is a natural focal disease closely connected with freshwater ecosystems. The culinary traditions of cooking fish and effectiveness of the carried out veterinarysanitary measures influence the frequency of the population's with this helminthiasis. In recent times, stable foci of this invasion were reported in the European part of Russia in the basins of the Oka and the Upper Don. In the basin of the Lower Don (Rostov region) in the last decades, sporadic cases of opisthorchiasis were registered, which were regarded as either a chronic invasion in people who had come from disadvantaged regions, or casuistically associated with the use of contaminated fish brought from opisthorchiasis-endemic areas.

Objectives: In this regard, the observation of a family case of acute opisthorchiasis, associated with the use of slightly marinated fish cooked at home, caught in the downstream of the river Don has practical interest.

Methods and Materials: The diagnosis was established by detection of felineus eggs in faeces using formalin-ether sedimentation method.

Results: As a result, 4 adults from the same family have fallen ill. The incubation period ranged from 14 to 30 days. In all patients, fever was recorded from 37 to 40 degrees C, eosinophilia from 23% to 66%, leukocytosis up to 18 x 109/l, increased activity of serum transferases. Three patients had jaundice and hepatomegaly up to 3,0 cm. The diagnosis in all patients was confirmed by detection of felineus eggs in faeces

The attention was drawn to the lack of correlation between the intensity of infection, the duration of the incubation period and severity of clinical manifestations of the disease.

All patients received anthelmintic treatment by praziguantel (75 mg/ kg/day divided in 3 doses) on the background of desensitizing agents. The patients underwent the above treatment satisfactorily, side effects have not been reported.

Conclusion: The presented data indicate the preservation of natural opisthorchiasis focus in the Lower Don. The physicians of clinical specialties should be aware of this infestation in the differential diagnosis of the diseases that occur with syndromes of fever, jaundice, eosinophilia. In carrying out preventive and anti-epidemic measures, special attention should be paid to health education.

International Meeting on Emerging Diseases and Surveillance 2013

22.154 Recurrent echinococcosis in the Rostov region of Russia

L. Ermakova¹, N. Pshenichnaya², Y. Kirtanasov³,

T. Tverdokhlebova¹

¹Rostov Research Institute of Microbiology and Parasitology, Rostov-on-Don, Russian Federation, ²Rostov State Medical University, Rostov-on-Don, Russian Federation, ³Rostov Regional Hospital #2, Rostov-on-Don, Russian Federation

Background: Echinococcosis occupies a special place in the structure of biohelminthosis due to a long asymptomatic disease, development of menacing surgical complications, frequent occurrence of relapse after surgical treatment. The attitude to echinococcosis as the exclusively surgical pathology, the absence of approved in the Russia standart of antihelminthic therapy of echinococcosis, is one of the reasons for the frequent recurrence of this helminthiasis.

Objectives: The aim of research is to estimate reasons and frequency of RE in the Rostov region of Russia.

Methods and Materials: In 2006–2010, 68 patients with echinococcosis, 7 to 84 years-old, were under medical supervision, of whose 75% of patients were in the working age (20 to 60 years-old).

Results: Echinococcosis of the liver was detected in 51 patients, pulmonary echinococcosis —in 5, rare localizations of hydatids (spleen, heart) were observed in 3 patients, the combined echinococcosis (liver and abdominal cavity) —in 4 patients, multiple echinococcosis with the simultaneous affect of two and more organs—in 5 patients.

The primary echinococcosis of different localizations was registered in 55 patients, recurrent in 13 patients (19%). Among the cases of the RE, women were registered 69% (9 patients), whereas in the gender structure of all patients women were 53%. The recurrence of pulmonary echinococcosis was registered in 2 patients, of liver in 11 persons. Five patients in 2–3 years after surgical treatment of isolated echinococcosis of the liver had multiple cysts of the liver. In one patient, a solitary cyst of the liver appeared 28 years after echinococcectomy, and in another patient after 33 years. Two patients had 4 operations for RE with an interval of 2–3 years. One patient within 1987–2008 years had 9 surgeries for pulmonary and liver echinococcosis. In 2010, this patient had inoperable disseminated echinococcosis of the lungs, mediastinal organs, liver, abdominal cavity, pelvic organs.

It should be noted that none of the patients with RE was prescribed antirecurrent treatment after the primary or re-performed surgical procedures.

Conclusion: The interaction of physicians of all specialties: surgeons, infectious disease specialists, therapists are necessary for the successful treatment of patients with echinococcosis and for the reduction of risk of recurrence

22.155 Mosquito surveillance of West Nile and Usutu viruses in Emilia-Romagna region, Italy, 2008–2012

M. Calzolari¹, P. Bonilauri¹, R. Bellini², M. Tamba³, P. Angelini⁴, M. Dottori¹

¹IZSLER, Reggio Emilia, Italy, ²CAA, Crevalcore, Italy, ³IZSLER, Bologna, Italy, ⁴Regione Emilia-Romagna, Bologna, Italy

Background: In recent years human diseases due to mosquito-borne viruses were increasingly reported in Italy and in Emilia-Romagna region.

Objectives: To evaluate the activity of West Nile (WNV) and Usutu (USUV) viruses a surveillance system, including mosquito-based surveillance, was established in this region since 2008 and gradually improved over the years until 2012.

Methods and Materials: More than one million of mosquitoes were sampled in georeferenced sites, pooled according date of collection, location, and species, and analyzed by reverse transcription polymerase chain reaction (RT-PCR) to detect the presence of RNA belong to Flavivirus genus and, more specifically, to WNV and USUV.

Results: From 2008 to 2012, a total of 1.176.885 mosquitoes. sampled between May and October, were tested: the large part of these mosquitoes were Cx. pipiens (86.4%), WNV was detected in 32/6,926 Cx. pipiens pools, while USUV was detected in 304 mosquito pools (species: 290/6,926 Cx. pipiens, 10/640 Aedes albopictus, 3/1,741 Aedes caspius, 1/85 Anopheles maculipennis s.l.). In February-March 2009-2011, 5,993 hibernating mosquitoes were manually sampled, out of which 80.1% were Culex pipiens, none of these mosquitoes tested positive. The two surveyed viruses showed a different pattern of activity during the period 2008-2011. WNV was detected in 2008, 2009 and 2010, but not in 2011 and 2012. USUV however, was continuously active throughout 2009, 2010, 2011 and 2012. Spatial analysis performed on mosquito collecting stations posed in a 10x10 km greed on the surveyed area, allowed to evaluate the influence of meteorological factors on the circulation of USUV, indicating an unexpected association of viral circulation and more drought environment.

Conclusion: The data obtained highlight the possible role of *Cx. pipiens* mosquito as the main vector both for WNV and USUV in Northern Italy. The lack of positive hibernating mosquitoes, and the presence of positive birds which were sampled early in the season, supports the hypothesis that the viruses may overwinter in birds rather than in mosquitoes. The output produced by the surveillance system demonstrated its usefulness and reliability in terms of early warning, risk assessment and planning of public health measures.

22.156 Seroprevalence of West Nile virus antibodies in poultry and risk factors associated with their occurrence at live bird markets in Kaduna, Nigeria

W. S. Mshelia, J. Kabir, J. Umoh, B. D. J. George Ahmadu Bello University Zaria, Kaduna, Nigeria,

Background: West Nile Virus (WNV; *Flavivirus*, Flaviviridae) is arthropod-borne zoonoses of public health importance.

Objectives: The study was designed to determine the prevalence of West Nile Virus (WNV) antibodies in poultry, in six (6) live bird markets of Kaduna metropolis, Nigeria and the possible risk factors associated with the occurrence of the infection.

Methods and Materials: A total of four hundred and seventy (470) sera samples were collected from the following bird species; indigenous breed (199), Improved breeds (broilers (141), layers (86), cockerels (13)), pigeons (7), Guinea fowl (19), turkey (1), and ducks (4), using systematic random sampling method. Competitive Enzyme Linked Immunosorbent Assay using ID Screen® kit from ID-VET Innovative diagnostic (Montpellier-France) was used to test the sera samples. Structured assessment forms were used to assess the possible risk factors to the infection in and around the bird markets.

Results: The result showed an overall prevalence of 6.4% (30/470) and individual prevalence of 10.6% (21/199) for indigenous breeds, 0.7% (1/141) broilers, 4.7% (4/86) layers, 42.9% (3/7) pigeons, 5.3% (1/19) Guinea fowl, and no reactors in cockerels, turkey and ducks. There was an association between the presence of the antibodies and types of birds sampled (p<0.05). Possible Risk factors for the occurrence of the infection were identified as; open shade buildings with bird cages attached to the main market, lack of pipe-borne water, use of open dark plastic containers for water storage and presence of stagnant water in drainages around the markets.

Conclusion: The presence of WNV antibodies in poultry in Kaduna state has been established in this study and this is the first time birds are screened for WNV antibodies in Nigeria. There is dearth of information and lack of awareness of the disease and its possible risk factors. The role of mosquitoes in transmitting this disease cannot be overemphasized. Therefore, there is the need to enlighten the populace about the disease and its zoonotic implication. Also, a more detail study on the isolation of the infective agent and is epidemiology is required in Nigeria.

International Meeting on Emerging Diseases and Surveillance 2013

22.157 Detection and characterization of first outbreak of chikungunya, Papua New Guinea, 2012

B. I. Pavlin¹, S. Jimmy², R. Dagina³, P. Horwood⁴, B. Ropa³ ¹World Health Organization, Port Moresby, Papua New Guinea, ²Vanimo General Hospital, Vanimo, Papua New Guinea, ³National Department of Health, Port Moresby, Papua New Guinea, ⁴PNG Institute for Medical Research, Goroka, Papua New Guinea

Background: Chikungunya virus (CHIKV) is a mosquito-transmitted Alphavirus in the family Togaviridae. Papua New Guinea (PNG) has never experienced an outbreak of chikungunya. In June 2012, Vanimo (pop. ~10,000), Sandaun Province, PNG began experiencing an outbreak of fever and arthralgia.

Objectives: To describe the detection and characterization of the first outbreak of chikungunya virus in PNG.

Methods and Materials: Beginning in late June, The PNG National Department of Health (NDOH) detected a rise in 'unexplained severe disease' and 'prolonged fever of three or more days' from the Vanimo General Hospital (VGH) site of the PNG Mobile Phone-based Surveillance system (MPS), a syndromic sentinel surveillance system currently active in three sites in PNG.

The NDOH supported VGH by developing a case investigation form and assisting with referral of serum specimens to the PNG Institute for Medical Research for testing by PCR for a variety of arboviruses.

After confirmation of etiology, patients with completed investigation forms, who met the case definition of acute fever and arthralgia, were analyzed for epidemiologic characteristics.

Results: The outbreak was initially characterized by fever, nausea, vomiting and arthralgia, with convalescent patients returning with persistent/recurring arthralgia. Chikungunya virus was confirmed by PCR on October 3rd.

Between June 25-November 25, 2012, a total of 1590 cases (combining 'unexplained severe disease' and 'prolonged fever') were recorded through the MPS. As of now, the outbreak is ongoing.

Patient data were available for only 98 cases. Of these, 54 (55%) were female. The age range was 2-60 years (median 24). The most common symptoms were: fever (100 %), arthralgia (100%), headache (83%), cough (31%), and nausea (26%).

Conclusion: This report describes the first outbreak of chikungunya in PNG. The origin of this outbreak remains a mystery; phylogenetic characterization of the virus is underway to determine its source.

The MPS proved a valuable way to identify this outbreak. For the system to be useful for detecting public health events throughout the country, it is now being expanded to 25+ sentinel sites.

22.158 Dirofilariosis in Slovakia M. Miterpakova, A. Iglodyova

Institute of Parasitology, Slovak Academy of Sciences, Kosice, Slovakia

Background: Environmental and climatic changes that occurred in recent decades caused the spread of parasites into new areas. In Central Europe, canine subcutaneous dirofilariosis caused by Dirofilaria repens is regarded as arthropod-born infection with the fasted spread. In Slovakia, canine dirofilariosis in dog was for the first time recorded in 2005.

Objectives: The objective of our study was to map the presence of subcutaneous dirofilariosis and heartworm disease in dogs in ecologically different regions of Slovakia.

Methods and Materials: Between 2007 and 2012 nearly 3000 dogs from all regions of Slovakia were examined. Modified Knott test and PCR were used for the parasite diagnostics.

Results: Microfilariae were detected in more than 12 % of blood samples. The results of our research show that D. repens is the predominant species circulating in Slovakia. Using PCR D. repens was detected in all infected animals; in 8 animals co-infection with D. immitis (heartworm) was present. Autochthonous origin of infection has been confirmed in all infected dogs. Great regional differences in prevalence were recorded: the majority of infected dogs came from southern regions of the country (the mean prevalence over 20 %); the lowest prevalence (2-4 %) of canine dirofilariosis was detected in northern part of Slovakia.

Conclusion: Our research revealed the occurrence of highly endemic areas of dirofilariosis in Slovakia and certified that climatic conditions are favourable for the parasite development and for further spread of this zoonotic infection. Transmission of the infection to people was also confirmed-during the last five years 5 human cases of dirofilariosis have been diagnosed.

The work was supported by the Science Grant Agency VEGA2/0011/12 (0.5) and project "Application Centre for Protection of Humans, Animals and Plants against Parasites" (code ITMS: 26220220018), supported by the Research & Development Operational Programme funded by the ERDF (0.5).

22.159 22.159 Bioecological study of malaria vector Anopheles balabacensis in one of the buffer areas of Merapi Mountain

N. I. Hariastuti¹, A. Tunissea², B. Yunianto³

¹National Institute of Health Research and Development, Jakarta Pusat, Indonesia, ²National Institute of Health Research and Development, Banjarnegara, Indonesia, ³Surakarta Health Polytechnic, MoH Indonesia, Klaten, Indonesia

Background: Anopheles balabacensis is known as a potential vector of malaria. It lives in the forest or mountain area. The density of An. balabacensis in Turi, Sleman, Yogyakarta was very high. Turi is one of the malaria sporadic sub-district that affected by the volcanic erruption of mount Merapi.

Objectives: The aim of this study was to identify An.balabacensis bioecology in this region which has not been known specifically, include the resting places, breeding places and biting habit.

Methods and Materials: The research conducted by entomological surveys that covered dry season and rain season. Man landing collection was conducted to study the biting habit. The investigation of An. balabacensis resting habit and breeding places was conducted by observation and identification.

Results: There were nine species of Anopheles found in this study; An.aconitus, An.maculatus, An.balabacensis, An.barbirostris, An.vagus, An.flavirostris, An.kochi, An.subpictus, and An.bengalensis. Anopheles balabacensis larvae were found in ponds, irrigation pipe leaks, wellsprings with physical quality of pH 6.85-7.34, DO 4-7.25 and temperature between 24.4 and 24.84°C.

Commonly An.balabacensis found to rest around sheep pens, while the morning resting habit around embanks and bough of salak trees. Pens were located apart from houses (2-3m). ELISA test showed there was no mosquito infected with Plasmodium falciparum and Plasmodium vivax sporozoit.

Conclusion: Biting activities of An.balabacensis on human was very low if being compared with An.balabacensis density caught around pens. The pens were able to make a cattle barrier to evade An.balabacensis that prefer human blood to look for food around pens.

22.160 Study of ticks infected with tick-borne encephalitis virus in the southern and southeastern regions of Kazakhstan

P. Deryabin¹, T. Nurmakhanov¹, J. Hay², B. Atshabar³, A. Vilkova¹ ¹M. Aikimbaev's Kazakh Scientific Center for Quarantine and Zoonotic Diseases (KSCQZD), Almaty, Kazakhstan, ²State University of New York SUNY, Buffalo, NY, USA, 3M. Aikimbayev's Kazakh Scientific Center for Quarantine and Zoonotic Diseases, Almaty, Kazakhstan

Background: Tick-borne encephalitis annually registered in the eastern and south-eastern regions of Kazakhstan. In the southern regions of Kazakhstan of tick-borne encephalitis is not registered.

Poster Presentations II

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: To study TBE virus in ticks in the southern (non-endemic) and southeast (endemic) regions of Kazakhstan and to visualize obtained data using geographic information system (GIS) technology.

Methods and Materials: Ticks infectiousness was assessed by detecting viral antigen using ELISA and viral RNA using RT-PCR («European» subtype TBE). All ticks were initially divided into separate pools, containing 3 to 56 insects. We investigated 13253 ticks (549 pools), including 3158 (157 pools) from Southern-Kazakhstan, 6200 (268 pools) from Kyzylorda region, 2200 (76 pools) from Zhambyl region and 1695 ticks (48 pools) from Almaty region. 3385 ticks (175 pools) belonged to genus Hyalomma, mainly H.asiaticum, 9696 (370 pools) to genus Dermacentor, mainly D.marginatum and D.niveus, 168 ticks to genus Haemaphysalis (3 pools) and 4 ticks (1 pool) to *I. persulcatus*.

Results: In Southern Kazakhstan TBE virus was detected in 44 (28.0%), in Kyzylorda region in 16 (6.0%), in Zhambyl region in 29 (38.2%) and in Almaty region in 8 (16.7%) of tested pools. TBE virus was detected in 175 (25.7%) of *Hyalomma* ticks, and in 370 (14.1%) pools with *Dermacentor* ticks. GIS applications such as Arc Catalog, Arc Map and Arc Toolbox were used to map points of collection of ticks and locations with TBE positive samples.

Conclusion: Ticks infected with TBE were detected both in endemic (Almaty region) and non-endemic areas (Southern Kazakhstan, Zhambyl and Kyzylorda regions) where TBE incidence was not previously registered. Ticks were detected significantly more often (p<0.05) in the south of Kazakhstan, especially Zhambyl region, compared to Almaty region. Significantly more TBE positive ticks were among *Hyalomma* pools. Mapping of areas with TBE positive ticks will facilitate more effective implementation of preventive measures and evaluation of biological risks.

22.161

Serological and molecular detection of tick borne pathogens in horses from Central Italy

M. Diaferia¹, F. Veronesi¹, F. Laus², E. Paggi², M. Cerquetella², B. Tesei², D. Piergili Fioretti¹

¹University of Perugia, Perugia, IT, Italy, ²University of Camerino, Matelica, IT, Italy

Background: Tick borne pathogens

Objectives: The present study is aimed to conduct a cross-sectional survey to analyze the presence and prevalence of tick borne pathogens infections in indigenous horse populations reared in different areas of Central Italy by using serological and molecular methods.

Methods and Materials: Between February 2010 and September 2011, blood samples from 300 horses were analyzed for the presence of antibodies against *Babesia caballi, Theileria equi, Anaplasma phagocytophilum* and *Borrelia burgdorferi* using the IFAT. The blood samples were also subjected to PCR assays in order to detect pathogen DNA.

Results: A total of 78 (26%) and 123 (41%) horses were found to be seropositive for *B. caballi* and *T. equi*, respectively, while 41 (13.44%) and 21 (7%) horses were, respectively, seropositive for *A. phagocytophilum* and *B. burgdorferi*. Seropositivity for more than one agent was detected in 76 horses. The most common association observed was between *T. equi* and *B. caballi* (14.66%). In addition, 54 horses (18%) were found to be positive for one or more tick-borne pathogens (TBP's) using PCR testing. Among these, 28 (9.33%) harbored single infections, while 26 (8.66%) were found to be co-infected with two or more pathogens. The correlation (K value) between IFAT and PCR results was 0.32 for *T. equi*, 0.34 for *B. caballi*, 0.62 for *B. burgdorferi*, and 0.48 for *A. phagocytophilum*.

Conclusion: This study represents the first documentation of multiple equine TBP infections in Italy using both serologic and molecular methods. Specifically, multiple TBP exposures were ascertained using IFAT and PCR testing in 25.33% and 8.66% of the total sample population, respectively. The most common associations observed consisted of *T. equi* and *B. caballi* followed by *B. burgdorferi* and *A. phagocytophilum*. The consequences of TBP co-infections in horses

have not yet been well established. Simultaneous infection with multiple agents may account for some of the differences observed clinically in comparison with infections involving a single pathogen. Public and private health providers both in Italy and abroad, particularly veterinary practitioners and physicians, should be aware of the potential for tickborne diseases in horses, especially where large numbers of animals are maintained for recreational purposes and many ticks are present.

22.162 *Culicoides*—Potential vectors of viral diseases in Eastern Slovakia

A. Sarvašová¹, A. Kočišová¹, I. Sopoliga²

¹University of Veterinary Medicine and Pharmacy in Košice, Kosice, Slovakia, ²University of Veterinary Medicine and Pharmacy, Rozhanovce, Slovakia

Background: In recent years, explosive outbreaks of *Culicoides*-borne pathogens have been noticed in Europe; in August 2006 Bluetongue outbreaks in Western Europe, and five years later, in August 2011 an unexpected appearance of new disease caused by *Schmallenberg* virus. Moreover the Epizootic hemorrhagic disease was reported in countries bordering the European Union in autumn 2006.

Objectives: The aim of this entomological survey was to obtain the baseline data on vector occurrence in Eastern Slovakia, predominantly the species from Obsoletus and Pulicaris complexes.

Methods and Materials: The entomological monitoring has been performed on two farms with cattle (Michalany, Tulcik) and one farm with fallow deer and muflons (Rozhanovce) from April 2011. Midges were collected weekly using blacklight traps. The samples were morphologically identified using the key of Delécolle (1985) and subsequently the females were age-graded as nulliparous, parous, gravid and freshly engorged.

Results: In total, 45125 midges were caught on three farms from April 2011 to September 2012. The most abundant species were the potential vectors of Obsoletus complex that comprised 33 % (2011) and 25% (2012) in Michalany, 68% and 89% in Tulcik and 65 % and 68% in Rozhanovce out of the total catches. The second most abundant were species of Pulicaris comlex, representing 29% and 31% in Michalany, 21.5% and 6% in Tulcik and 15% and 7,5% in Rozhanovce. On the farm Michalany, the species from Nubeculosus complex were caught in high number 21% and 19% in comparison with Tulcik and Rozhanovce, where they were present only in small number (1 and 4 specimens) in 2011. The midges were active from April to October.

Conclusion: Results confirmed the presence of both potential vector complexes and demonstrated that the vectors are highly abundant not only on farms with livestock but also on farm with wild animals. Although no outbreak of *Culicoides*-borne diseases have been observed in Slovakia yet, the parous midges of potential vector complexes will be processed in PCR for EHD virus detection to observe the potential subclinical infections of animals.

The work was supported by the Slovak Grant Agency VEGA No. 1/0236/12, under the basic research project NRL UVLF for pesticides.

22.163 *Borrelia* in immature *Ixodes ricinus* feeding on lizards in Algeria

H. Soualah-Alila¹, I. Bitam², **Z. Bouslama³**, A. Beneldjouzi⁴ ¹Mouhamed Chérif Messadia University-Souk-Ahras-Algeria, Laboratory of Ecology Terrestrial and Aquatic Systems, Department of Biology, Annaba University, Annaba, Algeria, ²Service d'Ecologie des Systèmes Véctoriels,Institut Pasteur d'Alger,Annexe Ruisseau, Algiers, Algeria, ³University of Badji Mokhat, Laboratory of Ecosystem Aquatic and Terrestrial, Annaba, Algeria, ⁴Service d'Ecologie des Systèmes Véctoriels,Institut Pasteur d'Alge, Algiers, Algeria

Background: Borrelia is one of the important emerging infectious diseases. It is a zoonotic spirochetal disease of global importance.

Objectives: This disease continues to have a major impact on people living in rural area.

IMED 2013

Poster Presentations II

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: Study Area: The study was conducted in Séraïdi, Annaba (North East of Algeria) humid bioclimatic zone. Tick and Lizard Collection: This survey was conducted from 2010 to 2011. Lizards were hand captured in the site or using a special pitfall in the complex zone. Ticks were removed from each lizard using forceps and stored in 70% ethanol for later identification to species and life stage using taxonomic keys (IPTM, version1.0 "AFPMB" and confirmed by Pasteur Institute of Algiers). DNA Extraction: DNA was extracted from ticks composed of males and unfed females, using the QIAmp DNA Mini Kit (QIAGEN GmbH, Hilden, Germany) and Sequencing was done in Marseille laboratory (unite des Rickettsies).

Results: 198 lizards were captured belonging to tree species: Psammodromus algirus, lacerta pater, Podarcis hispanica, were checked for attached ticks. In total 120 nymph and larval ticks were removed and further identified as I. recinus. We report here for the first time the detection of the Borrelia, from a total of 89 ticksnfrom 20 lizards (Psammodromus algirus).

Conclusion: Ticks on lizards should be a subject of further observation and contributed not only to recognize further epidemiological studies on geographical distribution of zoonosis which pathogens are spread by ticks.



22.164 Tick-borne encephalitis surveillance in the Czech Republic focused on the areas of the Czech/Austrian border in the decade 2002-2011

B. Kriz. M. Daniel, C. Benes

National Institute of Public Health, Praha 10, Czech Republic

Background: The reported incidence of tick-borne encephalitis (TBE) in Austria (A) and Czech Republic (CR) differs significantly. Most of the natural foci of this infection are located in the south part of CR and present a potential problem for visitors from abroad.

Objectives: To define the risk areas of CR/A border and present the epidemiological situation in the whole CR in the last decade.

Methods and Materials: In the CR, infectious diseases are reportable by law. Detailed data are reported electronically to the National Institute of Public Health, Prague.

Results: In 2002-2011, tick-borne encephalitis(TBE) continued the upward trend observed since the early 1990s. TBE incidence rates ranged between 5.0 and 10.0/100,000 population. The most affected administrative regions were the South Bohemian (23.1/100,000), and Highlands(12.6/100,000) Regions. They and the South Moravian Region (5.1/100,000) are located on the Czech/Austrian border.

Seven districts with an overall population of 734223 are direct neighbours ofAustria. TBE cases showed a downward trend in three districts, a plateau in two districts and an upward trend in two districts. The ten-year average TBE incidence rates in these border districts varied from 1.4/100,000 to 45.2/100,000.

On long-term average, the onset of the largest proportion of TBE cases occurs in July. Nevertheless, the incidence curve shows relatively often two peaks, with the second peak observed in autumn months. In the last decade, the highest numbers of TBE cases were reported in 2006 (1029-the highest number of TBE cases in the whole period 1971-2011) and in 2011 (861-the second highest number of TBF cases)

In 2006, the first TBE peak (79 cases) was seen in week 29 and the second one (88 cases) in week 36. In 2011, the respective peaks (60 and 53 cases) were observed in weeks 26 and 33. It is evident that the annual pattern of TBE onset peaks can vary widely between years.

Conclusion: Considerable part of the border areas between two states comprise a TBE risk areas for visitors. They should be aware of this fact and respect the preventive measures during their outdoor activities.

This study was supported by Czech Ministry of Health IGA project grant NT 11425-5/2010.

ellular factors needed for the functions of the Rift Valley fever virus virulence factor NSs

M. Kainulainen¹, M. Habjan², L. Busch¹, S. Lau¹, A. Pichlmair³, G. Superti-Furga³, F. Weber¹

¹Philipps-University Marburg, Marburg, Germany, ²University of Freiburg, Freiburg, Germany, 3CeMM, Vienna, Austria

Background: Rift Valley fever virus (RVFV, Phlebovirus / Bunyaviridae) is an arbovirus causing large epizootics and epidemics in Africa and on the Arabian Peninsula. In humans, symptoms vary from mild selflimiting disease to haemorrhagic fever and death. The spectrum of clinical symptoms in humans seems not to be caused by differences in infecting RVFV strains. It is therefore likely that host factors related to RVFV life-cycle play a role. We are looking into RVFV pathogenesis by studying how the main virulence factor of the virus-non-structural protein NSs-uses cellular factors to exert its functions.

Objectives: RVFV virulence factor NSs triggers proteasomal degradation of the general transcription factor IIH subunit p62 and the pattern-recognition receptor PKR (Kalveram et al., J. Virol. 2011, Ikegami et al., PLoS Pathog. 2009, Habjan et al., J. Virol. 2009). This results in inhibition of the antiviral interferon response and rescue of virus protein translation. The objective is to identify cellular factors that NSs uses to degrade p62 and PKR.

Methods and Materials: Co-IP/MS was used to identify cellular proteins interacting with NSs. The function of these factors was studied using confocal microscopy and siRNA experiments.

Results: We found that NSs interacts with a specific targetrecognizing E3 ubiquitin ligase component. The factor is required for NSs induced degradation of p62, but not for the degradation of PKR. Partial rescue of the type I interferon response is seen in RVFV infected knock-down cells. This indicates that the factor is relevant regarding the virulence mechanism of NSs.

Conclusion: An E3-ubiquitin ligase required for type I interferon antagonism by RVFV NSs has been identified. Ongoing work will identify the factors NSs uses to degrade its other target, PKR. We are also interested in studying the sequences and expression levels of the identified factors in patient samples, correlating these data with p62 and PKR degradation status, and comparing the findings with clinical outcomes. Understanding what determines the variability of RVFV pathogenicity in humans might enable limiting the impact of outbreaks by identifying individuals at elevated risk of severe disease.

22.166

Outbreak of West Nile virus infection in humans and horses, Croatia, 2012

T. Vilibic-Cavlek¹, L. Barbic², I. Pem-Novosel¹

I. Gjenero-Margan¹, E. Listes³, N. Pandak⁴, L. Peric⁵,

V. Stevanovic², G. Mlinaric-Galinovic¹, G. Savini⁶

¹Croatian National Institute of Public Health, Zagreb, Croatia, ²Faculty of Veterinary Medicine University of Zagreb, Zagreb, Croatia, ³Croatian Veterinary Institute, Split, Croatia, ⁴General Hospital "Dr Josip Bencevic", Slavonski Brod, Croatia, ⁵Clinical Hospital Centre Osijek, Osijek, Croatia, ⁶L'Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, Teramo, Italy

Background: During the last two decades, several West Nile virus (WNV) outbreaks have occurred throughout the world. In Croatia, clinical cases of WNV infection have not been documented until now, although cases have occurred in the neighboring countries (Italy, Hungary, Romania and Greece). Moreover, in July 2012, the first outbreak of WNV disease occurred in Serbia with 44 laboratory diagnosed cases and six deaths.

Objectives: We are reporting the first outbreak of WNV neuroinvasive infection in humans and evidence of acute WNV infection in horses in Croatia (August-September 2012).

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: WNV IgM/IgG testing and IgG avidity were performed using commercial ELISA and confirmed by plaque-reduction neutralization test (PRNT) and micro-neutralization test (micro-NT). Samples were also tested for other flaviviruses (tick-borne encephalitis virus-TBEV, dengue virus-DENV and Usutu virus-USUV) to rule out cross-reactions.

Results: Seven human cases of WNV neuroinvasive disease were laboratory confirmed between 06 and 21 September 2012 in Croatia. The median patient age was 62 years (range 48-77 years). Five patients presented with meningoencephalitis and two patients with meningoencephalitis followed by acute flaccid paralysis. Most of them had underlying diseases, the most common being hypertension. In six patients, WNV-specific IgM antibodies with low IgG avidity antibodies were detected while one patient showed only IgM antibodies. Crossreactivity was seen mainly for DENV IgG. WNV infection was confirmed by PRNT and micro-NT in all samples. Patients with WNV neuroinvasive disease are residents of three counties located in eastern part of Croatia, near the Serbian state border. The first case was imported from Serbia while the others represent the first autochthonous WNV cases. Five patients fully recovered. Before human cases were reported, acute WNV infection had been demonstrated by detection of IgM antibodies in twelve asymptomatic sentinel horses in counties where human cases occurred.

Conclusion: In September 2012, WNV neuroinvasive disease in humans was documented for the first time in Croatia. Asymptomatic acute infection in sentinel horses had been reported in the same geographic region before human cases occurred. Adulticidal and larvicidal treatments were administered immediately in the respective place of residence. Epidemic control measures prevented further spreading of disease.

22.167

Rapid spread of Schmallenberg virus in Austrian domestic ruminants P. Schiefer, A. Steinrigl, E. Wodak, F. Schmoll

Austrian Agency for Health & Food Safety (AGES), Mödling, Austria

Background: After observation of stillbirth as well as arthrogryposis hydranencephaly syndrome (AHS) in neonates and the identification of Schmallenberg Virus (SBV) as the source of these findings in Germany, Austria started routine monitoring of cattle, sheep and goat samples for SBV antibodies (AB) in the first half of 2012. In addition, retrospective analysis of cattle samples going back to the last quarter of 2011 was perfomed. Approximately 1200 serum samples were analyzed without detection of SBV AB in Austrian livestock until end of June 2012.

In September 2012, SBV AB were first detected in Austrian cattle, followed a view weeks later by detection of SBV genome in an aborted cattle fetus not showing AHS.

Objectives: The aim of this study was to get an overview about the extent of SBV spread in Austria in the period from mid-October to mid-November 2012

Methods and Materials: Samples for analyses performed in autumn 2012 were taken from a risk based monitoring program for Bluetongue virus in cattle, Brucella melitensis surveillance in sheep and goats and routine testing of cattle, sheep and goat samples. Screening for SBV AB was carried out with a monophasic ELISA Screening Test and questionable results were confirmed by biphasic ELISA (both IDvet); both test systems had been validated using serum neutralization test.

Results: Between mid-October and mid-November 2012, 630 bovine blood samples were analyzed, of which 562 samples (89.2 %) were seropositive. Samples from small ruminants collected in the same time period showed a remarkably lower seroprevalence: SBV AB were detected In 339 out of 608 blood samples (55.8 %).

Conclusion: This preliminary study shows a very high prevalence of SBV AB in Austrian cattle, which had been naïve to SBV until early to mid-summer 2012. This indicates rapid and extensive spread of SBV infection in Austrian cattle within a few months' time. The lower level of seroprevalence observed in small ruminants needs to be investigated further. As most small ruminants in Austria are-like cattle-pastured during summer, one would expect a similar risk of SBV infection in both small ruminants and cattle.

22.168 Ecoepidemiology of Anaplasma phagocytophylum in horses in France

A. Leblond¹, A. Chastagner², X. Bailly², S. Masseglia³, G. Vourc'h³ ¹Vetagrosup INRA, Marcy L'Etoile, France, ²INRA, Saint Genès Champanelle, France, ³INRA, Saint Genes Champanelle, France

Background: Anaplasma phagocytophilum is a tick-borne pathogen mainly transmitted by the tick Ixodes ricinus in Europe, but the bacterium has also been detected in Rhipicephalus and Dermacentor. Besides. A. phagocytophilum has a large genotypic diversity, which may depend on the species of ticks, infected animals or geography.

Prevalence studies conducted in horse's populations in the south of France (Camargue), showed that the infection is emerging in this area. Moreover Ixodes ricinus is thought to be rather rare in this Mediterranean ecosystem.

Objectives: The first objective of our study was to identify potential vectors of A. phagocytophilum in horses in Camargue. Then, we aimed at comparing the phylogenetic analysis of strains of A. phagocytophilum in Camargue with other ones isolated in a more northern region, around Lvon. on horse's cases.

Methods and Materials: Ticks were collected on 1450 horses and 20 pastures in Camargue. Besides, at the equine clinic of the veterinary university of Lyon, blood and ticks were collected on 3 diseased horses. Ticks were identified and all samples were tested for the presence of A. phagocytophilum by nested PCR of the 16S ARN gene. Phylogenetic analysis of the positive samples was then conducted and results were compared with sequences published in the GeneBank database

Results: In Camargue, 326 ticks were collected on horses and 81 on pastures. Six species were identified and among them Rhipicephalus bursa, Rhipicephalus sanguineus and Dermacentor marginatus were positive for A. phagocytophilum. No Ixodes ricinus was found. In Lyon, the two Ixodes ricinus collected on horse's cases were positive.

The phylogenetic analysis of the strains, using the AnkA and msp4 coding sequences, suggested that the same strain is circulating in the different species of ticks in Camargue. This strain is akin to a human strain isolated in USA and to other strains isolated in the Mediterranean region. The genotype identified in Lyon grouped with strains isolated on domestic or wild hosts in central Europe.

Conclusion: A strain potentially akin to a human strain of A. phagocytophilum is circulating in Camargue and potential vectors could be of the genus Rhipicephalus and/or Dermacentor.

22.169 First description, molecular and phylogenetic analyses of Barkedji virus isolated from Culex perexiguus in Israel in 2011

J. Kolodziejek¹, K. Pachler¹, K. Sekulin¹, H. Lussy¹, H. Bin²,

N. Nowotny¹

¹University of Veterinary Medicine, Vienna, Austria, ²Ministry of Health, Tel Hashomer, Israel

Background: Data regarding genetic evaluation and phylogenetic positioning of Barkedji virus within the family Flaviviridae were missing so far. The first Barkedji virus sequence of the isolate ArD86177 from Senegal was submitted to GenBank already in 2007 and was later included in a study on molecular evolution of 'insect-specific' flaviviruses (Cook et al., 2012), however without details on Barkedji virus.

Objectives: In the present study, Barkedji virus was identified in a pool of Culex perexiguus mosquitoes collected in Israel in 2011. The almost complete polyprotein gene sequence was determined and detailed molecular and phylogenetic analyses were conducted.

Methods and Materials: Thirty-eight mosquito pools collected in Israelbetween 2001 and 2011 were investigated for the presence of flaviviral nucleic acid. The samples were tested by two published universal RT-PCRs. While most of the samples were positive for West Nile (WN) viruses, one of them exhibited close relatedness to Barkedji virus strain Senegal. For determination of the almost complete genome sequence, 29 primer pairs were designed and the obtained PCR fragments were sequenced. The determined Barkedji virus sequence was aligned with

International Meeting on Emerging Diseases and Surveillance 2013

other flaviviral sequences from GenBank. Subsequently, phylogenetic analysis on altogether 36 selected mosquito-borne flaviviral sequences was conducted using the neighbour-joining method of the MEGA 5 program. Proteins were characterized employing Pfam and Prosite protein profile and alignment tools.

Results: The two Barkedji virus strains exhibit 97% and 99% identities to each other at the nucleotide and amino acid level, respectively. The Israeli Barkedji virus polyprotein sequence comprises 3420 aa (10588 nt); the three flavivirus structural proteins and eight flavivirus non-structural proteins could be localized. Phylogenetic analysis of the selected 36 polyprotein gene sequences exhibits two major clades. Barkedji viruses belong to the clade, which comprises *Culex*-associated viruses like WN, Japanese Encephalitis, St. Louis Encephalitis viruses as well as *Stegomyia*-associated Dengue viruses, however, they represent a distinct subclade. Comparison of protein sequences of Barkedji viruses with six other mosquito-borne flaviviruses mirrors the phylogenetic analysis.

Conclusion: The present study emphasizes a distant relationship of Barkedji virus to other known flaviviruses, suggestive of a novel lineage within the family *Flaviviridae*.

22.170 Mediterranean spotted fever a reemerging tick-born disease inBulgaria

I. G. Baltadzhiev

Medical University, Plovdiv, Bulgaria

Background: In Bulgaria Mediterranean spotted fever (MSF) is an endemic tick-borne rickettsiosis caused by *Rickettsia conorii conorii* and transmitted to humans by the brown dog tick *Rhipicephalus sanguineus*.

Objectives: Although it was not found in the country for a period of more than 20 years (1972–1992), MSF re-emerged unexpectedly at the beginning of the 90-s and was characterized by staggering rapid progression and severe course. The disease affected thousands of people and caused the death of tens of them. In the largest endemic Plovdiv-region inBulgaria re-emerging MSF demonstrated two phases in its development—of rapid and steep growth during the 1st and of drop in its dissemination during the 2nd phase.

Methods and Materials: The study compares the results of the first phase of upward growth (1993–2003) and the second phase of a downturn (2004–2011) of MSF in Plovdiv-region. The number of patients infected and treated from MSF for 1993–2011 is 1254. The disease has been confirmed etiologically in 549 patients in the first and 334 patients in the second phase by indirect immunofluorescence assay carried out in the Referent Rickettsial Laboratory, so that 883 MSF patients were enrolled in this study.

Results: We realized a comparative study and found out that independent of the reduced indexes of morbidity (11.88 vs. 9.56 per 100000 peoples) and lethality (3.46% vs. 1.19% p<0.05) during the 1st and the 2nd phases respectively,re-emerging MSF kept on with the classic clinical manifestations and the general clinical-epidemiological characteristics which were typical for the first phase. Those characteristics referred to the ways and modes of contamination, the endemic character of the disease, its seasonal appearance, the age, gender and social structure of the patients and the severity of the clinical forms. These were presented as mild (41.16 vs. 35.62% p>0.05), moderate (32.79 vs. 43.11% p<0.01), severe (16.03 vs. 11.37% p=0.05) and malignant (6.56 vs. 8.68% p>0.05) for the 1st and 2nd phases respectively.

Conclusion: It was concluded that MSF is a disease which is far away from elimination. It remains topical and dangerous for the health of people regardless of the decreasing indexes of morbidity and lethality.

22.171 Detection of SBV Antibodies in wild ruminants in Austria, 2012

P. Schiefer¹, A. Steinrigl¹, E. Wodak¹, A. Deutz², F. Schmoll¹ ¹Austrian Agency for Health & Food Safety (AGES), Mödling, Austria, ²Steiermärkische Landesregierung, St. Lambrecht, Austria

Background: Mid of September 2012 SBV antibodies (AB) were detected in Austrian livestock for the first time, followed by first detection of SBV genome in an aborted cattle fetus. Wide-spread detection of SBV AB in Austrian livestock raised the question about the situation concerning SBV infections in wild ruminants.

Objectives: Aim of this study was to provide a preliminary analysis of SBV seroprevalence in Austrian wild ruminants.

Methods and Materials: Blood samples from wild ruminants, farmed game and zoo animals such as red deer, row deer, fallow deer, reindeer, sika deer, moufflons and chamois were analyzed for the presence of SBV AB with the monophasic ELISA Screening Test of IDvet, which is registered for cattle, sheep and goats. To validate the ELISA for wild ruminants, presumably SBV AB-negative samples from deer from 2010 and SBV AB-positive samples from chamois from 2012 were revised by serum neutralization test—both test systems showed congruent results. Since most tested animals were shot, blood quality often was poor due to hemolysis. The blood was taken either out of the heart or the pectoral cavity.

Results: 66 blood samples of wild ruminants were taken from end of September until end of November 2012 and analyzed for SBV AB. One sample was not analyzable, 6 samples delivered questionable results, 27 were negative according to the cut-off value of the test kit and 32 samples (49.2 %) showed a positive reaction in ELISA. Positive SBV AB results were detected in red deer (6), row deer (15), sika deer (1), reindeer (4), fallow deer (2) and chamois (4). Some of the negative results showed an increased OD-value which should be further investigated.

Conclusion: In this study, SBV AB were detected in wild ruminants from very different regions in Austria and from places ranging in sea level from 200 up to 1.400 meters. The detection of SBV AB in chamois in higher alpine areas also provides evidence that arthropod vectors of SBV could also be present in higher alpine areas—either because vectors naturally inhabit alpine sites or because they were dispatched by wind drift.



Dengue virus seroprevalence survey in the inhabitants of the Croatian southern Adriatic coast

I. Pem-Novosel¹, I. Gjenero-Margan¹, T. Vilibic-Cavlek¹,

M. Ljubic², S. Kurecic Filipovic¹, T. Nemeth-Blazic¹ ¹Croatian National Institute of Public Health, Zagreb, Croatia, ²Dubrovnik-Neretva County Institute of Public Health,

Dubrovnik, Croatia

Background: Dengue is one of the major mosquito-borne viral infectious diseases considered an important global public health concern. France is the first country in Europe with autochthonous transmission of dengue infection. After a German patient with dengue fever had been reported after returning from the Croatian peninsula of Peljesac, health professionals and the public in Croatia were alerted to enhance surveillance of dengue. This has resulted in the diagnosis of the second autochthonous disease case as well as in the detection of recent dengue infections in residents of the same area, without travelling history.

Objectives: The aim of the study was to assess the seroprevalence of dengue IgG antibodies among the inhabitants of the Dubrovnik-Neretva County located at the southern Adriatic coast in Croatia, where autochthonous dengue cases were detected in August–September 2010.

International Meeting on Emerging Diseases and Surveillance 2013

Methods and Materials: A cross-sectional serologic survey was performed among the inhabitants of the Croatian Adriatic coast during 2011. A total of 139 sera samples were collected from healthy, anonymous residents of Dubrovnik-Neretva County. Samples are tested for the presence of dengue virus (DENV) IgG antibodies. Serological testing was performed using commercial ELISA. Positive and borderline results were confirmed using commercial indirect immunofluorescence assay (IFA). Reactive samples were further tested for West Nile virus (WNV) IgG and Chikungunya virus (CHIKV) IgG antibodies to rule out cross-reactions.

Results: Three out of 139 participants (aged 36, 32 and 7 years) were found positive for DENV-specific IgG antibodies by ELISA and IFA tests with the seroprevalence rate of 2.16%. Samples were negative for WNV and CHIKV IgG antibodies. Antibodies to tick-borne encephalitis virus (TBEV) were not analyzed because Adriatic coast is not endemic region for TBEV.

Conclusion: Results of this study indicate low DENV seroprevalence rate at the Croatian southern Adriatic coast. Larvicidal and adulticidal treatment had been implemented in the affected area as outbreak control measures. Preventive mosquito control measures have been regularly performed in Croatia, especially in the areas where a competent vector had been established. There were no new suspect dengue cases since 2010 in Croatia.

22.173 Possible involvement of Schmallenberg virus in ruminant abortions and early embryonic death in cattle

A. Steinrigl¹, P. Schiefer¹, W. Peinhopf², S. Revilla-Fernández¹, F. Schmoll¹

¹Austrian Agency for Health & Food Safety (AGES), Mödling, Austria, ²Dr. VET-Die Tierärzte, Lebring, Austria

Background: Schmallenberg virus (SBV), an orthobunyavirus of the Simbu serogroup, emerged in summer/autumn 2011 in north-western Europe. Since then, SBV has been continuously spreading over large parts of Europe, including Austria, where antibodies to SBV were first detected in September 2012.

Objectives: Existing studies have mainly focused on detection of SBV genome in malformed ruminant foetuses and new-borns, showing pathologic changes consistent with arthrogryposis hydranencephaly syndrome (AHS). Little is known about potential short-term consequences of SBV infection on ruminant fertility. Thus, this study was initiated to provide data about the possible contribution of SBV infection to ruminant abortions and early embryonic death in cattle observed around and after the time of first detection of SBV antibodies in Austrian ruminants.

Methods and Materials: Detection of SBV genome by RT-qPCR was attempted in foetal or placental tissue obtained from 151 cases of abortion in cattle and sheep, as well as in 7 bovine allantoic fluid samples, which were collected following ultrasound-assisted diagnosis of early embryonic death.

Results: SBV genome was detected by RT-qPCR in 37 of 135 (27%) cattle and 1 of 13 (8%) sheep abortions received from September to November 2012. Interestingly, SBV genome was detected in 2 of 7 bovine allantoic fluids sampled from October to November 2012.

Conclusion: Around and after the first detection of SBV antibodies in Austria in summer/autumn 2012, SBV genome was detected in a significant proportion of cattle abortions. Prevalence of SBV genome in contemporaneous ovine abortions was apparently lower; however, this difference should be interpreted with caution, as only a very limited number of sheep abortions were received for analysis. Furthermore, we present first evidence that SBV infection of pregnant cattle could also be involved in early embryonic death, as shown by detection of SBV genome in allantoic fluid.

S. Bilk¹, C. Schulze¹, F. Hühn², A. Hlinak¹, B. Hoffmann³, W.-I. Bock²

¹State Laboratory Berlin-Brandenburg (LLBB), Frankfurt (Oder), Germany, ²Thuringian State Authority for Food Safety and Consumer Protection (TLLV), Bad Langensalza, Germany, ³Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany

Background: In autumn 2011 a novel Orthobunyavirus, called Schmallenberg Virus (SBV), was discovered in domestic ruminants in Europe. Identification of the first SBV-induced malformed lambs was reported from the Netherlands in December 2011. From January 2012 onwards malformed lambs were submitted to the federal veterinary state laboratories of Thuringia and Brandenburg. At the beginning of the epidemic, only limited information was available about the organ distribution of the virus within the malformed lambs.

Objectives: The aim of this study was to define the most suitable organs for reliable, accurate and cost-effective diagnosis of SBV in lambs with typical malformations under routine diagnostic conditions.

Methods and Materials: From January until mid-March 2012 123 lambs (65 at TLLV and 58 at LLBB) with and without typical malformations (arthrogryposis, malformations of the brain, cerebellum and/or vertebral column) were tested for the presence of SBV RNA using RT-qPCR. The following organs and body fluids were investigated: cerebrum, cerebellum, spleen, spinal cord, bone marrow, skeletal muscle, thymus, lung, liver, kidney, heart, thyroid, meconium, umbilical cord, rib cartilage and external placental fluid.

Results: In 76 of the lambs SBV genome sequences were detected in at least one organ (40 at TLLV and 36 at LLBB). 75 of these foetuses showed typical malformations, whereas one was an amorphous globosus (twin of a typically malformed and SBV-RT-qPCR positive lamb). External placental fluid, umbilical cord, cerebrum, cerebellum and spinal cord were the organs with the highest detection rates. For 3 lambs SBV-RNA was not detected in any of the analysed organs, although the malformations looked like SBV-induced.

Conclusion: Our results show, that beside cerebrum, cerebellum and spinal cord, both external placental fluid and umbilical cord are suitable samples for the detection of SBV in malformed lambs. There was a good correlation concerning typical malformation and detection of SBV genome sequences, as nearly all animals (75 of 78) with typical malformation were SBV positive in at least one of these organs. The detection of SBV in an amorphous globosus might be an incidental finding. Using pooled samples including external placental fluid and umbilical cord in lambs seems to be an easy-sampling and cost-effective strategy for routine diagnosis.

22.175 Pulmonary involvement of Crimean–Congo haemorrhagic fever

L. Berisha-Ajazaj, S. Ahmeti, S. A. Namani, E. Qehaja-Bucaj, H. Ramadani, A. Vishaj

UCCK, Prishtina, Kosovo, Republic of (under UNSCR 1244/1999)

Background: Kosovo is an endemic region for Crimean-Congo hemorrhagic fever (CCHF) with sporadic cases and epidemic outbreaks being observed every year.

Objectives: The objective of the study was to analyze the respiratory involvement during the course of CCHF in patients treated at the Infectious Diseases Clinic in Prishtinë (Kosova) during years 2006-2011.

Methods and Materials: In this retrospective study were collected data from medical records of 87 patients confirmed for CCHF by laboratory findings. We analyzed respiratory involvement confirmed with pulmonary symptoms, pulmonary pathologic findings on physical examination and chest radiography.

Poster Presentations II

International Meeting on Emerging Diseases and Surveillance 2013

Results: During a six year study period there were 87 patients (range 2-75 years) confirmed for CCHF by reverse transcription- PCR. The overall mortality rate was 16% (fourteen cases of death). Male gender dominated with 58 cases (66.6%). The highest incidence of patients with CCHF was recorded from May to August. Of the 87 patients, 29 patients (33.3%) were diagnosed for pulmonary involvement of CCHF. Respiratory involvementdeveloped twice frequently in males (15/29; 51.7%) compared to females (14/58; 24.1%). Most frequent symptoms of patients with respiratory involvement were dyspnea/ tachypnea (62%), hemoptysis (6.9%), chest pain (6.9%), pulmonary edema (6.9%) and ARDS (3.4%). Chest radiographs showed unilateral pathology in 11 cases and bilateral pathology in 18 cases. Radiologic findings were bronchopneumonia (6 cases), pleural effusion (4 cases), pulmonary infiltrates (15 cases) paratracheal lymphadenopathy (2 cases), pneumonia (1 case) and abscessus pulmonum (1 case). Four patients died due to pulmonary haemorrhage (pleuritis haemorrhagica) and haemorrhagic syndrome (haematemesis, melena, epistaxis, haematoperitoneum). Of the 29 patients with respiratory envolvement of CCHF, 8 patients have died (27.6%).

Conclusion: Pulmonary involvement occur frequently in patients with CCHF and very often are associated with mortality.

22.176 First autochthonous dengue virus infections in Madeira Island, Portugal in 2012

L. Ze-Ze¹, F. Amaro¹, H. C. Osório¹, P. Parreira¹, T. Luz¹,

G. Andrade², P. L. Fernandes², M.-J. Alves¹

¹National Institute of Health Dr. Ricardo Jorge, Águas de Moura, Portugal, ²Hospital Dr. Nélio de Mendonça, Funchal, Portugal

Background: The last Dengue epidemic in Europe vectored by Aedes aegypti was reported, in 1927-1928 in Greece. In Madeira Island, Portugal, this mosquito species was detected for the first time in 2005 in Funchal, and the mosquito population and dispersion trough the island has been increasing since then.

Objectives: This work reports the molecular diagnosis of the outbreak autochthonous cases of dengue virus infections in Madeira Island in October 2012 and the virus serotype identification.

Methods and Materials: The first sera and whole blood human samples of clinically suspected patients from Madeira Island were tested by IFA and conventional RT-PCR (using Pan-flavi and Dengue specific assays) and confirmed by Real-time PCR for Dengue virus detection. The obtained amplicons by conventional PCR were purified, sequenced and identified by homology searches within the GenBank database using Blast algorithm.

Results: A total of 182 patients samples were analysed at CEVDI, 172 serologically and 43 by PCR in the first two months of the unset of the outbreak, of which 52.2% were positive, 74.7% IgM, 65.3% IgG and 61.1% for both dengue IgM and IgG. Regarding RT-PCR, 46.5% of the blood samples were found to be positive. In all PCR positive samples DEN1 virus was identified by sequence analysis of at least 450 nt of C-prM region. Preliminary sequence analyses ascertain this virus as related to sequences circulating in Latin America, namely Colombia, Venezuela and Roraima region in Brazil.

Conclusion: The first two autochthonous human cases of dengue virus in Madeira Island were reported on October 3rd 2012 and by the end of November Madeira Health authorities confirmed almost 2000 cases. Several cases in mainland Portuguese (10) and other European countries (Germany, U.K., France, Sweden and Finland) visitors have also been reported so far. The rapid expansion of dengue cases in Madeira Island highlights the importance of the maintenance of adequate surveillance systems, namely by the detection of the vector and human cases (especially in European regions where Aedes albopictus is already present) in a way to allow the implementation of adequate and prompt control actions.

2010–2011 Re-emergence of Chikungunya virus infection in National capital territory of India

P. K. Singh, M. Mir, L. Dar, S. Broor

all India Institute of medical Sciences, Delhi, India

Background: Chikungunya virus(CHIKV) is an emerging arboviral infection of public health importance. First reported 1952 in Tanzania. Presently CHIKV persist many parts of world including Africa, India and South East Asia. There were major outbreaks of chikungunya in 2006 in islands of Indian Ocean. In India recently major epidemics of chikungunya fever were reported in 2008, 2009 and 2010 from south India

Objectives: To study the epidermologic and Phlogenetic pattern of CHIKV during June 2011-Dec 2011 in national capital territory of India.

Methods and Materials: During study period 2346 blood samples were collected from outpatients and inpatients attending AIIMS New Delhi during the period from June 2010-Dec 2011. Serum samples were tested for IgM antibodies to chikungunya virus by mu-capture ELISA. RT-PCR was performed using primers from the envelope (E1) gene, C6/36 cell line were used to isolate CHIKV in tissue culture, E1 gene was sequenced for phylogenetic analysis and amino acid variations.

Results: IgM ELISA positivity of 38.45% (n=902) was seen (total=2346) with 43.1% (n=475) females and males 34.32% (n=427). Female:male ratio 1.1:1. RT-PCR targeting E1 gene for CHIKV shows positivity of 47.9% (n=168) with 42.3% (n=74) males and 53.41% (n=94) females. The age range of patients was 6 months-85 years, median of 32 years with most affected patients belong to age group >30-45. Maximum positivity was seen in Oct-Nov of both years. Using tissue culture CHIKV was successfully isolated from patient samples. Sequencing confirms samples clustering with Central East and South Africa (CESA) Genotype.

Conclusion: Chikungunya virus has emerged in Delhi during 2010 and contributed to about 30-40% of fever and arthralgia. Females are more affected than males. CHIKV prevalence is highest in post monsoon month of October. The virus is similar to CESA genotype prevalent in rest of India

22.178

Clinical and epidemiological aspects of Lyme borreliosis from Mures County, Romania

B. Tilea. I. Tilea

University of Medicine and Pharmacy, Tirgu Mures, Mures, Romania

Background: Lyme borreliosis (LB) is the most frequent infection transmitted by ticks from the Ixodes genus, both in the United States of America (USA), and in Europe.

Objectives: The objectives of this study were the monitoring of the incidence and clinical manifestations of the disease in Mures County.

Methods and Materials: The study underwent for two years, January 1, 2010–December 31, 2011, on a number of 120 consecutive patients. The definite or probable diagnosis of LB was established on the Center for Disease Control (CDC) Atlanta, USA criteria, and on the European Union Concerted Action on Lyme borreliosis (EUCALB). For the identification of IgM and IgG antiBb from the serum and CSF ELISA and Western-Blot techniques were used.

Results: In 2010 there were 44 cases and in 2011, 76 cases. According to the case definition, 106 cases were confirmed and 14 were probable. LB was more frequently diagnosed in children, young adults and adults, compared to the over 60 years old age group. The incidence of this disease was higher in women, 68 (56.66%) patients compared to men 52 patients (43.33%), with a higher proportion in people coming from an urban setting, 78 patients (65%), compared to people coming from a rural setting 42 patients (35%). The clinical manifestations were acute, like erythema migrans (EM) in 64.16% of the patients, neurological in 22.5% of the patients, joint related in 1.66% of the patients and cardiac in 0.83% of the cases.

Conclusion: In Mures county we have observed an increasing incidence of this disease in 2011 vs. 2010. The predominant clinical manifestations were the acute dermatological and neurological ones.

International Meeting on Emerging Diseases and Surveillance 2013

22.179 Genetic characterization of Chikungunya virus causing outbreaks in the Philippines

A. K. Sy¹, I. A. Medado¹, M. Saito²

¹Research Institute for Tropical Medicine, Muntinlupa, Philippines, ²Tohoku University Graduate School of Medicine, Sendai, Japan

Background: Chikungunya has caused large outbreaks in several countries throughout the world. In 2011, several provinces of the country started reporting outbreaks caused by Chikungunya. Nevertheless, while its neighboring countries have experienced massive outbreaks caused by Central/East African genotype in recent years, there is limited information about the genotype circulating in the country except for the report in 1985 in which the Asian genotype was detected.

Objectives: To study the molecular epidemiology of the current Chikungunya outbreak in the Philippines.

Methods and Materials: Serum samples collected from patients presenting with fever, rash, and joint pains during outbreak investigations in several provinces in 2011 to 2012, were tested using one-step reverse transcriptase polymerase chain reaction (RT-PCR) and followed by direct sequencing. Phylogenetic analysis was performed using maximum likelihood method on partial E1 gene sequences of 257 bp length.

Results: Chikungunya virus RNA were detected in 10 serum samples, and upon sequencing and analysis, it was grouped into Asian genotype belonging to the same branch and with high similarity to the Indonesian strains reported recently, with the Northern Mindanao strains forming a small cluster.

Conclusion: The Chikungunya virus genotype currently causing outbreaks in the Philippines is of the Asian genotype.

22.180 Estimation of some biologic values with regards to prognostic outcome of patients suffering from Crimean-Congo Haemorrhagic Fever

T. Kalo¹, P. Biberaj², A. Pilaca³, S. Kurti⁴, K. Shkurti⁵,

E. Puca⁶, D. Kraia³

¹University Hospital Center "Mother Theresa", Tirana, Albania, ²Faculty of Medical Sciences, University of Tirana, Tirana, Al, Albania, ³U.H.C."Mother Teresa" Tirana, Tirana, Albania, ⁴U.H.C."Mother Teresa", Tirana, Albania, ⁵UHC "Mother Teresa", Tirane, Albania, ⁶U.H.C., Tirana, Albania, ⁷Faculty of Medicine, Tirana, Albania, Albania

Background: Crimean-Congo Haemorrhagic fever (CCHF) is a tickborn and a fatal viral infection disease described in 30 countries around the world. The Balkan Peninsula is an endemic region for the disease, but the first case inAlbaniawas discovered in 1985.

Objectives: The objective of this study is to estimate some significant biologic values for CCHF, with regards to the predilection of its outcome. Methods and Materials: Study is based in a thoroughfully screening of 8 patients hospitalized during the last outbreak of CCHF inAlbania(May-June 2010). CCHF was confirmed with ELISA-test positive for anti-IgM.

Results: Based on the laboratory data of blood samples during the first week of clinical manifestation of CCHF, the following phenomena have been noticed: Thrombocytopenia was noted in 87.5% of cases, with a platelet count of 106.8×10^{9} /litre (normal range, 140×10^{9} - 400 × 10⁹/litre). Leucopenia was noted in 75% of cases. AST was elevated in 50% of cases, with an average level of 926.5UI/dl ranging from 13-6250UI/dl (normal level 0-35 UI/dl). ALT was elevated in 50% of cases with an average level of 528.1UI/dI ranging from 3-3150UI/dI (normal level 0-40UI/dl). The average Prothrombine Level was 76.7% ranging from 33.6-97.6%, and none of PL was below 30%. Fibrinogen was below normal level only in one case. The outcome of CCHF after an intensive supportive therapy was excellent for all of them.

Conclusion: Leucopenia, Thrombocytopenia, Elevation of AST and ALT do not have the same significance for the CCHF outcome as they have for its diagnosis.

22.181

BTV serotype 14 detection in Catalonia (Spain) in imported cattle from the Baltic Area

R. Rosell¹, M. Domingo¹, J. Pujols¹, I. Selga², A. Sanz², I. Mercader², E. San Miguel³, A. Rochas³, M. Aguero³

¹Centre for Research in Animal Health (CReSA), Bellaterra (Cerdanyola del Valles), Spain, ²Generalitat de Catalunya, Barcelona, Spain, ³Laboratorio Central de Veterinaria, MARM, Algete, Madrid, Spain

Background: As for December 2012, the whole peninsular Spain is a restricted zone for BTV-1, and some smaller zones in the southwest of the country are restricted for BTV-4 and BTV-8. Balearic and Canary Islands are both BTV-free zones, and according to EU regulation, imported animals to these regions have to be free of infection showed by quarantine and testing or by vaccination.

During testing of cattle for movement into the Balearic Island, a BTV-RT-PCR positive animal recently imported from Lithuania was found. BTV was classified as BTV-14. As BTV-14 is not present in Spain, it was concluded that the animal was infected in origin or at transport

Objectives: To describe the epidemiological and laboratory investigations performed in a BTV-positive bovine originating from Lithuania, finally classified as BTV-14

Methods and Materials: Generic RT-PCR for BTV was used for screening of blood samples. Serum from the positive animal was tested by serum-neutralization test against BTV-1, BTV-8, BTV-2, BTV-4, and BTV-14. Partial genomic sequence was done for genes of the NS1, NS3, and VP2 proteins. Isolation was attempted by inoculation of the sample in chicken embryo

Results: A group of 216 calves arrived on 6/Aug/2012 from Lithuania to a farm in Catalonia, and mixed together with other calves. On the 26/Sept/2012 a RT-PCR BTV positive sample was found in a batch tested for movement to the Balearic Islands (BTV-free zone). The positive bovine came from Lithuania. Remaining cattle in the farm gave a negative RT-PCR result, but three additional cattle imported from Lithuania gave a positive BTV-ELISA result. Blood was inoculated in chicken embryo, and BTV was isolated. RT-PCR protocols based on vp2 design to detect BTV-1, BTV-2, BTV-4 and BTV-8 gave a negative result. A BTV-14 RT-PCR resulted positive. In serum of this bovine VN antibodies were found against BTV-14, but not against other common serotypes in Spain. Surrounding farms did not show BTV-infection.

Conclusion: A bovine from Lithuania arrived to Catalonia viremic for BTV-14. The risk of establishment of BTV-14 in other MS by import of ruminants from affected areas is high. Partial sequencing of this BTV-14 showed high homology with South African BTV-14 reference strain

22.182

Partial genetic characterisation of orthobunyavirus Sedlec, Europe

T. Bakonyi¹, Z. Hubalek², I. Rudolf², R. L. Bercic³, N. Nowotny⁴ ¹Viral Zoonoses, Emerging and Vector-Borne Infections Group, Institute of Virology, Vienna, Austria, ²Institute of Vertebrate Biology v.v.i, Brno, Czech Republic, ³Faculty of Veterinary Science, Szent Istvan University, Budapest, Hungary, ⁴University of Veterinary Medicine, Vienna, Austria

Background: The genus Orthobunyavirus is one of the largest viral genera encompassing more than 170 viruses. Many orthobunyaviruses are significant human and animal pathogens. InEurope the presence of Tahyna virus, Inkoo virus, Snowshoe hare virus, Batai (Calovo) virus, Lednice virus, Schmallenberg virus and Sedlec virus has been reported so far.

Sedlec virus (strain AV 172) was first isolated from the blood of a clinically healthy reed warbler (Acrocephalus scirpaceus) in July 1984 in South Moravia, Czechland. Pathogenicity studies revealed its moderate virulence in mice (it killed suckling and adult mice when given intracerebrally, but not when inoculated intraperitoneally). Serological studies could not detect cross-reactivity to any bunyaviruses and other arboviruses.

International Meeting on Emerging Diseases and Surveillance 2013

Objectives: This study describes the first genetic data on Sedlec virus and gives an estimate on its phylogenetic relatedness to other members of the genus.

Methods and Materials: Partial genome sequences of the S and L genome segments of the Sedlec virus prototype strain were amplified using degenerated consensus primers in RT-PCR assays. The amplification products were sequenced, and a 387 nucleotide long sequence of the S segment (nucleocapsid protein genes), and a 1788 nucleotide long sequence of the L segment (RNA-dependent RNA polymerase gene) were determined. They were aligned with all in GenBank database available orthobunyavirus nucleotide sequences, and alignments were subjected to phylogenetic analyses.

Results: The phylogenetic tree based on the S segment indicates the closest genetic relatedness of Sedlec virus to Leanyer virus and Simbu group viruses, while the L segment phylogeny indicates the closest genetic relationship of Sedlec virus to two unclassified orthobunyaviruses I612045 virus (isolated in India in 1961) and Oyo virus (isolated in Nigeria in 1964).

Conclusion: Considering the genetic distances, Sedlec virus might be classified into a novel serogroup of the *Orthobunyavirus* genus.

22.183 A systematic approach to revealing the phylogeography of Rift Valley Fever Virus

C. A. Hercik Georgetown University, Washington, DC, USA

Background: Rift Valley Fever (RVF) virus is an arbovirus in the *Bunyaviridae* family that has caused extensive outbreaks of severe human and livestock disease. This zoonotic virus is endemic to Kenya yet has demonstrated a capacity to emerge in new territories, as exemplified in the outbreaks in Egypt (1977), Western Africa (1988) and the trans-continental jump to the Arabian Peninsula (2000).

Objectives: This study utilizes molecular phylogenetic methods to compare genetic profiles of RVFV isolates as they emerged in distinct settings across the continent of Africa and the Arabian Peninsula.

Methods and Materials: The RVFV nucleotide sequences were obtained from GenBank and used to compare viral isolates based upon S and L segments of the RVFV tripartite genome. The multiple sequences were aligned using the program *ClustalW2 and* model testing was completed using jModelTest2.1.1. The data was then analyzed using Bayesian Inference in the *Mr. Bayes* software program, with the GTR + I + gamma model. The *Markov Chain Monte Carlos* method was selected for ancestral state reconstruction and provided two consensus trees.

Results: From the maximum clade credibility trees produced in this analysis, one can infer that there is generally low genetic diversity observed amongst RVFV isolates, particularly seen in the isolates derived from the 2007-08 RVFV outbreak in Kenya and Tanzania. It can also be interpreted from this output that specific viral profiles correlate more with outbreak periods, rather than outbreak localities. This is exemplified in the large 2006-08 RVFV outbreak that spanned from the island country of Mayotte to Kenya. In addition, the results from this study also suggest that multiple viral profiles may exist within specific outbreak events. Finally, the cladograms suggest that specific strains can be disseminated over vast areas in relatively short periods of time, as demonstrated in the molecular homology seen in the viral strains derived from Southern Africa, and those that emerged in Egypt and Saudi Arabia shortly after.



Figure 1. RVFV L Segment Maximum Clade Credibility Tree.



Figure 2. RVFV S Segment Maximum Clade Credibility Tree.

Conclusion: The ability of RVFV to rapidly spread and adapt to diverse ecological settings across the continent of Africa and the Arabian Peninsula carries the implication of potential risks for its introduction into new regions.

International Meeting on Emerging Diseases and Surveillance 2013

22.184 Dengue infection outbreak among travelers at Koh Lanta, Krabi province, Thailand January–May 2012

K. Suwanna¹, **R. Buathong²**, H. Kanjanasombut², P. Kleaw-orm¹, P. Klabpadung³, W. Manee⁴, P. Huayleuk⁵

¹Disease Control and Prevention Office Region 11 Nakhon Si THammarat, Nakhon Si Thammarat, Thailand, ²Bureau of Epidemiology, Nonthaburi, Thailand, ³Krabi Provincial Health Offices, Krabi, Thailand, ⁴Lanta Hospital, Krabi Provincial Health Offices, Krabi, Thailand, ⁵Koh Lanta Health Offices, Krabi Provincial Health Offices, Krabi, Thailand

Background: On April, 2012 a private hospital in Phuket notified an increasing number of dengue cases among travelers. Initially 39 cases were diagnosed during January 1–April 23, 2012. The Bureau of Epidemiology and local heath authorities, Ministry of Public Health started epidemic investigation during April to May 2012.

Objectives: The investigation's objectives aimed to confirm diagnosis and existing the outbreak, to describe the characteristic of dengue outbreak among traveleres and to implement specific control and prevention measures during April to May 2012.

Methods and Materials: We reviewed medical records in the hospitals where the travelers sought medical care in Phuket and Krabi. Active case finding was done in the hotels and communities at Koh Lanta, Krabi. The case definitions was applied by WHO 1997. Laboratory investigation was done by Dengue PCR. Adult moquito was collected at the hotels and then identified species and testing PCR for Dengue virus.

Results: Total 55 foreigner cases were met case definition (33 DF, 15 DHF, 2 DSS, 5 unspecify) during January–May 2012. No fatal case was reported. There were 26 reported to the surveillance and 29 cases from active case finding. Male:Female ratio was 1:1. Median age was 33 years old (1–65). Age between 35 and 44 years old was the highest proportion (32.7%). Tourist/traveler was highest reported (87.3%). Swedish was the highest affected (49%) followed by German (7.3%), British (5.4%) and Danish (5.4%). The most common clinical presentation was fever, headache, myalgia and skin rash respectively. The highest reported case stayed at Saladan sub-district (67.3%). Three cases were positive Dengue serotype 1 and one case was positive for Dengue serotype 2. Four hotels were surveyed for adult mosquito collection. A hundred adult mosquitos was all *Ae. eagypti* (92 female vs 8 male) and found outside hotels (82%). All female mosquitos were Dengue negative.



Age Group



Conclusion: There was confirmed Dengue outbreak among traveler/ tourist. Multiple dengue serotype was observed. High number of DHF/ DSS was observed and was possibly secondary infection. Delay containment was a crucial factor due to unreporting of first few cases to the surveillance. Warning message and repellent recommended in the hotels. Sentinel surveillance in private clinics/hospitals already conducted.

22.185 New data on distribution and abundance of *Aedes aegypty* in Santiago Island (Cape Verde)

H. Spence da Costa Lima¹, M. C. Pou Barreto², R. Melero Alcibar³, **A. Fernandez-Alvarez²**, I. Monteiro de Pina Araujo¹, R. Molina³, B. Valladares²

¹University of Cape Verde, Praia, Cape Verde, ²University of La Laguna, San Cristóbal de La Laguna, Spain, ³Carlos III Health Institute, Madrid, Spain

Background: Dengue is an emerging disease in the Cape Verde archipelago (2009) where *Aedes aegypti* is its main vector. Abundance and distribution data of the *Aedes aegypti* populations, necessary to know the risk in an area, are currently unknown in the archipelago.

Objectives: The aim of this study was to set abundance and distribution of *Aedes aegypti* in Santiago Island where have been reported the most of the cases of dengue.

Methods and Materials: A random sampling was realized during the rainy season (September 2012). Larvae were captured by pipetting and classified using taxonomic keys.

Results: During the study were captured 282 larvaes, being *Aedes aegypti* the species most abundant (91.5%) and distributed in the island. Other species were identified: *Anopheles preporiensis, Culex tigripes, Culiseta longiareolata* and *Culex quinquefasciatus*. This last was the second most abundant (5.7%) and distributed species in the island. It is known as main vector of lymphatic filariasis which it presents in the island.

Conclusion: The information obtained will analyze with particular environmental and meteorological factors with the aim of create a map of risk of transmission of the disease. The building of map will be useful to develop much more rational strategies of surveillance and control in this zone.

This work was funded by the Project "Estudio medioambiental de vectores y reservorios de zoonosis en Cabo Verde" (A1/035356/11) from AECID.

190 IMED 2013

International Meeting on Emerging Diseases and Surveillance 2013

presenter = **bold** faced, abstract number: e.g. 10.019 = 10 is session number, 019 is presentation number within session

Aangenend H. 21.151 Abdel-Monem O. A. 21.101 AbdelHaleim M. M. 21.123 Abdelrahman M. B. 22.069 Abdu P. A. 21.076 Abdukhalilova G. 21.016 Abdul Wahab A. 21.185 AbdulAziz N. 22,116 Abedin J. 05.001 Abernethy D. 21.063 Abia-Bassey L. N. 21.150 Abramova F. 17.001 Abreu Santos C. 08.006 Abreu-Acosta N. 22.080 Abson F. 05.003 AbuBakar S. 22.082 Abutidze A. 21.160 Aceti A 22 062 Achappa B. 21.119, 21.122, 22.064, 22.078 Achilla B 22 017 Achour N. 22.081 Acs B. 22.054 Acutis P. L. 22.148 Adam V. Y. 22.117 Adamczyk M. 22.059 Adams N. 21.178 Adedeji A. 22.005 Adewuyi P. B. 22.126, 22.110 Adhikari P. 21.122 Adhikari R. P. 22.118 Adone R. 22.062 Aengwanich W. 22.056 Afonso A. 17.002 Aghaii M. N. 21.154 Agrafa I. 21.018 Agricola E. 22.044 Aguero M. 22.181 Ahmad H. 22.147 Ahmed A. 21.187 Ahmed J. 19.001 Ahmed K. 22.060 Ahmeti A. 22.134 Ahmeti S. 22.175 Ahumibe A. 12.001, 22.114 Aichinger G. 22.137 Ajack Y. 22.138 Ajazaj L. 21.130 Ajazaj Berisha L. 21.142 Ajogi I. 21.132 Ajumobi O. 22.126 Akhmedov I. 21.016 Akhvlediani T. 21.074, 21.073 Akpan H. 22.126 Akpede G. 21.156, 21.148, 21.152, 21.161, 21.145 Akpede N. 21.152, 21.156, 21.148 Al lankawi M. 21.185 Al-Eryani S. M. A. M. 22.116 AL-Harbie A. M. S. A. 21.170 Al-Samei A. 22.116 Alban L. 21.109, 21.021

Alborali L. 22.019 Alborzi A. 22.143 Aleman Aguilar E. 21.143 Alexander D. 21.129 AlGodair A. I. 21.007 Ali T. 21.096 Ali Raja S. 21.157 Aliyu A. A. 22.124 AlKohlani A 22 116 Allen H. 12.005, 21.081 Allerberger F. 21.035, 21.146, 22.087, 21.051, 21.111 Alm E. 22.020 Almeida O. P. 21.121 Almeida V. 21.021, 21.109 AlMuzrkchi A. 21.185 Alonso W. J. 21.112 Aloosh O. 21.027 Alves M.-J. 22.176 Alwi K. 21.174 Amalya M. 22.106 Amaro F. 22.176 Aminianfar M. 21.031, 21.030 Aminnezhad S. 21.006 Amuguni H. M. 22.133, 12.004 Amwayi S. 22.138 Anastacio S. 22.075 Andrade G. 22.176 Andrews N. 22.042 Andriushenko A. 21.067 Angelini P. 22.155 Angkititrakul S. 22.072, 21.013, 21 015 Antoci S. 21.108 Antolova D. 21.053 Apidechkul T. 21.116, 21.120 Araújo W. 08.004 Aribodor D. N. 21.144 Aromdee C. 21.025 Arriaga-Pizano L. A. 22.009 Arteaga G. 22.009 Artiushin S. 21.094 Arvelo W. 08.007 Asamneh N. 21.187 Asghar A. 21.005 Aslam S. 22.037 Aslam S. 21.157 Asogun D. 21.161 Asogun D. A. 21.148, 21.156, 21.145, 21.152 Assam A. 21.076 Asuquo A. E. 21.150 Athanasiou L. 21.085, 22.077 Atshabar B. 22.160 Auer H. 22.065 Avian A. 22.006 Awan S. 21.138 Ayazbayev T. 21.067 Avele W. 22.015 Backx A. 22.050 Baghery O. 21.006 Bagó Z. 21.059

Bago Z. 21.066 Bailly X. 22.168 Bajardi P. 12.009 Bakamutumaho B. 22.003 Baker J. 21.112 Bako B. S. 21.169 Bakonyi T. 10.002, 22.182 Balasubramaniam V. 22.147 Balasuriya U. 21.094 Balishev V. 21.087 Ballardini M. 22.148 Balogun M. S. 22.005 Baltadzhiev I. G. 22.170 Baltesiu L. 21.040 Bányai K. 22.092 Barbic L. 22.166 Barboza P. 22.050 Bardosh K. L. 22.086 Barisani-Asenbauer T. 21.153, 22.131 Barisic M. 21.001 Barrett N. 22.137 Barry G. 22.146 Baruah P. J. 22.016 Basanisi M. G. 21.107 Bashir D. 22.109 Bashorun A. T. 22.114, 12.001 Bassey B. E. 21.154 Bast J. 17.005 Basuno F 22.090 Bau A. 17.002 Baumgärtner W. 22.146 Baylis M. 21.075, 21.045, 21.043, 22 097 Bazzucchi M. 22.129, 22.128 Beato M. S. 21.071 Becker I 22 083 Bedenic B. 21.001 Beeler E. 21.065 Beeler E. 21.149 Beer M. 10.001, 17.003, 22.146 Belas A. 21.022, 21.021, 21.023, 21.024, 21.109, 21.014 Belashova T. 21.127 Belij S. 22.131 Belkhou R. 21.097 Bellali H. 21.042, 22.081 Bellini R. 22.155 Bello M 21 090 Bello M. 21.132 Belonojkina L. 21.067 Beltrán-Alcrudo D. 04.004, 21.095 Ben Alaya N. 22.081 Beneldjouzi A. 22.163 Benes C. 22.164 Bennani L. 21.097 Bercic R. L. 22.182 Bercini M. 08.004 Bercot B. 17.008 Bergstrom J. 17.007 Berisha-Ajazaj L. 22.175 Berthe F. 17.002

Bevene T. J. 21.096 Biberaj P. 21.078, 22.180 Bidashko F. 21.067 Bilk S. 22.152, 22.174 Billinis C. 22.077 Bin H. 22.169 Bin Abdulhak A. 21.007 Bin Zahur A. 21.092 Bino S. 22,149 Bino S. 22.134, 21.078, 21.163, 21.070, 22.048 Bintner N. 22.131 Birtsas P. 22.077 Bisia M. 21.105 Bisias A. 21.085 Biswas D 22.016 Bitam I. 22.163 Biya O. 21.169, 21.155 Blake J. 22.037 Blechova Z. 22.014 Bock W.-I. 22.174. 22.152 Bocková E. 21.039 Bogaardt C. 12.008 Boin C. 22.148 Bonacic Marinovic A. A. 22.095 Boni A. 22.020 Boni A. 22.019 Bonilauri P. 22.155 Boniotti M. B. 22.019 Bonnet G 21 079 Boone I. 22.088 Boonpornprasert P. 22.142 Borkakoty B. 22.016 Born B 05 004 Böröcz K. 21.139 Bos M. 05.006 Bosco-Garate I. 22.009 Bosnjak Z. 21.001 Bouslama Z. 17.006, 22.163 Bousquet V. 22.050 Boutsini S. 21.105 Boutsini S. 21.085 Bouwknegt M. 22.070 Bouwstra R. 17.003 Boye M. 21.089 Braden Z. 21.064 Bratasena A. 22.106 Bray N. 21.135 Brazil J. 22.049 Breuer O. 21.114 Brindle R. 22.025 Brooks | 22.054 Broor S. 22.023, 22.177 Brown K. A. 21.137 Brownstein J. 21.179, 16.001 Bruhn S. 05.004 Bruno R. 05.007 Buck P. A. 05.010 Budhathoki B. 21.113 Bulimo W. 22.017 Bumburidi Y. 22.040 Burattin A. 21.071

IMED 2013



International Meeting on Emerging Diseases and Surveillance 2013

Burdakov A. 22.030 Burgmann H. 21.111, 21.159 Busch L. 22.165 Byaruhanga T. 22.003 Cabrera L. 22.089 Cabrera Ruiz L. 21.143 Cadena B. 22.083 Cagiola M. 22.128, 22.129 Calistri P. 21.108, 05.007 Callahan M. V. 07.003 Calzolari M. 22.148, 22.155 Cambau E. 17.008 Camia P. 21.009 Campbell T. 22.029, 22.039 Campbell-Lendrum D. 02.003 Camus-Bouclainville C. 21.183 Caporale M. 22.146 Capua I. 21.071 Carrada G. 22.084, 22.083 Carroll D. 21.048 Carroll D. 19.003 Carvelli A. 05.007 Casalone C 22 148 Caserio-Schönemann C. 22.050 Catchpole M. 22.042 Cattani S. 21.009 Cattoli G. 21.071 Čechvala P. 22.132. 21.082 Centeno M. M. 21.024, 21.109, 21.021.21.023 Cerbulo-Vazquez A. 22.009 Cerquetella M. 22.161 Cerrel Bazo H. 21.009 Chadjichristodoulou C. 22.077 Chahed M. K. 21.042, 22.081 Chai J. Y. 21.099 Chaicom K. 21.115 Chaintoutis S. C. 12.007 Chaiprasert A. 21.025 Chan H. C. 22.053 Chang L.-Y. 22.082 Chantima K. 21.099 Chapman R. 21.055 Charlett A. 22.042 Charoenphan P. 21.086 Chaskopoulou A. 12.007 Chastagner A. 22.168 Chawla Y. 08.001, 08.008 Cheng H. 22.043, 22.045 Cheng L. 22.011, 22.035, 22.036 Chepkorir E. 17.005 Chiavacci L. 22.148 Chiiza R. 22.003 Chiocco D. 21.107 Chitadze N. 21.074 Chkhartishvili N. 21.160 Chotivichien S. 15.002 Chovancova B. 21.054 Christodoulopoulos G. 21.085 Chua M. S. H. 08.002 Chua P. 09.003 Chuang T.-W. 21.041 Ciancio B. 22.049

Ciontea M. I. 21.003, 21.028, 21 004 Ciorba V. 21.009 Cito F. 21.108 Claes F. 04.002 Cleton N. 21.172 Coates D. 02.002 Coberly J. 22.029 Como N. 21.163. 21.078 Concepcion J. L. 22.141 Conrahts F. 10.001 Conti S. 22.051 Cooper M. J. 22.039 Cordioli P. 22.020 Cordioli P. 22.019 Cork S. 12.011 Corrales-Aguilar E. 21.072 Cortinas Abrahantes J. 17.002 Costa F. 08.004 Coulombier D. 12.008 Courcier E. 21.063 Couto I. 21.022 Couto N. 21.109, 21.014, 21.022, 21.021, **21.024**, 21.023 Craig P. 11.003 Cremer J. 22.059, 22.136 Croville G. 21.183 Cruz A K 08 002 Cruz-Cureño G. 22.009 Curina G. 22.129, 22.128 Cutler R. 21.140 Cvetnic Z. 21.034 D'Agaro P. 21.166 D'Aurelio R. 21.108 d'Onofrio A. 18.002 da Silva A. V. 21.026 da Silva G. J. 22.075 Daaboub J. 21.042 Dagina R. 22.157 Dahiru T. 22.124 Dakić Z. 22.099 Damon I. 08.005, 21.064 Dan Á. 22.027 Daneman N. 21.137 Daniel M. 22.164 Danis K. 12.007 Dankoli R. 22.124 Dar L. 22.177 Darvishi M. 21.030, 21.031 Daszak P. 05.002, 19.003 Dauphin G. 04.002 Davidson J. 21.069 Dawainavesi A. 22.012 De Angelis V. 21.166 De Giuseppe A. 22.129 de Jong M. 21.172 De Massis F. 21.108, 05.007 De Mia G. M. 22.128, 22.129 de Paula F. 08.004 De Roda Husman A. M. 22.070 De Vincenzi M. 22.044 Defi G. B. B. B. 22.100 del Rio C. 21.160 Deriabin O 21 049

Deryabin P. 22.160 Deshmukh A. 21.185 Despres P. 21.184 Deutz A. 21.066, 22.171 Devaux I. 22.049 Dewé T. 22.079 Di Sabatino D. 05.007 Di Taranto A. 21.107 Di Trani L. 22.019 Di Trani L. 22.020 Diaferia M. 22.161 Dilanchian P. 21.135 Dimech G. S. 21.177, 22.085, 05.011 Ding Y. 22.035 Distler E. 22.137 Diwan V. K. 22.043, 22.036, 22.011, 22.047 Doe kouskouni E. 21.018 Dohmen W. 05.006 Doiphode S. 21.185 Domingo M. 22.181 Donduashvili M. 21.164 Dong H. 22.036 Donnadieu C. 21.183 Dottori M. 22.155 Douidah L. 22.073 Dovas C. I. 12.007 Dover A. S. 21.098 Downing R. G. 09.001 Drescher M. 22.006, 21.010 Dridi S. 22.081 Droller D. 21.135 Drosten C. 05.008 Dubey V. K. 22.145, 22.139 Dublineau A. 08.003 Ducatez M. 21.183 Duengkae P. 07.003 Duettmann W. 21.051, 22.065, 21.010, 21.134, 21.186 Dumbadze O. 22.153 Dünser M. 21.066 Dupuy C. 22.051 Durrheim D. 22.034 Duse A. 19.002 Duvnjak S. 21.034 Dzikwi A. A. 21.090 Dzupova O. 22.014 Ebuk J. G. 21.154 Eckerle I 05 008 Edwards W. 22.054 Efstathiou P. 21.018 Egemberdiyeva R. 21.068 Egorova I. 21.091, 21.087 Ehnert K. 21.065, 21.149 Eigelsreiter S. 21.175 Ekwunife C. A. 21.144 FI Marnissi B 21.097 El ouali lalami A. 21.097 El-Sukhon S. N. 21.017 El-Tras W. 21.101 Elbahi A. M. 22.101 Elbers A. R. W. 22.144 Elduma A. H. 22.071

Elfakhei M. 21.162 Elhassan A. M. 22.069 Elhassan T. M. A. A. 22.069 Elhussein A. M. 22.069 Elsherif B 21 123 Engels M. 05.004 Engstrom K. 22.045 Ennigrou S. 22.081 Epstein J. H. 07.001 Erdman D. 22.023 Erdman M. 21.094 Erhart L. M. 22.010 Ermakova L. 22.154, 22.153 Esan O 12.010 Estevez V. 12.008 Estrada A. 05.008 Ezeunala M. N. 21.144 Faas A. 21.159, 21.111 Faccini S. 22.019 Fajardo L. 22.022 Fapohunda V. 22.110 Faraji S. 21.031, 21.030 Farooq U. 21.092 Farouk A. 21.123 Fasanella A. 22.062 Fawole O. 22.126 Fee S. 21.063 Feierl G. 21.020 Feierl G. 21.010 Feighner B. 22.029 Felarca M. 22.054 Feliu C. 22.080, 21.079 Feliziani F. 22.129 Ferland L. 22.049 Fernandes L. 21.109 Fernandes P. L. 22.176 Fernandez-Alvarez A. 21.079. 22.080, 22.185 Ferraz M. L. G. 22.076 Ferraz M. M. G. 21.026 Fidhow A. 08.007 Fields B. 08.007 Fierro M. 22.022 Filioussis G. 21.032 Fingerle V. 21.141 Fisher M. 06.001 Fisman D. 18.004, 21.137, 21.129 Fleming D. M. 12.006 Flick H. 22.006, 21.051 Foni E. 22.027 Fonseca-Ford M. 22.022 Formenty P. 09.004 Foronda P. 22.080, 21.079 Forti K. 22.129, 22.128 Fouillet A. 22.051 Franchi D. 21.166 Fraser G. 22.046 Freed J. 22.042, 22.049 Freeman R. 22.042 Friães A. 21.002 Friedrich A. 21.151 Frye L. 21.135 Fuchsini E. 05.004 Galella M. 22.062

International Meeting on Emerging Diseases and Surveillance 2013

Galler H. 21.020 Gallo T. 21.166 Garay L. 08.004 Garbati M. A. 21.118, 21.007 Garcia Vera J. A. 22.001 Garuchava N. 21.074 Gbolahan A. O. 22.110 Gentilcore A. 22.037 Georgakopoulou T. 21.102, 21.103 George B. D. J. 22.156 Gervelmeyer A. 21.047 Gesser-Edelsburg A. 22.033 Gesualdo F. 22.044 Getso K. I. 21.155 Gewehr S. 12.007 Ghanghro A. A. 22.140 Gherasim A. M. 12.003, 21.061 Ghinai I. M. P. 22.119 Giammarioli M. 22.129 Giannakopoulos A. 22.077 Gidado S. 22.126, 21.155, 21.169 Gillespie T. 05.008 Giriputro S. 22.008 Gjenero-Margan I. 22.166, 22.172 Glawischnig W. 21.062, 21.056 Goeijenbier M. 22.066 Goh G. K. 22.053 Goldstein T. 05.002 Golenko C. 22.022, 22.010 Golob M. 21.034 Golovko A. 22.055 Golovko A. 21.049 Gomes Dias J. 08.006 Gomoiu M. T. 21.040 Gondak R. 21.121 Gonfiantini M 22 044 Goodman S. 21.045 Goris M. 22.066 Gossner C. 21.047 Goubard A. 17.008 Graeden E. 22.094 Granato C. H. 22.076 Grazhdanov A. 21.067 Green M. S. 22.033 Grigoryan V. 22.037 Grinberg L. 17.001 Grisold A. J. 21.010, 21.134 Grossel G. 22.052 Guedez F. 22.107 Guérin J.-L. 21.183 Gunther S. 21.145, 21.156, 21.148 Guo H. 08.002 Gupta P. K. 21.113 Gupta V. 22.023 Gura Z. 22.138 Gurley E. 05.001 Guthrie J. 21.129 Gyuranecz M. 22.092 Haas D. 21.020 Habjan M. 22.165 Hadjichristodoulou C. 21.102 Hakawi A. M. 21.118 Halán M. 21.039 Hall D. 21.069

Hallanvuo S. 21.106 Halsby K. 21.125 Hamal P. 21.025 Hamer M. 21.114 Hamid M. E. 22.071 Happi C. 21.145. 21.152 Hara T. 22.135 Harati A. 22.059 Hariastuti N | 22.159 Hartskeerl R. 22.066 Haruna E. G. 21.132 Hasan S. 21.135 Hassan S. S. 22.147 Hassan S S 22 007 Hautvast J. 21.151, 05.005 Havlickova M. 22.014 Hawkes I. 22.097 Hay J. 22.160 Heederik D. 05.006 Hemachudha T. 07.003 Hensgens M. 05.006 Henttonen H. 21.037 Hepworth P. J. 21.043 Hercik C. A. 22.183 Heringer T. P. 22.076 Herkner H. 21.159, 21.111 Hernandez-Hernandez V. A. 22.026 Herr W. 22.137 Herrmannova K. 22.014 Hesketh T. 22.119 Hewson R. 22.091, 22.063 Hjertqvist M. 21.061 Hla T. T. W. 22.119 Hlinak A. 22.174, 22.152 Hobelsberger D. 05.008 Hoenigl M. 21.010, 21.134, 21.186, 21.051, 22.065, 22.006 Hoeper D. 10.001 Hofer E. 21.066, 21.052 Hoffmann B. 10.001, 22.174 Hoffmann M. 17.004 Hofrichter J. 21.066 Höhne M. 22.113 Holmes A. 22.042 Holsteg M. 10.001 Hopkins S. 22.042 Horwood P. 22.157 Hoshina T. 22.135 Hosokawa N. 22.068 Hossain M. J. 05.001 Houf K. 22.073, 21.181 Hrčková G. 21.053 Hruba F. 22.046 Hu Y. 21.019 Huayleuk P. 22.184 Hubalek Z. 22.182 Huemer H. P. 21.056 Hufnagl P. 21.035 Hühn F. 22.152, 22.174 Hulth A. 22.051 Humphrey A. R. G. 22.123 Hurnikova Z. 21.054 Hussain M 21 092

Hutse V. 21.050 lannetti S. 21.108 Ibeneme E. O. 21.150 Ibragimov A. 21.016 Ibrahim N. A. 22.069 Ibrahimagić A. 21.012 Idris S. H. 21.155 Igansi C. N. 08.004 Iglodyova A. 22.158 liaz S. 21.157 ljaz T. 21.157 Ilham N. 22.090 Imari S. 21.174, 12.002 Indra A. 21.035. 21.146 Inic-Kanada A. 22.131 Inoue S. 21.176 Irene I. 22.028 Ishikawa H. 22.098 Isibasi A. 22.009 Ismail A. A. A. I. 22.071 Ivanytska L. 21.083 lvers L. 18.001 lyiola O. 22.110 Izumi C. 22.004 Jaakkonen A. 21.106 Jafar F. L. 22.082 Jaisuda S. 21.176 Jakab F. 22.092 Jamieson F. 21.129 Jansa J. 12.008, 08.006 Javadian E. 21.027 Javadian F. 21.027 Jian S.-W. 22.087, 21.147 Jiang W. 21.019 Jima D. 22.015 Jimenez A 22 083 Jimenez C. 21.072 Jimmy S. 22.157 Jirincova H. 22.014 Johnson C. K. 05.002 Johnson G. 12.011 Jolv D. 05.002. 21.179 Jonach B. 21.084, 21.089 Juliana A. M. 21.165 Junglen S. 05.008 Kaartinen L. 22.027 Kabamba J. 08.005 Kabir J. 22.156 Kadlec K. 21.022 Kainulainen M 22.165 Kakar R. 22.060 Kallimani A. 21.102 Kalo T. 22.180 Kalvatchev N. 22.092 Kamano H. 22.004 Kamberović F. 21.012 Kandun N. 12.002, 21.174 Kanieff M. 22.051 Kanitz E. 22.113, 22.087 Kanjanasombut H. 22.184 Kanokmedhakul S. 21.025 Kapadiya B. 21.173 Kapoor P. 21.131 Karageorgou K. 21.018

Kardoush M. I. H. I. 21.046 Kåre Jensen T. 21.089 Karem K. 21.064 Karesh W. 19.003, 05.002, 02.001 Karhemere S. 08.005 Kasper M. 21.124 Kato T. 22.151 Kayiwa J. T. 22.003 Kayuni S. A. 21.136 Kazeem M. O. 22.117 Kazi S. K. 21.167 Kdyrsikh B. 21.067 Keessen E. 05.006 Keikhaee N 21 027 Kelam S. H. 21.029 Kellam P. 22.027 Kemenesi G. 22.092 Kempker R. 21.160 Kerlic J. 22.049 Kermanshahi K. 21.006 Keshavarz M. 22.143 Kessler H. 22.006 Ketusing N. 22.142 Khamadi S. 17.005 Khan S. U. 21.064 Khawplod P. 21.176 Khaytovych O. B. 22.120, 21.036 Kheuanrat W. 21.176 Khosravi M. 21.031 Khurana J. 21.113 Kim L. W. 12.006 Kirkbride H. 21.125 Kirtanasov Y. 22.154 Kitazono H. 22.068 Kitchen M. 21.056 Klaassen C. H. 21.185 Klabpadung P. 22.184 Klang A. 21.175 Kleaw-orm P. 22.184 Klement E. 10.003 Klenk J. 22.037 Klier C. 21.141 Klinzing D. C. 08.002 Klopp C. 21.183 Klugman K. 14.003 Kochhar R. 21,131 Koci B. 21.130 Koci R. 21.130 Kočišová A. 21.039, 22.162 Köck R. 21.151 Kohayagawa Y. 21.168 Kohl A. 22.146 Koidl C. 21.186 Koido Y. 21.168 Kojima K. 22.098 Koka H. 17.005 Kokaia N. 21.074, 21.073 Kokhreidze M. 21.164 Kokkinos P. 21.103 Kokotovic B. 21.089, 21.084 Kolodziejek J. 22.169, 10.002 Kolodziejek J. 21.088 Komalaminsra N. 22.150 Kondo H. 21.168

IMED 2013



International Meeting on Emerging Diseases and Surveillance 2013

Kongsted H. 21.084, 21.089 Kontos V. 22.093 Kooi B. 22.144 Kool J. L. 22.012 Koopmans M. 17.003, 22.066, 21.172 Kopp A. 05.008 Koreta E. 21.078 Kornschober C. 21.062. 22.087 Korytár Ľ. 22.132, 21.082 Kota M. 22.134, 21.078, 21.163 Kovalenko I. S. 21.036 Krafft T. 22.051 Kraja D. 21.078 Kraja D. 22.180 Krammer W. 21.134 Krause R. 21.134, 21.186, 21.051, 21.010, 22.065, 22.006 Kreil T. R. 22.038 Kretzschmar M 22 095 Kridaningsih T. N. 22.112 Kriner P. 22.022 Krishnan A. 22.023 Krismawati H. 22.112 Kritas S. 21.032 Kriz B. 22.164 Kroneman M. 12.006 Krüger N. 17.004 Kudi C. A. 21.132 Kugoh T. 22.004 Kühlmann-Berenzon S. 21.061 Kuijper E. 05.006 Kunarac M. 21.012 Kungsang P. 21.115 Kurecic-Filipovic S. 22.172 Kurti S. 22.180 Kuspanov A. 21.067 Kusuhara K. 22.135 Kuznetsova G. 21.127, 21.128, 21,126 Kvell K. 22.092 Kyncl J. 22.014 La Ruche G. 17.008 Ladychuk M. 21.127 Lagan J. 22.025 Lagler H. 21.159 Lal R. 22.023 Lam K. 21.129 Lambertini C. 21.026, 21.044 Lamielle G. 21.149, 21.065 Lamsal A. 21.041 Lane C. 12.010 Langat D. 22.138 Lange M. 22.141 Lara G. H. B. 21.026 Larsen L. E. 22.027 Latif A. 21.092 Lau S 22 165 Laus F 22 161 Le Q. B. 21.069 Leal V. 22.083 Leal Moran P. 21.143 Leblond A. 22.168 Leça A. 08.006

Leclercq I. 08.003 Lecollinet S. 12.007 Lederer I. 22.113 Lederman E. 21.064, 21.178 Lee B. 21.129 Lee S. 22.133 Lee S. 22.150 Leendertz F. 05.008 Leite D. D. S. 21.044, 21.026 Leitner E. 21.134, 21.010 Lelli D. 22.019 Leneweaver K. J. 21.135 Lewis S. 22.029 LiC 22 024 Li X. 22.043, 22.108 Li Y. 21.064 Liais E. 21.183 Lilja M. 17.007 Lillakou E. 21.102, 21.103 Linchongsubongkoch W. 21.086 Lindh J. 17.007 Linge J. 22.050 Linina I. 12.003 Lipkin W. I. 19.003 Lipman L. 05.006 Listes E. 22.166 Listoni F. J. P. 21.026 Liu L. 22.035, 22.036 Ljubic M. 22.172 Lluch J. 21.183 Loeffen W. 22.027 Logothetis E. 21.018 Loitsch A. 21.066 Loncaric I. 21.175 Lopes Dias S. 05.011, 22.085, 21.177 Lopez-Macias C. 22.009 Lu X. 22.047 Lubroth J. 04.001 Luby S. P. 05.001 Luby S. 21.064 Lucey D. 17.001 Lucey D. 21.033 Lukwago L. 09.001 Lundkvist Å. 21.061 Lundström H. 21.106 Lunney M. 21.069 Lushima R. S. 08.005 Lussy H. 22.169, 10.002 Lustig R. 12.006 Lutomiah J. 17.005 Lutwama J. J. 22.003 Lutwick | 15.003 Luz T. 22.176 Lyon A. 22.052 Lysyk T. J. 12.011 Lyytikäinen O. 21.106 Ma J. 21.129 Macario E. M. 08.004 Machado J. 21.133 Madi D. 22.078, 21.119, 22.064, 21.122 Magee M. 21.160 Magid A. 22.033

Mahanta J. 22.016 Majanja J. 22.017 Majtan J. 21.100 Majtan V. 21.011, 21.100 Majtanova L. 21.100, 21.011 Majumdar M. 08.001, 08.008, 21.113 Makaula P. 21,136 Makio A. 17.005 Maksimović Z. 22.099 Makumbi I. 09.001 Malakani J. 21.048 Malania L. 21.074, 21.073 Malimbo M. 09.001 Malone F. 21.063 Maltez F. 21.133 Mamisahsvili E 21 073 Mancilla J. 22.009 Mancin M. 21.071 Mandola M. L. 22.148 Manee W. 22,184 Maneeorn P. 07.003 Manfredi P. 18.002 Maniero S. 21.071 Mankad S. 21.173 Manning D. 21.077 Manolidou Z. 21.018 Mansinho K. 08.006 Mansour M. E. A. 22.069 Mantero J. 12.003 Manuguerra J.-C. 08.003, 21.184 Marchand-Austin A. 21.129 Maresova V. 22.014 Mari M. 22,128 Mariano F V 21 121 Mariette J. 21.183 Marinkovic E. 22.131 Maritschnik S. 22.087, 22.113 Markowska-Daniel I. 22.027 Marrama Rakotoarivonv L. 12.008 Marshall S. 12.011 Martelli P. 21.166 Marth E. 21.020 Martin V. 04.002 Martín-Alonso A. 21.079, 22.080 Martina B. 22.066 Martindah E. 22.090 Marushchak L. 21.049 Maruyama S. 22.098 Masseglia S. 22.168 Massolo A. 12.011 Masuda E. T. 21.177, 05.011, 22.085 Matros L. 21.004, 21.003, 21.028 Matsuda S. 21.117 Matsuo S. 22.098 Mauad T. 21.121 Mazet J. 19.003, 05.002 Mc Nabb S. 22.049 McBride K. 21.063 McCollum A. 08.005 McConnell M. 22.057 McCormick B. 21.112 McCotter O. 22.022, 22.010

McIntyre K. M. 22.097, 21.043 McKeown I. 21.063 Medado I. A. 22.179 Medina S. 22.051 Medina-Pestana J. 22.076 Mehmeti M. 21.142. 21.130 Meis J. 21.185 Meiswinkel R. 22.144 Mejdoubi L. 21.153 Melero Alcibar R. 22.185 Mellou K. 22.049, 21.102 Mellou K. 21.103 Melo-Cristino J. 21.002 Memish Z. 03.001 Mendez I. 22.089 Menzies F. 21.063 Mercader I. 22.181 Mersini K. 21.070 Metcalf T. 21.124 Mettenleiter T. 10.001 Mihara Y. 22.135 Mingomataj E. 22.149 Mir M. 22.177 Mirino Y. Y. R. 21.165, 22.112 Misaki T. 22.115, 21.104 Miterpakova M. 21.053, 22.158, 21.054 Mkrtchyan H. 21.140 Mlinaric-Galinovic G. 22.166 Modrof J. 22.038 Mohammadi M. 21.027 Moinedden R. 21.137 Molina R. 22.185 Molinari L. 22.128 Mollet T 22 046 Mondal U. K. 05.001 Monne I. 21.071 Monroe B. 21.048 Montanaro J. 22.131 Montano S. 21.124 Monteiro de Pina Araujo I. 22.185 Montgomery J. 08.007 Moonpo M. 21.176 Mooseder G. 21.159, 21.111 Morales Vargas R. E. 22.150 Morand S. 22.097, 21.043Moreira B 08 004 Moreira-Soto A. E. 21.072 Moreno A. 22.019 Moreno Martin A. M. 22.020 Moreno-Valencia Y. 22.026 Morgan D. 21.125 Mori T. 22.004 Morse S. 19.003 Moses C. 21.048 Mounts A. W. 12.006 Mourelatos S. 12.007 Mpimpa A. 22.093 Mrabet A. 21.042, 22.081 Mshelia W. S. 22.156 Mudura R. 21.040 Mueller M. 05.008 Muir P. 22.025 Mukunzi S 22 017

International Meeting on Emerging Diseases and Surveillance 2013

Müller L. 22.051 Müller M. 21.111 Muné M. D. L. C. 22.021 Munir Ahmad B. 21.157 Murakami C. 22.004 Muranaka K. 22.068 Murgia C. 22.146 Muriu N. M. 22.138 Murk J - 1 21 172 Murphy D. 22.136 Musila L. 17.005 Musoke R. 09.001 Musto J. 22.012 Mutisva J. 17.005 Muyembe J. J. 08.005 Muzyka D. 21.060 Nadeem Shah Syed M. 22.105 Naeem K. 21.092 Nagira M. 22.115, 21.104 Nahar N. 05.001 Nakamura N. 21.110 Namagambo B. 22.003 Namani S. A. 22.175, 21.142, 21.130 Namukose E. M. 09.001 Nanyunja M. 09.001 Natalia E. 22.112 Natividad F. F. 08.002 Nauma R. 12.004 Nawar N. 21.123 Ndreu A 22.149 Ndreu A. 21.078 Nedorost N. 21.058 Németh V. 22.092 Nemeth-Blazic T. 22.172 Neri D. 21.108 Nguete B. 08.005 Nguku P. 21.155, 22.124, 22.114, 21.154, 12.001, 21.169, 22.005, 22.126 Nguyen A. M. 22.013, 22.024 Nguyen Q. 15.002 Nicolescu G. M. 21.040 Nicolotti D. 21.009 Nie S. 22.036, 22.035 Nielsen J. P. 21.084 Nigsch A. 22.079 Nikolaishvili M. 21.164 Nishibuchi M. 22.096 Njenga K. 08.007 Njeru I. 22.138 Noda M. 21.117 Nogoudalla M. 22.109 Nogoudalla M. 22.109 Noguchi A. 21.176 Noguera T. 21.098 Nor'e S. S. 22.082 Nouiri I. 21.042 Nowotny N. 22.182, 21.088, 22.169 Nowotny N. 10.002 Noymer A. 22.013, 22.024 Nozaki A. 22.004 Nunes A. 08.006 Nunes T. 21.109, 21.021

Nurmakhanov T. 22.160 Nutravong T. C. 21.013, 22.072 Nwachukwu W. E. 21.154 Nychyk S. 22.055 Obadi M. 22.116 Obonyo M. O. 08.007 Ocepek M. 21.034 Odoch T. 12.004 Ofula V. O. 08.007 Ogbaini E. 21,152 Ohnishi T. 21.110 Oishi K. 21.104, 22.115 Okabayashi T. 22.150 Okabe N 21 104 Okabe N. 21.110, 22.115 Okafor C. I. 21.144 Okeke L. A. 22.126 Okogbenin S. 21.148 Okokhere P. 21.145, 21.161 Okot C. L. 09.001 Oktavian A. 21.165 Oldal M. 22.092 Oliveira W. 08.004 Oliveira W. A. 21.177, 22.085 Olorundare I. 22.005 Olugbon S. 22.114, 12.001 Omar A. R. 22.007 Ondrejka R. 21.082, 22.132 Ondrejková A. 21.082, 22.132 Opaschaitat P. 22.142 Opot B. 22.017 Ordun C. 22.037 Orii N. 22.150 Orola M. J. 21.111 Orozco-Sanchez C. O. 22.026 Osadebe L. U. 08.005 Osman N. 22.071 Osório H. C. 22.176 Ossai O. 22.124 Osterhaus A. 22.066 Osuna F. 22.017 Othman I. 22.007 Othman I. 22.147 Oukharov A. 22.030 Ounpomma D. 21.086 Ozin-Hofsaess A. J. 22.107 Pace L. 22.062 Pachler K. 22.169, 10.002 Pachón D. 22.089 Paes A. C. 21.026 Paget J. W. 12.006, 21.151 Paggi E. 22.161 Pai S. 22.078 Paine Hallström L. 12.003 Pak M. 21.067 Palaeng B. 21.115 Palei M. 21.166 Palfner M. 22.065 Palm L. 22.031, 22.011 Palmarini M. 22.146 Panagiotopoulos T. 12.007 Pandak N. 22.166 Pandey B. 22.023 Pandolfi E. 22.044

Pandrea S. L. 21.004, 21.003, 21.028 Pane M. 12.002 Pane M. 22.058 Pane M. 21.174 Panomai N. 22.072 Pant G. R. 22.127, 22.067 Panteli A. 21.105 Pantin-Jackwood M. 21.060 Paolotti D. 12.009 Papa A. 21.163 Papanastassopoulou M. 12.007 Papanikolaou S. 21.018 Papaspyropoulos K. 22.077 Papatsiros V. 21.085, 21.105 Parker D. 22.059 Parreira P. 22.176 Parrish C. 19.003 Parrish J. S. 21.178 Passos A. M. 22.076 Pate M. 21.034 Patel L. 22.010 Patel N. G. 21.179 Patel S. 22.029 Paterson B. J. 22.034 Paulous S 21 184 Pavlenko O. L. 22.120 Pavlin B. I. 22.012, 22.157 Pedale R. 21.107 Peeling R. 21.136 Peinhopf W. 22.173 Peletto S. 22.148 Pem-Novosel I. 22.166 Pem-Novosel I. 22.172 Penttinen P. 12.003, 22.046 Pereira Vasconcelos de Oliveira P. 22.085, 05.011, 21.177 Perez Hernandez N. 21.143 Peric L. 22.166 Perosa A. 21.166 Peters T. 12.010 Petersen B. 21.114, 22.125 Petridou E. 21.032 Petrovska L. 22.077 Petsophonsakul W. 21.176 Petternel C. 21.020 Pezzetti F. 21.009 Pfaff G. 22.088 Pfeiffer S. 21.146 Philen R. M. 22.022 Phippard A. 22.022 Phornwisedsirikun S. 21.176 Phumala-Morales N. 22.150 Pichlmair A. 22.165 Picone J. 22.059 Piergili Fioretti D. 22.161 Pierson A. 22.107 Pihlajasaari A. 21.106 Pilaca A. 22.180 Piñon A. 22.021 Pintawong W. 21.086 Pinto J. 04.003 Pirš T. 21.034 Pitenko C. 22.040

Pizzuto M. S. 21.071 Planitzer C. 22.038 Plecko V. 21.001 Plicka H. 21.052 Podsiadlowski L. 05.008 Poeppl W. 21.111, 21.159 Polgreen L. A. 18.003 Polgreen P. 22.136, 18.003, 22.059 Pollack M. 15.001 Polpakdee A. 21.015 Pomba C. 21.109, 21.014, 21.021, **21.023**, 21.024, 21.022 Portsmouth D. 22.137 Portuguese Group for the Study of Streptococcal Infections P. 21.002 Posch J. 21.020 Potamiti-Komi M. 21.102, 21.103 Pou Barreto M. C. 22.185 Póvoas D. 21.133 Praptiningsih Y. 22.106 Prariyachatigul C. 21.025 Prattes J. 22.006 Prearo M. 22.148 Prencipe V. A. 21.108 Preza I. 22.134 Pringle C. 15.001 Priotto G. 22.049 Prokeš M. 21.082, 22.132 Prüller F. 21.134 Pshenichnaya N. 21.126, 22.153, 22.154, 21.128, 21.127 Pu Z. 22.043 Puca E. 22.180 Pujols J. 22.181 Pukuta E. 08.005 Purcarea-Ciulacu V. 21.040 Qasim A. M. M. 22.117 Qehaja E. 21.130 Qehaja Bucaj E. 21.142 Qehaja-Bucaj E. 22.175 Raab V. 21.114 Racic I. 21.034 Raggam R. 21.186, 21.134 Rahardjo M. 22.112 Rahim M. 22.060 Rahimi F. 21.031 Rai S. 22.023 Raizenne M. 05.010 Raj S. 21.122 Rakhshani F. 21.027 Ramadani H 22 175 Rambeloson Z. 21.055 Ramirez M. 21.002 Ramishvili M. 21.074 Ramosaco E. 22.149 Ranjbar R. 21.006 Rao S. 22.054 Rasmussen Z. 21.112 Rasouli M. 22.143 Ratho R. 21.113, 08.001, 08.008 Ratthanophart J. 22.142 Récky A. 21.082 Reffett C. 22.037



International Meeting on Emerging Diseases and Surveillance 2013

Reid S. 22.027 Reimerink J. 22.066 Reinthaler F. 21.020 Reisp K. 21.052 Reusken C. 17.003, 21.172 Reusken C. 22.066 Reusken C. 22.070 Revilla-Fernández S. 21.052, 22.173. 21.066. 21.059 Reyes Mar J. 21.143, 22.001 Reynolds M. 08.005, 21.048, 21.064 Ribeiro M. G. 21.026 Riccò M. 21.009 Rich A. 21.075 Richardson J. 17.002 Richter S. 21.059 Rijnders M. I. A. 21.012 Rimhanen-Finne R. 21.106 Rimi N A 05 001 Rimseliene G. 12.003 Risley C. L. 21.075, 21.045 Rizzo F. 22.148 Rizzo G. 22.129, 22.128 RMT Balasubramaniam V. 22.007 Robinson E. 12.008 Robles Hernandez M. D. L. 21.143 Rochas A. 22.181 Rodriguez A. 22.089 Rodriguez B. 21.072 Rodriguez Zulueta P. 22.001 Rojo Gutierrez L. 21.143 Rollin P. 07.003 Romani N. 21.056 Romanova E. 21.128, 21.126, 21.127 Ropa B. 22.157 Rose A. 21.035 Rosell R. 22.181 Rosidi N. 22.037 Rosin P. 22.046 Rudoler N. 21.057 Rudolf I. 22.182 Ruiz Hernandez C. Y. 21.143 Rumetshofer R. 21.153 Ruscio M. 21.166 Rushton J. O. 21.088 Russell E. 05.003 Rutjes S. 22.070 Sabatinelli G. 22.060 Sabitu K. 12.001, 21.169, 22.114, 21.155 Saeed E. S. 22.071 Saghinadze S. 21.074 Saial D. 21.023 Saipov F. 22.041 Saito M. 22.179 Sakkijha H. 21.007 Sala Soler M. 22.051 Saleh M. 22.116 Salerno T 21 026 Salmenlinna S. 21.106 Samaan G. 21.174, 12.002, 22.058, 22.106

Samji N. 21.112 San Miguel E. 22.181 Sanchez B. 22.083 Sang R. 17.005, 08.007 Sanodze L. 21.073, 21.074 Santarelli G. A. 21.108 Santillan Lopez G. 21.143 Santon D. 21.166 Santos M. É. 21.177, 05.011, 22.085 Sanz A. 22.181 Sardelic S. 21.001 Sariwati E. 22.008 SarvaDová A. 21.039, 22.162 Sathian B. 22.118 Saudagar P. 22.145 Sauermann R. 22.137 Savini G. 22.166 Sawoo L. I. O. 21.184, 08.003 Sazzad H. S. 07.002 Schiefer P. 22.173, 22.171, 22.167 Schillinger S. 22.030 Schimmer B. 05.005 Schirrmeier H. 10.001 Schmid D. 22.113 Schmid D. 21.147 Schmid D. 22.087, 21.146 Schmidt D. 21.158 Schmidt-Chanasit J. 17.003 Schmoll F. 21.066, 22.171, 22.167, 21.052, 21.059, 22.173 Schmuth M. 21.056 Schneeberger P. 05.005 Schnettler E. 22.146 Schoepf K. 21.062 Schotten N. 05.005 Schuchat A. 01.001 Schulze C. 22.152, 22.174 Schwarz S. 21.022 Scott T. 21.149, 21.065 Sednaoui P. 17.008 Seeber K. 21.010, 21.134, 22.006, 21.186, 21.051, 22.065 Seidel B. 21.035 Sekulin K. 22.169, 10.002 Selga I. 22.181 Selyaninov Y. 21.087, 21.091 Sepehri Z. 21.027 Serrecchia L. 22.062 Setiawaty V. 22.008 Setzkorn C. 21.043 Severi G. 22.128, 22.129 Shapiyeva Z. 21.068 Sharker M. A. Y. 05.001 Sharvadze L. 21.160 Shaw A. 22.146 Shelton M. 22.037 Shigematsu S. 08.003 Shirafuji H. 22.151, 22.142 Shirakawa K. 22.096 Shkurti K. 22.180 Shuto Y. 22.151 Sideroglou T. 21.103, 21.102 Sidi-Boumedine K. 22.075

Signorelli C. 21.009 Signorini A. 20.001 Siitonen A. 21.106 Silva A. C. 08.006 Silva-Costa C. 21.002 Simaku A. 22.048, 21.163, 22.134 Simon G. 22.027 Simons E. J. 21.146, 22.087, 22.113 Simonsen I 12 006 Simusika P. 22.002 Singh M. P. 08.001, 21.113, 08.008 Singh P. K. 22.177 Siqueira A. K. 21.026 Siqueira A. K. 21.044 Sirisukeepradit C. 22.142 Sithamparanathan K. 22.025 Sitorus M. 22.106 Slepecká E. 21.082, 22.132 Sloet van Oldruitenborgh-Oosterbaan M. 22.144 Smiley T. W. 05.002 Smith G. J. D. 08.002 Smith J. 22.022 Smith K. 02.004 Smolinski M. 16.002 Soleimani E. 21.030. 21.031 Soletti R. 08.004 Song X. 22.108, 22.047 Sonricker Hansen A. 21.179 Sopoliga I. 22.162 Soria J. 21.124 Soto L. E. 21.143 Soualah-Alila H. 17.006, 22.163 Spanakos G. 22.093 Spence da Costa Lima H. 22.185 Spergser J. 21.175 Spicic S. 21.034 Sponseller J. 21.158 Spreeuwenberg P. 12.006 Spyrou V. 22.077 Sridhar R. 22.053 Srijun M. 21.176 Sripanya T. 21.176 Srisawat R. 22.150 Stärk K. 22.079 Stark K. 21.141 Stecchina M. 21.166 Steele J. A. 21.158 Stegniy A. 21.060 Stegniy B. T. 21.060 Stein E. 22.131 Steinrigl A. 22.171, 22.167, 22.173, 21.066 Stephan C. 22.137 Stevanovic V. 22.166 Stobberingh E. E. 21.012 Stojanovic M. 22.131 Stojicevic I. 22.131 Stougiou D. 21.105 Stougiou D. 21.085 Strenger V. 21.020 Struelens M. 22.107

Su Y. C. F. 08.002 Sudre B. 08.006 Sugita-Konishie Y. 21.110 Sulbaran Romero E. 22.141 Suleiman A 21 090 Süli J. 22.132 Sullender W. 22.023 Sulo J. 21.070, 21.163 Sultana R. 05.001 Sun X. 22.133 Superti-Furga G. 22.165 Suradhat S. 07.003 Surov V. 21.067 Sutrisna B. 22.008 Suwanna K. 22.184 Suwannarong K. 21.055 Swaan C. 22.095 Sy A. K. 22.179 Sytyuk M. 22.055 Szabó R. 21.139 Szönyi A. 21.139 Tack D. 21.048 Tada Y. 21.104, 22.115 Taj-Aldeen S. J. 21.185 Taju A. 12.001 Takada H. 22.135 Talyor R. J. 12.006 Tamba M. 22.155 Tambyah P. A. 22.053 Tan K. K. 22.082 Tan L. 22.035, 22.036 Taniguchi K. 22.115, 21.110, 21.104 Tantilertcharoen R. 07.003 Tao T. 21.019, 22.045, 22.011, 22.031, 22.043 Tatarchuk O. 21.087 Tattiyapong M. 22.142 Tayel A. A. 21.101 Taylor A. 21.081 Taylor L. M. 21.072 Tejo B. A. 22.007 Telama H. K. 22.074 Telo da Gama L. 21.022 Tesei B. 22.161 Thabet A. A. Q. 22.116 Tham H. W. 22.147 Thamm M. 21.141 Thapa B. R. 21.113 Thomas Y. 05.004 Thongsri Y. 21.025 Thornton C. 21.186 Thulke H.-H. 22.141 Tian L. 22.035 Ticona E. 21.124 Tilea B 22.178 Tilea I. 22.178 Tilley P. 21.022 Tobin E. A. 21.148, 21.156, 21.145, 21.152 Tobli S. 21.070, 21.163 Toikkanen S. 21.106 Toledo L. F. 21.044 Toleman M. 19.004

International Meeting on Emerging Diseases and Surveillance 2013

Wallner A. 21.062

Tomickova D. 22.014 Tomiie K. 22.004 Tomini E. 22.048, 21.078, 21.163, 21.070 Torgerson P. 11.001 Torres B. C. 08.002 Torres J. 15.002 Touloudi A. 22.077 Tovilo K. 22.006 Toyokawa T. 21.110 Tozzi A. E. 22.044 Trapaidze N. 21.074, 21.073 Tripathy M. 21.122 Trojanek M. 22.014 Troppan K. 21.186 Tsai A. Y. 22.039 Tsampalis P. 21.085 Tseroni M. 21.018 Tsertsvadze T. 21.160 Tugumizemu V. 09.001 Tuite A. 21.129 Tulamo R.-M. 22.074 Tunissea A. 22.159 Tuychiev L. 21.016 Tverdokhlebova T. 22.154, 22.153 Tzipori S. 22.133, 21.158 Tzivara A. 21.032 Ukaga C. N. 21.144 Ullah A. 21.092 Ulqinaku D. 22.048 Umoh A. N. 21.150 Umoh J. 22.156 Ushijima R. 05.009 Uwamino Y. 22.068 Uzunović S. 21.012 Uzzaman T. 21.162 Vaccari G. 22.019 Vaccari G. 22.020 Vaillant L. 22.050, 16.003 Vainio A 21 106 Vaishnavi C. 21.131 Vakalis N. 22.093 Valastro V. 21.071 Valdez Vazguez R. 22.001 Valentin T. 21.051, 21.010, 22.065 Valiakos G 22.077 Valladares B. 22.185, 21.079, 22.080 Vallat B 13.001 Van den Abeele A.-M. 21.181 van den Kerkhof H. 17.003 van den Wijngaard C. 17.003 van der Eijk A. 21.172 van der Giessen J. 22.070 van der Plas S. 22.049

van der Poel W. 17.003 van der Velden M. 22.137 van Duynhoven Y. 05.005 Van Eldere J. 14.002 van Gorp E. 22.066 Van Gucht S. 21.050 Van Kerkhove M. D. 12.006 Van Reeth K. 22.027 Van Steenbergen J. 22.095 van Weezep E. 22.144 Vander K. 22.006 Vanhomwegen J. 21.184 Vanskike F. 22.010 Vantarakis A. 21.103 Varco J. 22.122, 21.033 Varda-Brkic D. 21.001 Varela M. 22.146 Vargas P. A. 21.121 Vasconcelos P. 08.006 Vasili A. 22.048 Vassalos C. 22.093 Vassalou E. 22.093 Vaughan M. 22.054 Vaz J. I. M. 22.107 Vazquez-Perez J. A. 22.026 Velardi P. 22.044 Velden van der K. 21.151 Velez Perez F 22 001 Vellema P. 17.003, 05.005 Venkatachalam I. 22.053 Verloo D. 17.002 Verner Carlsson J. 21.061 Veronesi F. 22.161 Vicenzi E. 21.071 Vila J. 14.001 Vilibic-Cavlek T. 22.166, 22.172 Vilkova A. 22.160 Virtala A.-M. 22.074 Vishaj A. 22.175 Vlizlo V. 21.083 Voss A. 21.151 Vourc'h G. 22.168 Vranes J. 21.001 Wacharapluesadee S. 07.003 Wadegu M. 22.017 Wagenaar J. 05.006 Wagenaar J. 22.066 Wagner E. M. 22.137 Wagner J. 21.186, 21.134, 22.065, 21.051 Wagner-Wiening C. 22.088 Wahl T. 22.030 Wai T. H. 22.007 Waitzl B. 21.186 Wallensten A. 21.061 Wallensten A. 17.007

Wallner C. 21.051 Walsh A. 21.125 Wamala J. F. 09.001 Wang W. 21.019 Wangui J. 22.017 Ward B. 21.046 Watanabe T. 22.098 Waterman S. H. 22.022 Wattanamethanont J. 22.142 Wautier M. 21.050 Weber F. 22.165 Wei S. 22.035, 22.036 Weinberger H. 21.059 Weissenbacher-Lang C. 21.058 Weissenböck H. 10.002 Weissenboeck H. 21.175, 21.058 Welsh F. 05.010 Wenham C. 22.032 Wernike K. 10.001 Whelan M. 21.129 Widerstrom M. 17.007 Wigh B 22 023 Wilde H. 07.003 Wilke T. 22.125, 21.114 Wilking H. 21.141 Willgert K. 17.002 Willingham A. L. 11.002, 11.004 Wimberly M. 21.041 Windisch A. 21.056 Winkler A. 09.002 Winkler H.-M. 21,159 Wodak E. 22.167, 21.066, 22.171 Wojcik R. 22.029 Woldehanna S. 21.055 Wolk D. M. 22.010 Wongsawad C. 21.099 Woodall J. 15.004 Woolhouse M. 19.003 Wouters I. 17.003 Woyessa A. B. 22.015, 21.187 Wudie A. W. 21.096 Wurapa E. 22.017, 17.005, 08.007 Wutte N. 22.065 Xu B. 22.047, 22.031, 22.043, 22.045, 22.108, 21.019, 22.011 Yadav H. 21.077 Yadav K. 22.016 Yahata Y. 21.104 Yahata Y. 21.110, 22.115 Yamakawa M. 22.151 Yan W. 22.031 Yan W. 22.036 Yan W. 22.035, 22.036 Yan W. 22.031

Yan W. 22.035 Yanase T. 22.142, 22.151 Yang F. 22.031 Yang J. 22.045 Yano T. 21.086 Yap G. 21.182, 21.038 Yasseen A. S. 05.010 Yazaki R. 22.151 Yenjai C. 21.025 Yu M. 22.031. 22.011 Yuan H. 22.047, 22.108, 22.031 Yuill T. 15.004 Yunianto B. 22.159 Yusdja Y. 22.090 Zaccaria G. 22.020 Zaccaria G. 22.019 Zaichenko A. 21.083 Zajc U. 21.034 Zakalashvili M. 21.073 Zakareishvili M. 21.164 Zakharov A. 21.067 Zambrana-Torrelio C. 19.003 Zarfel G. 21.010 Zarfel G. 21.020 Zaria L. T. 21.090 Zdovc I. 21.034 Ze-Ze L. 22.176 Zeglam H. 22.101 Zeitlinger M. 22.137 Zeller H. 08.006 Zeller H. 12.008, 22.092 Zemelak E. 22.015 Zeweld S W 22.061 Zewude G. 21.096 Zghenti E. 21.073 Zhang J. 22.036, 22.035 Zhao G. 22.043, 22.011 Zhao H 21 064 Zhao Q. 22.045. 22.047. 22.011, 22.043, 22.108, 21.019, 22.031 Zheng H. 05.010 Zholshorinov A. 22.040 Zhou C. 22.108, 22.047 Zhou J. 22.045 Zhu Y. 22.045, 22.011 Ziemann A. 22.051 Zientara S. 12.007 Zimicki S 21 055 Ziros P. 21.103 Zobl A. 21.056 Zollner-Schwetz I. 22.065, 21.051 Zuliani A. 12.011 Zunt J. 21.124 Zurak I. 21.008



 •••••••••••••••••••••••••••••••••••••••
 •





 •••••••••••••••••••••••••••••••••••••••
 •



••••••
••••••









•••••••••••••••••••••••••••••••••••••••
•••••••••••••••••••••••••••••••••••••••



Don't miss out on the latest WILEY research published by Wiley

Register and opt to receive New Content Alerts from our Infectious Disease and Microbiology journals

www.wileyonlinelibrary.com/subject/infectiousdiseases



Edited by **Mary Torrence**

Impact factor 1.895

(2011 Journal Citation Reports[®], Thomson Reuters)

Exploring Public Health at the Interface of Humans, Animals, and Environment

Zoonoses and Public Health brings together veterinary and human health researchers and policy-makers. Papers focus on collaborative, multidisciplinary and global research in zoonoses and public health. This journal provides rapid publication of original papers, reviews, and discussion papers embracing this collaborative spirit. Papers should advance the scientific knowledge of the sources, transmission, prevention and control of zoonoses and be authored by scientists with expertise in areas such as microbiology, virology, parasitology and epidemiology.

Submit at: http://mc.manuscriptcentral.com/zph www.wileyonlinelibrary.com/ journal/zph

Transboundary and Emerging Diseases

Edited by **Paul Kitching**

Impact factor 1.809

(2011 Journal Citation Reports®, Thomson Reuters)

Transboundary and Emerging Diseases brings together in one

place the latest research on infectious animal diseases considered to hold the greatest economic threat to animals worldwide. The journal provides a venue for global research on the sources favoring their diagnosis, prevention and management, and for papers on veterinary public health, pathogenesis, epidemiology, statistical modeling, diagnostics, biosecurity issues, genomics, vaccine development and rapid communication of new outbreaks. Papers should include timely research approaches using state-of-the-art technologies. The editors encourage papers on socio-economic and environmental factors influencing the management of the bio-security threat posed by these diseases, including risk analysis modeling, as long as a science-based approach is adopted.

Submit at: http://mc.manuscriptcentral.com/tbed www.wileyonlinelibrary.com/ journal/tbed



INFECTION AND DISEASE DO NOT STOP AT BORDERS Neither should your research!

DACTION



INFECTION ECOLOGY & EPIDEMIOLOGY

is a peer-reviewed Open Access journal aiming to be a truly international forum for the free exchange of original, crossdisciplinary, high quality papers from researchers in multiple medical and ecological disciplines engaged in describing the complexity of zoonotic infections and what exactly happens at the interface between wild and domestic animals, and humans. Of particular interest at present is the growing global problem of antibiotic resistance. Learning water for an energy direction of a constraint of a co

EMERGING HEALTH THREATS JOURNAL

is an international, peer-reviewed journal publishing the latest and best research on emerging threats to human health. Its focus is threats from any source, including the environment, chemicals, radiation, pathogens, and society. It welcomes papers on the preparedness and response to natural or man-made disasters, including those that involve the deliberate release of chemical, biological, or radio-nuclear material.



GLOBAL HEALTH ACTION

is an international peer-reviewed Open Access journal affiliated to the Umeå Centre for Global Health Research (UCGHR) at Umeå University, Sweden. The journal aims to contribute to fuelling a more concrete, hands-on approach to global health challenges. Articles from low- and midincome countries as well as those resulting from South-South and South-North collaborations are particularly welcomed. All papers are expected to address a global agenda and include a strong implementation or policy component.

SEBLES

www.GlobalHealthAction.net

www.InfectionEcologyandEpidemiology.net

COACTION

www.EHT-Journal.net



www.co-action.net

