Invited & Oral Presentations – IMED 2016

Session 01 (Plenary Session)

Plenary: One World - One Health: Trans-Boundary Emerging Diseases in Humans, Animals and Wildlife

Friday, November 4, 2016

Room: Park Congress

14:20-17:15

01.001 AIDS, Avian flu, SARS, MERS, Ebola, Zika …what next?

A. Osterhaus
Artemis One Health Foundation, Hanover, Germany

Complex relationships between humans and animals have created an interface that allowed cross-species transmission, emergence and eventual evolution of a plethora of human pathogens. Until 1900, infectious diseases were the major cause of mortality of humankind, causing an estimated fifty percent of all deaths. In the western world, this decreased to only a few percent, due to the implementation of public health measures and the introduction of vaccines and antimicrobial compounds. This prompted policymakers and scientists to speculate that soon human infectious diseases would be brought under control. Paradoxically, soon thereafter the world was confronted with an ever-increasing number of (re-)emerging infectious diseases, like AIDS, Avian flu, SARS, MERS, Ebola, and Zika spilling over from animal reservoirs. A complex mix of predisposing factors in our globalizing world, linked to major changes in our societal environment and global ecology, collectively created opportunities for viruses and other pathogens to infect and adapt to new animal and/or human hosts. This paved the way for the unprecedented spread of infections in humans and animals with dramatic consequences for public and animal health, animal welfare, food supply, economies, and biodiversity. It is important to realize that due to the complex and largely interactive nature of the predisposing factors, it is virtually impossible to predict what the next pathogen threat will be, from where it will come and when it will strike. However better understanding of the underlying processes may eventually lead to predictions that would improve our preparedness for outbreaks in humans and animals. Investment in a better understanding the human-animal interface will therefore offer a future head start in the never-ending battle against infectious diseases of humans. Importantly, the increased emergence of viral infections is largely paralleled by medical, veterinary, technological, and scientific progress, continuously spurred by our never-ending combat against pathogens. Especially the establishment of vaccine development platforms, widely applicable to both known and unknown viruses will further contribute to an R&D based response preparedness.

01.002 Evidence for a risk-based strategy to detect viral spillover and spread

C. Kreuder Johnson
University of California - Davis, Davis, CA, USA

Emerging zoonotic viruses present persistent threats to global health, and a collaborative transboundary approach is needed for early detection of zoonotic viruses that have high potential to spread among humans. USAID's Emerging Pandemic Threats PREDICT project is one of many projects globally using a risk-based strategy to investigate emerging diseases threats. Here we examine common animal hosts and convergent mechanisms involved in spillover of zoonotic viruses in the past in order to identify high-risk interfaces for surveillance activities and interventions aimed at prevention. We also analyze previous outbreak reports to test several assumptions regarding common traits among zoonotic viruses that have amplified spillover by human-to-human transmission. We find that viruses transmitted to humans during circumstances that facilitated mixing of diverse animal species had significantly higher host plasticity (in that they have been reported in a taxonomically diverse host range). Viruses with higher host plasticity were more likely to amplify viral spillover by secondary human-to-human transmission and have broader geographic spread. We also provide evidence for a strong linear relationship between species abundance and viral spillover, with the more common species, especially those increasing in abundance, having transmitted more viruses to humans. PREDICT activities have thus focused on high-risk interfaces that facilitate mixing of animal species in areas with high biodiversity, dense human populations, and land use change that allows frequent contact between people and wildlife,

particularly highly adaptable species increasing in abundance. Our data to date highlight viral traits and epidemiologic circumstances likely to facilitate future disease emergence, and our findings add to ongoing efforts to guide global disease surveillance.

01.003 Satisficing control options for influenza

G. M. Leung
The University of Hong Kong, Hong Kong, China

Drawing on real-life examples from past influenza outbreaks, particularly 2009 H1N1pdm and 2013 H7N9, this talk will highlight the state of the science in influenza preparedness research, in mitigation of annual epidemics, the next pandemic and newly emerging outbreaks otherwise. It will draw on the multiple disciplines of ecology, evolutionary biology, virology, epidemiology, and mathematical sciences. A “One Health” approach that recognises the zoonotic driver of epidemics will be emphasised. Particular attention will focus on the multiple strands of global health initiatives contributing to the common goal of health and human security against influenza and its sequelae.

01.004 Zoonotic diseases at the human-domestic animal - Wildlife interface in Southern and Eastern Africa

R. R. Kazwala
Sokoine University of Agriculture, Morogoro, Tanzania, United Republic of

Southern and East African Countries are rich in ecosystems where human, livestock and wildlife populations are in close proximity and serviced by the ecosystems services such as water, land and fauna resources. In the course of mingling there are possibility of sharing pathogens which consequently may lead to outbreaks of zoonotic agents in the concern populations. In Tanzania various studies were conducted in the past decade which were determining the presence of zoonotic agents, the burden in individual populations, the dynamics and drivers of disease transmissions at the human-livestock-wildlife interfaces.. Using serological and molecular biological techniques, a cross sectional studies were conducted in human and animal populations at an various ecosystems neighbouring wildlife conservation areas of Tanzania. The selected agents studied included bacterial and viral zoonotic agents.
Microscopic Agglutination Test (MAT) was carried out to test for leptospira antibodies in 1,351 livestock and 42 wildlife. The overall seroprevalence was 26.35% and 28.57% with serovars of Leptospira Interrogans; Hardjo, Hebdomadis, Grippotyphosa, Sokoine and Lora were common. Similarly, 30% of 267 human samples tested positive, for almost similar serovars. Sequencing alignment on 16S ribosomal DNA gene, suggested that serovars of Leptospira interrogans were common among human and animal populations. Using Rose bengal as a screen test, a total of 5.57% and 11.9% of sera from domestic animal and wild animals were found to be positive respectively. The IDEXX Q Fever ELISA for the detection of antibodies against Coxiella burnetii was employed and 40 of 587 (6.8%) cattle and 15 of 22 (68.2%) of wild animals were found to have antibodies against C. brunetti. RVF virus testing conducted IgG and IgM ELISA revealed, thirty two out of 800 (4%) and eight out of 42 (19%) from domestic animals and wildlife tested positive for IgG respectively. Of the 440 sera from domestic animal tested for IgM only 15 (3.4%) had IgM, while all wild animal samples were negative. Under the PREDICT Project protocol, a total of 268 wildlife animal species (Bats, Rodents and Non human primates) were subjected to molecular virology diagnostic tests and revealed the presence of 64 viruses including 48 novel viruses. The identification of the novel viruses is still underway to determine the peculiar genus and species. Using the geographical information system, the locations for infected animals and humans congregated at same coordinates putatively indicate cross infections between two populations.
Findings from the present studies are providing important insight on presence of zoonotic agents which potentially may cause febrile illness among persons in frequent contact with animals and their products in the poor resources rural communities not only of Tanzania but across the developing world.

01.005 Global early warning signs for health threats at the human animal ecosystem interface

J. Pinto
FAO, Rome, Italy

Diseases are emerging and remerging rapidly in different ecosystems and regions. Disease surveillance is an approach widely used for detecting new pathogens through event-based or indicator surveillance efforts. We should ask ourselves why, as a global community, do we

not implement a robust global surveillance and early warning system capable of detecting early signals of disease emergence? In addition, why is it that we continue to incur high costs of crisis mitigation, as in outbreaks of H5N1 HPAI, Nipah, MERS-CoV, Zika, Ebola, etc., particularly in regions associated with poor indicators of development and high vulnerability? A new mindset is required to change the way that the international community coordinates and manages disease emergencies. Lessons learned from HPAI H5N1 outbreaks indicate that many affected countries continue to suffer disease impacts because of failures in implementation of technical strategies, poor practices and inadequate policies for disease prevention and control. A better understanding of the drivers of disease emergence is needed to help identify prompt actions that will tackle the issues at their source. A multidisciplinary approach is required to build a strong network of institutions and coordinate incidents at the complex human/animal/ecosystem interface. This approach also necessitates local capabilities and networks with epidemiologists or public health specialists capable of conducting disease outbreak investigations with the support of national or regional laboratory networks. Strengthening local capacities in epidemiological analysis, and the use of open analytical tools and GIS platforms, and new technologies (e.g. mobile devices, rapid diagnostics) are opening a new window of opportunities to enhance the quality and speed on how disease information is reported, detected, verified and communicated.
Disease information is available and circulating every day from the media, social networks, informal surveillance systems and official systems. Health information should be recognized as a public good and we should all practice due diligence to share publicly our data and information collectively. The international community should no longer wait for official reports to respond to disease threats. This new approach, however, requires a coordinated and joint effort among governments, communities, donors and international networks to invest in prevention systems with capability to identify early signals for the emergence, spill over and spread of animal pathogens (livestock production dynamics, trade issues and markets, climate change, civil unrest, consumer behaviors, etc.). A global and intelligent early warning system is needed to capture, analyze and transform data and information that can be used effectively for early detection of signals related to the disease emergence, spillover and spread at the interface.

Session 02 (Invited Presentation)

Flaviviruses - An Expanding Global Threat

Saturday, November 5, 2016

Room: Park Congress

08:30-10:30

02.001 Teratogenic viral infections of the fetal central nervous system in animals: Timing and pathogen genetics are critical

N. J. MacLachlan
University of California, Davis, Davis, CA, USA

Congenital infections of domestic animals with viruses in several families, including *Bunyaviridae, Flaviridae, Parvoviridae,* and *Reoviridae*, are the cause of naturally occurring teratogenic central nervous system defects. Congenital infections of ruminant livestock with bluetongue virus (BTV), a midge- transmitted arbovirus, have clearly shown the critical role of gestational age in determining outcome; specifically, fetuses infected prior to midgestation that survive congenital BTV infection are born with cavitating central nervous system defects that range from severe hydranencephaly to cerebral cysts (porencephaly). Generally, the younger the fetus (in terms of gestational age) at infection, the more severe the teratogenic lesion at birth. Fetuses infected after midgestation are often normal. Whereas congenital infection is characteristic of certain BTV strains, notably live-attenuated vaccine viruses that have been passaged in embryonating eggs, transplacental transmission is not characteristic of many field strains of the virus. Akabane and related teratogenic Bunyaviruses (e.g. Cache Valley, Aino, Schmallenberg and Rift Valley fever viruses, amongst others) also cause age-dependent teratogenesis in fetal ruminants but, in addition to cavitating central nervous system defects, affected fetuses are born with contracted limbs (congenital hydranencephaly/arthrogryposis syndrome). Pestiviruses are non- arthropod-transmitted members of the family *Flaviridae* that can cause teratogenic central nervous system defects in congenitally infected livestock, specifically bovine viral diarrhea virus in cattle and Border disease virus in sheep. Age-dependent virus infection and destruction of neuronal and/or glial cell precursors that populate the developing central nervous system is responsible for these

naturally occurring virus-induced congenital defects of animals, thus lesions are most severe when progenitor cells are infected prior to their normal migration during embryogenesis. Although teratogenic congenital viral infections of animals have been recognized for many years, much remains to be determined regarding the virological and animal host determinants of transplacental transmission of individual viruses. Importantly, in distinct contrast to primates, maternal immunoglobulins do not cross the ungulate placenta so that fetal ruminants are dependent on their own innate and acquired immune responses, which are acquired sequentially during gestation.

02.002 Congenital Zika Syndrome

V. Van der Linden
Recife, Brazil

The Zika virus (ZIKV) is a RNA virus in the family Flaviviridae, genus Flavivirus. ZIKV carries the name of a forest close to Kampala in Uganda, where it was first identified in Rhesus monkeys in 1947.1 In 1952 it was isolated in humans in Africa for the first time. In 2014, the Zikv arrived in South America, notably in Brazil. Since then, a dramatic increase in cases of microcephaly was detected in several states, especially in the Northeast of Brazil. In April 2016, the causal relationship between microcephaly and Zika virus was proved.
After World Health Organization advised that the clusters of microcephaly and other neurological disorders and their possible association with Zika virus constitutes a Public Health Emergency of International Concern efforts are been made to describe and understand the syndrome.
A Congenital Zika Syndrome has as a main characteristic the brain impairment, with microcephalus, however it is still little known about this entity and its clinical spectrum that includes newborns with normal head circumference.
In addition to congenital microcephaly, a range of manifestations including craniofacial disproportion, spasticity, seizures, irritability, brainstem dysfunction such as swallowing problems, limb contractures, including arthrogryposis, hearing and ocular abnormalities, and brain anomalies detected by neuroimaging have been reported among neonates where there has been in utero exposure to Zika virus.
The pattern of brain images abnormalities in congenital Zika syndrome has been fully described by Aragão et al (2016). Brain calcification and disorder of cortical development are the most frequent findings. Cerebellar atrophy and malformations of the brainstem may also occur. The pattern of calcifications at the junction between cortical and subcortical white matter, in addition to the cortical developmental disorders predominantly on frontal regions confers highly suggestive pattern of Zikv congenital infection.
The rare and unusual arthrogrypotic joints did not result from abnormalities of the joints themselves and are likely to be of neurogenic origin, with chronic involvement of central and peripheral motor neurons, leading to intrauterine fixed postures and consequently deformities.
The ophthalmological abnormalities were already described by Paula Freitas et al and Ventura et al (2016) and Leal et al (2016) described sensorineural hearing loss associated with congenital zika syndrome.
There is a lack of studies regarding the consequence of congenital ZIKV infection at the third trimester of pregnancy. It is important to health professionals be alert to the changes in the neurodevelopment during the first years of life, especially if mothers describe record of cutaneous rash during pregnancy.
The complete neurological picture requires the central nervous system maturation and it will only become clear after, at least 18 months, so to a better definition of congenital Zika syndrome we need a longer follow-up.

02.003 Mathematical models to elucidate the transmission dynamics and control of vector-borne disease

G. Chowell
Atlanta, GA, USA

Mathematical modeling offers a powerful toolkit to improve our understanding of infectious disease transmission and control. In particular, carefully calibrated mechanistic models of disease transmission can be used to forecast trajectories and likely disease burden of epidemics. This talk focuses on the key ingredients that need to be incorporated into mechanistic models in order to characterize the transmission dynamics of vector-borne infectious diseases such as dengue, chikungunya and Zika. I will discuss some of the insights that mathematical modeling has provided on the effectiveness of reactive interventions and the role of spatial heterogeneity. For instance, analyses have revealed important associations between the role of climatological variables, spatial scales, and the timing of dengue

epidemics. In the context of the ongoing Zika epidemic, these tools are shedding light into the role of asymptomatic infections and the contribution of sexual transmission on outbreak size and duration.

02.004 Flaviviruses - An expanding global threat

O. Tomori
Redeemer's University, Lagos, Nigeria

Yellow fever (YF), probably evolved in Africa about 3,000 years ago, but was only introduced into the Americas on slave ships of the 1600s carrying humans and mosquitoes. In 1648, Mayan manuscripts describe the first report of YF disease in Yucatan and Guadaloupe. Between 1668 and 1699, YF outbreaks were reported in the USA. In the 1700s, YF spread to Europe, with reports in 1730 of YF outbreak in 1730, in Cadiz, Spain. This was followed by other outbreaks in France and Britain. Back in the US, the disease continued to ravage the populations of New Orleans between 1839 and 1860. The demonstration that *Ae. aegypti* mosquitoes transmit YF to humans, led the US Army, to carry out the sanitation programme in Panama and Havana, led to the eradication of the disease in these areas. The death in 1778, of British soldiers stationed in St Louis, Senegal is the first recorded report of YF outbreak in Africa. The research activities by the Rockefeller Foundation, which began in 1925, led to significant findings on YF disease in West Africa, including the development of YF vaccines in the 1930s.The conduct of mass preventive vaccination campaigns between 1948 and 1960, resulted in the control of YF disease in parts of West Africa. There was a resurgence of YF outbreak in West Africa between 1958 and 1970 and from 1980 to 2000. Consequently, a GAVI-led YF control initiative was implemented between 2005 and 2012. Through the implementation of mass preventive campaigns and introduction of YF into routine immunization, there has been zero report of YF outbreaks in West Africa since 2006. On the other hand, YF is re-emerging in countries of the East and Central Africa, that have not yet implemented the GAVI plan of action. Between 1992 and 2016, YF outbreaks were reported in seven countries of eastern and Central Africa. To successfully control YF in Africa, the YF endemic countries of Eastern and Central Africa should adopt and implement the strategies currently being implemented by the countries of West Africa to keep YF at bay. The absence of YF in Asia, despite the presence of an appropriate vector for urban transmission of the disease, remains an enigma.

Session 03 (Oral Presentation)

What's New? Novel and Re-Emerging Pathogens & Hackathon Winning Ideas

Saturday, November 5, 2016

Room: Klimt 2 & 3

08:30-10:30

03.001 Health hackathons

C. Lee
MIT Hacking Medicine, Cambridge, MA, USA

Institutional obstacles to clinical translation of novel technologies frequently prevent bench research advances from reaching patients. Training in rapid innovation methods is not broadly accessible to most clinicians and researchers, and structured opportunities for interdisciplinary collaboration and co-creation of innovations addressing clinical needs remain relatively uncommon. MIT Hacking Medicine is a student, academic, and community led innovation group that uses systems-oriented “healthcare hacking” to address the challenges in innovation adoption. By connecting diverse minds across the healthcare ecosystem to solve significant healthcare challenges, this has led to the development of new medical devices, digital health tools, and solutions improving patient experience. To foster this process, MIT Hacking Medicine brings together engineers, scientists, clinicians, entrepreneurs, and designers to collaborate around shared interests, and develop novel solutions over a 2-day hackathon with potential for greater impact in the healthcare industry. Participants are trained to address needs from the perspective of multiple stakeholders and emphasize utility and implementation viability of proposed solutions. By following this outlook, over the past 5 years, MIT Hacking Medicine has facilitated over 80 hackathons and healthcare design thinking events across 11 countries and 9 US states. Our largest annual event brought together 500+ participants representing 320 distinct healthcare organizations from 22 different countries. Teams coming out of our events have had successes joining

prestigious accelerators (e.g., TechStars, Y Combinator, Healthbox, and Rock Health), raising significant investment funding, and partnering with healthcare institutions or companies towards implementing their hack ideas. To date, we are proud to say we have helped launch nearly 20 active companies that have raised over $120M in financing. Our efforts were recently honored with a 2016 Stanford MedicineX Healthcare Design award, in the category of *Education in Healthcare*.
The MIT Hacking Medicine model is a method to integrate collaboration and training in rapid innovation techniques into academic centers, corporations, and non-profit organizations. Built upon a systems approach to healthcare innovation, the time-compressed but expertly guided nature of the events could enable more widely accessible preliminary training in systems-level innovation methodology, as well as creating a structured opportunity for interdisciplinary congregation and collaboration.

03.002 Identifying the next Zika: An analysis of zoonotic potential in Flaviviridae
K. Olival[1], K. Wiens[2], C. Rosenthal[3], A. Willoughby[4], C. Zambrana-Torrelio[5], N. Ross[4], P. Daszak[1]
[1]EcoHealth Alliance, New York, NY, USA, [2]New York University, New York, USA, [3]Trinity College, New York, USA, [4]EcoHealth Alliance, New York, USA, [5]EcoHealth Alliance.org, New York, NY, USA

Purpose: The viral family Flaviviridae contains several viruses known to cause human disease and recent widespread epidemics (e.g. Zika, West Nile, Dengue, and Yellow Fever viruses). Yet, many viruses in the family are little studied and the ecological, viral, and genomic factors that contribute to zoonotic potential are unknown.
Methods & Materials: Through an extensive review of the literature we compiled all known vertebrate hosts and arthropod vectors for each of the 63 ICTV-recognized (2015) viruses in the family Flaviviridae. For each host and vector species, we compiled ecological and life history traits and geographic range information where available. Viral genomes for 40+ available viral species were downloaded and phylogenies were reconstructed for the following genes with potential involvement in expanded host range and zoonotic potential: envelope (E), premembrane (prM), capsid (C), NS1, NS2AB, NS3, NS4AB, and NS5. A novel approach utilizing Generalized Additive Models and a combination of ecological and phylogenetic traits was used to identify ecological and genetic factors that predict whether or not a virus is zoonotic.
Results: We found 40/63 (64%) of ICTV recognized Flaviviridae species are zoonotic -- with evidence of infection in humans and at least one other vertebrate host -- with a mean of 21 (range 1-413) known host species per virus. Including a control for research effort, the phylogenetic breadth of non-human hosts was a significant predictor of whether or not a virus is zoonotic. We map the natural geographic 'hotspots' of flavivirus diversity based on the distribution of known hosts and also show non-random patterns in the distribution of zoonoses across the each gene specific viral phylogeny.
Conclusion: These analyses can be used to target future surveillance for flaviviruses to the host species and geographic regions most likely to harbor them. We show that viral and ecological factors can predict zoonotic potential in this important group of human pathogens, and identify specific genetic factors of interest for further characterization to better understand zoonotic potential.

03.003 Exploiting viral pseudotypes for emerging virus research
K. Grehan[1], E. Bentley[2], S. Mather[3], R. Kinsley[3], G. Carnell[1], S. D. Scott[3], **E. Wright** [2], N. Temperton[4]
[1]University of Kent, Chatham, United Kingdom, [2]University of Westminster, London, United Kingdom, [3]University of Kent, Chatham Maritime, Kent, United Kingdom, [4]University of Kent, Chatham Maritime, United Kingdom

Purpose: It is widely recognised that zoonotic virus infections represent a significant threat to global human and animal health. In addition to established infections, emerging zoonotics are increasing in prevalence due to changes in climate and global travel patterns. These have a primary impact on resource limited countries, as ecological factors result in outbreaks predominantly occurring in these countries. Virus infection via influenza, lyssa-, corona- and filoviruses, represent a significant proportion of emerging diseases in these settings. One of the principal bottlenecks for screening animal/human serum samples against such viruses is the paucity of expensive, high-containment facilities.
Methods & Materials: Lentiviral pseudotypes (PV) were prepared via 3 plasmid transfection methodology. For transfection in a cell culture dish, the transfection mix for each plate of HEK 293T/17 cells was prepared with: 0.5-1 µg of pI.18-ENV-GP, 1 µg of *gag-pol* construct

(pCMV-Δ8.91) and 1.5 µg of reporter gene construct (e.g. pCSGW for GFP, pCSFLW for firefly luc or pCSRLW for renilla luc). For neutralization assays, input was set at 10e6 RLU of PV and IC50 values were calculated using GraphPad Prism.
Results: We have developed a panel of safe, replication-defective PV for influenza, lyssa-, corona- and filoviruses. We have used these to undertake epitope mapping and immunogenic hierarchy of viral envelope protein epitopes/domains. We have shown that PV are very stable over a range of temperatures and humidities, and can be freeze-dried, allowing for efficient deployment to end-users in resource limited counties. We have incorporated a range of reporters (GFP, firefly and renilla luc) that increases the assay flexiblity so it can be tailored to individual laboratories. Finally we have shown that virus neutralisation performed using PV are also serum and antigen sparing and enable the study of functional responses, which correlate strongly with those measured using cognate wild-type virus assays.
Conclusion: PV represent flexible and powerful tools for the study of many facets of emerging virus epidemiology and for therapeutic development. They are facililative for epitope studies due to their ease of manipulation (plasmid-directed production) and are effective surrogates for use in serological assays for a wide range of pathogenic RNA viruses.

03.004 Outbreak of *Candida auris* in a tertiary care hospital in Karachi, Pakistan

J. Q. Farooqi[1], **A. Soomro**[2], S. Sajjad[2], M. A. Baig[3], K. Jabeen[1], K. Etienne[4], N. Nasir[1], S. F. Mahmood[5], A. Zafar[5], R. J. Asghar[6]
[1]Aga Khan University, Karachi, Pakistan, [2]Field Epidemiology and Laboratory Training Program, Pakistan, Karachi, Pakistan, [3]FELTP, Islamabad, Pakistan, [4]Centers of Disease Control and Prevention, Atlanta, USA, [5]Aga Khan University Hospital, Karachi, N/A = Not Applicable, Pakistan, [6]Field Epidemiology and Laboratory Training program, Islamabad, Pakistan

Purpose: Starting in September 2014, a tertiary care hospital in Karachi, Pakistan, diagnosed 3-5 cases/month of *Saccharomyces spp*. The hospital sent isolates to the US Centers for Disease Control and Prevention (CDC) for confirmation; CDC identified the isolates as *Candida auris*. The Pakistan Field Epidemiology and Laboratory Training Program (FELTP) investigated the outbreak in three phases spanning 6th April 2015- 6th January 2016.
Methods & Materials: Medical records, nursing schedules, and infection control practices were reviewed. A case was defined as any patient admitted at hospital yielding a positive culture for *Candida auris* from 1st September 2014 – 30th November 2015. Sixty two age and sex matched hospital controls from same wards were identified. Bivariate and multivariate logistic regression analyses and odds ratios were calculated. Seventeen isolates were sent to CDC for DNA sequencing. Environmental sampling was conducted in areas of hospital where multiple cases were associated.
Results: Thirty cases (17 males) were identified. Mean age 51.6 years (range: 2-91), case fatality rate 53%. Twenty eight were admitted through the ER (OR 9.2; 95% CI 2.3-62), 15 had surgery within 90 days of diagnosis (OR 6.5; 95% CI 2.3-19.3), 23 had a central venous catheter (OR 5.4; 95% CI 2.0-15.6), 10 had a chronic kidney disease (CKD)(OR 4.5; 95% CI 1.5-15.2), 11 had a previous fungal infection (OR 4.4; 95% CI 1.5-14), 26 had a urinary catheter inserted (OR 4; 95% CI 1.3-15), 16 had a stay in the ICU (OR 3.8; 95% CI 1.5-10) and 24 had an endotracheal tube (OR 2.9; 95% CI 1.0-8.9). Multivariate Logistic regression showed that a history of surgery within 90 days of diagnosis, ER admission and history of chronic kidney disease (CKD) were significantly associated with *Candida auris* infection. Among 17 isolates available, 15 were confirmed as *Candida auris*, one *Candida parapsilosis* and one *Saccharomyces spp*. *Candida auris* was not detected in environmental samples.
Conclusion: *Candida auris* is a nosocomial organism that may spread within the hospital especially among patients with invasive procedures. Review of infection control protocols and a refresher for staff on infection control practices was recommended

03.005 Emergence of non-candida albicans in ICU patients–A one year study of changing trends of candidemia in a tertiary care centre in North India

P. Sharma[1], M. Sharma[2]
[1]Kailash Hospital, Greater Noida, India, [2]Kailash Hospital,Noida, Noida, India

Purpose: During recent decades, the spectrum of candidiasis has changed with the emergence of non-albicans candida species especially in critically ill patients.The progressive shift observed towards non-albicans candida species also demonstrate reduced susceptibility to commonly used antifungal drugs.This study was undertaken to analyze the prevalence of non-albicans Candida species among Candida isolates from various clinical specimens and their antifungal susceptibility profile.

Methods & Materials: In the present study, 98 Candida isolates collected from patients admitted to ICU over a period of one year from April 2015 to May 2016 were characterized and identified to the species level by standard procedures and antifungal sensitivity was performed by disc diffusion method.
Results: Among all candida isolates from ICU patients,71.42 % were identified as non-albicans candida species and 28.58 % as candida albicans. The most common isolate among non-candida albicans was C.tropicalis (31.42 %) followed by C.dublinensis (21.42%) and others.Overall, 8.16%, 10.20 %, and 5.10% of all the isolates were resistant to Amphotericin B, Fluconazole and Voriconazole.
Conclusion: In the recent years there has been increasing trend in the emergence of non-candida albicans species as a potential pathogen, particularly in ICU patients. These non-candida albicans species are found to be more resistant than Candida albicans to antifungal drugs. The changing epidemiology of Candidiasis, therefore highlights the need for close monitoring of Candida species distribution and susceptibility in order to optimize therapy and outcome.. *Candida* non-albicans species were more resistant to azoles compared to albicans, information that can be useful for clinicians dealing with non - responding cases. Thus, eliciting history of exposure to these drugs may be important in choosing appropriate therapy

03.006 Novel astrovirus and calicivirus identified in migratory birds in Brazil
W. M. Souza[1], M. F. Romeiro[1], M. J. Fumagalli[1], J. Araujo[2], L. La Serra[1], L. C. Vieira[1], E. L. Durigon[2], P. R. Murcia[3], L. T. M. Figueiredo[1]
[1]University of São Paulo, Ribeirão Preto, Brazil, [2]University of São Paulo, São Paulo, Brazil, [3]MRC- University of Glasgow Centre for Virus Research, Glasgow, United Kingdom

Purpose: Examining the viral diversity present in domestic and wild birds in Brazil. To this end we applied a metagenomic approach to clinical specimens derived from different birds species in various geographical locations.
Methods & Materials: We sampled 100 individuals that represented eight different birds species. The samples of poultry (*Gallus gallus, Cairina monchata*) were collected in Breves city, Pará State, whereas samples from migratory birds (*Arenaria interpres*, *Thalasseus sandvicensis*, *Calidris pusilla*) were collected in Coroa do Avião Island, Pernambuco State, and wild residents birds (*Hilophilus amaurocephalus*, *Sarkesphorus cristapus* and *Coryphospingus pileatus*) in São José do Egito, Paraíba State. Samples were distributed in pools based on species, sample type (i.e. cloacal swabs and sera), date and capture location. Viral RNA was extracted and followed by synthesis of double-stranded cDNA prior to Illumina sequencing. Sequence reads were quality-filtered, removed the adapter sequences and remaining reads were assembled *de novo*. Obtained contigs were submitted to BLAST-based searches to identify viruses and further subject to phylogenetic analyses.
Results: We found nine viruses that showed similarity to known caliciviruses and astroviruses. A complete genome and two partial genomes of astrovirus were obtained from two pools of *Arenaria interpres*. The genome organization of Arenaria interpres astrovirus (AiAstV) was similar to that of other Astrovirus, and phylogenetic analysis reveals that the AiAstV is a member of Avastrovirus genus. AiAstV was most closely related to a recently characterized chicken avastrovirus with their genomes sharing ~60% amino acid identity. On another hand, four contigs and a complete genome of a calivirus were obtained in four pools from *Cairina monchata*, *Arenaria interpres* and *Hilophilus amaurocephalus*. A complete full-length genome sequence of approximately 8kb in length was obtained from samples from *Arenaria interpres*, showing a genomic organization typical of caliciviruses. Phylogenetic analysis reveals that Arenaria interpres calicivirus is a potential member of Nacovirus genus. Interestingly, both novel viruses were detected exclusively from cloacals swab, strongly suggesting the excretion of these viruses in nature.
Conclusion: Based on our results we found two novel astrovirus and calicivirus species in the Avastrovirus and Nacovirus genera, respectively. Further studies should aim to characterize their host range and pathogenic potential.

03.007 Crimean congo hemorrhagic fever, 2013 and 2014 Sudan
C. Kohl[1], M. Eldegail[2], I. Mahmoud[2], L. Schrick[1], A. Radonic[1], P. Emmerich[3], T. Rieger[3], S. Gunther[3], A. Nitsche[1], A. A. Osman[2]
[1]Robert Koch Institute; Center for Biological Threats and Special Pathogens 1 (ZBS-1), Berlin, Germany, [2]National Public Health Laboratory, Karthoum, Sudan, [3]Bernhard-Nocht-Institute for Tropical Medicine, Hamburg, Germany

Purpose: The German Partnership Program for Excellence in Biological and Health Security was launched in 2013 and is funded by the German Federal Foreign Office. Currently, the program funds projects in 18 countries in the fields of infectious disease surveillance,

detection & diagnostics, biosafety & biosecurity, capacity building and networking. In Sudan one focus of the partnership is the detection of highly pathogenic viruses and identification of known and yet unknown etiological agents in outbreak situations.
Methods & Materials: In 2014 an outbreak of hemorrhagic fever in humans was reported from different states of Sudan (South Darfur, West Kordofan, South Kordofan). The NPHL investigated the cases and forwarded 29 sera samples from patients suffering from hemorrhagic fever to the RKI. The sample-set included a panel of 10 sera collected during former hemorrhagic fever outbreaks in the same region in 2013. All sera were tested with qPCR assays for Marburg virus, Ebola virus and CCHFV. Additionally all samples were subjected to metagenomic deep sequencing on an Illumina MiSeq sequencer.
Results: CCHF was identified by two independent qPCR assays in a sample from November 2013 and November 2014, respectively. Deep sequencing confirmed these results. Based on the available sequences the novel CCHFV strain 'Sudan 2014' shares 96% identity (na) with its closest relative CCHFV SPU 187/90 from South Africa.
Conclusion: CCHFV is reported to be transmitted by ticks in Europe, Asia and Africa and known as etiological agent of severe hemorrhagic fever in humans and livestock. Beside insect-repellent no preventive measures are available. The pathogenicity and characteristics of this novel strain have yet to be determined by cell-culture isolation and serology. Further molecular analysis will contribute to clarify the divergence of the CCHFV strains detected in 2013 and 2014. First results including possible co-infections will be presented.

03.008 An epidemiological investigation of a multisource outbreak of Crimean-Congo hemorrhagic fever in Karachi, from January– 15th September 2016

M. A. Syed[1], H. Jhatyal[2]
[1]FELTP-Pakistan, Karachi, Sindh, Pakistan, [2]FELTP-PAKISTAN , Karachi, Pakistan

Purpose: In Pakistan Crimean–Congo haemorrhagic fever (CCHF) is an emerging life-threatening viral disease with case fatality rates up to 50%. With the increase in number of CCHF confirmed cases in the Karachi by December 2015, we decided to focus attention on disease in 2016. An epidemiological investigation was conducted in District Karachi to estimate the magnitude and associated risk factors for infection.
Methods & Materials: From January- September 2016 an outbreak investigation was conducted. Cases were identified through an active surveillance in health care facilities by using World Health organization recommended case definition. Information was collected by in personal interview with cases/attendant and review of hospital records. Human blood sample was collected for ELISA followed by PCR. Contact tracing was also done for identification of susceptible cases. Data were analyzed using Epiinfo version 7.0.
Results: Twenty-five suspected cases were identified by using WHO recommend cases definition out of them 08 were confirmed on IgM followed by PCR. The mean age for confirmed cases was 34.6 years (range: 16-65); all were male. Persons aged 30-39 years were the most severely affected n=5 (62.5%). Overall cases fatality rate (CFR) was n=6 (75%). The most frequent clinical features was fever n=8 (100%) followed by body pain n=7 (87.5%) and hemorrhagic manifestations n=6 (75%). When the cases were evaluated in terms of risk factors, the majority of the cases (n=4; 50%) were engaged in trading of animals. (n=2; 25%) has history of contact with animals. Two cases (25%) were medical doctor had history of operation of CCHF infected patient. Fifty percent (n=4) cases were reported in the month of August. Thirty three close contacts were traced and followed for 14 days no symptomatic evidence of the disease was reported.
Conclusion: Failure to implement CCHF preventive measures have contributed to the outbreak with high CFR. Community based health education campaigns were done, and strict compliance of infection control practices were instituted in the hospital. Establishment of prevention and control program on CCHF with efficient surveillance will be helpful for future outbreak.

Session 04 **(Plenary Session)**

Plenary Session: Epidemics Without Borders: From Challenges to Opportunities for Better Emergency Response

Saturday, November 5, 2016

Room: Park Congress

11:00-11:45

04.001 Epidemics without borders: From challenges to opportunities for better emergency response

M. Tatay
MSF International, Geneva, Switzerland

Over the last decade, MSF responded to outbreaks in countries where internal and external constraints hindered a proper and timely epidemic response. This failure to respond means excess mortality linked with the disease causing the outbreak. We are concerned about adequate investment in preventing and responding to outbreaks of cholera, malaria, measles, meningitis, and other often-overlooked emerging diseases, likely to pose greater threat to people's health in the years ahead. Current strategies to prevent major outbreaks of disease show limited success. Epidemics continue to occur with devastating consequences for less developed countries. They open cracks in national health systems and exhaust available resources. Communicable diseases with epidemic potential stand the main mortality cause in children ages one to 59 months worldwide, predominantly related to vaccine-preventable and infectious diseases. The yellow fever epidemic sweeping through Angola and DRC illustrates gaps still remain: limited supplies of vaccines, no specific treatment, no rapid diagnostics. In Europe and the Middle East, some countries cannot afford to vaccinate refugees and displaced populations to protect them and their hosting community (i.e. PCV).
The reality is that not all epidemics are viewed equally. The global health security concept at the heart of IHR defines protection against a threat as the main trigger for international action. External help seems to reach out only when wealthy nations feel under threat. The global fear Ebola generated triggered initiatives for reform. Health crises propelled onto the global political agenda, locking national security with health. However, making all of us healthier depends on making each of us healthier.
Public health surveillance alone is meaningless without a capacity to deliver direct care to affected populations. Emergency response needs to be prioritized not in competition with long-term goals. Epidemics are a consequence of global health priorities, where the overarching policy is prevention and health systems strengthening, rather than emergency response. Rapid urbanization, mass population movements, climate change, and resistance to pesticides and available treatments can and will increase the risk of epidemics in the future. Closing the gap between theory and practical implementation is one of the main challenges for emergency response. An efficient emergency response is to translate threats and gaps into opportunities and actions.

Session 05 (Invited Presentation)

Tracking Emerging Diseases

Saturday, November 5, 2016

Room: Park Congress

14:30-16:00

05.001 Innovations in participatory disease surveillance

M. Smolinski
Skoll Global Threats Fund, , USA

Citizen engagement in public health is being transformed through systems that enable users to directly report on symptoms of disease via email and smartphone technology. Innovative surveillance systems encourage routine, voluntary submission of syndromic health information by the general public. Reported data are aggregated and shared in near real-time with users and health authorities. Rapid collection and dissemination of disease data provide early warning as clusters of symptoms are identified in time and space. Engagement in participatory systems provides avenues for risk communication during health and other crises and a flexible platform for data collection and other innovative public health approaches. Most participatory surveillance systems obtain basic user demographic information upon

registration, including age, sex, and geographic location. Systems may collect additional baseline information about health risk factors. Users are prompted with a frequency that ranges from once per week to daily reminders. Many systems allow registered users to report for household members, who may include children or dependent adults. Syndromic data is collected from a range of pre-identified symptoms. Systems have been designed for both routine and mass gathering surveillance.
Nine participatory disease surveillance systems are currently operating in at least seventeen countries on six continents, including 10 Western European nations, Australia, Brazil, Thailand, Tanzania, and North America. These systems currently allow 11 percent of the globe to directly participate in disease surveillance.
Participatory surveillance systems are a scalable, sensitive approach for engaging communities, monitoring population health, and providing early warning for outbreaks and other health and safety issues. These systems can provide dynamic surveys that can be tailored to population subgroups, or emerging incidents and have potential to transform rapid risk assessment and epidemiologic studies.

05.002 UpToDate: Using clinicians' searches to track outbreaks

A. Thorner
UpToDate, Wolters Kluwer Health, Waltham, MA, USA

UpToDate is an online clinical decision support resource that is used widely by clinicians around the world. Digital surveillance techniques have shown promise for aiding with the detection and monitoring of infectious disease outbreaks. We sought to determine whether significant increases in UpToDate search activity for selected infectious diseases predate or coincide with infectious disease outbreaks.
We analyzed daily searches related to Middle East respiratory syndrome (MERS) in Jeddah and Riyadh, Saudi Arabia during three hospital-based outbreaks in these cities in 2014 and 2015 and compared them with reported cases during the same periods. We also compared UpToDate MERS searches in the affected cities to those in a composite of four negative control cities for the two outbreaks in 2014. UpToDate MERS searches during all three MERS outbreaks in Saudi Arabia showed a correlation to reported cases. In addition, UpToDate MERS search volume in Jeddah and Riyadh during the outbreak periods in 2014 was significantly higher than the concurrent search volume in the negative control cities. UpToDate search activity for specific infectious diseases also increased during outbreaks of salmonellosis, measles, dengue, West Nile virus, and influenza in Arizona, USA, and cyclosporiasis in Texas, Iowa, and Nebraska, USA. For outbreaks of salmonellosis, dengue, and measles in Arizona, UpToDate search activity increased before cases were reported or confirmed, suggesting that UpToDate search log data could be used as a complementary method for the early detection of new outbreaks. Analysis of UpToDate search logs is also a promising tool for monitoring ongoing outbreaks.

05.003 Tracking activity to improve the sensitivity of the OIE's monitoring and early warning systems for human and animal diseases

P. Caceres
OIE, Paris, France

One of the important attributes that define the quality of a surveillance system is its sensitivity (ability to detect all animal disease events). The sensitivity of the OIE World Animal Health Information System (WAHIS) is mainly ensured by the legal obligation of Member Countries to report OIE-listed diseases and emerging diseases, as indicated in the *Terrestrial* and *Aquatic Animal Health Codes*. In addition, in 2002, the OIE introduced a tracking activity for non-official information relating to animal and public health. The OIE tracking activity covered more than 250 sources of information disseminated by the media, animal and public health networks, scientific journals, and reports from OIE Reference Laboratories. Finally, in 2006, jointly with its partners, the World Health Organization and the Food and Agriculture Organization of the United Nations, the Global Early Warning System (GLEWS) was created to combine public health and animal health surveillance. For 2015, more than 5,000 rumours were tracked by the OIE. Information was collected for 167 countries and 100 diseases (85% of the 118 OIE-Listed diseases). The results of this activity were used to evaluate the impact of tracking on WAHIS sensitivity in 2015, using two indexes: i) *Monitoring system index*: % of reports where tracking added sensitivity (number reports with tracking confirmed / total number reports submitted); *Early warning system index*: % of events notified following tracking (number events notified after tracking / total number of events notified) The results for the monitoring system show that 23% of the reports submitted contained information confirmed through the tracking activity. For the early warning system, the index shows a value

of 8-13%, with significant variation due to the geographical area (highest values observed in Europe with only 4-6% of the reports following tracking activity) and the disease reported (percentage lower than 10% observed for bluetongue, low pathogenic avian influenza, foot and mouth disease, African swine fever). The analysis shows an overall good sensitivity of WAHIS, but more resources will need to be invested to increase its performance and to sensitize the countries to report disease events spontaneously and in a timely manner.

Session 06 **(Invited Presentation)**

The Farthest Reach: The Challenge of Nomadic and Remote Populations to Emergency Response, Emerging Disease Surveillance, and Eradication

Saturday, November 5, 2016

Room: Klimt 2 & 3

14:30-16:00

06.001 The challenge of nomadic and remote populations to emergency response, emerging disease surveillance, and eradication

J. Montgomery
CDC, Atlanta, GA, USA

Itinerant and remote populations can be important sentinels for emerging pathogens, as well as vectors or reservoirs of diseases such as malaria and polio. However, these populations – by dint of their perceived "disconnectedness" – are typically under-represented in surveillance data and surveys, and often untouched by services reliant on "outreach" paradigms or targeted service delivery campaigns. Why are these populations considered so "hard to reach"? The effectiveness of healthcare systems, designed foremost to serve sedentary populations, is modulated by the features of their immediate surroundings: geography, infrastructure, climate, and primary means of livelihood, to name a few. In remote or sparsely settled areas, service delivery is doubly-encumbered by these challenges. Thus, the concept of "poor access" defined by proximity is a common (and convenient) trope to rationalize suboptimal service uptake among geographically marginalized groups, while ignoring the social, environmental and economic realities that offer relevant countervailing narratives. In this symposium, we will explore common research narratives involving these populations and will illustrate the complex environs in which public health practitioners must navigate effectively and collaboratively to succeed. We will consider constraints to emergency response for diseases such as ebola, the role of climate change on population movement, and access to care for nomadic groups. The presentations will address systematic exclusion under wide-ranging circumstances, in an effort to expand both the narratives around "access" and the solution space to incorporate tools and perspectives from other fields.

06.002 The impact of climate change and population mobility on neglected tropical disease elimination

J. J. Amon
Neglected Tropical Diseases at Helen Keller International, New York, NY, USA

The WHO has established targets for the global or regional eradication or elimination of 11 neglected tropical diseases (NTDs) diseases by 2020. Other NTDs, such as soil transmitted helminths (STH), are the focus of intensified control efforts in specific countries. Two key strategies are being implemented to achieve these goals: preventive chemotherapy through repeated community-based mass drug administration (MDA) and intensified disease management. This presentation will present an update on NTD elimination efforts in sub-Saharan Africa, examining in particular the challenges posed by climate change and migration on MDA campaigns, including for lymphatic filariasis, onchocerciasis, schistosomiasis, STH and trachoma. While increasingly researchers are identifying (and predicting) health impacts from climate change (notably, how changes in temperature, precipitation and vegetation phenology impact malaria and certain arbovirus vectors), relatively less attention has been paid to the impact of climate change on NTDs in particular, or the challenges climate change related migration, which may also be associated with conflict or shifting labor migration, may pose to NTD elimination efforts. In addition to challenges in achieving high coverage rates for MDA, migration can complicate the assessment of transmission interruption and post-MDA disease surveillance, putting in doubt the verification of elimination. Achieving high coverage rates of mobile populations, whether for surveillance or MDA efforts, is a broader concern than for NTD programs. In the context of increasing health impacts of climate change, and in support of sustainable development goals and the push for universal health coverage, more emphasis should be put on the development of effective strategies to reach mobile populations across various public health,

outbreak response, disease control and elimination programs and on documenting and sharing lessons learned.

06.003 Interdisciplinary approaches to evaluate vaccination coverage among nomadic pastoralists in northeastern Kenya for polio eradication

V. Gammino
US Centers for Disease Control and Prevention, Atlanta, GA, USA

BACKGROUND. As polio eradication draws near, immunization and surveillance of remote and itinerant populations who are potential virus reservoirs become increasingly important. In 2013 and 2014, wild poliovirus imported from an endemic country in West Africa caused outbreaks in Somalia, Ethiopia and Kenya. Some cases were found among nomadic pastoralists, traditionally characterized as having limited access to health care including vaccination. We aimed to measure vaccination coverage and characterize its geospatial and socio-economic determinants among both settled and nomadic pastoralists in northeastern Kenya.
METHODS/ MATERIALS. Utilizing a mixed-methods approach and remote sensing to create a more robust sampling frame, we surveyed 12 households (HH) in each of 25 permanent ("settled") and temporary ("nomadic") pastoralist clusters. We utilized bi-lingual interviewers and a combination of tablet-based data collection tools to complete the survey; quality assurance checks were conducted onsite and using remote sensing methods.
RESULTS. We surveyed mothers in 235 settled and 263 nomadic pastoralist HHs. HHs were located, on average, 2 and 19 km from the closest clinic and/or co-located market for settled and nomadic HHs respectively. We obtained vaccination coverage data for 353 settled and 405 nomadic children < 5 respectively. Oral poliovirus vaccine (OPV3) coverage in settled pastoralist children < 5 was 85%; in nomadic children, coverage was 28% in children 1-4, and 10% among infants <1 year. Among nomadic mothers, 71% knew that vaccine protected children from disease; only 15% knew when a child should begin receiving vaccine. In contrast, 94% of settled mothers understood the purpose of vaccination, and 67% knew when a child should receive his/her first vaccine. Vaccination was reported as either somewhat or very important by 94% of settled mothers and 74% of nomadic mothers. Among mothers of either group whose child had never been vaccinated, distance to health facility was cited as a barrier. The diseases of principal concern across both groups of mothers were malaria, respiratory diseases and diarrhea in rank order.
CONCLUSIONS. OPV3 coverage was suboptimal in this sample of nomadic pastoralist children. Increasing the saliency of vaccination by increasing knowledge and reducing barriers to access may strengthen polio eradication efforts among remote and itinerant populations.

Session 07 (Invited Presentation)

Pandemic Preparedness and What we Learned from Ebola

Saturday, November 5, 2016

Room: Park Congress

16:30-18:00

07.001 Vaccine trials during outbreaks: The Sierra Leone trial to introduce a vaccine against Ebola (STRIVE) experience

B. Mahon
CDC, Atlanta, GA, USA

West Africa's Ebola epidemic was unprecedented in size and complexity. In September 2014, exponential increase in cases raised concern that timely control might not be achievable without a vaccine, so vaccine development was accelerated. By late 2014, Phase 1 studies of candidate vaccines started, and multiple organizations began planning phase 2/3 studies with collaborators in Ebola-affected countries. The US Centers for Disease Control and Prevention sponsored STRIVE, a phase 2/3 trial in Sierra Leone, in collaboration with the College of Medicine and Allied Health Sciences, University of Sierra Leone, and the Ministry of Health and Sanitation. STRIVE was designed as an individually randomized trial to simultaneously evaluate safety and efficacy of recombinant vesicular stomatitis virus Zaire Ebola vaccine (rVSV-ZEBOV) in healthcare and frontline Ebola response workers ; no placebo was used. Participants were randomized to immediate (within 7 days) or delayed (within 18-24 weeks) vaccination and followed for 6 months after vaccination for serious adverse events and Ebola

infection. Sub-studies collected detailed safety, reactogenicity, and immunogenicity data. STRIVE established 7 enrollment and vaccination sites in 5 districts, 3 data centers, and a -80^{o} C vaccine cold chain. STRIVE staff conducted >100 outreach sessions targeting potential participants, community members, and health leaders and trained >350 Sierra Leone staff. The study design evolved in response to the changing epidemiologic situation. A stepped wedge design (sequential vaccination after full enrollment) was initially considered but was replaced by phased enrollment to allow earlier vaccination in the context of the ongoing outbreak. After another trial demonstrated likely efficacy, some participants in the delayed vaccination group were vaccinated before 18-24 weeks. From April to December 2015, >8,650 participants were enrolled and >8,000 vaccinated. Ebola response measures successfully interrupted transmission, so vaccine efficacy could not be assessed. Preliminary analysis of safety data indicates no vaccine-related deaths or other serious adverse events; these data will be critical to application for licensure. Implementing STRIVE without detracting from the response to an epidemic of a highly lethal virus, in the face of limited infrastructure, high community concern, and changing epidemiology required extensive partnership-building, creativity, collaboration, and flexibility.

07.002 The Ebola commissions and international health regulations

D. Lucey
Georgetown University Medical Center, Washington, DC, USA

This presentation will offer a synopsis of: (A) the extensive information contained in a series of Ebola Commissions (July 2015-January 2016) and (B) recommendations of the Review Committee on the role of the International Health Regulations (IHR) in the Ebola Outbreak and Response (13 May 2016 A69/21) including a more recent draft global implementation plan for these recommendations. (A) While there were many Ebola Reports and Commissions, an analysis by authors of four of these major global commissions was published May 19, 2016 (Gostin et al. PLOS Medicine). They provide discussion with 10 tables and 3 figures comparing the four Commissions on key issues e.g., National Health Systems strengthening and financing , WHO Reform, UN Reform, and Research and Development acceleration. (B) At the World Health Assembly in May 2016 a list of 12 recommendations was presented in the report of the Review Committee on the role of the IHR in the Ebola outbreak and response. The first recommendation stated “There is neither the need for, nor benefit to be drawn from, opening up the amendment process for the IHR, at this time.” Instead, the emphasis is on implementation of the IHR. Accordingly, soon afterwards the WHO posted on their website a ‘Draft global implementation plan for the recommendations of the Review Committee on the Role of the IHR in the Ebola Outbreak and Response’, with six proposed area of action. WHO has already created a new Health Emergencies Programme headed by Dr. Peter Salama. A WHO synopsis of this new Programme, dated June 2016, stated that scale-up in terms of people and financing will occur over the 36 months starting 1 July 2016 “to become fully operational to the field level”. These actions are essential as epidemics and “pan-epidemics” will occur increasingly in our era that could be called the “Epidemic Anthropocene”. On 1 Feb. and 19 May, 2016 WHO convened two IHR Emergency Committees, as called for beforehand by Lucey and Gostin (JAMA Jan 27, 2016 (Zika) and JAMA May 9 (Yellow Fever). The “preventable tragedy” of Ebola must not be repeated.

07.003 Ebola survivors: Insights on complications of EBV disease

M. Fallah
PREVAIL/NIH, Monrovia, Liberia

no abstract received by presenter

Session 08 (Oral Presentation)

Zika & Other Vectorborne Diseases

Saturday, November 5, 2016

Room: Klimt 2 & 3

16:30-18:00

08.001 Guillain-Barré syndrome during an outbreak of Zika virus in Bangladesh: A case-control study

C. Geurts van Kessel[1], Z. Islam[2], B. Jacobs[1], S. Kamga[1], C. Reusken[3], R. Mogling[1], B. Islam[2], D. Mohammed[4], M. Koopmans[5], H. endtz[1]

[1]Erasmus MC, Rotterdam, Netherlands, [2]ICDDR,B, Dhaka, Bangladesh, [3]Erasmus Medical Center, Rotterdam, Netherlands, [4]Dhaka Medical College Hospital, Dhaka, Bangladesh, [5]Erasmus Medical Centre, Rotterdam, Netherlands

Purpose: Zika virus (ZIKV), a mosquito-borne flavivirus, is currently causing a large outbreak in the Americas. Until 2013, ZIKV infection was associated with only mild disease. Since an increasing number of severe neurological complications have been associated with ZIKV e.g. Guillain-Barré syndrome (GBS) and congenital malformations, the World Health Organization has declared the cluster of microencephaly and other neurological disorders a global health emergency in February 2016.
The purpose of our study is to verify the proposed assocation between ZIKV and GBS in a large cohort of well-defined GBS patients in Bangladesh during an outbreak of ZIKV in the population.
Methods & Materials: During a 5-year period from 2011-2015 420 patients with GBS were diagnosed by internationally standardized criteria. All patients were followed up until complete recovery or up to one year after presentation. Multiple specimens were collected during this period allowing longitudinal analysis of antibody responses against ZIKV. Virological investigations included RT-PCR, ELISA and seroneutralization assays for ZIKV and dengue virus.
Results: Analyses show evidence for an outbreak of ZIKV in Bangladesh in 2013-2014. This corresponds to the timing of the outbreak in French Polynesia. We show an increase in the number of GBS patients with virus neutralizing antibodies against Zika virus in this period. The majority of people with virus neutralizing antibodies against ZIKV also had antibodies against dengue virus, emphasizing the need of virus neutralization. PCRs were all negative in these patients.
Conclusion: Our data suggest that during the ZIKV outbreak in 2013-2014 in Bangladesh ZIKV may be associated with GBS. We will present detailed clinical and epidemiological data on the association between ZIKV infection and the putative severe neurological complication.

08.002 Infectome, diseasome and comorbidities of Zika infection

M. Moni[1], **P. Lio**[2]

[1]Garvan Institute of Medical Research, University of New South Wales, Sydney, Sydney, Australia, [2]University of Cambridge, Cambridge, United Kingdom

Purpose: The mosquito-borne Zika flavivirus (ZIKV) causes a mild or asymptomatic dengue-like disease that usually lasts two to seven days. Symptoms may include fever, headache and rash that are often either unrecognized or misdiagnosed as dengue, West Nile fever (WNF), chikungunya or other viral infections. ZIKV infection may also be associated with a risk for development of neurologic complications including Guillain-Barré syndrome (GBS). Zika infection is often associated to infectome, diseasome and comorbidity.
Methods & Materials: We present a quantitative framework to compare and explore infectome, diseasome and comorbidity of Zika infection. We have analysed several gene expression microarray data from Zika, WNF, chikungunya, dengue, other flaviviruses and GBS, with respect to healthy and control data sets.
Results: The differential gene expression profiling of ZIKV infection shows that a large number of genes (1197 genes) are statistically dysregulated. We also observed that 47 genes are commonly highly expressed between ZIKV and dengue infections. However, ZIKV shares only 12, 15 and 10 significant genes with chikungunya, WNF and GBS respectively. Notably, one significant gene *SELENBP1* is commonly dysregulated among ZIKV, Dengue and GBS, 2 significant genes *AF5* and *BAMB1* are commonly dysregulated among ZIKV, Dengue and WNF and 2 significant genes *NAMPT* and *PMAIP1* are commonly dysregulated among ZIKV, GBS and WNF. By using neighbourhood based benchmark and multi layer network topology methods, we have built infectome, diseasome and comorbidity relationships network based

on the OMIM and our identified significant genes. Then based on the gene expression, PPI and signalling pathways data, we investigate the infectome, diseasome and comorbidity association among the Zika, chikungunya, WNS, dengue infections and GBS.
Conclusion: Here, we describe the infectome and diseasome of ZIKV with dengue, chikungunya, WNS and GBS. We believe that our results will be important for comprehensive modelling and analysis of the systems level properties associated to Zika virus infections, molecular association analysis of these five symtomatic and pathological similar infections and disorders and for translational medicine aims. Our methods and pipeline will be useful for advancing our current knowledge on disease mechanism and predicting infectome, diseasome and disease comorbidities in a quantitative way.

08.003 Arbovirus epidemiology in pregnant women in Pernambuco state, Brazil

M. Eder[1], L. C. Bezerra[2], F. S. Outtes[2], G. S. Dimech[2], R. A. Ximenes[3], R. Dhalia[4], D. M. Cordeiro[4], E. T. Marques[5], C. M. T. Martelli[6]
[1]London School of Hygiene and Tropical Medicine, London, UK, London, United Kingdom, [2]Pernambuco State Health Department (SES-PE), Recife, Brazil, [3]Federal University of Pernambuco, Recife, Brazil, Recife, Brazil, [4]Aggeu Magalhães Research Center, Recife, Pernambuco, Brazil, [5]University of Pittsburgh, Pittsburgh, PA, USA, [6]Centro de Pesquisa Aggeu Magalhaes - Fiocruz Pernambuco, Recife, Pernambuco, Brazil

Purpose: Chikungunya (CHIKV), Dengue (DENV) and Zika (ZIKV) viruses are co-circulating in North-East Brazil and other parts of the world. All three are known to cause adverse pregnancy outcomes. Zika causes severe birth defects in neonates, Chikungunya a clinical syndrome in newborns delivered by mothers viraemic at birth, whereas Dengue is associated with prematurity and low birth weight.
In Pernambuco State, a protocol is in place for women developing exanthema during pregnancy to present to their health services, where they are notified, and tested for mosquito-transmitted viruses. We present Arbovirus prevalence data about pregnant women for Pernambuco State, and discuss their clinical and public health relevance.
Methods & Materials: Ministry of Health national Arbovirus notification data (2016) were retrieved online. A database including nearly 4000 pregnant women with exanthema during pregnancy, notified to the Pernambuco State Secretary of Health since November 2015 was reviewed for laboratory evidence of acute DENV, CHIKV (positive virus-specific IgM and/or viral RT-PCR) and ZIKV (RT-PCR only) exposure.
Results: Ministry of Health notifications since 1st January until 10th May 2016 show Pernambuco reporting CHIKV 17.417 out of 83.678 (21%) cases of Brazil, DENV 57.098/1.227.920 (5%) and ZIKV 496/138.108 (0.4%). In Pernambuco State, amongst 3986 pregnant women with rash between November 2015 and beginning of May 2016, evidence of acute CHIKV was detected in 200/595 (34%) women tested, DENV in 189/1.527 (12%), and ZIKV in 11/150 (7%).
Conclusion: There is a large proportion of laboratory confirmed acute Arbovirus exposure in Pernambuco State found among women with exanthema during pregnancy, and significant overall transmission of CHIKV, as well as DENV and ZIKV during the first half of 2016. Limitations include reporting, timing of laboratory testing in relation to onset of symptoms (testing outside viraemic period resulting in negative PCR/ falsely-low ZIKV case numbers). There is a huge need for research on Arbovirus epidemiology in pregnant women, in particular cohort studies for characterising and quantifying risk of adverse pregnancy outcomes as a result of maternal Arbovirus infections. This will guide clinical diagnosis and management for women at risk or exposed, public health decisions and, research initiatives on effective post-exposure prophylaxis, treatment or vaccines.

08.004 Evaluation of the Euroimmun Zika Virus IgG and IgM ELISA kits

L. Hueston
Pathology West-ICPMR, Westmead, NSW, Australia

Purpose: The diagnosis of Zika virus infections has been of increasing importance to many nations in the Asia Pacific region. Until 2016 the ability to diagnose Zika virus infection serologically was restricted to a small number of reference laboratories. In 2016 Euroimmun released an IgG and IgM ELISA for Zika virus antibody detection, however independent assessment the kits specificity and sensitivity was not available. This presentation examines the sensitivity and specificity of these kits and determines their suitability for routine diagnostic use in the Asia Pacific region.
Methods & Materials: Neutralisation using a 90% endpoint was used as the gold standard. All neutralisation positive samples were tested for the presence of IgM using in house IFA and repeat testing by neutralisation following removal of IgG. 310 samples were tested for

IgG and 320 samples were tested for IgM. Specificity was challenged by testing the kits against samples positive for other flaviviruses including dengue (primary and secondary); JEV; YFV; MVEV; KUNV; KOKV; ALFV; STRV; EHV and samples from patients with EBV, CMV, Q fever infections and samples positive for ANA and ANF.
Results: IgG: sensitivity 92%
IgG: specificity 89%
IgM: sensitivity 90%
IgM: specificity 93%
Conclusion: The use of recombinant nonstructural antigen did not provide the specificity claimed by the manufacturer. Cross reactions were more common with IgG than IgM but were found in both. This is concerning in the Asia Pacific region as multiple flaviviruses co-circulate and there is high flavivirus seroprevalence. In addition early infections were missed in some cases - which may be due to the choice of antigen or the setting of the cut-off. However, these kits have the potential to be used as a first line test to screen out negatives particularly if two suitably timed samples are used. Any positive sample should be submitted for confirmatory testing. Additional care needs to be taken in interpretation of IgG positive only samples and it is suggested that comments include the following or similar: "These results may suggest past infection with Zika virus. Cross reaction with another flavivirus or flavivirus vaccination cannot be excluded. If further differentiation is required neutralisation testing may be required"

08.005 High levels of exposure of Zika and Dengue infections detected using plaque reduction neutralization assay in Brazil

C. M. T. Martelli[1], P. Castanha[2], F. Cortes[2], L. Rodrigues[3], E. T. Marques[4]
[1]Centro de Pesquisa Aggeu Magalhaes - Fiocruz Pernambuco, Recife, Pernambuco, Brazil, [2]Fiocruz Pernambuco, Recife, Brazil, [3]LSHTM, London, United Kingdom, [4]University of Pittsburgh, Pittsburgh, PA, USA

Purpose: To assess the frequency of Zika (ZIKV) and dengue (DENV1-4) viruses among mothers and neonates (microcephaly cases and controls) using the plaque reduction neutralization assay ($PRNT_{50}$) in an ongoing study in Brazil.
Methods & Materials: Seroprevalence was assessed in an ongoing case-control (1:2) study conducted in Northeast Brazil (January-May 2016). Neonates were prospectively recruited at delivery in public hospitals in metropolitan Recife. Cases were neonates with microcephaly, defined according to Brazilian guidelines (head circumference 2 SD below mean for sex and gestational age). Controls were live neonates without microcephaly and with normal brain imaging by transfontanellar ultrasonography. Informed consent, clinical interview and blood samples were obtained from mothers; umbilical cord blood from all children in the delivery room, cerebrospinal fluid (CSF) in cases only. Serum and CSF samples underwent RT-PCR and ZIKV-specific-IgM antibody testing. Presence of neutralizing antibodies to ZIKV/DENV was assessed by plaque reduction neutralization assay ($PRNT_{50}$) in Vero cells (Lavite-Fiocruz PE/Brazil).
Results: We tested 94 mothers, 32 with microcephalic neonates (cases; 35% severe >3SD below mean) and 62 controls. 40% of cases were positive for either RT-PCR or Zika-specific IgM in CSF or serum with 8 cases being positive specific-ZIKV IgM confirmed by $PRNT_{50}$ assay.
Seventy percent of mothers had ZIKV neutralizing antibodies ($PRNT_{50}$) with similar results in neonates, and 55% of mothers (cases and controls) specific antibodies of multitypic ZIKV/DENV infections. ZIKV PRNT positivity among mothers reflects the high frequency of ZIKV infection attack rate during the first viral introduction in naïve population in Brazil.
Conclusion: This is the first report on combined ZIKV and DENV seroprevalence in Brazil. We found a higher frequency of multitypic *Flavivirus* infections including ZIKV and DENV-3/DENV-4 serotypes, in agreement with the predominant DENV profile in the study region. The question of flavivirus cross-reactivity, particularly for dengue, may not be relevant in neonates, as intrauterine infection with dengue is unlikely (maternal IgM not crossoing the placental barrier). This ongoing case-control study will allow assessing whether previous Dengue exposure increases the risk of ZIKV infection or severity of neonatal outcomes.
Ethical approval by PAHOERC #2015-12-0075 and CEP/CONEPE/CAAE #1.380.943.
Financial support: PAHO, Brazilian MoH and ERAES.

08.006 Regional surveillance for arbovirus in Lazio Region, Italy during the ZIKV epidemic in Latin America

F. Vairo[1], S. Valle[1], A. Mammone[1], C. Castilletti[2], E. Nicastri[2], V. puro[1], M. Capobianchi[2], G. Ippolito[2], P. scognamiglio[1], A. SERESMI TEAM[1]

[1]National Institute for Infectious Diseases "L.Spallanzani", Rome, Italy, [2]National Institute for Infectious Diseases INMI “L. Spallanzani”, Rome, Italy

Purpose: Due to the presence of a competent vector, mainly *Aedes Albopictus*, and to the experience of an outbreak of Chikungunya in 2006, Italy has implemented an integrated surveillance system for chikungunya fever, dengue fever and ZIKV fever. We describe temporal trends and geographic origins of vector-borne diseases in the Lazio Region, Italy.
Methods & Materials: We analyzed all the notifications for suspected arbovirus infection reported to the Regional Infectious Disease Surveillance System (SERESMI) from December 2014 to April 2016. Routine surveillance data on demographics, clinical features, origin of infection were integrated with data from the Regional Reference Laboratory for Arbovirosis. Confirmed cases are defined as positivity to serological tests and/or molecular detection of the virus in serum samples by PCR, as appropriate.
Results: During the reported period, 131 suspected cases of arbovirosis were reported; all suspected cases were returning travelers. Of these, 63 (48.2%) cases were confirmed as arboviral infections: 16 (25.4%) were chikungunya cases, 32 (50.8%) were dengue fever cases and 14 (22.2%) were ZIKV cases. One case of Toscana virus infection was reported. Imported cases of chikungunya fever primarily returned from South America (9/16, 56.3%). Southeast Asia (10/32, 31.3%) contributed the largest proportion of dengue fever cases, followed by Caribbean, Central and South America. Finally, ZIKV infected travelers were returning from South America (9/14, 64.3%), followed by Caribbean (5/14, 35.7%). Main clinical findings were fever, rash, headache and joint pain. Fever was present in the majority of chikungunya and dengue patients, but only in one third of ZIKV patients. Among ZIKV patients, rash was the most frequent clinical finding (12/14, 85.7%). Most of the patients had been already symptomatic during the travel. Starting from January 2016 there was a marked increase in the reporting of suspected cases.
Conclusion: The incidence of arboviral infections due to Aedes spp mosquitoes in the Lazio Region, a region densely colonized by *Ae. albopictus*, should be closely monitored. To date, no secondary autochthonous cases have been identified. The increase in suspected cases in parallel with the media coverage of the ZIKV outbreak in Latin America highlights the importance of risk communication to health care workers.

08.009 Development of models for Zika virus infection in mice and Rhesus macaques using a contemporary virus strain

D. Boltz[1], P. Curry[1], R. Baker[2]
[1]IIT Research Institute, Chicago, USA, [2]IIT Research Institute, Chicago, IL, USA

Purpose: Zika virus is a zoonotic pathogen that recently emerged in North and South America. Zika virus infections in humans can cause severe birth defects. There is an urgent need for animal models to study viral pathogenesis and to test vaccine and therapeutic medical countermeasures against this imprtant pathogen.
Methods & Materials: Zika virus strain PRVABC59 was used for all studies in this project. For mouse studies, AG129 mice were infected with various doses of Zika virus via the subcutaneous route. For NHP studies, sexually-mature male Eighteen Rhesus macaques were infected with $1x10^4$ PFU of Zika virus via the subcutaneous route. Animals were monitored for clinical signs including weight loss, rash, body temperature, and survival, as well as viral load in blood samples, oral swabs and semen samples (NHPs). Methods for the electro ejaculation of NHPs were developed for the collection of semen samples.
Results: AG129 were found to be extremely susceptible to infection with Zika virus. The LD_{50} was found to be less than 100 PFU, with mice exhibiting a dose-dependent hange in the mean time to death. Mice showed few clinical signs until a few days before death, at which point the exhibited severe weight loss and hypothermia.
Rhesus macaques exhibited few slinical signs of infection, much like humans. There was equivocal observations of rash on a few animals, but no observed change in body weight, body temperature or activity levels. However, viral genomes were easily detected by qRT-PCR extracts of blood samples for as much as a week after infection. Viral load was also assessed in oral swabs and in semen samples for up to two months after infection.
Conclusion: We conclude that the lethal AG129 mouse model is likely a useful model for early screening of medical countermeasures against Zika virus infection, especially for therapeutics and provides very clear endpoints in a less-expensive model. The mouse model may be less useful for vaccine and immunomodulatory drug testing due to the Type I and II interferon receptor knockout background in these mice. The Rhesus macaque model likely mimics the human disease more closely, but suffers from less clear endpoints and higher costs.

08.010 Development of a Zika vaccine using a novel MVA-VLP platform

F. Guirakhoo[1], A. Domi[2], N. McCurley[2], H. Robinson[2]
[1]Geovax, Melrose, MA, USA, [2]Geovax, ATLANTA, USA

Purpose: Zika is a rapidly spreading, emerging infectious disease linked to infant microcephaly, Guillain Barre Syndrome, and other neurological disorders putting half of the world's population at risk of infection. No approved preventive or therapeutic products are currently available.
To rapidly develop a Zika vaccine, GeoVax is leveraging its 4th generation MVA-VLP technology, improved for transgene stability and designed to produce VLPs in vaccinated individuals, for the construction of a Zika virus (ZIKV) vaccine.
Methods & Materials: Two MVA-VLP vaccine candidates have been developed from ZIKV strain Suriname 2015 sequences: one expressing pre-Membrane and Envelope (prME) genes, and the other expressing prME + Non-Structural protein 1 (NS1) genes. These antigens were chosen based on documented evidence that flavivirus prME and NS1 proteins are sufficient to elicit protective immune responses.
Results: The production of ZIKV prME VLPs was demonstrated by EM in after infections of DF1 cells with MVA-PrME virus. VLP were produced at high concentrations in production cell lines. ZIKV-specific antibodies detected both E (54kD) and NS1 (40kD) proteins in cell lysate and supernatant (only E) of infected cells. Research stocks were made from sucrose gradient purified MVA-VLP viruses at titeres of >10e8 TCID50/ml and being used for immunizations of various strians of mice at our collaborators' laboratories at CDC and University of Georgia.
Conclusion: This is the first report that a viral vector (replication competent or replication deficient) has produced a vaccine candidate for Zika that forms VLPs in vivo. Induction of VLPs in the host cells of the vaccine recipients not only eliminates the need for VLP purifications during manufacturing, but also generates a potent single dose vaccine (as shown with our MVA-VLP Ebola vaccine) that induces strong humoral and cellular immune responses similar to that of a natural Zika virus. Being tested safely in more than 120,000 subjects, including immunodeficient individuals, MVA based vaccines will be appropriate to be used in women of child bearing age, elderly or infant population. A potential single dose MVA-VLP Zika vaccine can be used for stockpiling by governments as well as for an immediate response to an ongoing epidemic.

Session 09 (Invited Presentation)

A Refugee's Journey from Insecurity to Stability

Sunday, November 6, 2016

Room: Park Congress

08:30-10:30

09.001 Cross border infection surveillance in mobile European population—GeoSentinel and more

P. Schlagenhauf
University of Zürich, Zurich, Switzerland

The flow of migrants and refugees throughout Europe is governed by complex geopolitical and social factors. More than 800,000 asylum applications have been filed and numbers are growing. Some processes are in place for screening migrants for infectious disease (ID) at the point of arrival but on-going, cross border ID surveillance remains an important challenge. This presentation proposes a matrix approach to sustained surveillance of migration related infection. It suggests the use of existing surveillance systems such as GeoSentinel and the European subnetwork of GeoSentinel sites, EuroTravNet . Here clinicians at 22 sites in Europe provide surveillance data on diagnoses in travellers who present at one of the network's tropical and travel medicine specialist sites. To be eligible for inclusion in the database, the patient must have crossed an international border before presentation and the diagnosis must be considered to be travel/migration related. A strength of this approach is that the infection data are linked to country of origin, travel/migration route and possible area of illness acquisition. Other surveillance approaches include analyses of existing systems such as ProMED-mail, a rapid reporting system of emerging diseases in humans and HealthMap, a service that uses web-crawling to find information on disease outbreaks and place it in a detailed Google map. Systematic reviews (according to PRISMA guidelines) can also be pivotal in identifying illness profiles in specific migrant groups and guiding screening and care guidelines. Migrants themselves, using mobile devices and novel tech, such as ITIT,

may soon contribute to the surveillance of travel related infections. Cross border infection surveillance of migrants within Europe necessitates a mosaic approach, using available resources and innovation for new approaches.

09.002 German experience with screening and healthcare in refugee and asylum seeker reception camps

W. Kern
University Hospital & Medical Center, Freiburg, Germany

The burden of disease among refugees and asylum seekers (refgs) has been in three areas: chronic preexisting non-communicable diseases (diabetes etc.), infections (preexisting/latent – depending on geographic/socioeconomic origin, and acute – depending on transmission risks during migration and in reception/transit camps [cmps]) as well as mental illness and psychosocial disorders. All three types may be highly relevant for healthcare organization (HCO) during migration, at arrival in cmps and thereafter. In addition two groups merit special consideration: unaccompanied or separated children/minors (UASC) and pregnant women. Screening upon arrival can identify only a part of these diseases and needs to take into account the dynamics of the risks associated with the different periods of flight/migration. Major limitations have included communication/language problems, registration processes disconnected to housing/accommodation capacities and with asynchronous health screening. Germany´s experience in the phase of the overwhelming influx of refgs in 2015 (0.9-1.0 million, most from Syria) and in (first half of) 2016 (0.2-0.3) has clearly pointed to a strong need for integrated HCO with on-the spot or camp-near health units and early access to primary care as well as specialized care. The demand for special woman&child and UASC care was unexpectedly high as was the need for counselling, psychosocial support and mental healthcare which tended to increase rather than decrease after arrival. Apart from initial X-ray screening for pulmonary tuberculosis among adults there has been no uniform infectious disease screening in Germany states and counties. Also, vaccination coverage within the first 4 weeks after arrival has been highly variable. Surveillance and monitoring has shown that there were several outbreaks of chickenpox and measles in cmps and a clear increase in the number of tuberculosis cases in the country so far restricted to the refgs population. Other complex/complicated infections were sporadic and not a major part of disease burden.

09.003 Tracing antibiotic resistance genes along the migration pathways

G. Cornaglia
University of Verona, Verona, Italy

no abstract received by submitter

09.004 Managing health and infections in refugees: Turkey's experience

N. Tulek
Ankara Training and Research Hospital, Ankara, Turkey

Continuing conflicts near the borders led to massive population flows, Turkey has followed an open door policy and accepted them as ‘’guest’’. Turkey is currently hosting the largest number of Syrian refugees in the World.
According to the official numbers 2,726,980 (Aug 2016) Syrians are staying at Turkey but it is difficult to give the exact numbers (1). Nearly half of them are children, and 152,000 Syrian refugees were born in Turkey (Feb 2016). A limited number of refugees (269,672; Sep 2016) are sheltered in 26 camps located around the border cities, and others are living throughout Turkey (2). Camps are coordinated by Prime Ministry Disaster and Emergency Management Authority of the Republic of Turkey which provide accommodation, health, food, education, and other services. Local hospitals have been enlarged and equipped to cover the most acute needs.
A lot of legal, administrative and institutional arrangements have been made, some are underway. Currently, each registered Syrian refugee has free access to healthcare services under the Ministry of Health like as Turkish citizen. Emergency healthcare is provided free to unregistered Syrians and to all migrants. Recently, 85 Migrant Health Units have been organized in 16 provinces. In general, preventive health services to refugees are delivered by Public Health Directorates.
Active surveillance for cutaneous leishmaniasis and malaria is initiated. According to the data of Ministry of Health; 825 cases of cutaneous leishmaniasis were detected in 2015. Totally 1022 cases of tuberculosis were diagnosed and treated between 2012-2015 years. Tuberculosis prevalence rate was found as 18.7/100000, similar to Turkish population. Any

malaria case was not detected. Syndromic surveillance for food- and waterborne diseases is being conducted at the camps. Syrian children were also affected recent measles outbreak due to interruption of vaccination on civil war condition. Considering the polio cases in Syria, measles and polio vaccination campaign were launched promptly. All the Syrian children are included into the national childhood immunization programme of Turkey.
Nevertheless there are still some problems to access to health care services resulting from communication barriers and cultural differences. Educational activities for healthcare workers and Syrians are in progress.

Session 10 (Oral Presentation)

One Health - Diseases Across Species Boundaries

Sunday, November 6, 2016

Room: Klimt 2 & 3

08:30-10:30

10.001 Intense human-animal interaction and limited capacity for the surveillance of zoonoses as drivers for Hepatitis E virus infections among animals and humans in Lao PDR

M. Pauly[1], C. P. Muller[1], A. P. Black[2], **C. J. Snoeck**[1]
[1]Luxembourg Institute of Health, Esch-sur-Alzette, Luxembourg, [2]Institut Pasteur du Laos, Vientiane, Lao, People's Democratic Republic of

Purpose: In Lao People's Democratic Republic (PDR), overlapping habitats of the population and livestock create a propitious environment for zoonoses. Insufficient hygienic measures in slaughterhouses and in rural settings further increase the risk for zoonotic transmission. Limited laboratory capacity as well as lack of background knowledge prevent timely control of disease oubreaks. Here, we assess the occurrence and transmission of Hepatits E virus (HEV), as well as public awareness of zoonoses.
Methods & Materials: In 2015 and 2016, samples were collected from ruminants in rural areas (n=211), as well as from slaughterhouse workers (n=129) and slaughter pigs (n=290) in Lao PDR. Using commercial ELISAs, presence of antibodies (IgG, IgM and IgA) against HEV was assessed. Fecal shedding of HEV by animals was investigated using a generic real-time PCR. Detected viruses were characterized by Sanger sequencing if feasible. Using a standardized questionnaire, data on risk factors for zoonotic pathogen transmission and awareness on zoonoses were captured. Much emphasis was placed on collaborating with local actors and on strengthening laboratory capacities.
Results: Anti-HEV antibodies were detected in 13 % of ruminants in rural settings and in 46 % of slaughter pigs. 7 % of the ruminants and 2 % of the pigs shed HEV that were thus far not characterizable. While anti-HEV antibody seroprevalence was of 33% in people exposed to pigs, only 15% of the non-exposed control group were seropositive (p= 0.001). Awareness of zoonoses among farmers and slaughterhouse workers was low. Wearing protective equipment was associated with a decrease in anti-HEV antibody detection (p=0.024). Limiting the consumption and use of groundwater and cooking of meat further reduced the risk for HEV infection in a domestic context.
Conclusion: We could show that people who are exposed to livestock and pigs are at higher risk for contracting HEV than the general population. Although shedding rates were relatively low, animals may represent an infection source that can be controlled by applying personal protective equipment. Building the capacity for the detection and prevention of infectious diseases and increasing awareness about zoonoses in developing countries is a prerequisite for combating infectious disease outbreaks in future.

10.002 The Vietnam Initiative on Zoonotic Infections (VIZIONs): An interim analysis of the epidemiology and aetiology of central nervous system infections

H. E. Brindle[1], M. Choisy[2], M. P. Tran[3], R. van Doorn[4], B. Nadjm[4], R. Christley[1], M. Griffiths[1], H. D. T. Nghia[3], G. Thwaites[3], S. Baker[3]
[1]University of Liverpool, Liverpool, United Kingdom, [2]Institut de recherche pour le développement, Hanoi, Viet Nam, [3]Oxford University Clinical Research Unit, Ho Chi Minh City, Viet Nam, [4]Oxford University Clinical Research Unit, Hanoi, Viet Nam

Purpose: The Vietnam Initiative on Zoonotic Infections (VIZIONs) is a nationwide multi-centre study of which aims to assess the aetiology and epidemiology of patients hospitalised with one of four syndromes.

Methods & Materials: An interim analysis of seven hundred and seventy-eight cases of central nervous system infection admitted to six hospitals from December 2012 until March 2016 was performed. Patients aged one month and over with a suspected CNS infection were recruited according to clinical criteria.
Results: A pathogen was detected in 31.5% (95%CI 28.3-34.9%). Of the pathogens identified the most common included *Streptococcus suis* (35.1%; 29.2-41.5%) followed by Japanese encephalitis virus (JEV) (26.9%; 21.6-33.0%), *Streptococcus pneumoniae* (18.0%; 13.5-23.5%) and dengue virus (DENV) (7.8%; 4.9-12%). However, of those with *S suis,* significantly more were adults (aged 16 years and over) compared to children (82.4%; 72.3-89.5% versus 17.6%; 10.5-27.8% p<0.001) and with JEV, significantly more children (75.8%; 63.4-85.1% versus 24.2; 14.9-36.6% p<0.001). There was a significant difference between males and females with *S. suis* (80.2%; 70.0-87.7% versus 19.8%; 12.3-30.0% p<0.001), *S. pneumoniae* (70.5%; 54.6-82.8% versus 29.5%; 17.2-45.4%, p=0.01), JEV (65.2%; 52.3-76.2% versus 34.8%; 23.8-47.7% p=0.02) and where the aetiology was unknown (65.9%; 61.6-69.8% versus 34.1%; 30.2-38.4%, p<0.001). 41% (37.5-44.6%) of cases raised, kept or handled an animal at home and 40.8% (37.3-44.4%) had eaten, cooked or handled raw meat, viscera or blood within two weeks prior to symptoms onset. Of those with no pathogen detected, 61.0%; 56.7-65.1% had a form of animal contact.
Conclusion: The common pathogens seen in this study are in keeping with similar previous studies in Vietnam. However, further analysis of the results of this study will be undertaken to determine the spatial-temporal distribution of the known and unknown pathogens and association of environmental and demographic variables.

10.003 Interspecies transmission of influenza A viruses at the human-swine interface, West Africa

O. A. Adeola[1], B. O. Olugasa[2], B. O. Emikpe[2]
[1]Bingham University, Nigeria, Jos, Nigeria, [2]University of Ibadan, Nigeria, Ibadan, Nigeria

Purpose: Seasonal influenza epidemics have been reported to cause significant morbidity and loss of man-hours while previous influenza pandemics resulted in high mortality and socio-economic losses. It is now becoming clearer that these epidemics and pandemics have been sustained, through the years, through continuous evolution of influenza viruses through mechanisms such as interspecies transmission and genetic reassortment. In particular, due to the role of the pig in reassortment of influenza viruses, human-to-swine interspecies transmission is uniquely significant. We therefore investigated the possibility and nature of transmission of influenza A viruses at the human-swine interface in two West-African countries.
Methods & Materials: Specimens were collected in 2008 and from 2013 to 2015. Nasal swabs were collected from 205 pigs at different locations in Ibadan, Nigeria and Kumasi, Ghana. Nasopharyngeal swabs were also collected from 31 pig handlers in the two West African cities. Some of these specimens were first cultured in 10-12 day old embryonated hen's eggs before testing, while most of them were tested directly by a sensitive Quantitative Solid Phase Antigen-detection Sandwich ELISA, using different anti-hemmaglutinnin monoclonal antibodies, and by RT-PCR using type-specific and subtype-specific primers. Amplicons were sequenced using ABI V3.1 Big dye kit. Sequence editing, alignment and phylogenetic analyses were also done. Serum specimens were collected from ninety-one pigs within Ibadan in 2008. Two strains of human influenza virus A: A/Brisbane/59/2007 (H1N1) and A/Brisbane/10/2007 (H3N2) were used in Haemagglutination-Inhibition (HI) Assay for antibody detection.
Results: Antigenic analyses revealed that a human strain of Influenza A(H1N1) and A (H3N2) circulated in swine populations in the study areas. Molecular characterization and phylogenetic analyses also revealed that these viruses had human origins. In addition, we also detected HI antibodies against Human H1 and H3 Strains of Influenza A Viruses in pigs in Ibadan, Nigeria.
Conclusion: Our results confirm the occurrence of interspecies transmission of influenza A viruses, especially human-to-swine, in Nigeria and Ghana. This may proceed even more rapidly because basic hygiene and biosecurity measures were generally poorly accepted by pig farmers. We recommend improvement on personal hygiene of pig handlers and enforcement of sick leave, particularly during the first few days of influenza-like illnesses.

10.004 Resurgence of influenza-A(H1N1) 2009 in Pakistan, November 2015-April 2016

M. A. Khan[1], J. ANsari[2], M. A. Ranjha[3], M. Salman[2], N. Hassan[4], U. Amir[4], S. Zaidi[4]
[1]NIH, Islamabad, Select a State, Pakistan, [2]National Institute of Health, Islamabad, Pakistan, [3]National Institute of Health, Islamabad, Pakistan, Pakistan, [4]NIH, Islamabad, Pakistan

Purpose: To describe the descriptive features and evaluate the risk factors of fatalities
Methods & Materials: A descriptive analysis on referred cases at NIH during November 2015 to April 2016 was conducted. Respiratory specimens were confirmed through RT-PCR. Standard WHO case definitions for Severe Acute Respiratory Illness (SARI) and Influenza Like Ilness (ILI) were followed. Information was gathered through a structured questionnaire and analyzed through Epi info-7.
Results: A total 1246 samples received from all over country. Out of which 338 (27%) were positive for Influenza. Most samples received from district Rawalpindi (n=512/41%), Islamabad (n=400/32%), Lahore (n=202/16%) and Peshawar (n=62/5%). Out of 338 positive cases, 286 (85%) were Influenza-A while 52 (15%) were Influenza-B. Out of 286 Influenza-A cases, 214 (75%) were positive for H1N1 pdm09 and 72 (25%) for Influenza H3N2. Among H1N1pdm09 positive cases, Islamabad reported 68 (31%), Rawalpindi and Lahore 27(13%) each and Peshawar were 17 (8%). The case fatality ratio (CFR) for H1N1 pdm09 cases was 8.3% with Islamabad as the most affected area accounting for 22 deaths. Major clinical symptoms were fever (n= 212, 88%), flu (n= 221, 92%), cough (n= 207, 86%), body aches (n=205, 85%), sore throat (n=132, 55%), shortness of breath (n=48, 20%) and respiratory distress (n= 19, 8%). Among the 68 positive cases of Islamabad, 21 (31%) had history of contact with positive case. 31 (46%) SARI cases were hospitalized, from which 22 (32%) died. Among the fatal cases 12 (55%) were males. Age groups of fatal cases are: <5yrs (2), 5-20yrs (01), 21-45yrs (02), 46-65yrs (7) and above 65yrs (10). All fatal cases had pre-existing medical conditions like chronic cardiac disease (n=6, 27%), chronic hepatitis (n=3, 13%), chronic respiratory disease (n=4, 18%), diabetes (n=3, 13%), infancy & pregnancy (n=2, 9%) ea
Conclusion: Present resurgence of H1N1 could be attributed to extreme cold/ dry weather, possibility of virus drift and absence of seasonal vaccination. Fatalities occurred among the patients with comorbidities. The results suggest that many deaths can be prevented with early diagnosis, timely supportive treatment and vaccination of high risk groups. Strengthening surveillance, predicting any resurgence and vaccinating high risk population are essential control measure.

10.005 Differential effect of pandemic H1N1/2009 virus introduction in pigs in Europe compared to West and Central Africa

C. J. Snoeck[1], O. Abiola[2], M. Okwen[3], A. Olubayo[2], A. Owoade[2], F. Wildschutz[4], C. P. Muller[5], J. Huebschen[1]
[1]Luxembourg Institute of Health, Esch-sur-Alzette, Luxembourg, [2]University of Ibadan, Ibadan, Nigeria, [3]district Hospital Bali, Bamenda, Cameroon, [4]4Administration des Services Vétérinaires de l'Etat, Luxembourg, Luxembourg, [5]Centre de Recherche Public de la Santé (CRP-Santé), Luxembourg, Luxembourg

Purpose: The emergence of pandemic H1N1/2009 shook up the epidemiology of influenza A virus in humans but also in other susceptible species, especially in pigs. At the heart of Europe, Luxembourg is a small agricultural country with strong interactions with neighbouring countries. Similarly to Luxembourg, influenza viruses circulating in swine in West and Central Africa are largely unknown, despite a growing porcine sector and their importance for public health.
Methods & Materials: Almost 1600 serum samples collected from pigs in Luxembourg (2009, 2012), Nigeria (2009, 2012) and Cameroon (2011) were tested by virus microneutralization against a panel of influenza strains including European, American swine and human influenza viruses for assessing the presence of influenza type-specific neutralizing antibodies. Nasal swabs were also collected in Nigeria (n=264, 2009; n=340, 2012) and Luxembourg (n=270, 2009; n=518, 2014-2015), screened by RT-PCR and the genome of the strains detected was sequenced.
Results: Our serological survey suggested that, before the 2009 pandemic, only rare swine and human H3N2 or human H1N1 infections occurred in Nigeria. However, in 2011–2012, 27.4% of pigs in Nigeria and 5.6% in Cameroon had antibodies against H1N1 viruses. Higher antibody titres against pandemic H1N1/2009 suggested that pigs were exposed to this or a similar virus, either by multiple introductions or sustained circulation, and that reactivity against American and European swine H1N1 viruses resulted from cross-reaction. In Luxembourg however, the antibody response was dominated by European H1N1 avian-like viruses in 2009 and 2012, while rare cases of exposure to pandemic H1N1/2009 were suspected in 2012. Our molecular survey found several types of influenza viruses in Luxembourg, including a case of seasonal human H3N2 and a new reassortant with internal genes from the pandemic H1N1 rarely reported elswhere in Europe.
Conclusion: Taken altogether, our results suggest that the pandemic H1N1/2009 may have been successfully transmitted and spread more easily in countries where previous circulation

of other swine influenza viruses was low, compared to countries with pre-existing endemic swine influenza virus circulation. The introduction of pandemic H1N1 also permitted the generation of new reassortants whose fitness and zoonotic potential are still unknown.

10.006 Monoclonal antibody-mediated clearance of rabies virus from the central nervous system: Implications for future approaches to rabies therapy

P. De Benedictis[1], A. Minola[2], E. Rota Nodari[1], R. Aiello[1], A. Lanzavecchia[3], H. Bourhy[4], D. Corti[2]
[1]Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (PD), Italy, [2]Humabs BioMed SA, Bellinzona, Switzerland, [3]Institute for Research in Biomedicine, Università della Svizzera Italiana, Bellinzona, Switzerland, [4]Institut Pasteur, Paris, France

Purpose: Current rabies post-exposure prophylaxis (PEP) currently includes the administration of equine or human rabies immunoglobulins (RIG). The replacement of these products with at least equally potent and safe products is strongly encouraged. Of note, PEP efficacy diminishes progressively when PEP administration is delayed, being ineffective when symptoms appear. We have recently identified a cocktail of two anti-rabies human monoclonal antibodies (RVC20/RVC58) with unprecedented potency and breadth, that can be combined with vaccination (PEP) or even administered alone as a late post-exposure treatment (late-PET).
Methods & Materials: Syrian hamsters were firstly challenged intramuscularly (IM) with CVS-11 (0.05ml) and treated IM at day 0 with vaccine + mAbs (expPEP), or vaccine + HRIG (stPEP) or left untreated. Second, animals were PEP-treated without challenge, to assess whether the administration of RVC20/RVC58 may influence the hamster response to vaccination. Third, animals were challenged IM with a 100-fold higher dose of CVS-11, administered IM with a high dose of RVC20/RVC58 late post infection (d2 pi and d3 pi), with stPEP or left untreated. Animals were observed over 340 days. Mortality, clinical signs and CNS viral load were assessed.
Results: RVC20/RVC58-administered Syrian hamster successfully survived to the lethal CVS-11 challenge, in both exp-PEP and late-PET experiments. Interestingly, RVC20/RVC58 did not affect the endogenous post-vaccination antibody response. As for the late-PET experiment, viral mRNA was present in the CNS of challenged animals from day 2 pi. Untreated and PEP animals all succumbed at day 5 pi. Late-treated animals survived over 340 days (100% in d2 pi and 58.33% in d3 pi), showing clinical signs from d4 pi and recovering by d24 pi. Significant differences were observed in viral loads between untreated and late-treated groups.
Conclusion: Despite the mAb-driven clearance of rabies virus from the CNS has long been investigated in the past, scarce data are available in literature to support its efficacy. Our data provides evidence for the potential efficacy of mAbs, alone or in combination with other antiviral drugs, to treat rabies infection. Further studies are needed to explore alternative routes of administration possibly extending the therapeutic window.

10.007 Host-symbionts interactions between bats and coronaviruses

S. Leopardi[1], L. Tassoni[1], P. priori[2], M. Gastaldelli[1], D. Scaravelli[3], P. De Benedictis[1]
[1]Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Italy, [2]S.T.E.R.N.A., Forlì, Italy, [3]Università degli studi di Bologna, Forlì, Italy

Purpose: Alpha and beta Coronaviruses (CoVs) show highest diversity and geographical range in bats, suggesting a long-standing host-symbiont association and a key-role of these animals as reservoir. This study investigates the evolutionary dynamics shaping CoVs evolution in their bat hosts, which influences their potential to cross the species barrier.
Methods & Materials: We investigated the phylogeny of alpha and beta-CoVs through the Bayesian approach implemented in MrBayes v3.2.4 using two separate datasets, including *RdRp* sequences either from bats only (461) or from all mammals (561). We tested CoVs compartmentalization using BaTS_beta_build2 and evaluated the phylogenetic congruence between hosts and symbionts using the Parafit_Test implemented in R v3.2.5. Spills-over between different bat genera and sustained transmissions within the recipient host were defined as previously described.
Results: Our data supported CoV's speciation upon the bat host genus, while species-specific clusters were not consistent with distinctive CoV species. However, CoVs also showed compartmentalization upon the bat species, particularly in genera highly diversified in alimentation, reproduction and roosting ecology (i.e. *Myotis*). Similarly, we detected intra-specific geographical structuring of bat CoVs, especially in non-migrant species. These findings suggest CoV's adaptation in bats rather than the concomitant speciation of hosts and symbionts. Highest CoV diversity was detected in the genera *Rhinolophus, Pipistrellus* and

Hipposideros, associated with both alpha and beta CoVs. Genetic analyses supported 24 spills-over between bat genera, also disproving co-speciation as the major evolutionary mechanism of CoVs. Of note, spills-over were particularly frequent in Rhinolophids, bats that usually co-roost with species from different genera. Spillover between related genera was more likely to lead to sustained within-species transmission in the recipient host. This data, coupled with the phylogenetic congruence between bats and CoVs as derived by distance-based analyses, suggest a preferential host shift towards phylogenetically related hosts. **Conclusion:** Our study suggests host shift rather than co-divergence as being the major evolutionary force shaping CoV diversity in bats. This would suggest high potential for bat CoVs to emerge in new hosts through host jumps. We suggest that the risk might be enhanced in bats showing alpha and beta CoV co-infections, which might lead to a higher chance for recombination.

10.008 Nipah virus ecology and infection dynamics in its bat reservoir, *Pteropus medius,* in Bangladesh

J. H. Epstein[1], S. J. Anthony[2], A. Islam[3], A. M. Kilpatrick[4], S. Ali Khan[5], N. Ross[1], I. Smith[6], J. Barr[6], C. Zambrana-Torrelio[7], Y. Tao[8], A. Islam[9], P. L. Quan[10], K. Olival[7], E. Gurley[11], M. J. Hossain[11], H. E. field[12], M. Fielder[13], T. Briese[14], M. Rahman[15], G. Crameri[6], L.-F. Wang[16], S. Luby[17], W. I. Lipkin[18], P. Daszak[7]
[1]EcoHealth Alliance, New York, USA, [2]Columbia University, New York, NY, USA, [3]EcoHealth Alliance, Dhaka, Bangladesh, [4]University of California, Santa Cruz, Santa Cruz, USA, [5]Chittagong Veterinary and Animal Sciences University, Chittagong, Bangladesh, [6]CSIRO Australian Animal Health Laboratory, Geelong, Australia, [7]EcoHealth Alliance, New York, NY, USA, [8]Penn State University, State College, USA, [9]International Centre for Diarrheal Disease Research, Bangladesh, Dhaka, Bangladesh, [10]State University of New York, Stony Brook, Stony Brook, USA, [11]icddr,b, Dhaka, Bangladesh, [12]EcoHealth Alliance, Brisbane, Australia, [13]Kingston University, London, London, United Kingdom, [14]Columbia University, New York, USA, [15]Institute of Epidemiology, Disease Control & Research (IEDCR), Dhaka, Bangladesh, [16]Duke NUS, Singapore, Singapore, [17]Stanford University, Stanford, CA, USA, [18]Columbia University Mailman School of Public Health, New York, NY, USA

Purpose: Nipah virus (NiV) is an emerging zoonotic virus that causes seasonal outbreaks of encephalitis in Bangladesh with >75% mortality. Little is known about NiV dynamics in *Pteropus medius,* the putative bat reservoir in Bangladesh. Date palm sap consumption is the primary route of transmission to humans. The aim of this study was to determine whether seasonal dynamics or distribution of NiV in bats accounts for human outbreak patterns.
Methods & Materials: Between 2006 and 2012, urine, blood, feces and saliva was collected from 100 *P. medius* from each of eight districts across Bangladesh. Additionally, 100 bats from Faridpur were sampled quarterly for 6 years. Samples were screened for NiV RNA by PCR. Sera were screened for anti-NiV IgG antibodies by ELISA and Luminex. Serological data was modelled to identify seasonal trends.
Results: 2,790 bats were sampled. NiV RNA was detected in 0 - 3.8% of bats per sample (n ~ 100) and was detected outside the Nipah Belt and outside the human NiV season. Bats were sero-positive throughout Bangladesh (seroprevalence: 20% - 56%). Models showed recurring outbreaks within the study population approximately every two years, following periods of waning immunity. Adults drive outbreaks in bats and appear to become susceptible to reinfection after ~ 7 years. Phylogenetic analysis of N, P, and G gene regions from the same population over time showed >98% sequence homology. A divergent strain of NIV (~80% homology) was identified in eastern Bangladesh.
Conclusion: *Pteropus medius* is the reservoir for Nipah virus in Bangladesh and likely to be an ongoing source of human infection. NiV detection was not restricted to the Nipah Belt, suggesting spillover is possible anywhere in Bangladesh if a suitable strain and bat-human interface were present. Different strains in disparate locations and high homology in one location over time, suggests that there may be localized strains persistently circulating in bats. Human activities such as date palm sap harvesting, concurrent with viral circulation in local bat populations are likely to be the major driver of human outbreaks in Bangladesh. Viral dynamics in bats, which include years with no outbreaks, may explain years when no human NiV cases have been detected.

10.009 Global correlates of emerging zoonoses: Anthropogenic, environmental, and biodiversity risk factors

T. Allen[1], K. Murray[2], C. Zambrana-Torrelio[3], S. Morse[4], C. rondinini[5], V. Di Marco Lo Presti[6], K. Olival[7], P. Daszak[7]
[1]EcoHealth Alliance, New York, USA, [2]Imperial College London, London, United Kingdom, [3]EcoHealth Alliance.org, New York, NY, USA, [4]Columbia University, New York, NY, USA,

[5]Sapienza Università di Roma, Rome, Italy, [6]Istituto Zooprofilattico Sperimentale of Sicily , Barcellona P.G. (Messina), Italy, [7]EcoHealth Alliance, New York, NY, USA

Purpose: Human infectious diseases originating from wildlife represent a significant threat to global health, security and economic growth. Efforts to identify the geographic origins and underlying causes of disease emergence are essential to move interventions closer to the source, more effectively limiting subsequent impacts.
A previous study (Jones et al. 2008) used logistic regression to model the association between "EID events" and various factors, and found different distribution and driver associations for different categories of EID event.
We aim to better analyze the mechanistic underpinnings of disease emergence and address some methodological limitations of previous work. We focus on zoonotic EIDs and predictor datasets for specifically hypothesized mechanisms of emergence.
Methods & Materials: We used boosted regression trees to model associations between an updated set of zoonotic EID events and spatial predictors, selected for their relevance to a priori hypotheses about mechanisms of emergence. We included improved measures of mammal species richness, land use, land-use change and land cover. We constructed a novel measure of relative publication effort as a proxy for observation bias, and used a bootstrap resampling regime to account for spatial uncertainty in EID event data.
Results: Biodiversity, land cover and land use were the most important factors in predicting locations of disease emergence events, after accounting for observation bias and the baseline distribution of the human population. We found that disease emergence was more likely in areas of high mammal biodiversity and heavily forested areas. Weaker, but still important, factors included high levels of urbanization, and rapid land conversion to and from pasture.
Conclusion: The global distribution of zoonotic EID risk (EID 'hotspots') is concentrated in tropical regions where wildlife biodiversity is high, human populations dense and growing, and land use change is occurring rapidly. These regions are most likely to produce the next EID event, and therefore most valuable for surveillance in wildlife, livestock or people.
Directions for future research include: fitting and pooling separate models for different diseases; 'ground truthing' using data from wildlife to measure factors such as pathogen diversity and human contact with wildlife.

10.010 Prevalence and risk factors of seropositivity to C.burnetii infection in dairy farms and dairy farmers, Chiang-Mai, Thaialnd 2015

P. Doung-ngern[1], P. Padungtod[2], M. Emch[3], D. Weber[4], G. Kersh[5], G. Koch[4], S. Meshnick[4]
[1]Bureau of Epidemiology, Mueang, Nonthaburi, Thailand, [2]Thai-MOPH - US.CDC, Nonthaburi, Thailand, [3]University of North Carolina Chapel Hill, Chapel Hill, NC, USA, [4]University of North Carolina at Chapel Hill, Chapel Hill, USA, [5]Center for Disease Control and Prevention, USA, Atlanta, USA

Purpose: A one year longitudinal study of Q fever among dairy farms and farmers was conducted in June 2015 in the areas of Chiang-Mai where Q fever was reported. This study was conducted by the collaboration between public health and animal health sectors. We reported a preliminary analysis of baseline information to describe the magnitude and factors associated with *C.burnetii* infection in this high risk population.
Methods & Materials: Two-stage random sampling of the farms and farmers was performed to identify cohort of dairy farms farmers. We conducted face to face interview with farmers, and collected blood for baseline assessment. Bulk tank milk samples from each farm were screened and specimens were collected from cows, other animals, and farm environment in the farms with milk positive. Farmer sera were tested using Indirect Immunofluorescense Assay (IFA). Milk and cow sera were tested using Enzyme-Linked Immunosorbent Assay. Vaginal swabs and environmental samples were tested using Polymerase Chain Reaction. Descriptive statistics and multivariate logistic regression were performed to describe baseline seroprevalence and factors associated with milk positive. This cohort of farms was followed up at 6 and 12 month after the baseline assessment.
Results: Totally, 282/306 (92.2%) randomly selected farms, and 532/637 (83.5%) randomly selected farmers participated. The overall seroprevalence of antibodies to *C.burnetii* was 40.8% (115/282) in milk, and 16.9% (90/532) in farmers (IFA cut-off value 1:64). We visited 99 from115 positive farms and collected samples from 790 cows. In the milk positive farms, seroprevalence to *C.burnetii* infection was 28.4% (224/790) at the individual cow and 91.9% (91/99) at the herd level. Multivariate logistic regression model showed that every 10 increase in number of cows age ≥ 2 years (OR 1.32, 95%CI 1.15-1.52), farms located in 1 kilometer from milk positive farm (OR 2.8, 95%CI 1.15 – 6.84), ever clean birthing area after calving

(OR 0.31, 95%CI 0.91 – 0.99), and quarantine newly purchased animals (OR 0.54, 95%CI 0.35 – 0.97) were associated with milk positive.
Conclusion: Farm practices were associated with the presence of *C.burnetii* infection. Further assessment is needed to determine the incidence of seroconversion and other risk behavior among dairy farmers.

10.011 Tuberculosis in captive elephants and mahouts: Implications to health policy
D. Abraham[1], K. Venugopal[2], S. Cork[3]
[1]Veterinary Dispensary, Kozhikode, Kerala, India, [2]Government Medical College Hospital, Kottayam, India, [3]University of Calgary, Faculty of Veterinary Medicine, Calgary, AB, Canada

Purpose: In southern India, there are nearly a thousand captive Asian elephants and not less than 3,000 mahouts (traditional elephant keepers). Tuberculosis among the elephants and mahouts presents the risk of both inter and intra-species disease transmission. As part of a long term research project, we undertook tuberculosis screening of nearly 800 captive elephants and their mahouts.
Methods & Materials: Screening of elephants was done using serological tests and mycobacterial isolation on Lowenstein Jensen medium by culture of trunk wash from live animals and lung nodules from dead animals by a team of veterinarians. A team of medical physicians completed the tuberculosis screening of mahouts by clinical examination, chest X-ray evaluation, sputum culture and tuberculin skin testing.
Results: Our preliminary results suggest evidence for inter-species tuberculosis transmission. We examined three different scenarios of tuberculosis transmission. First is the risk of infection from a diseased mahout to an elephant. Second is the risk of infection from a diseased elephant to a mahout and third is that from a diseased elephant to another elephant. Under the tropical climatic conditions in southern India, the risk of infection to a captive elephant from a diseased mahout seems to far outweigh the risks of infection to a mahout from a diseased elephant. Also, there seems to be little evidence to suggest elephant-to-elephant transmission of human tuberculosis.
Conclusion: There are ethical as well as political consequences to the outcomes in each of the three scenarios, which are both complex and diverse. Mahouts and captive elephants in southern India are highly migrant and hence contact tracing and follow-up testing of the subjects are difficult. In the existing cultural and religious contexts in southern India, implementing the policy guidelines for prevention and control will be an even bigger challenge. In the long term, with the help of evidence based results, we intend to formulate specific policy guidelines to mitigate the risk of intra and inter species tuberculosis infection among captive elephants and mahouts.

10.012 The first reported human Rift Valley Fever outbreak in Uganda, 2016
H. Kyobe Bosa[1], R. Majwala[2], S. Kabwama Ndugwa[2], R. G. Downing [3], H. Kibuuka[4], N. Kiwanuka[2], J. J. Lutwama[5]
[1]Uganda Virus Research Institute, Entebbe, Uganda, [2]Makerere University , Kampala, Uganda, [3]Centres for Disease Control and Prevention Uganda, Entebbe, Uganda, [4]Makerere University Walter Reed Project, Kampala, Uganda, [5]Uganda Virus Reseacrh Institute, Entebbe, Uganda

Purpose: On 7th March 2016 a case of suspected viral hemorrhagic fever, a middle-aged abattoir worker hospitalized at Kabale Regional Referral Hospital was reported to Uganda Ministry of Health. Two cases were subsequently confirmed as Rift Valley Fever Virus (RVFV) by RT-PCR at Uganda Virus Research Institute, Entebbe. A subsequent RVF sero-survey of 1051 domestic animals in the districts neighboring Kabale showed evidence of previous RVF infection in cattle (27%), goats (6.5%) and sheep (5.7%).
Here we report the findings of an epidemiological investigation of the first reported human RVF outbreak in Uganda.
Methods & Materials: A suspect RVF case was defined as acute onset of fever (>37.5^{o}C), negative malaria test, and at least two of the following three symptoms: headache, muscle or joint pain and any gastrointestinal symptom. A confirmed case was a suspected case that was laboratory confirmed by detection of RVF nucleic acid by RT-PCR or demonstration of serum IgM antibodies by ELISA. Case finding was conducted through community interviews in the affected communities, abattoir workers and review of clinical records at health facilities in the areas of the confirmed cases.
Results: 24 suspect cases were line-listed from active case-finding. Except for the two confirmed cases, no other confirmed cases were identified. The dates of onset of symptoms for a 16-year old school-boy and the 42-year old butcher were February 13th and 18th 2016 respectively.

Infection of the index case appears to be vector-borne transmission as opposed to meat handling in the second case. There was no clear epidemiological link between the two cases. Moreover, there was no evidence of suspect RVF cases among abattoir workers. For 5 months prior to infection of the primary case, multiple cow and goat abortions were reported in nearby farms.
Conclusion: We report the first two independent cases of human RVF infections in Uganda. They appear to have been random spillovers from a missed RVF outbreak among the livestock into the human population. Zoonotic disease surveillance at the human-livestock interface is critical for early identification of RVF transmission from livestock. We recommend sentinel surveillance amongst abattoir workers for detection of RVF in humans in the area.

10.013 Determining hotspots of human exposure to rodents, bats and monkeys in Bangladesh

I. S. Shanta[1], S. P. Luby[2], K. Hossain[1], S. S. U. Ahmed[1], T. Rahman[1], E. Kennedy[3], M. A. Y. Sharker[4], A. M. Kilpatrick[5], J. R. C. Pulliam[6], E. S. Gurley[1]
[1]icddr,b, Dhaka, Bangladesh, [2]Stanford University, Stanford, CA, USA, [3]CDC, Atlanta, USA, [4]University of Florida, Gainesville, FL, USA, [5]University of California, Santa Cruz, Santa Cruz, USA, [6]Stellenbosch University, Stellenbosch, South Africa

Purpose: Bangladesh is at risk for emerging infectious disease transmission from wildlife to humans because of its extremely dense human population, wildlife diversity, deforestation, urbanization and habitat migration. There are some known examples of diseases that have been transmitted to humans from wildlife in Bangladesh, however, efforts to identify new emerging threats should be pursued. The objectives of this study were to identify the frequency of human exposures to rodents, bats and monkeys and to map human exposure to these animals across Bangladesh, to identify their seasonality, and to inform in-depth studies of disease transmission.
Methods & Materials: From 2013 through 2016, we conducted a cross sectional survey in a nationally representative sample of 9,512 households from 952 randomly selected urban and rural communities. The most senior household member between 18 to 60 years of age was interviewed about any household members' exposures to rodents, bats and monkeys within the past month. We performed kernel density estimation to measure intensity of each exposure geographically. The spatial dependence between exposure and longitude was examined by scatter plot and correlation coefficient.
Results: Throughout the country, 90% (95%CI: 89-91) of respondents reported observing rats/mice in their households, 51% (95%CI: 50-52) reported observing bats and 2% (95%CI: 1.6-2.2) reported observing monkeys close to their households. Among all households, 8.5% (95%CI: 7.9-9.1) reported direct contact with rodents, 0.5% (95%CI: 0.4-0.7) with bats and 0.05% (95%CI: 0.022-0.13) with monkeys. Contact with rodents was more commonly reported in the two largest metropolitan areas and their surroundings. Human exposure to bats was more common in the southwest and northern part of the country and exposure to monkeys was primarily clustered in the southwest and northeast. There was no seasonality in exposures.
Conclusion: Of the 160 million people in Bangladesh, 13.6 million are exposed to rodents every month, 800,000 to bats and 80,000 to monkeys. Diseases known to be transmitted through these exposure routes could be prevented by targeting high contact areas for surveillance and prevention efforts. Information about where these exposures cluster could be used to inform studies aimed at identifying emerging disease from rodents, bats and monkeys.

Session 11 (Plenary Session)

Plenary: Trends in Antimicrobial Resistance in Europe

Sunday, November 6, 2016

Room: Park Congress

11:00-11:45

11.001 Trends in antimicrobial resistance in Europe

D. L. Monnet
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Surveillance of antimicrobial resistance in Europe is mainly performed by the European Antimicrobial Resistance Surveillance Network (EARS-Net) hosted at the European Centre

for Disease Prevention and Control (ECDC). EARS-Net collects and reports data from the 28 EU Member States, Iceland and Norway on antimicrobial resistance in invasive isolates of eight bacterial pathogens. Data are collected by national networks following a standardised protocol and then uploaded into The European Surveillance System (TESSy) at ECDC. There were, however, large differences depending on the country. For example in 2014, the proportion of *Staphylococcus aureus* invasive isolates - mostly bloodstream infections - that were resistant to meticillin (MRSA) varied from <1% (Netherlands) to >50% (Romania). The next update of EARS-Net data on antimicrobial resistance in Europe will be available in November 2016.
In addition to EARS-Net, the Central Asian and Eastern European Surveillance of Antimicrobial Resistance (CAESAR), coordinated by the WHO Regional Office for Europe, collects data based on the same methodology in other countries in the WHO European Region.
Data on antimicrobial resistance in *Salmonella* spp. and *Campylobacter* spp. are collected by the European Food- and Waterborne Diseases and Zoonoses Network (FWD-Net) at ECDC and reported annually in a joint report together with the European Food Safety Authority (EFSA). In addition, the three EU agencies (ECDC, EFSA and the European Medicines Agency – EMA) published, in January 2015, a first Joint Interagency Antimicrobial Consumption and Resistance Analysis (JIACRA) report, comparing data from humans and food animals, and a second report is in preparation.
Data on antimicrobial resistance in *Neisseria gonorrhoeae* infections are available from the European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP). European data on multidrug-resistant (MDR) and extensively drug-resistant (XDR) tuberculosis are available from the annual report on Tuberculosis surveillance and monitoring in Europe and in the ECDC Surveillance Atlas of Infectious Diseases.

Session 12 (Invited Presentation)

Hot Topics in Emerging Infections

Sunday, November 6, 2016

Room: Park Congress

14:30-16:00

12.001 MERS-CoV

Z. Memish
Ministry of Health, Riyadh, Saudi Arabia

Coronaviruses have been known to cause human infection since the 1960s. In September 2012, a novel corona virus was isolated from a patient in Saudi Arabia presenting with acute respiratory distress and acute kidney injury. Soon after, similar clinical syndromes were described in additional patients in Saudi Arabia. Analysis revealed the disease syndromes to be due to a novel virus closely linked to the Middle East duly named the Middle East Respiratory Coronavirus (MERS-CoV). Since its initial discovery initially in 2012 a total of 1806 cases have been reported from 27 countries, with a case fatality rate of 36%. Zoonotic transmission is of significant importance and evidence is growing implicating the dromedary camel as the animal host. The clinical picture of MERS-CoV includes asymptomatic infections, mild or moderately symptomatic cases and fatal disease. Transmissions of MERS-CoV within healthcare settings are facilitated by overcrowding, poor compliance with basic infection control measures, unrecognized infections, the superspreaders phenomenon and poor triage systems. The actual contributing factors to the spread of MERS-CoV are yet to be systematically studied, but data to date suggest viral, host and environmental factors play a major role. Supportive care has been the mainstay of management for patients with MERS-CoV infection. To prevent spread of MERS-CoV within health-care settings, it is important to eliminate practice variation by adopting a respiratory screening program and to practice the best available infection control measures. Risk assessment and training of all HCWs on recognizing, isolating, and cohorting possible cases are of great importance to further decrease transmissions within the health-care facilities.

12.002 Transboundary animal diseases and social instability

L. Myers
Food and Agriculture Organization of the United Nations, Rome, Italy

The world is experiencing an increased risk of disease threats that are emerging or re-emerging at the human, animal, environment, and social interface. These threats can spread quickly and, if not mitigated, can evolve into major crises, seriously affecting animal and human health, food security and social stability. It is well documented that the poor and politically marginalized are disproportionately affected by all crises, including recurrent animal disease emergencies.
Social instability may occur as a consequence of recurrent or protracted crises and conflicts, or natural disasters such as earthquakes, floods, droughts and epidemics. Animal disease outbreaks, including zoonoses, can many times be the result of social instability, but disease can also precede, trigger and contribute to community hardship, which leads to wider social instability, particularly if they disrupt social infrastructure or reduce food availability. The relationship between disease and social instability may appear indirect but real, particularly in the hardest hit countries in the developing world. Coping mechanisms, such as sound policies, trust in government, and robust infrastructure quickly breakdown at times of civil instability. Such breakdown often leads to a decline in public health, medical care, food accessibility and affordability, marketing certification practices and food safety, or employment stability. Furthermore, the agricultural-livestock base is often undermined, which in turn creates a vicious cycle of inadequate nutrition, social fragmentation, threatened livelihoods, and further food insecurity. The complexity to isolate instability and health or disease as the interaction is a multifactorial circular argument.
Animal disease management experts myopically tend to focus on traditional veterinary specialties of epidemiology, laboratory diagnostics, risk assessment, and emergency management when assessing and analyzing disease events. The animal health sector would greatly benefit from fully recognizing and understanding the driving factors beyond the disease event itself that impact improved upstream prevention measures and disease management. Expanding the 'One Health' approach to embrace the social and economic sciences would likely yield great value in the way that the international community manages animal disease threats.
Every person has a daily need for accessible, affordable, and nutritious food; without this the social fabric unwinds and can become unstable. Attendance to animal health through professionally guided community-based involvement needs to be an increasing component of humanitarian assistance programmes to avoid consequential major epizootics and epidemics. Because food and agriculture production supports social stability and peace, the Food and Agriculture Organization of the United Nations believes that transformational change is required in the way humanitarian crises are approached.

12.003 Crimean-Congo hemorrhagic fever

O. Ergonul
Koc University, Istanbul, Turkey

The objectives of this presentation is updating all the information related to Crimean-Congo Hemorrhagic Fever (CCHF). The titles of the presentation will be epidemiology, pathogenesis, treatment, prevention and vaccination. CCHF is a fatal viral infection with the reported mortality rate of 3-30 %. Every year >1000 laboratory confirmed cases were reported from Africa, Asia and Europe. Recent autochthonous cases were reported from Spain in August of 2016. In pathogenesis of CCHF infection like in other viral hemorrhagic fevers, inflammatory processes are key elements of immune response, and the release of proinflammatory cytokines were suggested to be related with the disease course and clinical outcome. Since then, some other studies also reported the critical role of proinflammatory cytokines in disease course, however complete understanding of the pathogenesis of CCHF infection was needed. Many studies showed the beneficial effect of ribavirin previously, benefit was shown by a recent powerful study, which included 281 laboratory confirmed CCHF patients. Severity-scoring index was defined, and the patients were grouped as mild, moderate, and severe accordingly. The CFR among patients who received ribavirin was significantly lower than that among those who did not receive ribavirin (1.49% vs 17%; P = .001). Among severely ill patients, use of corticosteroid therapy was beneficial (P = .014). After stratifying patients on the basis of the SSI described here, ribavirin was found to be effective in reducing the CFR among moderately ill patients, whereas steroids were found to be beneficial among patients with more severe disease.
These findings support the theoretical hypothesis on the beneficial role of ribavirin therapy during the earlier, viremic phase of the disease course. In later phases of the disease, corticosteroids could be effective in severely ill patients, in whom enormous amounts of cytokines have been released. In summary, in CCHFV infection ribavirin was found to be effective in treatment, in post-exposure prophylaxis, and should be given as early as possible. In post-exposure prophylaxis ribavirin should be given. Other drugs like favipiravir were

studied in vitro and also could be considered in vivo. Vaccine studies are being performed in several centers, but there is no product yet.

12.004 Avian influenza viruses at the animal human interface: Progress and challenges in under resourced countries

G. Cattoli
International Atomic Energy Agency, Vienna, Austria

Before the emergence of the Avian Influenza (AI) H5N1 panzootic in 2003, highly pathogenic AI (HPAI) was considered an uncommon disease of poultry in many countries worldwide. However, in the last 15 years infections caused by HPAI zoonotic viruses belonging to the H5 and H7 subtypes have increasingly been reported in Africa, Australasia and the Americas, including many under-resource countries, where these viruses had never been detected before. Therefore, many countries were found completely unprepared and with limited technical and financial resources to properly face the emergence and spread of AI infections, which implied severe economical and public health potential threats. This prompted both governmental institutions and international organizations to promote research, mobilize resources and take actions to strengthen public health and veterinary services in under resource countries, particularly in Africa and Asia where HPAI virus infections have become endemic in some areas. My presentation will highlight some of the progress made to combat HPAI in these countries, as well as the challenges that still exist for an efficient control of this disease.

12.005 The sterile insect technique as a tool for control of insect vectors and vector-borne diseases

K. Bourtzis
Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria

The mosquito species *Aedes aegypti* and *Ae. albopictus* are responsible for the transmission of human pathogenic viruses including yellow fever, dengue (DENV), chikungunya (CHIKV) and Zika (ZIKV). According to the World Health Organization (WHO), dengue and chikungunya are still causing significant human health problems in over 100 countries, while Zika has recently spread to over 70 countries and territories, and has been associated with microcephaly and other central nervous system (CNS) malformations, and Guillain-Barré syndrome (GBS). Efficient, safe and low-cost drugs and vaccines to combat these diseases are yet to be discovered and therefore population control of the insect vector is considered as the most effective way of managing these diseases. Current vector control programmes are largely based on insecticides; however, concerns over the growing resistance to all major groups of insecticides, lack of sustainability and the impact on environment and human health calls for alternative, sustainable and environment-friendly approaches for controlling populations of *Aedes* mosquitoes. We propose the use of the combined sterile insect technique (SIT) and incompatible insect technique (IIT)-approach, as a component of a stakeholder-driven integrated vector management (IVM) strategy, to suppress *Aedes* mosquito populations below the threshold required for disease transmission. We will present recent advances in the development and application of the combined SIT/IIT package as an effective, safe and efficient approach to suppress populations of *Aedes* species, including proof-of-concept data.

Session 13 (Invited Presentation)

Data Sharing and Ethics of Big Data

Sunday, November 6, 2016

Room: Klimt 2 & 3

14:30-16:00

13.001 Round Table Discussion: Data Sharing and Ethics of the Big Data

K. Littler
The Wellcome Trust, London, United Kingdom

no abstract submitted by presenter

13.002 Sharing public health data saves lives

D. Harper
Centre on Global Health Security, London, United Kingdom

Since the turn of the 21st century, global disease outbreaks including SARS, pandemic influenza, MERS, Ebola and Zika show us clearly that a public health event in a remote location can rapidly spread to have a major international impact. Public health surveillance is a critical tool that helps achieve the control of infectious diseases - a global public good. Sharing public health surveillance data in a timely manner enables better preparedness and response, locally and globally.
Increasingly, online data that might not have been collected with an a priori health objective is used for public health purposes. Online technologies that provide data for disease or event detection - known as digital disease detection (DDD) systems - incorporate the use of established tools such as search engine queries and social media, as well as those that are emerging in this context such as crowd-sourced information, machine learning and geolocalization.
DDD is a rapidly evolving field with improving data quality and accuracy and new applications as the online technology matures. It will likely take a more prominent role, in particular in settings where the infrastructure to support more traditional public health surveillance systems is lacking. However, we are at the frontier of new ethical and legal challenges that need addressing before it can be fully integrated into more conventional surveillance systems and its undoubted potential realized.
The Centre on Global Health Security at Chatham House has been engaging with leading experts from around the world to develop a guide on how to create the right environment and achieve good practice for sharing public health data. There are seven principles to the approach: Articulating the Value; Planning for Data Sharing; Achieving Quality Data; Collaborating in Creating Data Sharing Agreements; Building Trust; Understanding the Legal Context; and Monitoring and Evaluation. Each of these incorporates the ethical concepts most relevant to data sharing, namely: social beneficence, respect, justice and transparency. The findings from the Chatham House research will be discussed in the context of Digital Disease Detection and Big Data.

13.003 Round Table Discussion: Data Sharing and Ethics of Big Data
V. Moorthy
World Health Organization, Geneva, Switzerland

no abstract submitted by submitter

Session 14 (Invited Presentation)

Managing the Next Outbreak

Sunday, November 6, 2016

Room: Park Congress

16:30-18:00

14.001 Metagenomics and molecular diagnostics for emerging infectious diseases
E. Rubin
Metabiota, San Francisco, CA, USA

The genomic revolution that began with the completion of the human genome program continues. The acceleration in DNA sequencing throughput and decrease in cost position us to increasingly consider unbiased metagenomics analysis as a diagnostic tool for emerging infectious disease. I will describe the trajectory of genomic technologies and their future application to the metagenomic based diagnosis of emerging infectious diseases. In addition, I will describe our analysis of metagenomic sequence data from environmental samples to identified infectious disease outbreaks in the past and to dramatically increase our knowledge of the Earth's DNA virome.

14.002 Therapeutic considerations for emerging viral infections
P. A. Tambyah
National University Health System, Singapore, Singapore

Emerging viral infections by definition present a huge challenge for the development of therapeutics and vaccines. Our track record in the development of novel therapeutics for

emerging viral infections is not good. Part of the reason is related to the need to isolate the virus, define its laboratory safety level and develop practical cell culture and animal models to understand the behaviour of the virus before even considering the development of therapeutics. In the modern era of molecular diagnostics, many laboratories especially in low and middle income countries may not be equipped to do these. Laboratory safety is a major concern especially with completely novel infections as there have been laboratory acquired infections in the past most notably with SARS. Animal models can also be a challenge to develop as many viral infections to date do not have very good animal models that replicate human disease. We have had the most success with reemerging viral diseases for which vaccines already exist such as yellow fever or polio where novel vaccine strategies can be employed to contain outbreaks. Also, there are some emerging viral infections such as avian influenza for which licensed antivirals are likely to have some efficacy. Many investigators are exploring re-purposing already licensed drugs for use in emerging viral infections and this has the potential to make a difference. With the increasing armamentarium of therapeutic agents targeting chronic viral infections such as hepatitis or HIV, there is the hope that some of these agents may be active against novel emerging viral infections. The use of high throughput screens and in silico models also promises to aid in the development of novel therapeutics.

14.003 Communicating during outbreaks: What works, what doesn't

H. Branswell
STAT, Boston, MA, USA

Emerging and re-emerging disease outbreaks are by their very nature times of high stakes and high stress, situations demanding clear and timely communications between health authorities and the public, through their surrogate, the media.
Each outbreak has its unique characteristics and communications quandaries, whether that's the efficient hospital spread of SARS and MERS, the fear factor of Ebola or the unexpected sexual transmission of Zika.
However, fast-changing facts and the crush of interest from a multitude of media outlets makes keeping the public apprised a daunting task. In a rapidly transforming media universe, the ranks of specialist reporters upon whom public health officials have relied are dwindling. Conversely the power of social media – with its astounding reach and lack of filters – is surging. But with that power comes peril. Tweeter is like RNA viruses – lacks a correct function and can spin a story in unexpected and unfortunate directions.
These evolving communications channels are creating both new opportunities and substantial challenges for those attempting to keep the public apprised of an ongoing outbreak.

Session 15 (Oral Presentation)

Lessons from Ebola - Preparing for the Next Pandemic

Sunday, November 6, 2016

Room: Klimt 2 & 3

16:30-18:00

15.001 An economic model for introducing a quadrivalent conjugate meningococcal vaccine among adolescents in South Africa

S. G. P. Lengana[1], A. von Gottberg[2], S. Meiring[3], C. von Mollendorf[4], J. Moyes[5], C. Cohen[3]
[1]National Institute for Communicable Diseases, Johannesburg, Gauteng, South Africa, [2]National Institute for Communicable Diseases and Medical Research Council, Johannesburg, South Africa, [3]National Institute for Communicable Diseases, Johannesburg, South Africa, [4]National Institute for Communicable Disease, Johannesburg, South Africa, [5]National Institute for Communicable Diseases, Nelspruit, South Africa

Purpose: Although rare, invasive meningococcal disease can have devastating long-term complications. Use of a quadrivalent conjugate meningococcal vaccine (MCV4) has the potential to prevent disease and associated costs.
Methods & Materials: A cost-effectiveness model was built using MS Excel (Microsoft, Redmond, Washington). Data to populate the model were obtained from GERMS-SA, a national laboratory surveillance programme, as well as published literature. We compared the cost-effectiveness of introducing MCV4 in school-based, routine distribution to 11 year-old children in South Africa over a 10 year period (2003-2012) to the current strategy of no routine vaccination. We evaluated the benefits from a governmental perspective using the following health effects: cases, sequelae, deaths, disability-adjusted life-years (DALYs)

averted, and life-years saved as well as the following costs or savings: direct medical costs, costs of vaccination programme, costs of treating moderate and severe adverse events. All costs were converted to the 2012 rand dollar exchange rate (R8.53/ 1$).
Results: The model estimated a 49% (1674/3477 cases) reduction in vaccine-preventable invasive meningococcal disease in the presence of routine vaccination of 11 year-old children during 2003-2012. Furthermore, the model estimated a 47% (287/615) reduction in vaccine-preventable deaths and 7,987 life-years saved of a possible 17,132 life-years that would have been lost due to death. The reduction would equate to a R62 million (USD$7.3 million) savings in direct medical costs; however, the vaccine campaign would have a net cost of R2.4 billion ($290 million) over the 10 year period; with a cost per DALY saved of R880,000 ($103,000).
Conclusion: Routine vaccination of 11 year-olds in a school-based programme with MCV4 could potentially reduce the number of meningococcal cases by half, however the progamme would be extremely costly.

15.002 Point-of-care molecular diagnostics for epidemic-prone viruses

C. Escadafal[1], A. Kwasiborski[1], L. Magro[2], B. Jacquelin[3], P. Garneret[2], F. Monti[2], P. Tabeling[2], P. Lafaye[3], J.-C. Manuguerra[1], J. Vanhomwegen[1]
[1]Institut Pasteur, Paris, France., Paris, France, [2]ESPCI Paris, Paris, France, [3]Institut Pasteur, Paris, France

Purpose: Inexpensive, portable and easy-to-use diagnostic tools are urgently needed to ensure rapid detection of epidemic-prone viruses, such as Ebola virus (EBV) and Zika virus (ZIKV). Detection of nucleic acids (NA) allows early, sensitive and specific diagnostics for viral diseases. Unfortunately, the availability of molecular diagnostics in high disease-burden areas is limited by cost, accessibility, infrastructure and personnel constraints. This project aims to develop NA testing with stable, ready-to-use reagents and affordable, robust and portable devices able to provide rapidly reliable results directly at the point-of-care.
Methods & Materials: Isothermal amplification technologies such as LAMP (loop-mediated isothermal amplification) and RPA (recombinase polymerase amplification) are more robust, simple and rapid assays than PCR-based NA detection methods and therefore more suited to field-use. We developed both Reverse Transcriptase (RT)-RPA and RT-LAMP assays for RNA detection in a microtube-format on a portable real-time amplification device. An interdisciplinary approach enabled us to develop a more innovative, simple and miniaturised technology by applying isothermal amplification to paper microfluidics. A RT-LAMP in microtube-format and a paper-based RT-RPA assay for the detection of EBV were developed and evaluated in Guinea, to detect the presence of EBV in human plasma RNA extracts. Furthermore, isothermal assays for ZIKV detection were developed to propose multiplex assays for epidemic-prone viruses.
Results: Technical validation of RT-LAMP assays for the detection of EBV and ZIKV demonstrated a detection limit of 10 and 5 RNA copies/reaction respectively and a time-to-result of 20 minutes. Field evaluation of the EBV RT-LAMP assay demonstrated a sensitivity and specificity of 100% compared to the reference RT-PCR method while the EBV RT-RPA paper-based assay demonstrated a sensitivity of 94.7% and specificity of 60%. To enable multiplex detection on paper microfluidics, a multi-layered device was developed achieving parallel detection of three distinct RNA targets.
Conclusion: The EBV and ZIKV microtube-assays demonstrated to be highly accurate, fast, easy-to-use, and applicable at the point-of-care. Although further developments are required to simplify sample preparation and improve paper-based test performances, our results show that rapid and sensitive NA amplification is achievable on paper-based devices and that both test formats are promising tools to bring molecular diagnostics closer to the field.

15.003 Effectiveness of masks and respirators against respiratory infections in healthcare workers: A systematic review and meta-analysis

V. Offeddu[1], C.-F. Yung[2], M. S. F. Low[1], C. Tam[3]
[1]National University Singapore, Singapore, Singapore, [2]Tan Tock Seng Hospital, Singapore, Singapore, [3]Saw Swee Hock School of Public Health, Singapore, Singapore

Purpose: This systematic review and meta-analysis assessed the effectiveness of personal respiratory protective equipment, such as medical masks and respirators, in protecting healthcare workers (HCWs) from respiratory infections.
Methods & Materials: The databases Pubmed, EMBASE and Web of Science were searched for relevant randomized controlled trials (RCTs) and observational studies with no language or time restrictions. We included published RCTs and observational studies assessing the effectiveness of medical masks and respirators in protecting HCWs from

clinical or laboratory-confirmed respiratory outcomes. Editorials, press articles, reviews, guidelines, mathematical models, ongoing studies and non-peer-reviewed reports were excluded. Fixed- or random-effects model meta-analyses were conducted with appropriate combinations of RCTs or observational studies to calculate pooled risk ratios (RRs) or odds ratios (ORs), respectively. To facilitate an appropriate interpretation of the findings from our meta-analysis of observational studies, we calculated a range of plausible RRs for each summary OR, assuming a baseline risk of SARS-CoV infection ranging from 20% to 60%, as estimated from the available cohort studies.
Results: Six RCTs and twenty-three observational studies were included into this review. Meta-analysis of RCTs indicated a protective effect of masks and respirators against clinical respiratory illness (CRI) (RR=0.59; 95%CI: 0.46 to 0.77) and influenza-like illness (ILI) (RR=0.34; 95%CI: 0.14 to 0.82), but not laboratory-confirmed viral infection (VRI). Compared to masks, N95 respirators conferred superior protection against CRI (RR= 0.47; 95%CI= 0.36 to 0.62) and laboratory-confirmed bacterial infection (RR= 0.46; 95%CI= 0.34 to 0.62), but not ILI or VRI. In the meta-analysis of observational studies, there was fairly consistent evidence of a protective effect of both N95 respirators (OR= 0.12; 95%CI: 0.06 to 0.26) and medical masks (OR= 0.13; 95%CI: 0.03 to 0.62) against SARS. Evidence for a protective effect of masks or respirators against pandemic H1N1 influenza infection was not consistent.
Conclusion: Overall, this systematic review and meta-analysis supports the use of respiratory protection to prevent clinical symptoms of respiratory infection among HCWs when used consistently during non-epidemic scenarios. In addition, both N95 respirators and medical masks were effective against SARS, but not pandemic H1N1 influenza, although additional studies will be required to validate these findings.

15.004 Utility, feasibility and acceptance of an online platform for tropical diseases contact tracing

P. E. PANTOJA[1], J. Gomez-Junyent[2], N. Serret[1], J. MUÑOZ-GUTIERREZ[2], A. VILELLA[1], A. TRILLA[1]
[1]HOSPITAL CLINIC, Barcelona, Spain, [2]ISGlobal, Barcelona, Spain

Purpose: At the outbreak control of Ebola Virus Disease (EVD), the World Health Organization has proposed a new methodology for contact tracing, including Information and Communication Technologies (ICTs).
In order to evaluate using multiple approaches using mobile platforms for monitoring contact EVD, during April 2015 and March 2016. Six centers of the CIBERESP Spain perform a prospective follow-up in four cohorts of risk with the mobile web platform for Tropical Diseases Clinical Management (TDCM).
Methods & Materials: 43 Health workers, 25 aid workers, 20 travelers and 20 immigrants, a total of 108 subjects were recruited. On the first visit, they were given a mobile phone and a digital thermometer to follow up. Monitoring was based on the use of the application, completing two tasks twice a day for 21 days, looking for symptoms of EVE. TDCM creates real-time alerts and send SMS for investigators to follow up. We evaluate the utility with iSYScore scale and feasibility with tracing data quality and adherence of the subjetcs. Acceptability evaluation was made with a satisfaction survey given on the second and last visit.
Results: The iSYScore (27/47) considered the application useful. We found that 50% of the alerts generated were due to adherence. The total adherence was 73%, greater in health workers (81%) and aid workers (75%) rather than inmigrants (56%, ANOVA $p < 0.05$). Moreover acceptance was between 41.2% - 47.4%. Finally contact tracing acceptance decrease 9 % after follow-up.
Conclusion: TDCM is a useful platform for developing better model based on self monitoring and real-time monitoring systems. Presents a better adherence in health and aid workers, both groups feels better with self monitoring. Acceptance was superior to other Android applications, with differences between groups.

15.005 Building specimen referral networks to support outbreak response

S. K. Lakiss[1], J. Fischer[2], C. Standley[3], R. Muhayangabo[4], **W. Heegaard**[5]
[1]Gouvernement de la Republique de Guinee, Conakry, Guinea, [2]George Washington University Milken Institute of Public Health, Washington, DC, USA, [3]Georgetown University, Washington D.C., USA, [4]International Medical Corps, Conakry, Guinea, [5]International Medical Corps, Los Angeles, California, USA

Purpose: This case study identifies lessons learned from efforts to support the Guinean Ministry of Health to refer and transport clinical samples from local-level community health

centers to diagnostic laboratories during the WHO-designated Phase 3 of Ebola surveillance and recovery.
Methods & Materials: This study consists of a review of associated literature, followed by a compare/contrast analysis of specimen referral networks in Haiti, Uganda and Guinea. Data on Guinea's pilot referral network comes from International Medical Corps' specimen transport pilot program, launched in collaboration with Georgetown University. The study includes quantitative evidence on sample referral in Guinea (facility assessments, number/type of samples referred, training results, etc.), as well as qualitative information (beneficiary interviews, program workshop reports, capacity statements etc.).
Results: Guinea's context of Ebola response and recovery creates unique challenges to replicating pre-existing models of clinical specimen referral. "Hub and spoke" laboratory networks in Haiti and Uganda offer useful pictures of success, but do not wholly address the fundamental needs arising from Guinea's unprecedented epidemic disaster. These needs include 1) harmonizing protocols and training modules across response, recovery and development projects, 2) filling infrastructure and equipment gaps for safe, secure, and reliable sample management, and 3) assuring health workers' skill and confidence to collect samples for targeted disease surveillance in the post-Ebola setting.
Conclusion: Guinea's pilot program provides valuable lessons learned for other initiatives working to bridge the gap between epidemic disaster response and health systems strengthening. Interventions that seek to strengthen specimen referral systems during or immediately after infectious disease outbreaks must ensure that 1) guidelines for sample collection and transport are in line with response messaging, 2) facilities are equipped to manage samples of diseases targeted for surveillance, and 3) health workers receive regularly updated trainings during the transition from response to recovery. Evidence from Guinea supports a flexible approach to network development, one that offers clinicians the capacity to urgently refer samples of public health risk, while also installing regular transport circuits for non-urgent clinical testing. Coordination between partners working at different levels of the specimen referral system is critical for insuring policies and practices evolve in sync.

15.006 Establishing EVD testing at a mobile laboratory using GeneXpert Technology in Liberia - Impact on Surveillance System, Outbreak Detection and Patient Management

P. Raftery[1], C. Wasunna[2], J. Kpaka[3], R. Zwizwai[4], O. Condell[5], V. Katwerra[6], P. Hardy[7], P. Sahr[7], A. Gasasira[1], T. Nyenswah[7]
[1]World Health Organisation, Monrovia, Liberia, [2]PREVAIL, Monrovia, Liberia, [3]ACCEL, Monrovia, Liberia, [4]FIND, London, United Kingdom, [5]WHO, Dublin, Ireland, [6]WHO, Monrovia, Liberia, [7]Ministry of Health, Monrovia, Liberia

Purpose: The Ebola Virus Disease (EVD) outbreak in West Africa 2014-15 highlighted the necessity for sustainable, rapid, point-of care diagnostics. In October 2015, Xpert Ebola Assay was approved by the Minister for Health of Liberia, for use as a stand-alone EVD test for whole blood specimens. We describe implementation of GeneXpert technology at an Ebola Treatment Unit (ETU) mobile laboratory in Liberia and subsequent impact on surveillance of EVD, outbreak detection and patient management.
Methods & Materials: GeneXpert technology was established at a mobile laboratory and local laboratory technicians trained to conduct EVD diagnosis. Site coordination, management and oversight of operations was provided through successful collaborations between Ministry of Health and international partners.
Results: The EVD laboratory has capacity to test 64 blood specimens per day, requiring two technicians. Over 8000 specimens were analysed between October 2015 and June 2016. Sample turn-around-time with the Xpert Ebola Assay is two hours compared with six for conventional RT-PCR and allows for single specimen testing. Specimens taken from patients during subsequent flare-ups in November/December 2015 and April 2016 were analysed at the laboratory and Ct values of consecutive specimens compared, indicating trends in the viral load of patient specimens. This information was used by the case management team to inform clinical management of patients.
Conclusion: The mobile laboratory for EVD diagnostics contributed significantly to the surveillance activities in Liberia over an eight month period. In November 2015, a new case of EVD was identified during routine surveillance. The resulting cluster of cases, were closely monitored at the on-site laboratory using Ct values from the RT-PCR assay informing clinical care and patient management. In addition, during the flare-up in April 2016, two confirmed EVD patients at the ETU were monitored by real-time testing at the on-site laboratory. The GeneXpert platform is easy to use, has relatively low running costs and can be easily integrated into other national diagnostic and testing algorithms; a sustainable system for

Liberia. The strategic placement of GeneXperts to complement isolation facilities and establishing an integrated network of GeneXpert laboratories would strengthen epidemic preparedness and response capabilities for flare-ups of EVD clusters.

15.007 Potential impact of sexual transmission on Ebola virus epidemiology: Sierra Leone as a case study

J. Abbate[1], C. L. murall[2], H. Richner[3], **C. Althaus**[3]
[1]Institute for Research of Development (IRD), Montpellier, France, [2]Max-Planck Institute for Dynamics and Self-Organization, Gottingen, Germany, [3]University of Bern, Berne, Switzerland

Purpose: Sexual transmission of Ebola virus disease (EVD) 6 months after onset of symptoms has been documented, and Ebola virus RNA has been detected in semen of survivors up to 9 months after onset of symptoms. As it remains unclear what threat is posed by rare sexual transmission events that could arise from convalescent survivors, we assessed the potential impact of this secondary transmission route on the EVD epidemic in Sierra Leone using a mathematical transmission model.
Methods & Materials: We devised a compartmental EVD transmission model that includes sexual transmission from convalescent survivors. We fitted the model to weekly incidence of EVD cases from the epidemic in Sierra Leone, and performed sensitivity analyses and Monte Carlo Simulations.
Results: Assuming a per sex act transmission probability of 0.1% and a 3-month convalescent period, we found that sexual transmission would extend the epidemic by 83 days (95% CI: 68-98 days) on average. Strikingly, a 6-month convalescent period extended the average epidemic by 540 days (95% CI: 508-572 days), despite an insignificant rise in the number of new cases generated.
Conclusion: Our results show that reductions in the per sex act transmission probability via abstinence and condom use should reduce the number of sporadic sexual transmission events, but will not significantly reduce the epidemic size and may only minimally shorten the length of time the public health community must maintain response preparedness.

15.008 Promoting safe sex and condom use among Ebola virus disease (EVD) survivors to mitigate risk of sexual transmission through clinic-based education and semen testing in 3 districts in Sierra Leone

J. Garland[1], **A. Myers**[2], A. Oxner[2], E. Headrick [3], K. Tekuyama[4], J. Gottesfeld[5], K. Dierberg[5], M. Calderon[6], K. O'Neil[7], S. Bangura[8]
[1]University of California Los Angeles, Los Angeles, USA, [2]University of South Florida, Tampa, USA, [3]Emory University , Atlanta, GA, USA, [4]Partners In Health, Kono, Sierra leone, [5]Partners In Health, Freetown, Sierra leone, [6]World Health Organization, Freetown, Sierra leone, [7]Republic of Sierra Leone Ministry of Health and Sanitation, Freetown, Sierra leone, [8]Sierra Leone Association of Ebola Survivors (SLAES), Port Loko, Sierra leone

Purpose: Beginning in December 2013, the largest known outbreak of Ebola virus disease (EVD) began in West Africa with Sierra Leone as the most widely affected country, resulting in a total of 14,124 cases and 3,956 confirmed deaths. The decline in new cases in the three most affected countries, Sierra Leone, Guinea, and Liberia suggested that epidemiological containment strategies were successful and WHO declared Sierra Leone to be EVD free on Nov 7, 2015. However, there is growing evidence that EVD survivors can harbor and transmit EVD through sexual contact many months after recovery, with at least 3 reported cases of sexual transmission in the literature.
In order to mitigate risk of sexual EVD transmission, the National Ebola Response Centre (NERC) in collaboration with the Ministry of Health & Sanitation (MOHS) and others, Partners In Health assisted with implementation of Project Shield in 3 highly EVD affected districts within Sierra Leone: Port Loko, Kono, and Kambia
Methods & Materials: A four phase approach was used to implement Project Shield for eligible male EVD survivors ages >15 in the 3 districts. Phase 1: Planning, Phase 2: Identification, registration, & mapping of EVD survivors, Phase 3: Community education & sexual risk-reduction counseling to survivors and their partners, and Phase 4: Quantitative reverse transcriptase-polymerase chain reaction (RT-PCR) semen testing. Phase 4 testing began in Port Loko District in December 2015, in May 2016 in Kono District, and in June 2016 in Kambia District. Identities of EVD survivors, test results, and other identifying data are maintained in a secured location in each district by a staff member dedicated to data monitoring for Project Shield.

Results: After two consecutive negative RT-PCR samples are collected one month apart, EVD survivors are discharged from the program and advised to resume normal sexual practices in accordance with the most recent WHO guidelines for EVD survivor care.
Conclusion: Project Shields offers male survivors the opportunity to have their semen tested for viral persistence in order to inform them of their status and allows the scientific community to gather important data on viral persistence to further guide treatment and policy decision making.

15.009 First data in African subjects for the monovalent Janssen Ebola Zaire heterologous prime-boost vaccines, combining Ad26.ZEBOV and MVA-BN-Filo

O. Anzala[1], G. Mutua[1], B. Nyaoke[2], C. Robinson[3], K. Luhn[3], B. Callendret[3], R. Thiebaut[4], M. Snape[5], D. Watson-Jones[6], M. Douoguih[7]
[1]University of Nairobi, Nairobi, Kenya, [2]University of Kenya, Nairobi, Kenya, [3]Janssen Vaccines & Prevention B.V., Pennsylvania, USA, [4]University of Bordeaux, Bordeaux, France, [5]University of Oxford, Oxford, United Kingdom, [6]London School of Hygiene & Tropical Medicine, London, United Kingdom, [7]Janssen Vaccines & Prevention B.V. , Pennsylvania, USA

Purpose: The West African Ebola outbreak (2013-16) was the first emergence of Ebolavirus Zaire (ZEBOV) in a high-density urban population, and resulted in rapid, widespread and prolonged viral transmission. Although this epidemic is over, vaccines are needed to prevent and mitigate future Ebola outbreaks. This study provides first data from sub-Saharan Africa on safety and immunogenicity of investigational heterologous prophylactic prime-boost vaccine regimens based on Ad26.ZEBOV and MVA-BN-Filo.
Methods & Materials: A phase 1, randomized, placebo-controlled, observer-blind trial assessing replication-defective Ad26.ZEBOV ($5x10^{10}$ vp) and MVA-BN-Filo ($1x10^{8}$ $TCID_{50}$) administered in heterologous prime-boost vaccination schedules was conducted in 72 healthy adults in Kenya. Volunteers were randomized 1:1:1:1 to one of four groups, and further randomized in a 5:1 ratio to vaccine or placebo. Volunteers were vaccinated at baseline with MVA-BN-Filo (Groups 1&2) or Ad26.ZEBOV (Groups 3&4), followed by boost with the heterologous component on Day 29 (Groups 1&3) or Day 57 (Groups 2&4). EBOV GP-specific immune responses were assessed by total IgG ELISA, IFN-γ^{+} T-cell ELISpot and intracellular cytokine staining up to 180 days after prime vaccination.
Results: Following prime or boost immunization, only transient and mild local and systemic reactions were observed. This was the case in 80% and 68% of participants, respectively, following MVA-BN-Filo, and 64% and 75% following Ad26.ZEBOV. 28 days following primary immunization, EBOV GP-specific IgG responses were seen in 15/30 of MVA-BN-Filo (50%; 95%CI: 31.3%-68.7%) and 28/29 (97%; 95%CI: 82.24%-99.91%) of Ad26.ZEBOV recipients. 21 days post-boost, IgG was detectable in all vaccinees, with geometric mean (95%CI) concentrations of 8613 (5548-13371), 15,308 (9476-24729), 5156 (3426-7759) and 16,341 (10812-24697) ELISA units/mL in Groups 1 to 4 respectively. At Day 180 post-prime, 100%, 93%, 93% and 100% responded (assessed by IgG ELISA) to vaccination in Groups 1 to 4 respectively. Persisting polyfunctional $CD4^{+}$ and $CD8^{+}$ T-cell responses were induced.
Conclusion: All regimens were well tolerated. Ad26.ZEBOV prime MVA-BN-Filo boost regimen elicited immune responses early on, persisting to Day 180. Follow-up to confirm longer-term immunogenicity is ongoing. This regimen may be well-suited to preventive vaccination strategies to counter a new outbreak and was chosen for further evaluation in Phase 2&3 studies.

Session 16 (Invited Presentation)

Antimicrobial Resistance in the One Health Context

Monday, November 7, 2016

Room: Park Congress

08:30-10:30

16.001 Antimicrobial resistance in Lebanon from the food chain: A One Health perspective

G. M. Matar
American University of Beirut, Beirut, Lebanon

Antimicrobial Resistance (AMR), a global public health threat, is also a food safety issue. The food chain is considered to be an important route for emergence and spread of antimicrobial

resistance between animals and humans. Resistance is growing faster than new drugs are being developed.
To that purpose a nation-wide laboratory based surveillance of antimicrobial resistance on bacterial strains from clinical specimens, and animal food products, was done under the sponsorship of PulseNet International (CDC), WHO-AGISAR, MOH, and AUB, and aimed at determining the prevalence of serotypes, genotypes and antimicrobial resistance profiles of foodborne pathogens from clinical specimens and corresponding animal food products, to assess their potential origin from the food chain.
Foodborne isolates, namely *Salmonella* spp. and *E.coli* obtained from clinical specimens and animal food products were subjected to antimicrobial susceptibility testing, serotyping and genotyping by Pulsed Field Gel Electrophoresis and BIONUMERICS software analysis. A direct correlation between serotypes, genotypes and antimicrobial resistance profiles of *Salmonella* spp. and *E.coli,* obtained during the same period of time from clinical specimens and animal food products, was determined. Moreover, tracking the source of foodborne illness from animal food products in outbreaks settings was also performed.
Our data have shown that similar particular serotypes, genotypes and antimicrobial resistance profiles were detected in *Salmonella* and *E. coli* isolates from clinical specimens and corresponding animal food samples over a set period of time, denoting a direct transfer of resistant determinants in bacterial clones from animal food products to humans.
Generated data offered a better understanding of the emergence and spread of particular antimicrobial resistant *Salmonella* spp. and *E.coli* strains from the food chain in Lebanon and helped guiding MOH in taking appropriate preventive and control measures for food-borne diseases.

16.002 Colistin Resistance, MCR1
S. Granier
Anses, Maisons-Alfort, France

no abstract submitted by presenter

16.003 ResistanceOpen: A web application for global antibiotic resistance monitoring
D. MacFadden
University of Toronto, Toronto, ON, Canada

Background: Antibiotic resistance is a major public health concern. Despite this, we have a poor understanding of the burden and regional patterns of antibiotic resistance using existing techniques. Non-traditional approaches may be able to complement and support current programs for antibiotic resistance surveillance. We sought to use existing but disparate online antibiotic resistance data to monitor regional patterns of antibiotic resistance.
Methods: We developed a web-based and mobile compatible platform for identifying and analyzing regional patterns of antibiotic resistance using existing resistance indices. Antibiotic resistance indices were reviewed and abstracted by experienced data curators. Antibiotic resistance information was captured for up to 35 pre-specified bacteria and 27 pre-specified antibiotics. Additional variables identified included (1) year of index isolates, (2) laboratory standards employed, (3) specimen site, (4) hospital site, and (5) hospital/laboratory/surveillance body classification. Aggregated antibiotic resistance data for the United States and Canada were compared to existing national and state surveillance estimates for validation purposes. Measures of variability of antibiotic susceptibility were evaluated for the United States and Canada to determine magnitudes of differences within countries.
Results: Over 850 indices of resistance globally were identified and abstracted, with over 5 million total isolates, and from 340 separate locations. Indices spanned 41 countries, 6 continents, 43/50 US states, and 8/10 Canadian provinces. Aggregated resistance values for the United States and Canada for the years 2013 and 2014 showed agreement with reported values ranging from 94-97%. State-specific resistance estimates, for the United States, showed an agreement of 92%. Large differences in antibiotic resistance were seen within countries.
Conclusion: Utilizing non-traditional approaches, we created a web-based platform for aggregating antibiotic resistance indices to support antibiotic resistance surveillance globally. Estimates derived using these techniques generate estimates comparable to traditional surveillance data and may prove useful in under-resourced regions.

16.004 Ecology and environmental drivers of antimicrobial resistance
U. Theuretzbacher
Center for Anti-Infective Agents, Vienna, Austria

Given the multifaceted nature of the resistance problem, the focus of attention has expanded from human and animal antibiotic use to the human influence on resistance in the environment. The link between the animal and human sector are well studied and led to policy changes in some parts of the world. Such regulatory initiatives are still missing in the environmental field which is usually not included in the One Health approach to tackle the global resistance problem.

The direct release of multidrug resistant bacteria from healthcare settings and animal farms into the environment as well as the pollution of the environment with high concentrations of antibiotics create a dangerous resistance reservoir. Recent metagenomics studies highlighted the role of mobile genetic elements (mobilome) as environmental pollutants and their role in co-assembling of resistance determinants and horizontal transfer from environmental bacteria to pathogens and vice-versa. Phages are widely distributed in nature and may act as vehicles for such co-localized resistance cluster genes resistance genes with significant implications for the horizontal spread of antibiotic resistance. They are enriched in microbial genomes or independent of their bacterial host in hospital wastewater systems, animal husbandry and its wastes, aquaculture, and in wastewater treatment plants. This resistance gene pool (environmental resistome) has been described in natural waters, sediments near effluent pipe openings, and in soil especially agricultural farm land due to irrigation with contaminated water. High levels of antibiotic residues in wastewater plants, natural waters but also reclaimed water supply systems due to unregulated pollution from antibiotic manufacturing plants exert unprecedented selection pressure in nature. Addressing this problem requires concerted policy actions and needs to be included in the One Health approach of current global initiatives.

Session 17 (Oral Presentation)

Innovative Approaches to Emerging Disease Surveillance

Monday, November 7, 2016

Room: Klimt 2 & 3

08:30-10:30

17.001 Estimating FluNearYou correlation to CDC's ILINet

R. Arafat[1], E. Bakota[2], E. Santos[2]
[1]Houston Health Department, Houston, Texas, USA, [2]HHD, Houston, USA

Purpose: To provide evidence for the data quality of Flu Near You (FNY) by evaluating the national and Houston datasets against CDC influenza-like illness (ILI) data.
Methods & Materials: Each week, FNY users submit surveys that describe the symptoms experienced for the previous week. The survey tracks if and when a user has received a flu shot and experienced ILI. This study used those survey responses. The data were deidentified and provided by the Skoll Global Threats Fund to the Houston Health Department (HHD). The FNY data were compared to ILINet's national summary of ILI and influenza positive tests by estimating the correlation coefficient for the 2014-2015 influenza season. FNY total ILI counts were correlated to total positive influenza tests, and FNY percent ILI was compared to ILINet's unweighted percent ILI. Mean correlation coefficients for 1,000 bootstraps were estimated for a sequence of weekly user counts of 10 to 10,435 in increments of 10. Bootstrapped samples were stratified by ZIP code to account for fluctuations in weekly participation for both FNY and ILINet, as both datasets see an increase in user participation during influenza season. R version 3.2 was used for all analyses; HHD received the line-list dataset from FNY that contained nearly 400,000 entries. Each entry corresponds to a single person.
Results: •Correlation of the full FNY dataset against ILI & flu tests are very high (r^2 = .94 and .92 respectively).
•Weekly reports from < 200 weekly users have high variance in their correlation to ILINet and a moderate correlation coefficient (r^2 between 0.3 and 0.7).
•At low participation counts, (< 400 per week) FNY correlates better with positive influenza tests than percentage with ILI.
•Overall, FNY data correlates well with national ILINet data, even at limited participation levels.
Conclusion: Approximately two-thirds of the counties within the United States have a population of < 50,000. As such, FNY provides a simple, low-cost opportunity for public health officials within those jurisdictions to obtain data that reasonably mirrors ILINet. For larger

jurisdictions, FNY is another tool available to track and identify seasonal influenza and engage the public on prevention.

17.002 The first phase of PREDICT: Surveillance for emerging infectious zoonotic diseases of wildlife origin (2009-2014)

D. Joly[1], C. Kreuder Johnson[2], T. Goldstein[2], S. J. Anthony[3], W. Karesh[4], P. Daszak[4], N. Wolfe[5], S. Murray[6], J. Mazet[7]
[1]Metabiota, Nanaimo, British Columbia, Canada, [2]University of California - Davis, Davis, CA, USA, [3]Columbia University, New York, NY, USA, [4]EcoHealth Alliance, New York, NY, USA, [5]Global Viral Forecasting Initiative, San Francisco, CA, USA, [6]Smithsonian, Washington, DC, USA, [7]UC Davis, Davis, CA, USA

Purpose: Based on the premise that the majority of emerging infectious zoonotic diseases originate in wildlife species, the United States Agency for International Development created the Emerging Pandemic Threats Program to increase capacity in the developing world to detect and respond to emerging threats. A coalition of organizations led by the University of California at Davis, and including EcoHealth Alliance, Wildlife Conservation Society, Metabiota Inc., and the Smithsonian Institution, implemented the first phase of PREDICT (2009-2014), the component of the program tasked with developing the capacity for early detection of these emerging threats.
Methods & Materials: Based on an iterative process of field and digital data collection and statistical computer modeling, PREDICT identified geographic, taxonomic, and behavioural interfaces likely to lead to disease emergence.
Results: Between 2009 and 2014, over 250,000 samples from over 56,000 animals were collected from wildlife in close proximity to humans (46.6%), free-ranging wildlife and hunted wildlife (31.8%), traded and market wildlife (14.6%), and other sampling sources (7%). Family-level viral screening was conducted using consensus PCR, in 32 laboratories in 20 developing countries around the world. Over 800 hundred novel viruses were found, based on molecular characterisation and on the percentage sequence identity between established species, in addition to over a hundred known viruses.
Conclusion: Implementation of the PREDICT surveillance strategy and prioritization process has improved the capacity in hotspot countries to detect and respond to emerging disease threats.

17.003 Emerging and re-emerging infectious diseases in displaced populations 1998 to 2016: An analysis of ProMED-mail reports

J. W. Ramatowski[1], L. Madoff[1], B. Lassmann[1], N. Marano[2]
[1]International Society for Infectious Diseases, Brookline, MA, USA, [2]CDC, Atlanta, GA, USA

Purpose: Understanding the occurrence of emerging and re-emerging infectious disease outbreaks in displaced populations is important to ensure adequate control measures.
Methods & Materials: The 1994–2015 ProMED-mail record database was queried for records containing the term “refugee,” “asylum seeker,” and “displaced.” For the purpose of this analysis, together these groups are termed displaced populations (DPs). Of the 52,247 records, 600 were returned. Records containing one of the listed terms were then assessed for the following information: reported disease outbreak location, reported disease, origin of DPs, and number of people affected by the outbreak. Unique outbreak events were then identified. One outbreak event possibly contained multiple records. Rates of outbreak events, per total number of ProMED-mail reports each year, were calculated to ensure that any changes, over time, were not simply secondary to changes in the total number of reports posted on ProMED and were compared using a two-sided t-test; $P < 0.05$ was considered statistically significant.
Results: Of 600 records, 118 disease outbreaks spanning years 1998–2015 were identified for use by this review. The mean incidence of reported outbreak events increased across three, 5-year interval periods (Figure 1). Kenya, Uganda, and Sudan had seven or more outbreak events between years 1998-2015. The number of outbreak events in DPs per total ProMED-mail posts between the first and third 5-year interval increased by 277% ($P < 0.01$). In total, >559,000 cases of emerging and re-emerging infectious diseases were reported from the 118 events. Of these, >520,000 cases were related to the cholera outbreak in internally displaced people after the 2010 Haitian earthquake. Additionally, >14,000 vaccine preventable disease cases (measles, chickenpox, polio, and tetanus) and >10,000 Hepatitis E cases were reported. Less common outbreaks included malaria, dengue, hemorrhagic fevers, meningitis, leishmaniasis, louse-borne relapsing fever, anthrax and typhoid fever.

Time Period	Sum of Reports	Average Reports-Per-Year
2010-2015	65	11
2004-2009	33	6
1998-2003	17	3

Conclusion: As the number of displaced people grows, there has been an associated rise in reports related to emerging and re-emerging diseases in DPs. The results of this analysis underscore the importance of adequate infrastructure, human resources, clean water access, and ongoing support needed to prevent, diagnose, and treat infectious diseases in DPs, with particular emphasis in under-resourced countries.

17.004 Digital functions in a participatory One Health surveillance initiative aiming for pandemic averting

P. Susampao[1], K. Chanachai[2], P. Petra[1], T. Yano[3], S. Pattamakaew[3], E. Laiya[3], L. Srikitjakarn[3], A. Crawley[4], J. Olsen[4], M. Smolinski[5]
[1]Opendream Co., Ltd., Bangkok, Thailand, [2]Department Of Livestock Development, Bangkok, Thailand, [3]Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai, Thailand, [4]Skoll Global Threats Fund, San Francisco, USA, [5]Skoll Global Threats Fund, San Francisco, CA, USA

Purpose: A community-based Participatory One Health Disease Detection system (PODD) using smart phone technology was piloted in Chiang Mai, Thailand. Volunteers from 300 villages and 74 community governmental agencies were selected purposively to submit daily surveillance reports of poultry health and disease in their communities The primary objective of PODD in pilot phase was to detect abnormal deaths in backyard animal in order to elicit rapid investigation and response. Abnormal numbers or types of death can be a signal of zoonotic diseases which transmits to human and causes pandemic as a subsequence, such as abnormal death in poultry could be an early clinical sign of highly pathogenic avian influenza (HPAI), a potential precursor of an AI pandemic in humans. Use of smart phones and digital technology is one of the key factors making the PODD system workable.
Methods & Materials: The daily reports of poultry health and abnormal poultry death are automatically captured, filtered with predefined case and outbreak definitions, and projected onto a GIS mapping system. The real time analysis of incoming reports allows rapid detection of outbreaks and the generation of automatic SMS warning messages to activate community contingency plans. A disease investigation team is dispatched to confirm the outbreak by clinical examination and, as necessary, laboratory confirmation. The system follows up automatically until 3 weeks after the last report of sick animals or death in the affected area. All stakeholders are notified after complete recovery to normal.
Results: During the first 16 months of PODD system piloting 25 abnormal death outbreaks were detected. Eight of the outbreaks were laboratory confirmed with devastating epizootic pathogens, while 17 of the outbreaks unable to confirmed the causes. Within eight laboratory confirmed outbreaks, two of which resulted in almost all chickens in the villages dying. The other six outbreaks could be timely and effectively controlled by the communities.
Conclusion: Those early outbreak detection and rapid response demonstrated the potential to integrate this PODD surveillance system under their one health operation centres to prevent pandemic in their community.

17.005 Economics of One Health: Evidence of substantial benefits of integrated West Nile virus surveillance

G. Paternoster[1], S. Babo Martins[2], A. Mattivi[3], R. Cagarelli[3], P. Angelini[3], R. Bellini[4], M. Tamba[1], A. santi[1], J. Rushton[2], K. Stärk[2]
[1]IZSLER, Bologna, Italy, [2]Royal Veterinary College, University of London, London, United Kingdom, [3]Regione Emilia-Romagna, Bologna, Italy, [4]CAA, Crevalcore, Italy

Purpose: Enhanced cross-sectorial collaboration and sharing of surveillance information between the animal and the public health sectors are key to improve the management of zoonotic threats. However, there is little evidence on the costs and benefits of One Health (OH) surveillance for zoonoses. An integrated and multi-disciplinary West Nile virus (WNV) surveillance system (SS) has been implemented in Emilia-Romagna since 2009. The SS includes surveillance activities in the public health and in the animal health sectors. From 2013, surveillance information generated in the two sectors is shared, guiding targeted public health interventions to mitigate the risk of WNV transmission via blood transfusion. The objective of this work was to estimate the cross-sectorial costs and benefits associated with the OH approach to surveillance information of this SS.
Methods & Materials: We applied a conceptual framework to identify the cross-sectorial links between WNV surveillance and triggered interventions, and the associated costs and

benefits. Cost items included costs of human, animal, and entomological surveillance, linking of information, and triggered interventions. Benefits were quantified as the averted costs of potential human cases of West Nile neuroinvasive disease associated to infected blood transfusions. Evaluation of costs and benefits of surveillance designs was conducted considering two scenarios: OH and a uni-sectorial approach that does not integrate animal health information.
Results: The OH scenario was estimated to represent a reduction of 184'619 EUR in the overall costs of surveillance in the 2009-2015 period. The main cost components were blood donation screening activities in both the OH and uni-sectorial scenario. The OH approach allowed savings of 1.24 million EUR in blood donations screening activities. These savings compensated the cost of animal health surveillance and linking of information. Benefits of the OH approach due to avoided short term cost-of-illness and avoided compensation for transfusion-transmitted infections were estimated to be 3.0 million EUR.
Conclusion: Overall, the OH approach to WNV surveillance in Emilia-Romagna region is estimated to be economically beneficial. These results can further contribute to bring evidence on the economic aspects of OH surveillance for zoonoses and contribute for the prioritization of resource allocated to zoonoses mitigation.

17.006 Developing a transdisciplinary database for operationalization of One Health surveillance for Japanese Encephalitis in India

E. T. rogawski[1], **P. Chatterjee**[2], M. Kakkar[3]
[1]University of Virginia, Charlottesville, USA, [2]Public Health Foundation of India, Gurgaon, Haryana, India, [3]Public Health Foundation of India, New Delhi, Delhi, India

Purpose: Vector borne diseases like Japanese Encephalitis (JE) result from the convergence of multiple factors, including, but not limited to, human, animal, environmental, economic and social determinants. To combat these problems, it is essential to have a systematic understanding of drivers and determinants based on a surveillance system that systematically gathers and analyzes data emanating from across multiple disciplines. We developed and deployed a database for collection of transdisciplinary data, obtained both through cross-sectional and longitudinal approaches, across various biotopes, which can function as an affordable surveillance database.
Methods & Materials: A multidisciplinary group of experts, representing epidemiology, human health, veterinary public health, microbiology, GIS, social sciences, and entomology, was assembled to develop a conceptual framework through collaborative iterations. A unique identifier was developed to construct a relational database to organize data from multiple sources, collected in multiple rounds: animal testing, human testing, questionnaire-based surveys, demographic data, GPS data, environmental and metereological data, vector collection and entomological data. The database was developed using Microsoft Access.
Results: The unique ID based system spanned multiple strate; data points could be identified from a macro (state or district) level to a micro (individual) level. The relational database allowed comparisons across and within strate, allowing us to tease out the determinants that had interactions at various levels. Recognition of factors like changing feeding/biting preference of JE vector mosquitoes could be identified only due to the transdisciplinary nature of the relational database. Presence of JEV in both pig-owning and non-pig-owning villages indicated local factors playing at a higher strata. This database allowed us to connect drivers which were previously studied only within their sectoral enquiries.
Conclusion: Developing an affordable, simple, and efficient database that could collate transdisciplinary data, allowed us to not only identify unique insights in JE epidemiology, but also provided us with a template to develop One Health surveillance database for vector borne diseases.

17.007 Analyzing a hepatitis A outbreak by integrating space-time distances and network approach as evidences-based assessment of vaccination policy

M.-H. Lin, W.-C. chen, Y.-L. Liu, H.-W. Kuo, J.-K. Wang, D.-P. Liu
Centers for Disease Control, Taiwan, Taipei, Taiwan, R.O.C.

Purpose: Acute hepatitis A (AHA) is one of notifiable diseases in Taiwan, and a significant decrease in incidence was documented after vaccination to high risk children in 1995. However, a rapid increase in AHA was noted since June 2015 which signaled an outbreak. Hepatitis A Virus (HAV) vaccine has been considered as a main measure for disease prevention. Past researches indicate the effectiveness of vaccine to interrupt an outbreak largely depend on targeting right groups and immunization coverage rate. This study proposes a framework to identify the epidemiological patterns of AHA in order to predict the effectiveness of vaccination on different groups.

Methods & Materials: A total of 128 laboratory-confirmed AHA patients reported to Taiwan Centers for Disease Control in 2015 were investigated and information on sexual risk behaviors, history of sexual transmitted diseases (STDs), and HAV viral sequence were collected. We divided the patients into two groups, case group was defined as patients with identical HAV sequence (n=81) and others were control group (n=47). This study identified clustering patterns by local indicators of spatial autocorrelation. Space-time distances and social network analysis (SNA) were integrated to assess potential effects of vaccination under different scenarios by centrality indices.
Results: In case group, all were male, 51(63.0%) had been infected with HIV, syphilis or gonorrhea, and 33(40.7%) of the cases performed anilingus during communicability period, whereas none of the controls did. Moreover, the cases compared with the controls demonstrated a spatial cluster pattern (Moran's I: 0.39 and 0.14, respectively). By means of SNA, our finding indicated that vaccination to cases with STDs history would not significantly diminish the efficiency of transmission. Only when provided vaccination to all the people at risk and reached at least 20% coverage rates would abate an epidemic of AHA effectively (2% lower compared with no intervention, $p<0.05$).
Conclusion: This study demonstrates a framework not only to recognize the epidemiological patterns but also as an instrument for assessing vaccination policy in hepatitis A outbreak. These results suggest that the effectiveness of interventions integrated with immunization delivery deserved further investigation.

17.008 Emergence and surveillance of hepatitis E in humans, EU/EEA, 2005–2015

C. Adlhoch[1], E. Aspinall[2], J. Takkinen[1]
[1]European Centre for Disease Prevention and Control, Stockholm, Sweden, [2]2 Glasgow Caledonian University, Glasgow, United Kingdom

Purpose: Hepatitis E virus (HEV) is one of the most common causes of acute hepatitis in the EU/EEA. HEV is currently not under EU-wide surveillance and populations under surveillance, case definitions and reporting systems, are set by Member States. The purpose of this study was to obtain a picture of national surveillance systems and numbers of confirmed HEV cases across the EU/EEA.
Methods & Materials: Data on national surveillance systems, case definitions and case numbers were collected through a standardised questionnaire sent to the members of the EU/EEA Food- and Waterborne Diseases and Zoonoses network (FWD-Net) and participants at an HEV expert group meeting.
Results: Data were provided by FWD-Net members and HEV experts from 30 and 16 EU/EEA countries, respectively. Twenty (67%) countries reported having HEV-specific surveillance systems, and nine having syndromic viral hepatitis surveillance systems. Case definitions varied across countries with three having additional case definitions for chronic cases. Laboratory-confirmed cases were reported from 22 countries and showed a nearly 10-fold increase between 2005 and 2015 due to an increase of autochthonous cases. Three Western EU/EEA countries contributed more than 90% of the cases while lower numbers were reported in Northern and Southern European countries. The proportion of cases over 50 years of age increased between 2005 and 2015 from 28% to 61% and the proportion of male cases ranged between 55% and 69% overall. The pooled number of hospitalisations increased from 50 in 2005 to 861 in 2015 in thirteen reporting countries representing up to 69% of the confirmed cases reported overall from those countries. Twenty-six deaths associated with HEV infection were reported from 11 countries during the studied period. Infections were predominantly caused by HEV genotype 3, the most prevalent virus type in the European animal reservoirs.
Conclusion: This is the first overview of surveillance systems and data collected on hepatitis E infections across EU/EEA countries. Systems and case definitions vary and more information on testing practices and circulating virus subtypes is needed to better understand the epidemiology of the disease, especially the reason of the increase of locally acquired cases.

17.009 Validation of EGCRISC for HCV infection screening and risk assessment in the Egyptian population

E. M. El-Ghitany, A. Farghaly, **E. Abd El- Wahab** , S. Farag
High Institute of Public Health - Alexandria University, Alexandria, Egypt

Purpose: Chronic HCV infection, a highly endemic disease in Egypt, is usually asymptomatic for decades after infection. Prediction questionnaire tool was proofed to be a valuable, feasible and efficient instrument for the screening of several diseases. We previously

developed an Egyptian HCV risk screening tool (EGCRISC). This study aims to validate/modify EGCRISC.
Methods & Materials: A cross-sectional study testing 4579 individuals by EGCRISC as well as ELISA/PCR was performed. The sample was a stratified cluster sampling from urban and rural areas in Upper and Lower Egypt using a proportional allocation technique. The degree of agreement and positive and negative posttest probabilities were calculated. ROC curve was done and the cutoff points were customized for best performance. The total score was further classified into three levels according to the risk load.
Results: The mean age of the participants was 41.1±12.2 in whom HCV prevalence was 8.6%. EGCRISC, particularly after modifying the cutoff points, has a good discriminating ability. The degree of agreement was at least 68.1% and the positive posttest probability ranged from 5% to 37.2% whereas the negative posttest probability was in the range 1% to 17%.
Conclusion: EGCRISC is a valid tool that can be used to screen for HCV risk in Egypt and could diminish the need for mass serologic screening in those apparently at low risk. Widespread use of electronic and self- or interviewer-administered risk-based screening strategy may facilitate and increase overall screening and detection of HCV in diverse populations.

17.010 The role of phylogenetic lineage in Escherichia coli O157:H7 risk: Location, location, location

G. A. M. Tarr[1], S. Shringi[2], J. Wakefield[1], A. I. Phipps[1], T. E. Besser[2], P. I. Tarr[3], P. Rabinowitz[1], J. Mayer[1]
[1]University of Washington, Seattle, WA, USA, [2]Washington State University, Pullman, WA, USA, [3]Washington University in St. Louis School of Medicine, St. Louis, MO, USA

Purpose: Shiga toxin-producing *Escherichia coli* (STEC) O157 is an important zoonotic infection commonly transmitted via food, water, and animal contact. Washington State has historically experienced a substantial share of the United States' STEC O157 outbreaks and high incidence of sporadic infections. Some areas of the state appear to be at particularly high risk. Greater understanding of factors responsible for such geographic foci of STEC O157 could allow us to better interrupt transmission and prevent disease. To advance knowledge of the underlying causes of hot spots in Washington State, we assessed the geographic segregation of STEC O157 phylogenetic lineages.
Methods & Materials: We studied 1,160 culture-confirmed STEC O157 cases reported to the Washington State Department of Health, 2005-2014. A single nucleotide polymorphism assay of bacterial isolates was used to assign lineage according to the phylogenetic tree developed by Bono et al. (2012). Case addresses were geocoded to census block groups. The kernel method of Diggle et al. (2005) was used to estimate spatial segregation. A multinomial generalized additive model (GAM) was used to identify specific spatial effects by phylogenetic lineage.
Results: A single lineage, Ib, accounted for 53% of reported cases. Two additional lineages, IIa and IIb, accounted for 41% of cases. Each of these three was analyzed separately; remaining lineages accounting for 6% of cases were grouped as clinically rare lineages. Lineage-specific probabilities calculated through kernel estimation varied across the state, and the test for spatial segregation was statistically significant ($p=0.001$). Greatest overlap of lineages was observed in areas with large livestock populations and in urban areas, and substantial segregation was observed in coastal and mountainous regions. Using the multinomial GAM, we found that the smoothed risk surface of lineage IIb was not uniform across the state ($p<0.001$), with higher incidence in the western parts of the state, as compared to lineage Ib.
Conclusion: Different phylogenetic lineages of STEC O157 dominate in different geographic locations across Washington State. This suggests that STEC O157 lineages are associated with distinct exposures that cluster in particular areas and/or that a lineage becomes established and maintains its population in a local reservoir.

17.011 The efficacy of passive surveillance for HPAI H5N1 in Nigeria: Practices that affect early detection of disease outbreaks in poultry

A. E. Ojimelukwe[1], J. Rushton[2]
[1]University of Port Harcourt, Port Harcourt, Rivers State, Nigeria, [2]Royal Veterinary College, University of London, London, United Kingdom

Purpose: This study identified characteristics of poultry farming with a focus on practices that affect the detection of HPAI; and estimated the system sensitivity of passive surveillance for HPAI H5N1 in commercial and backyard chicken farms in Bayelsa-State, Nigeria.

Methods & Materials: Field studies were carried out in Yenegoa and Ogbia local government areas in Bayelsa state. A total of 26 (13 commercial ad 13 backyard) poultry farmers were surveyed. The sensitivity of passive surveillance for HPAI was assessed using scenario tree modelling. A scenario tree model was developed and applied to estimate the sensitivity, i.e. the probability of detecting one or more infected chicken farms in Bayelsa state at different levels of disease prevalence.
Results: Willingness to report HPAI was highest in commercial poultry farms (13/13) than in Backyard farms (8/13). Poor means of dead bird disposal was common to both commercial and backyard farms. Administering some form of treatment to sick birds without prior consultation with a professional was higher in backyard farms (8/13) than in commercial farms (4/13). Consumption of sick birds was reported in 4/13 backyard farms and sale of dead birds was recorded in one commercial farm. The model showed a median sensitivity of 100%, 67% and 23% for detecting HPAI by passive surveillance at a disease prevalence of 0.1%, a minimum of 10 and 3 infected poultry farms respectively. Passive surveillance system sensitivity at a design prevalence of 10 infected farms is increasable up to 86% when the disease detection in backyard chicken farms is enhanced.
Conclusion: Our estimates of the sensitivity of passive surveillance for HPAI at a design prevalence of 0.1% is high. However the present surveillance system is limited in its ability to detect HPAI at the early stages when one to ten farms are infected. Prohibiting such practices such as treatment of sick birds without prior consultation with a professional and the sale or consumption of sick birds will yield promising results in improving the efficacy of surveillance for infectious poultry diseases in Nigeria.

17.012 Comparing laboratory surveillance with the notifiable disease surveillance system in South Africa

F. G. Benson[1], L. Blumberg[2], L. Rispel[3]
[1]National Department of Health, Johannesburg, South Africa, [2]National Institute of Communicable Diseases, Johannesburg, South Africa, [3]School of Public Health, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg., Johannesburg, South Africa

Purpose: A functioning surveillance system is essential for the successful response to communicable diseases. The purpose of the study was to compare laboratory surveillance with the notifiable disease surveillance system (NDSS) in South Africa, as part of a broader evaluation of the NDSS.
Methods & Materials: A retrospective record review was conducted to analyse the attributes of data quality (percentage completeness of data), stability (reliability of the system in providing a diagnosis), representativeness (percentage of provinces represented in the system), sensitivity (proportion of cases detected by the system) and positive predictive value (PPV - proportion of reported cases that actually have the disease) of the national NDSS. We compared the data from the two systems on three tracer notifiable diseases- measles, meningococcal meningitis and typhoid- for 2013. A record review form extracted information on disease diagnosed or notified and patient demographics. All records with inconclusive diagnostic information were excluded from the study sample. We used the Wilcoxon and the Chi-square tests to compare the systems. All tests were conducted at 5% significance level.
Results: For all three tracers, fewer cases were notified than laboratory confirmed. The median completeness for the laboratory was higher than notified cases for both measles (63% versus 47%, $p<0.001$) and meningococcal meningitis (63% versus 57%, $p<0.001$) but there was no significant difference for typhoid (63% versus 60%, $p=0.0818$). Stability was higher in the laboratory (100% for all three diseases) compared to the notifiable diseases for measles (24%, $p<0.001$), meningitis (74%, $p<0.001$), and typhoid (36%, $p<0.001$). Representativeness was also higher in the laboratory (all 100%) compared to the notifiable cases where we found 67% for measles ($p=0.058$), 56% for meningitis ($p=0.023$), and 44% for typhoid ($p=0.009$). We found the sensitivity of the NDSS to be 38%, 81% and 50% and the PPV to be 4%, 35% and 41% for measles, meningococcal meningitis, and typhoid respectively.
Conclusion: Compared to laboratory surveillance, the NDSS performed poorly on most system attributes. The revitalisation of the NDSS in South Africa should address the completeness of data, as well as the stability, representativeness, sensitivity and PPV of the system.

17.013 Data sharing in public health emergencies

D. Mietchen
National Institutes of Health, Bethesda, MD, USA

Purpose: Public health emergencies caused by emerging diseases pose special challenges in terms of gathering relevant information and making it available to the research and public health communities as well as the public more broadly. In response, a growing number of initiatives are focusing on the role of data sharing under these circumstances.
Methods & Materials: In this contribution, I am reviewing existing efforts around data sharing in recent public health emergencies from around the globe, focusing on cases where emerging diseases played a major role, as in the ongoing Zika virus outbreak.

The underlying project is conducted by way of open notebook science that can be followed and contributed to via https://github.com/Daniel-Mietchen/datascience/blob/master/emergency-response.md .
Results: Data sharing can increase the speed of responses to emerging diseases. It may also affect the quality, the nature or the range of the responses and other variables. Conversely, a lack of adequate data sharing may pose a considerable barrier to effective responses.
Conclusion: Data sharing is becoming an important aspect of responses to public health emergencies, and strategies for communicating outbreaks and emerging diseases are evolving around this notion, complementing traditional means of research and public health communication with faster, more transparent, more collaborative and more responsive channels.

Session 18 (Plenary Session)

Plenary: The Global Virome Project

Monday, November 7, 2016

Room: Park Congress

11:00-11:45

18.001 The global virome project

P. Daszak[1], **D. Carroll**[2], N. Wolfe[3], J. Mazet[4]
[1]EcoHealth Alliance, New York, NY, USA, [2]USAID, Washington, DC, USA, [3]Metabiota, San Francisco, CA, USA, [4]UC Davis, Davis, CA, USA

The frequency of pandemics is increasing, driven by rapid demographic and environmental change and globalized trade and travel. Viruses of animal origin are a particular threat and have caused a series of significant recent outbreaks (e.g. SARS, pandemic influenza, MERS, Ebola and Zika). Recent work suggests only an estimated 1% of viral threats have been identified and fewer have had vaccines or counter measures developed. In the future, we will witness spillover from a pool of more than 500,000 currently unknown viruses into human populations. We need to be better informed about these threats to improve preparedness and reduce response times and associated costs. Here, we discuss the scientific and economic rationale, governance and technical framework for a global initiative to identify and characterize every significant viral threat available for spillover from animal reservoirs. We propose that such a step toward ending the pandemic era is achievable over the next ten years at a cost of less than $3.5 billion, and can be scaled up from current projects in a way that will provide rapid benefits to global health.