Oral Presentations - IMED 2018

Session 03 (Oral Presentations)
One Health – Emerging Threats Across Species Boundaries
Saturday, November 10, 2018
08:30 – 10:30hrs

_____

03.001
The persistent prevalence and evolution of cross-family recombinant coronavirus GCCDC1 among a bat population: a two-year follow-up

J. O. Obameso[1], W. J. Liu[2], G. F. Gao[3]; [1]Federal Polytechnic Ado-Ekiti, Science Technology Department, Akure Ondo State, OVERSEAS/NG, [2]College of Laboratory Medicine and Life Sciences Wenzhou Medical University Wenzhou, China, Key Laboratory of Medical Virology and Viral Diseases, Beijing/CN, [3]Institute of Microbiology, University of Chinese Academy of Sciences Beijing China, CAS Key Laboratory of Pathogenic Microbiology and Immunology, Beijing/CN

Purpose: Coronaviruses are one of the most common viruses discovered in bats, which were considered as the natural source of recent human-susceptible coronaviruses, i.e. SARS-COV and MERS-CoV. Our previous study reported the discovery of a bat-derived putative cross-family recombinant coronavirus with a reovirus gene p10, named as Ro-BatCoV GCCDC1. In this report, through a two-year follow-up of a special bat population in one specific cave of south China, we illustrate that Ro-BatCoV GCCDC1 persistently circulates among bats. Notably, through the longitudinal observation, we identified the dynamic evolution of Ro-BatCoV GCCDC1 in bats represented by continuously recombination events. Our study provides the first glimpse of the virus evolution in one longitudinally observed bat population cohort and underlines the surveillance and pre-warning of potential interspecies transmittable viruses in bats.
Methods & Materials: Sample collection, storage and transportation
Anal swab samples were collected from *Rousettus leschenaulti* (*R. leschenaulti*) bats captured in one cave
located in Xishuangbanna, Yunnan Province, China and transported in viral transport medium (VTM) to the laboratory further analysis.
RNA extraction
Total RNA was extracted using the RNeasy mini kit (Qiagen, Germany) according to the manufacturer's protocol.

Viral detection by nested-PCR
The extracted total RNA was transcribed to cDNA using reverse transcriptase enzyme (Thermo, USA) and then screened for the presence of coronavirus RNA using pancoronavirus RT-PCR degenerate primers.
Virus isolation
RT-PCR positive samples for coronavirus were cultured in five different cell lines, incubated at 37°C in 5% CO_2 and observed daily for viral cytopathic effect.
Results: The results from this study showed a persistent prevalence of Ro-BatCoV GCCDC1 in the bat population. The phylogenetic analysis of the RdRp sequences revealed two groups of Ro-BatCoV GCCDC1 characterized by p10 genes and mutation in the amino acid translation of both Groups. The cross-family recombinant p10 gene stably exists in the novel virus. Notably, we observed the dynamic evolution of this virus in the special bat population.
Conclusion: This study provides beneficial recommendation for the surveillance and pre-warning of potential interspecies transmittable viruses in bats. This study also benefits the understanding of dynamic virus evolution in special bat population and underlines the surveillance of potential interspecies viruses in bats.

03.002

A Mathematical Model of the Transmission of Middle East Respiratory Syndrome Coronavirus in Dromedary Camels (*Camelus dromedarius*).

A. Dighe[1], T. Jombart[1], M. van Kerkhove[2], N. Ferguson[1]; [1]MRC Centre for Outbreak Analysis and Modelling, London/UK, [2]WHO Health Emergencies Programme, Geneva/CH

Purpose: Middle East Respiratory Syndrome Coronavirus (MERS-CoV) remains an emerging disease threat, with regular reports of human cases on the Arabian Peninsula, driven by recurring camel-to-human transmission events. A prophylactic vaccine under development has been found to greatly reduce shedding in dromedaries, but there are major gaps in our quantitative understanding of the epidemiology of MERS-CoV in dromedary populations. The purpose of our work is to develop a mathematical model of MERS-CoV transmission in camels in order to address these gaps and to eventually inform the development of evidence-based animal vaccination strategies.

Methods & Materials: After reviewing publicly available data on camel demography and epidemiology of MERS-CoV in camels, we developed a stochastic, age-structured mathematical model of MERS-CoV transmission in single homogenous camel populations, and between coupled sub-populations.

Results: We show that if immunity is completely protective against future infection, a basic reproduction number (R_0) of 6 reproduces reported patterns of age-stratified seroprevalence observed in camel populations sampled in the Arabian Peninsula and North Africa. If immunity offers only partial protection, we estimate that R_0 is approximately 3. In large modelled populations where transmission persists long-term, epidemics are predicted to have an annual periodicity driven by seasonal births. Allowing reinfection (due to partial immunity) enhances persistence but disease extinction by chance is still expected in well-mixed populations of less than 1000 animals. Hence, we predict that single herds are unlikely to be able to sustain MERS-CoV transmission. Using a meta-population model of multiple coupled small populations, we show that transmission can persist in the population as a whole due to random reintroduction of virus into populations in which transmission has previously ceased via animal movements.

Conclusion: We conclude that the R_0 of MERS-CoV in camels is in the range 3-6, indicating moderate transmissibility. A meta-population model of MERS-CoV transmission reproduces the long-term persistence of MERS-CoV in camel populations in Africa and the Arabian Peninsula and may be useful for simulating camel vaccination strategies.

03.003

Ebola in Animals - Our Knowledge to Date: Assessing Human Exposure Risks

S. von Dobschuetz[1], X. C. R. Roche[2], C. Pittiglio[3], L. Plee[4], S. Shadomy[3], E. Palamara[3], M. Bruni[3], L. Myers[5], E. Bonbon[3], C. Ingabire[3], C. Bebay[6], C. Biaou[7], L. Wiersma[8], A. Saidouni[3], P. Kone[9], M. Ndenge Hello[9], V. Bonkela Isa Nkoy[10], S. Morzaria[3], J. Pinto[11], E. Raizman[12], A. El Idrissi[3], **G. Lamielle**[13], J. Lubroth[11]; [1]Food and Agriculture Organization, Animal Health Service, Rome/IT, [2]Food and Agriculture Organisation , Animal Health, Rome/IT, [3]Food and Agriculture Organisation, Animal Health, Rome/IT, [4]Food and Agriculture Organisation, Animal Health, Jerusalem/IL, [5]Food and Agriculture Organization of the United Nations, Crisis Management Centre – Animal Health (CMC-AH), Rome/IT, [6]FAO Emergency Centre for Transboundary Diseases for West and central Africa, , Bamako/ML, [7]Food and Agriculture Organisation, Animal Health, Libreville/GA, [8]EMPRES – UN FAO, Rome/IT, [9]Food and Agriculture Organisation, Animal Health, Abidjan/CI, [10]Food and Agriculture Organisation, Animal Health, Kinshasa/CD, [11]FAO, Rome/IT, [12]Food and Agriculture Organization of the United Nation , Animal Health Serivce, Rome/IT, [13]County of Los Angeles, Department of Public Health, Veterinary Public Health, Los Angeles, CA/US

Purpose: Many unknowns remain concerning the role of animal species in the epidemiology of ebolavirus (EBOV) and transmission risk to humans. The 2018 Ebola outbreak led the Food and Agriculture Organization of the United Nations (FAO) to update its qualitative risk assessment on EBOV release from animals or their products and human exposure.

Methods & Materials: A literature review identified recent publications (since January 2015, when FAO's last EBOV risk assessment was published). International scientists provided information from ongoing research, both laboratory and field studies. FAO colleagues from affected and at risk countries contributed field knowledge. Utilizing the information collected from various sources, the likelihood for human exposure to EBOV was assessed considering close contact, handling and consumption of (i) wild animal species or (ii) domestic animal species in areas where EBOV is present, as well as (iii) the likelihood of EBOV introduction into non-infected countries through trade, handling or consumption of meat from susceptible wild animals originating from affected areas.

Results: The likelihood for human exposure from susceptible wild animals, such as fruit bats, non-human primates and duikers, in areas where EBOV is present was assessed as low. For domestic animals in these areas, such as pigs and dogs, the likelihood was assessed as very low. The likelihood of EBOV introduction into non-infected countries through trade, handling and consumption of wild meat was also assessed as very low. Given limited availability of surveillance or field study data, the level of uncertainty in the assessment remains high.

Conclusion: Investigations of historic human outbreaks suggest that EBOV is initially introduced into human populations through contact with infected wild mammals or their meat. However, in line with the assessed low likelihood, this is considered a rare event. The public health impact of spillover, when occurring, is however devastating due to the huge consequences that human outbreaks entail. The risk assessment helped consolidating current knowledge on EBOV in animals and highlighted outstanding knowledge gaps, including EBOV survival in the environment, susceptibility of animal species in field settings, and information on wild meat trade movements.

03.004
Ebola West Africa, 2014-16: An Analysis Of A Filovirus Outbreak

A. Duse; NHLS & University of Witwatersrand, School of Pathology, Johannesburg/ZA

Purpose: Zoonotic infections are those that can be transmitted between animals and humans. Approximately two-thirds of human infections are zoonoses and caused by microorganisms as diverse as viruses, bacteria, fungi and parasites. Many of the pathogens causing zoonoses are considered to be either emerging or novel agents. Health of humans is inextricably linked to the health of animals and the environment. More broadly, the environment not only encompasses physical, geographical, climatic, ecological, agricultural and veterinary dimensions, but also the social, cultural, political and religious factors that influence those human behaviors that shape it.

Addressing the connections between health and the environment requires an urgent expansion of interdisciplinary collaborations and strong political and global will.Viral hemorrhagic fever agents pose serious challenges to human health due to the fact that: (i) Filovirus outbreaks are largely created by man and driven by human behavior, (ii) there is significant nosocomial (hospital) amplification of disease, (iii) there is an associated high morbidity and mortality, (iv) case management is difficult and, as yet, there are no *commercially*available vaccines and therapeutic agents, (v) prevention of infections is fraught with difficulties, and (vi) infection prevention and control strategies can be frustratingly unsuccessful.
Methods & Materials: Case study approach.
Results: The presentation focuses on the complexity of the 2014-16 West African Ebola outbreak in which there has been multi-country involvement (Guinea, Liberia and Sierra Leone) and is deemed to be the largest Ebola outbreak ever described. Challenges and controversies related to VHF outbreak responses, international health regulations, environmental and sociocultural factors, as well as lapses in infection prevention and control interventions are contextualized. Current knowledge gaps, and future research areas, are highlighted.
Conclusion: The viral hemorrhagic fevers (VHFs) of Africa, and more specifically, filoviral infections provide the perfect illustration of the interconnected nature of man, microbe and the environment. With the increasing frequency of filovirus outbreak reports and the threat that filoviruses pose to local, national and global health, knowledge gaps need to be urgently addressed with high quality interdisciplinary research. For this, the One Heath approach provides the perfect platform

03.005

The Detection of Diverse Coronaviruses, Including MERS-Related Coronaviruses, In South African Bat Populations And Their Associated Ecology in *Neoromica capensis*

N. Cronjé[1], N. L. Ithete[1], M. C. Schoeman[2], W. Preiser[3]; [1]Stellenbosch University, Medical Virology(Department of Pathology), Cape Town/ZA, [2]University of KwaZulu Natal, School of Life Sciences, Durban/ZA, [3]Stellenbosch University & National Health Laboratory Service Tygerberg, Medical Virology(Department of Pathology), Cape Town/ZA

Purpose: Coronaviruses are RNA viruses encompassing four genera. The alpha- and betacoronaviruses commonly cause mild disease in humans. However, outbreaks of severe respiratory disease in 2002 and 2012 led to the identification of highly pathogenic human betacoronaviruses, SARS- and MERS-CoV, respectively. Bats are believed to be the reservoir host from which all mammalian coronaviruses emerged.

Few studies have been published on South African bat coronaviruses; only 16 bat alphacoronavirus and two betacoronavirus sequences have been reported. Phylogenetic inference shows that the betacoronavirus sequences belong to the same viral species as MERS-CoV. Through a One Health approach, this study aimed to describe coronavirus diversity within South African bat populations as well as factors that might influence bat-coronavirus ecology.

Methods & Materials: During a general surveillance effort, 404 bat faecal pellets were screened using PCR assays targeting conserved regions of the coronavirus genome. An additional 183 faecal pellets, collected from *Neoromicia capensis* bats, were screened as part of a species-specific surveillance study. Using mixed effects logistic regression analyses, collected ecological sampling data were collated with screening results to identify possible predictors of coronavirus infection in *N. capensis* bats.

Results: Based on putative coronavirus species classification criteria, the general surveillance effort detected nine coronavirus species, eight alphacoronaviruses and one MERS-related betacoronavirus, from eight different bat species.

The species-specific surveillance detected three coronavirus species, including MERS-related betacoronaviruses, and identified several instances of coinfection with two different coronaviruses. The mixed effects logistic regression analyses indicated that female *N. capensis* bats and bats trapped at low altitude sites with low body condition scores were most likely to be coronavirus positive.

Conclusion: This study demonstrates that diverse coronaviruses are present in different South African bat species and lends additional support to an ongoing circulation of MERS-related betacoronaviruses in this region. The observed cases of coinfection indicate the potential for recombination that could lead to the emergence of a new coronavirus that might have zoonotic potential. The collation of ecological data with screening results revealed that both host and environmental factors may influence coronavirus ecology. These findings could assist the development of improved wildlife surveillance sampling strategies for better detection of novel bat coronaviruses.

03.006

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, Animal and Environmental Biology, Port Harcourt, RIVERS STATE/NG, [2]Royal Veterinary College, University of London, Production and Population Health, London/UK

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.

03.007

Long-term Wildlife and Human Disease Surveillance in Northern Congo: A Model for the Detection of Ebola Virus Disease Epizootics

E. Kuisma[1], S. Olson[2], P. Reed[3], A. Ondzie[4], V. Munster[5], C. Goma Nkoua[6], H.-J. Parra[7], W. Karesh[8], J.-V. Mombouli[7]; [1]Wildlife Conservation Society, Wildlife Health Programme, Brazzaville/CG, [2]Wildlife Conservation Society, Wildlife Health Program, Ney York/US, [3]Field Veterinarian, Cape Town/ZA, [4]Wildlife Conservation Society Congo, Brazzaville/CG, [5]Rocky Mountain Laboratories NIAID, Laboratory of Virology, Hamilton, MT/US, [6]Laboratoire National de Santé Publique , Service d'Epidémiologie Moléculaire, Brazzaville/CG, [7]Laboratoire National de Santé Publique, Brazzaville/CG, [8]EcoHealth Alliance, New York, NY/US

Purpose: We examine if local communities reporting great ape and other mammal carcasses are able to act as an effective wildlife mortality surveillance network for Ebola virus disease (EVD) with wide-coverage and low financial commitment.

Methods & Materials: Partnering with the Congolese Ministry of Health (MoH), the Wildlife Conservation Society (WCS) conducted wildlife mortality surveillance and community outreach campaigns in the Cuvette and Sangha regions of the Republic of Congo (RoC). As several recorded EVD epidemics have been preceded by epizootics and physical contact with wildlife carcasses, residents in the rural communities are visited by members of the WCS Wildlife Health Program for educational campaigns. The team meets with the community and provides information on the dangers of EVD and other zoonotic diseases, including how to reduce the risk of human exposure by changing behaviour. Advice includes avoiding contact with carcasses and building awareness of the best practice in the case of illness. The hunters and women foraging in the forest are then encouraged to report observations of carcasses to a hotline and posters are affixed to prominent locations in the village. Carcass notifications trigger a follow-up visit to reinforce the initial messaging, sampling, testing, and a return visit to relay the test results.

Results: Since 2006, our network engaged over **5,800** hunters in more than **290** villages, effectively covering more than **140,000 km^2** of landscape within Ebola endemic areas and high levels of human-wildlife cohabitation. To date, the network has safely sampled carcasses from 41 gorillas, 10 chimpanzees, and 6 mortalities of other species. In total, **16** national and international field staff have been trained in safe carcass sampling methods.

Conclusion: This decade-long disease surveillance effort continues to function as an early but untested warning system for epizootics and zoonotic spillover. The last positive detection of Ebola virus in RoC was June 2003. Surveillance of wildlife mortality, coupled with community education are fundamental tools that public health agencies can use to protect against future outbreaks.

03.008

Review of brucellosis in Albania: disease frequency in humans and animals, and one health efforts to control the disease, 1925 to present.

K. Mersini[1], L. Alla[2], A. Juma[3], X. Koleci[4], J. Crilly[3], S. Bino[5]; [1]South East European Centre for Disease Surveillance and Control, Tirana/AL, [2]Institute of Public Health, Surveillance and Control of Infectious Diseases, Tirana/AL, [3]Food Safety and Veterinary Institute, National Veterinary Epidemiology Unit,, Tirana/AL, [4]Agricultural University of Tirana, Faculty of Veterinary Medicine, Tirana/AL, [5]Institute of Public Health, Tirane/AL

Purpose: The aim of the current review is to provide frequency estimates and spatial distribution of brucellosis in humans and animals over a century.

Methods & Materials: Descriptive epidemiology of brucellosis in humans and animals is elucidated by a combined approach utilizing official data and literature review. Official data on disease occurrence from 1990 to present were collected from the Institute of Public Health and Food Safety and Veterinary Institute. A total of 77 national publications on brucellosis from 1938 to 2016 were reviewed and data were extracted.

Results: Results are divided in different time periods according to disease patterns and control measures applied on animal populations. The first period 1925 – 1960 was marked by a rapid increase of cases both in humans and animals. The prevalence in small ruminants was 4% - 8% and 0.2% - 9% in cattle, meanwhile average annual incidence in humans was 23 cases per 100.000. During the next period 1960 – 1990, the disease was almost eradicated due to intensive test and slaughter and massive vaccination of animals. As a result the prevalence in small ruminants in 1989 has fallen to 0.02% and 0.001% in small ruminants and cattle respectively. During the 80s only sporadic cases were recorded in humans. In the third period 1991 - 2004 a comeback of brucellosis has been documented with similar trend like in the 60s. Interestingly the number of cases in 2004 was 1.139 which is almost the double of 614 cases in 1960, however the incidence was identical with 37 cases per 100.000 pop which is explained by rapid demographic changes that occurred in the country. The fourth period 2005 -2015 is characterized by a rapid decline with 5 cases per 100.000 pop in humans. The fall of the disease presumably has occurred also in animal species but due to veterinary interventions with mass vaccinations the data are not reliable.

Conclusion: As shown by historical disease patterns the current risk for re-emergence of brucellosis is evident especially when veterinary activities are relaxed as a result of a false safety related to low rates of the disease.

03.009

"One Health" approach community of practice advocacy for Lassa fever outbreak and other emerging
pandemics public health emergencies surveillance and response in Africa

E. Tambo[1], O. A. Olalubi[2], X.-N. Zhou[3]; [1]Africa disease Intelligence and Response Institute,&
Universite des Mntagnes, Communication Unit, Yaounde, CENTRE/CM, [2]Kwara State University,
School of Public Health, Malete/NG, [3]National Institute of Parasitic Diseases, Chinese Center for
Disease Control and Prevention, WHO Collaborating Centre for Tropical Diseases, Shanghai , Global
Health Department, Shanghai/CN

Purpose: Recent Lassa fever outbreaks in almost 20 states in Nigeria led to 101 deaths and 175
suspected and confirmed cases since August 2015. Of the 75 laboratory confirmed cases, 90 deaths
occurred representing 120% laboratory-confirmed case fatality. It is shown that Lassa fever peak
endemicity incidence and prevalence overlap the dry season (within January to March) and reduced
during the wet season (May - November) annually in Sierra Leone, Senegal to Nigeria.
Methods & Materials: We assessed retrospectively Lassa fever outbreaks and other emerging
pandemics public health emergencies surveillance and response knowledge gaps and challenges in
promoting 'One Health community of practice advocacy implementation in Africa.
Results: One Health community of practice advocacy is essential in building and strengthening
effective and resilience of the affected community and its leadership in transforming its cultural and
socio-behavioural values to asset in increased community engagement and participation of all the
local stakeholders, e.g. department of health or government , laboratories, clinicians (doctors/nurses),
traditional and faith-based community leaders. This is essential in implementing improved community-
based programs to boosting knowledge and awareness outreach through secured SMS and social
media platform, understanding the importance of clear risk communication and resilience during
outbreaks/pandemics threats using contextually appropriate modes and methods, can help to correct
misunderstandings, myths/rumours, stigma and panic. Moreover, real time, trusted and timely
information sharing with adequate preparedness capacity integration is critical for community-
informed decision making in boosting community resource mobilization, scaling p access and uptake
of affordable for prevention and control interventions needs implementation, monitoring and
effectiveness in affected settings. Moreover, strengthening community's role in Lassa fever outbreak
and other emerging pandemics public health emergencies surveillance and response including health
risk factors education and contact tracing, sanitation and hygiene best practices and management as
well as accurate updates and feedback from the affected communities on the situation for planning
purposes and travel medicine is core.
Conclusion: The value of "One Health" approach community of practice advocacy and integration is
crucial in Lassa fever outbreaks and other emerging pandemics public health emergencies
prevention, preparedness and rapid response strategies, but also community participation and
programs ownership for sustainability are discussed.

03.010

Ten Outbreaks of Rift Valley Fever in Uganda 2016-2018:   Epidemiological and Laboratory Findings

L. Nyakarahuka[1], S. Balinandi[1], S. Mulei[1], J. Kyondo[1], A. Tumusiime[1], J. Klena[2], J. J. Lutwama[1], T. Shoemaker[2]; [1]Uganda Virus Research Institute, Arbovirology, Emerging and Re-emerging Diseases, Entebbe/UG, [2]US Centres for Disease Control and Prevention, Viral Special Pathogens , Atlanta/US

Purpose: After 50 years without an outbreak of Rift Valley Fever (RVF), Uganda has reported 10 sporadic outbreaks in the last 3 years. We investigated each of these outbreaks to establish the epidemiology of RVF and institute control and prevention measures.

Methods & Materials: Uganda established a Viral Haemorrhagic Fever (VHF) surveillance program since 2010 whereby VHF-suspected human and animal samples are submitted to the laboratory at Uganda Virus Research Institute (UVRI). At UVRI, samples are tested by both PCR and ELISA and results are sent to the National Taskforce for outbreak response. Working with National and District task forces, staff from the VHF surveillance program deploys to the outbreak areas and performs enhanced surveillance including the collection of both human and animal samples, entomological studies, health education and institution of control and prevention measures. Virus isolation and genomic sequencing are performed at the High Containment Laboratory of CDC's Viral Special Pathogens Branch, Atlanta, GA, USA.

Results: Since March 2016 to June 2018, 10 independent outbreaks of RVF have been detected in Uganda. The outbreaks occurred in 10 districts and involved 16 human cases of whom 7 died (CFR= 44%). From investigations conducted in Kabale district following RVF outbreak in 2016, cattle, goats, and sheep had a seroprevalence of 27% (86/324), 7% (40/569) and 4% (7/158), respectively. Of the 655 human blood samples that were collected, anti-RVFV IgG was detected in 78 (12%) human samples. Seropositivity for RVF was greater in participants who were butchers (OR =5.1; 95% CI 1.7-15.1) and those who reported handling raw meat (OR 3.4; 95% CI 1.2-9.8). Some mosquitoes collected during the investigations were RT-PCR positive for RVF. The RVF virus circulating in Uganda is similar to that of the East Africa 2006-2007 Kenya-2 outbreak lineage.

Conclusion: Rapid case detection, prompt laboratory testing at UVRI and presence of pre-trained, well-prepared National and District rapid response teams facilitated rapid containment and control of these outbreaks. These findings also indicate possible endemicity or re-emergence of RVF virus across many parts of Uganda.

03.011

The Discovery Of A New Ebolavirus, Bombali Virus, Adds Further Support For Bats As Hosts Of Ebolaviruses

T. Goldstein[1], S. J. Anthony[2], A. Gbakima[3], B. Bird[1], J. Bangura[4], A. Tremeau-Bravard[1], M. Belaganahalli[1], H. Wells[2], J. Dhanota[5], E. Liang[2], M. Grodus[2], R. Jangra[6], V. Dejesus[6], G. Lasso[7], B. Smith[5], A. Jambai[8], B. Kamara[8], S. Kamara[9], W. Bangura[10], C. Monagin[5], S. Shapira[7], C. Kreuder Johnson[1], K. Saylors[11], E. Rubin[11], K. Chandran[6], W. I. Lipkin[12], J. Mazet[13]; [1]University of California - Davis, Davis, CA/US, [2]Columbia University, Center for Infection and Immunity, MSPH, New York, NY/US, [3]Ministry of Education, Freetown/SL, [4]UC Davis, Freetown/SL, [5]University of California, Davis, Davis/US, [6]Albert Einstein College of Medicine, New York/US, [7]Columbia University, New York/US, [8]Ministry of Health and Sanitation, Freetown/SL, [9]Ministry of Agriculture, Forestry and Food Security, Livestock and Veterinary Services Division, Freetown/SL, [10]Ministry of Agriculture, Forestry and Food Security, Forestry and Wildlife Division, Freetown/SL, [11]Metabiota, San Francisco, CA/US, [12]Columbia University Mailman School of Public Health, Center for Infection and Immunity, New York, NY/US, [13]UC Davis, Davis, CA/US

Purpose: Despite more than 40 years of research and continued outbreaks, the reservoirs of ebolaviruses remain unknown and outbreaks continue to occur. We initiated a survey in Sierra Leone to identify hosts of Ebola virus (EBOV; species *Zaire ebolavirus*) and to identify any additional filoviruses that might be circulating in wildlife.

Methods & Materials: Oral, rectal, and/or blood samples were collected from 535 animals, including 244 bats, 46 rodents, 240 dogs, and 5 cats (total = 1278 samples). Consensus PCR (cPCR) targeting all filoviruses was used to screen for EBOV and any novel filoviruses. Samples positive by cPCR were sequenced by high-throughput sequencing and genome walking to recover the complete viral genome sequence. In vitro experiments using vesicular stomatitis virus (rVSV) encoding ebolavirus glycoproteins (GP) were used to evaluate viral ability to mediate entry into human cells.

Results: Of the 1278 samples, 3 oral and 3 rectal swabs were positive by cPCR for a novel ebolavirus. The six positive samples were from five free-tailed bats belonging to two species (*Chaerephon pumilus* and *Mops condylurus*), both living in close proximity to humans. Phylogenetic analyses showed that the virus is sufficiently distinct to represent the prototypic strain of a new species within the *Ebolavirus* genus; and has been named Bombali virus (BOMV; species *Bombali ebolavirus*). We did not detect EBOV in any of the samples. Using a rVSV system encoding the BOMV *GP* gene, we showed that the rVSV- BOMV GP was infectious in human osteosarcoma (U2OS) cells demonstrating that the BOMV $GP_{1,2}$ is fully competent to mediate viral entry.

Conclusion: This is the first full genome of an ebolavirus to be recovered from a bat, providing strong evidence that bats are a natural reservoir of these viruses. The BOMV surface GP was able to mediate entry into human cells via interaction with the Niemann-Pick C1 (NPC1) receptor, suggesting the virus has zoonotic potential. The bats were also found roosting inside houses, indicating the potential for human transmission. However, further studies are required to investigate whether exposure has actually occurred or if BOMV is pathogenic in humans.

03.012

Serological evidence of exposure to filoviruses and henipaviruses in wildlife, Malaysia

E. D. Laing[1], T. Hughes[2], M. H. Lee[2], F. T. Sitam[3], M. L. Abdullah[3], M. Gani[3], J. Lee[2], J. J. Rovie-Ryan[3], C. Broder[4], J. Epstein[5]; [1]Uniformed Services University, Microbiology, Bethesda, MD/US, [2]EcoHealth Alliance, Kuala Lumpur/MY, [3]Department of Wildlife and National Parks, Kuala Lumpur/MY, [4]Uniformed Services University, Microbiology, Bethesda/US, [5]EcoHealth Alliance, New York/US

Purpose: PCR and serological-based approaches have been used to identify henipavirus and filovirus (e.g. Nipah virus, Ebola virus) exposure or infection in bat populations in Bangladesh, China, and Southeast Asia. Our understanding of the diversity of these viruses in bat reservoirs, and the frequency of spillover to other animals or people, is extremely limited. We hypothesized that henipaviruses and filoviruses were circulating within multiple bat reservoirs and that spillover of these viruses to non-human primate populations has occurred in Malaysia.

Methods & Materials: We utilized a multiplex serological assay to screen sera for reactive IgGs that bound to antigens from henipaviruses and filoviruses. We produced virus attachment glycoproteins (GP) from sixteen virus species in the families Paramyxoviridae and Filoviridae. As part of our ongoing collaboration, we conducted in-country assay training and sera testing at the Department of Wildlife and National Parks, National Wildlife Forensic Laboratory. We screened sera from eight bat genera and sera from *Macaca fascicularis* populations.

Results: Sera samples from *Pteropus hypomelanus* (n=56) were reactive with Nipah virus GP (25%) and cross-reactive with GPs from closely-related henipaviruses. In these same *P. hypomelanus* samples we detected reactivity with Ebola virus and Sudan virus GPs (10% and 5%, respectively). Sera from several *Hipposideros* species and *P. hypomelaus* reacted with the *Henipavirus* species, Mojiang virus GP. Two *M. fascicularis* sera samples reacted with GPs from Ebola virus and Bundibugyo virus and *M. fascicularis* sera samples specifically reacted with Mojiang virus; all four samples exhibited median fluorescence intensity values > 10,000. We also detected reactivity to Ebola virus and Sudan virus GPs in sera samples collected from *Hipposideros*, *Cynopterus* and *Rhinolophus* species. We did not detect any samples that were reactive with Reston virus GPs.

Conclusion: We detected evidence of past exposure to virus(es) most antigenically-similar to Ebola virus, Bundibugyo virus, and Sudan virus in sera samples from bat and non-human primate populations collected in Malaysia. This is also the first sero-survey for Mojiang virus and the first evidence of exposure to Mojiang virus in bats and non-human primates. Our results suggest that there are different but antigenically related henipaviruses and filoviruses circulating in bats in Malaysia.

03.013

Zoonoses In The Bolivian Amazon: Alarming Initial Results From An NGO-led One Health Initiative

E. Alandia Robles[1], E. Martinez[2], D. Arteaga Voigt[3], P. Durán[2], T. Hald[4], E. Quispe[5], C. Salazar[6], A. Salas[6], L. R. Nielsen[7]; [1]Fundacion Teko Kavi, La Paz, La Paz, LP/BO, [2]Facultad de Medicina, Universidad Mayor de San Andrés, Instituto de Investigación en Salud y Desarrollo - IINSAD, La Paz/BO, [3] Instituto de Investigaciones Técnico Científicas de la Universidad Policial - IITCUP, Centro de Investigación Genética, La Paz/BO, [4]Technical University of Denmark, National Food Institute, Copenhagen/DK, [5]Servicio Nacional de Sanidad Agropecuaria e Inocuidad Alimentaria - SENASAG, Unidad de Sanidad Animal, La Paz/BO, [6]Servicio Departamental de Salud de La Paz - SEDES La Paz, Unidad de Epidemiología e Investigación, La Paz/BO, [7]University of Copenhagen, Department of Veterinary and Animal Sciences, Copenhagen/DK

Purpose: Building on prior surveillance experiences from the Bolivian Amazon region, a new initiative aims to improve the livelihood of rural communities by detecting, preventing and combating zoonotic diseases.

Methods & Materials: A new organisational approach has been chosen to develop sustainable health solutions for humans, domestic animals, wildlife and local ecosystems in remote indigenous communities with limited access to health services and whose territory is being affected by anthropogenic changes. The initiative is built on three pillars: research, capacity building and citizen engagement and is led by a local non-profit organisation, Teko Kavi, who works closely with Bolivian regional health and veterinary authorities, laboratories and universities as well as local indigenous community organisations, health centres and schools to improve awareness raising and building of networks and the much needed new capacities. The project is funded by a Danish social capacity building fund, and a Danish NGO-collaboration partner of Teko Kavi and two Danish universities provide One Health and capacity building expertise.

Samples were collected in 2018 from 76 humans and 84 domestic animals in addition to environmental and wildlife samples in two Tacana Indigenous Territory villages in the San Buenaventura municipality located in the Amazon region of La Paz Department, Bolivia. Also, health information was collected for data analysis by face-to-face interviews of the tested people and owners of the tested animals.

Results: The results are alarming: a high proportion of participating humans in the two villages were ill with fever, muscle pain, nausea and fatigue among other symptoms on or shortly prior to the day of sampling. Moreover, a high proportion (27%) of human serum samples were found to contain IgM antibodies directed against *Leptospira spp.*, indicative of acute infection, while 63.6% of PCR-tests of urine samples from humans and 50% from animals were Leptospira-positive. Besides this hitherto unreported disease in the area, other important zoonotic pathogens were also detected in the samples, including Hantavirus and *Aerococcus viridans*.

Conclusion: Information meetings have been held in the local communities as well as between the health institutions and workers, and a participatory integrated health intervention strategy is being discussed between partners in the initiative.

03.014
Hendra Virus in The Field – Risk Profiling And Management

N. Y.-H. Kung; Biosecurity Queensland, Department of Agriculture and Fisheries, Brisbane, QLD/AU

Purpose: Hendra virus is a zoonotic pathogen which was first identified in 1994 and spillover events in horses were sporadic in Queensland (QLD) and New South Wales (NSW), Australia until 2010. The predominant differences during 2011-2017 were the number of spillover events (46 incidents during 2011-2017 compared to 14 incidents during 1994-2010), the unprecedented number of incidents in NSW (19 incidents during 2011-2017 compared to one incident during 1994-2010) and the geographic clustering in southeast QLD and northern NSW (30 incidents in southeast QLD and north NSW compared to 16 incidents in central and northern QLD during 2011-2017). Detailed epidemiological investigations on infected property (IP) were conducted on all Hendra virus infected horse properties during 2011-2017 to find any risk factors related to these spillover events and better management recommendations for risk mitigation.
Methods & Materials: Profiling activities involved case history reviews, property visits and interviews with the horse and/or property owners focusing on the infected horse(s) (health, behaviour), husbandry (supplementary feeding, water), property (pasture condition, paddock/yard/stable), vegetation (location and stage of fruiting/flowering trees/shrubs), flying-fox activities (as evidenced by the presence of spats, faeces, partly-eaten fruit/flowers/seeds and/or infra-red/thermal camera photographs) and potential flying-fox - horse interaction site(s).
Results: Findings from IP profiling showed that all infected horses were paddock horses and that flying-fox activities were identified on most infected properties even when the owners reported no flying-fox sightings. Infected property profiling findings also indicated the management of the horses (locations of water/feed troughs, night yarding under flowering/fruiting trees) and horse behaviour may play a role in the Hendra virus transmission through the flying-fox - horse interaction.
Conclusion: Profiling findings have identified several high risk factors related to the horse and human behaviours. Horse personality such as dominance and inquisitiveness could have brought the horses closer to the environment with flying –fox foraging activities. Several human behaviours in related to the decision of horse husbandry could have also placed the horses under higher risk due to indirectly interaction with flying-fox activities. This results have reinforced Queensland government's recommendations to the horse owners on Hendra virus risk management and risk mitigation for animal and human health.

_____

08.001

One-Shot Immunization Using a Measles/Lassa Vaccine Fully Protects Cynomolgus Monkeys Against Lassa Fever

M. Mateo[1], S. Reynard[1], N. Baillet[1], X. Carnec[1], A. Fizet[1], M. Jourdain[1], C. Picard[1], J. Schaeffer[1], L. Barrot[2], S. Barron[2], A. Vallve[2], H. Raoul[2], C. Carbonnelle[2], F. Tangy[3], **S. Baize**[4]; [1]Institut Pasteur, UBIVE, Lyon/FR, [2]INSERM, US003, Lyon/FR, [3]Institut Pasteur, UGVV, Paris/FR, [4]Institut Pasteur, Lyon/FR

Purpose: Lassa fever is a major public health issue in Western Africa and there is still no licensed vaccine. Here we have used the Measles virus (MeV) vaccine platform to generate Lassa fever vaccine candidates expressing the Lassa virus (LASV) glycoprotein GPC alone or in combination with the nucleoprotein NP or the matrix protein Z. We have demonstrated that NP should be mutated to preserve a strong induction of the type I IFN response and activation of human antigen presenting cells in response to the vector. We selected two vaccines, MeV-NPmut/GPC and MeV-Z/GPC, for further testing in non-human primates

Methods & Materials: Cynomolgus monkeys were immunized with a single dose of MeV-NPmut/GPC, MeV-Z/GPC, or empty MeV vector as a control, one month before being challenged with a lethal dose of LASV. Animals were monitored for biological, clinical, virological, and immunological paramaters after immunization and challenge

Results: The two vectors were safe, did neither replicate in nor shed from vaccinees, and protected all cynomolgus monkeys while controls all died from Lassa fever. Interestingly, MeV-NPmut/GPC conferred almost a sterilizing immunity and animals only experienced a transient elevation in the body temperature but no biological alterations or clinical signs. On the contrary, MeV-Z/GPC –immunized monkeys developed more severe symptoms and a prolonged LASV viremia. Analysis of the immune responses showed that early and robust T cell responses against GPC are critical for enhanced protection after challenge and suggests that T cell immunity against NP may greatly enhance protection. Early transcriptomic and proteomic studies have also been performed after immunization to identify early biological markers correlated with vaccine efficiency. MeV-based vaccines induce a strong humoral response against MeV and could thus be used as bivalent vaccines to prevent Lassa fever and Measles in endemic areas where both MeV and LASV are circulating

Conclusion: The MeV-NPmut/GPC vaccine is safe, fully protects after a single shot cynomolgus monkeys against a lethal LASV challenge and could be used as a bivalent Measles-Lassa vaccine. Importantly, Themis Biosciences has been selected by the Coalition for Epidemic Preparedness Innovations (CEPI) to further develop the MeV-NPmut/GPC vaccine and test it in phase I and II clinical trials

08.002

Use of Pseudotyped Viruses for the Production of Reference Materials as part of Emerging Viral Outbreak Preparedness

E. Bentley[1], E. Wright[2], M. Hassall[3], S. Myhill[3], P. Rigsby[3], D. Wilkinson[3], L. Stone[3], M. Page[4], G. Mattiuzzo[4]; [1]NIBSC, Division of Virology, Potters Bar, HERTFORDSHIRE/UK, [2]University of Sussex, Brighton/UK, [3]NIBSC, Potters Bar/UK, [4]National Institute for Biological Standards and Control (NIBSC), Potters Bar/UK

Purpose: The recent public health emergencies of international concern (PHEIC), caused by Ebola and Zika virus, have highlighted the lack of prophylactic treatments and need for effective diagnostics for emerging viruses. In response to this, we established International Reference Reagents for antibody detection, which enables the comparison of results from laboratories worldwide undertaking treatment/vaccine efficacy clinical trials. The requirement for high containment facilities to handle viruses with outbreak potential, such as BSL4 for Ebola virus, is a constraining challenge. We have developed serological assays using replication defective pseudotyped viruses (PV) for the evaluation of reference material to avert high containment requirements.

Methods & Materials: The preferred candidate material is a pool of plasma or sera from convalescent patients as this provides a commutable standard. For the reference material for Ebola antibody, several donations were received at NIBSC and solvent-detergent treated to ensure inactivation of virus. Characterisation is performed in-house using both PV neutralisation assays and ELISA platforms. PV is produced via plasmid transfection of 293T cells, with plasmids encoding a lentiviral core component, a reporter gene which is packaged within the core and the sequence of the envelope protein for the virus of interest. The ability of candidate material to block PV entry into target cells is measured via reporter signal reduction.

Results: Following a WHO-sponsored International Collaborative study, the 1st WHO International Standard for Ebola virus antibodies was established in 2017. Participants in the collaborative study evaluated the candidate materials using assays available in their laboratories. Data from neutralisation assays employing PV with either a lentiviral or vesiculoviral core component was correlated with the wildtype assay and showed a better correlation coefficient when the vesiculovirus PV system was used.

Conclusion: To support preparedness activities, antibody reference materials are now being established for other WHO priority pathogens such as Lassa and Nipah virus. To characterise the serological material at a low containment level, we have established assays using PV generated with both the lentiviral and vesiculovirus platforms. The two systems are currently being investigated to determine the most appropriate for each high containment virus.

08.003

Global Flu View: A Platform to Connect Crowdsourced Disease Surveillance Around the World

A. W. Crawley[1], D. Paolotti[2], C. Dalton[3], J. Brownstein[4], M. Smolinski[1]; [1]Ending Pandemics, San Francisco, CA/US, [2]ISI Foundation, Turin, Turin/IT, [3]Hunter Medical Research Institute, Newcastle/AU, [4]Childrens Hospital, Boston, MA/US

Purpose: Participatory disease surveillance actively engages the public in reporting on symptoms of their health to provide community-level data that complements traditional healthcare-based surveillance. Participatory surveillance is timely, low-cost, can account for non-medically attended populations, and allows for direct engagement with local populations. Three examples of participatory surveillance systems – Flu Near You in North America, Influenzanet in Europe, and Flu Tracking in Australia and New Zealand – have recently collaborated to develop Global Flu View, a shared platform for aggregation and dissemination of crowdsourced data on influenza-like illness.

Methods & Materials: The collaborating surveillance systems have developed a shared application programming interface (API) for data exchange among systems. The API specifications outline specific variables that are called into a shared, cloud-based database. Data is processed via an ETL layer resulting in aggregate data at the postcode level. Key variables include reporting week, postal and country codes, user birth month and birth year, gender, vaccination status, and a series of symptom variables that include fever, cough, sore throat, headache, fatigue, and other indications of influenza-like illness. Processed data will be available to view in both graph and map formats on the website www.globalfluview.org.

Results: The Global Flu View platform connects community-level influenza surveillance efforts across 15 countries on 3 continents. Tens of thousands of weekly reports are made available for users to explore through graphs, maps, and various filtering tools. The Global Flu View database also serves as a repository of influenza surveillance data that can be shared with disease modelers, researchers, and epidemiologists around the world.

Conclusion: Global Flu View can highlight the value of the participatory surveillance approach, serving as a model for other countries. The platform is poised to incorporate data from additional countries with similar tools and serves as a case study for collaborative, multi-country data sharing for global health surveillance. As of July 2018 the platform is in beta-testing mode and will be made publicly available by late August 2018.

08.004

Novel platform (wEB) to study flu virus evolution and predict vaccine efficacy

S. Paessler[1], V. Veljkovic[2]; [1]University of Texas Medical Branch, Pathology, Galveston, TX/US, [2]BiomedProtection, LLC, Galveston, TX/US

Purpose: Flu epidemics and potential pandemics pose great challenges to public health institutions, scientists and vaccine producers. Creating right vaccine composition for different parts of the world is not trivial and has been historically very problematic. This often resulted in decrease in vaccinations and reduced trust in public health officials. To improve future protection of population against flu we urgently need new methods for vaccine efficacy prediction and vaccine virus selection.

Methods & Materials: We analyzed the hemagglutinin HA1 region from (i) 2,379 H3N2 viruses collected in Europe and North America from 2014 to February 2018, 804 human and animal H3N2 viruses collected in the US.

The informational spectrum method (ISM) is the virtual spectroscopy method for calculation of the long-range properties of biological macromolecules (Veljkovic et al., 1983). The ISM is based on the electron-ion interaction potential (EIIP) representing molecular descriptor which determines long-range interactions (interactions on distances >5Å) between biological molecules.

Results: Using the electronic biology platform, we predicted that flu vaccine in the flu season 2017/2018 in US could work as well as in the previous season (https://f1000research.com/articles/6-2067/v1). Our prediction has been recently confirmed through laboratory reports released by CDC (https://www.cdc.gov/mmwr/volumes/67/wr/mm6706a2.htm).

Conclusion: Using the electronic biology platform, we predicted that flu vaccine in the flu season 2017/2018 in US could work as well as in the previous season (https://f1000research.com/articles/6-2067/v1). Our prediction has been recently confirmed through laboratory reports released by CDC (https://www.cdc.gov/mmwr/volumes/67/wr/mm6706a2.htm). Of note is that this reported VE for the flu season 2017/2018 was remarkable higher (especially in children) than predicted by the NIH (https://www.nejm.org/doi/full/10.1056/NEJMp1714916).

We are expecting that this electronic biology approach will be used by other researchers for rapid and accurate analysis of different influenza A viruses and for VE prediction.

08.005

Comparison Of Seasonal Influenza Trends: Timeliness Validation of State Outbreak Reports in Mexico 2007-2014.

H. Lee[1], C. Castillo-Salgado[2]; [1]Johns Hopkins University, Epidemiology, Baltimore, MD/US, [2]Johns Hopkins University, Epidemiology, Baltimore/US

Purpose: Seasonal influenza is a common cause of acute respiratory infections with distinct annual epidemic characteristics. Monitoring temporal trends in different States is a key to understanding the national influenza activity and they can be used as predictors of national level high seasonal activity. Therefore, we used timeliness validation methods to compare temporal trends of seasonal influenza from 2007 to 2014 at the State level in Mexico.

Methods & Materials: National confirmed weekly seasonal influenza case reports were used in this trend analysis. Timeline of seasonal influenza defined from first year's 28 weeks to last year's 27 weeks by state/national trends. We used peak time difference, aberration time reporting difference by EARS and time-series correlation algorithms to quantify the time difference from states to the national report.

Results: We have a total of 5 years of complete surveillance reports by 32 states. For peak time difference method, the mean time difference for each state for 5 years ranged from -14.6 weeks to 3.8 weeks. Specifically states 12, 13, and 31 showed 5 years which had an earlier peak than the national level. For aberration time difference method (by EARS C3), the mean time difference for each state for 5 years ranged from -2.25 weeks to 14.75 weeks, -1 week to 5.8 weeks, and -1.4 weeks to 3.6 weeks by each algorithm. For correlation method (by cross-correlation function), the mean lag time difference for each state for 5 years ranged from -9.8 weeks to 1.3 weeks. Specifically states 4,5,7,12 and 31 show an earlier epi curve than the national level.

Conclusion: Each state shows different temporal trends of seasonal influenza activity compared to the national level, and some states show significant early outbreaks of seasonal activity by peak time and correlation. Public health professionals and state governments should focus on those states for an early sign of influenza activity. Furthermore, different aberration detection algorithms or different timeline definitions may apply to make validation outcomes consistent.

08.006

Comparison of characteristics of individuals hospitalised with acute and chronic respiratory illness testing influenza positive at two sites in South Africa, 2011-2016

T. L. Mkhencele[1], S. Walaza[1], J. Moyes[1], J. M. McAnerney[1], S. Mhlanga[1], A. Nguweneza[1], E. Variava[2], H. Dawood[3], O. Mekgoe[4], F. Naby[5], C. Cohen[1]; [1]National Institute for Communicable Diseases, Centre for Respiratory Disease and Meningitis, Johannesburg/ZA, [2]University of the Witwatersrand, Department of Internal Medicine, Faculty of Health Sciences, Johannesburg/ZA, [3]Greys Hospital, Department of Medicine, Piertermaritzburg/ZA, [4]Klerksdorp Hospital, Klerksdorp, North West Province/ZA, [5]Metropolitan Hospital , Department of Pediatrics, Piertermaritzburg/ZA

Purpose: The current World Health Organization (WHO) severe acute respiratory illness (SARI) case definition for global influenza surveillance includes hospitalized individuals with fever and cough, with onset within 10 days. In the South Africa pneumonia surveillance programme, we enrol individuals irrespective of symptom duration; however, the characteristics of influenza patients with chronic symptoms have not been described.

Methods & Materials: We conducted active syndromic surveillance for hospitalised patients with severe respiratory tract infection (SRI) of any duration in two provinces of South Africa during 2011-2016. Upper respiratory tract samples were tested for influenza A and B and eight other respiratory viruses e.g. RSV, adenovirus, rhinovirus etc. using a polymerase chain reaction assay. We compared the demographic and clinical characteristics of influenza-positive individuals with symptoms duration ≤10 (acute) and >10 days (chronic) using unconditional logistic regression.

Results: During the study period, we enrolled and tested 9861 patients with SRI, 38% had chronic (3769/9861) symptoms. Among children <5 years, influenza viruses were detected in 6% (208/3466) of individuals, (6% (186/3255) were acute and 10% (22/211) were chronic cases, p=0.006). Among individuals aged ≥5 years, influenza viruses were detected in 5% (337/6395) of individuals (7% (189/2837) were acute and 4% (148/3558) were chronic cases, p=0.001). In the multivariable analysis of influenza positive SRI cases <5 years old, chronic patients were less likely to present with fever ((aOR 0.3, 95% CI 0.1-1.0) and were more likely to have influenza type B infection (aOR 4.2, 95% CI 1.7-10.7). Among individuals age ≥5 years, chronic patients were less likely to have fever (aOR 0.4, 95% CI 0.2-0.7) and to have *S. pneumoniae* colonization (aOR 0.4, 95% CI 0.2-0.7) but more likely to be hospitalized for longer: 4-7 days (aOR 2.4, 95% CI 1.2-4.7) and 8 days or more (OR 3.3, 95% CI 1.7-5.4) compared to <4 days.

Conclusion: Influenza-positive patients with chronic presentation were more likely to be afebrile, and hospitalized for longer (≥5years). Patients with chronic presentation and older patients with less fever are more likely to be missed by WHO SARI case definition. In systems measuring influenza burden it may be useful to modify the WHO SARI case definition.

08.007

Full-genome Analysis of the Pandemic (H1N1) 2009 Influenza Viruses Isolated in Ukraine During 2009-2017 Years

O. Smutko[1], A. Fesenko[2], L. Radchenko[2], O. Onishchenko[2], L. Leibenko[2], I. Budzanivska[3], A. Mironenko[4]; [1]ESC "Institute of Biology", Taras Shevchenko National University of Kyiv, SI "Gromashevsky L.V. Institute of epidemiology and infectious diseases, NAMS of Ukraine", Kiev/UA, [2]SI "Gromashevsky L.V. Institute of epidemiology and infectious diseases, NAMS of Ukraine" , Kiev/UA, [3]ESC "Institute of Biology", Taras Shevchenko National University of Kyiv, Kiev/UA, [4]SI "Gromashevsky L.V. Institute of epidemiology and infectious diseases, NAMS of Ukraine", Kiev/UA

Purpose: New studies increasingly use an analysis of the entire genome of influenza viruses that can shed new light on the evolution of viruses and the process of selecting vaccine strains.
The purpose of our study was to carry out molecular-genetic and phylogenetic analysis of all genes of pandemic A (H1N1) influenza viruses which circulated in Ukraine during 2009-2017 years.
Methods & Materials: Samples were analyzed using real-time polymerase chain reaction (RT-PCR). The sequences of influenza viruses from other countries were received from web-site GISAID using BLAST analysis. The influenza A (H1N1) pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009-like virus. Phylogenetic analysis was performed using MEGA 7. 3D structures were constructed in Chimera 1.11.2rc software.
Results: We have analyzed viruses isolated in Ukraine in the period of 2009 - 2017 year. Over the last five years the HA genes have evolved and eight genetic groups have been designated, with A/California/7/2009 representing group 1. The viruses were isolated in Ukraine during 2009-2017 fell into genetic groups 1, 2, 6, 7 and 8. This study demonstrated mutation in all five HA antigenic sites. In the NA genes were observed mutations H275Y and D151X caused resistance to antiviral drugs in different years. NP genes had mutations N377S and V425I, which can influence the immune response. In 2015-2016 in NP genes emerged two mutations A22T and M105I. All isolates including the A/California/07/2009 vaccine strain had the D21G mutation in the M2 protein, which causes resistance to antiviral drugs such as amantadine and rimantadine. NS1 genes had few mutations: E55E, E125D and N205S, which can inhibit human immune response and increase virulence of the virus. In PA was mutation P560S that increases virulence. In addition, we found unique changes in all genes of the polymerase complex (PA, PB1, and PB2).
Conclusion: According to the literature review, mutations acquired in each genome segment, in combination lead to increased virulence of the pandemic A (H1N1) pdm09 influenza viruses. Their impact on the increasing of influenza viruses' virulence was demonstrated in the experiments on mice.

08.008

Global Origins Of African Highly Pathogenic Avian Influenza H5Nx Viruses And Intracontinental Spread

A. Fusaro[1], B. Zecchin[1], B. Vrancken[2], C. Abolnik[3], A. R. Ademun[4], Y. P. Akpeli[5], A. Alassane[6], J. A. Awuni[7], E. Couacy-Hymann[8], M. Coulibaly[8], E. Go-Maro[5], T. Joannis[9], S. D. Jumbo[10], G. Minoungou[11], C. Meseko[9], S. M. Moutari[6], D. B. Ndumu[4], A. Twabela[12], A. Wade[13], L. Wiersma[14], G. Zamperin[1], A. Milani[1], P. Lemey[2], I. Monne[1]; [1]Istituto Zooprofilattico Sperimentale delle Venezie, Research and Development, Legnaro/IT, [2]Rega Institute, KU Leuven, Louvain/BE, [3]University of Pretoria, Pretoria/ZA, [4]Ministry of Agriculture Animal Industry and Fisheries, National Animal Disease Diagnostics and Epidemiology Center(NADDEC), Entebbe/UG, [5]Laboratoire Central Vétérinaire de Lomé, Lomé/TG, [6]LABOCEL, Niamey/NE, [7]6VSD of Ministry of Food and Agriculture, Accra/GH, [8]LANADA, Abidjan/CI, [9]National Veterinary Research Institute, Vom/NG, [10]Laboratoire National Vétérinaire (LANAVET), Garoua/CM, [11]Laboratoire National d'Elevage de Ouagadougou, Ouagadougou/BF, [12]Veterinary Laboratory of Kinshasa, Kinshasa/CD, [13]Laboratoire National Vétérinaire (LANAVET), Yaoundé/CM, [14]EMPRES – UN FAO, Rome/IT

Purpose: In 2006, 2014 and 2016 Africa was hit by three intercontinental epidemic waves of the highly pathogenic avian influenza virus (HPAIV) belonging to three distinct genetic clades of the A/goose/Guangdong/1/1996 lineage, namely 2.2, 2.3.2.1c and 2.3.4.4, which substantially affected the local poultry industry. In this study we compared the global and intra-African HPAIV H5 transmission patterns of these clades to shed light on the spread of the virus within Africa and to explore the contributions of different avian host populations to virus introduction and dissemination.

Methods & Materials: For each of the three clades, two datasets of the hemagglutinin gene were generated: one including representative sequences from affected regions throughout the world and from different host species, and one comprising all the African sequences generated in this study or retrieved from public databases. We reconstructed the history of epidemic spread in space and time and the host switching patterns through Bayesian phylogeographic analyses in both discrete and continuous space for each dataset using the BEAST v1.8.4 program.

Results: We identified multiple introductions of clade 2.2 from Europe and of clade 2.3.4.4-B from South and North-Central Asia into the African continent, while a single virus spread from South Asia to Africa seems to have been responsible of the 2.3.2.1c incursion. Our results identify West Africa as the most important area of virus introduction into the continent. A joint analysis of host dynamics and continuous spatial diffusion indicates that the incursion of the H5 clades into Africa is driven by wild *Anseriformes* and domestic *Galliformes* hosts, suggesting that both migratory birds and live poultry trade may have played an important role in the spread of the virus into Africa.

Conclusion: This study shows that viral sources are not stable over time in the African continent, but can change at each epidemic wave, making it difficult to predict the source for the next incursion. In addition, our results indicate a strategic role of West Africa in the virus spread within the continent, which may be considered as a hotspot for H5 HPAIV surveillance.

08.009

Changing Epidemiology of Listeria Outbreaks and Recalls: A review of ProMED reports from 1996-2018

A. N. Desai[1], A. Anyoha[2], L. Madoff[3], B. Lassmann[3]; [1]Brigham & Women's Hospital, Infectious Disease, Boston, MA/US, [2]Tufts University, Boston/US, [3]ISID, Brookline, MA/US

Purpose: Given emerging data regarding large-scale outbreaks of listeriosis, the purpose of this study is to identify trends in global *Listeria* epidemiology using ProMED reports. ProMED is an informal, global outbreak reporting system, that, in the context of *Listeria* outbreaks, reports atypical findings such as larger than average case counts, events from unusual sources, and multinational outbreaks.

Methods & Materials: Keywords "listeria," and "listeriosis," were utilized in the ProMED search engine from 1996-2018. Issue date, countries involved, source, suspected and confirmed case counts, and fatalities were extracted. Data unique to each outbreak including commentary by content experts were evaluated. Three independent investigators manually reviewed the database. When multiple reports regarding the same outbreak were obtained, the last report pertaining to that outbreak was utilized. Number of events and countries involved over time were normalized to the total number of *Listeria* ProMED events each year and compared using a two sided t-test; $p < 0.05$ was considered statistically significant.

Results: From 1996 to 2018, 91 outbreak events and 29 recalls from 27 countries were identified. The implicated food source was identified in 105 events. 27/105 events (26%) were associated with atypical food sources and 2 events were associated with pet foods. Events associated with unusual food sources increased over the study period with 7 events reported from 1997-2007 to 20 events reported from 2008-2018 ($p<0.05$). Event size did not differ significantly over the two time periods. 17/120 reports described international events with more than one country involved in the outbreak or recall, most of which (14/17; 82%) occurred from 2008-2018 ($p<0.05$). 34 events (28%) resulted in large-scale recalls of food items. 8 outbreaks (6.6%) were hospital-acquired.

Conclusion: This study demonstrates that the epidemiology of *Listeria* infections has been changing over time. More events are now associated with atypical food sources. Informing high-risk individuals such as pregnant women and immunocompromised individuals of safe food handling practices is warranted. To ensure timely recall of contaminated sources, open data sharing and communication across borders is critical. Changes in food production and distribution and improved diagnostics may contribute to the observed changes.

08.010

Hantavirus *Puumala* Genetic Variation In The Patients With HFRS In Tatarstan, Russia

E. Kabwe[1], Y. N. Davidyuk[1], S. P. Morzunov[2], E. V. Martynova[1], **E. E. Garanina**[1], V. G. Shakirova[3], R. K. Ismagilova[4], S. F. Khaiboullina[5], A. A. Rizvanov[1]; [1]Kazan (Volga region) Federal University, Openlab "Gene and Cell technologies", Kazan/RU, [2]University of Nevada, Reno, Department of Pathology, Nevada, Reno/US, [3]Kazan State Medical Academy, Infectious Diseases, Kazan/RU, [4]Kazan (Volga region) Federal University, Research Laboratory "Omics technology", Kazan/RU, [5]University of Nevada, Reno, Department of Microbiology and Immunology, Nevada, Reno/RU

Purpose: Background: *Puumala* hantavirus (PUUV) can cause hemorrhagic fever with renal syndrome (HFRS), an acute infection characterized by hemorrhages and kidney insufficiency. The Volga Federal District, including the Republic of Tatarstan (RT), is the most active zoonotic region where HFRS accounts for 83.3% of all zoonotic registered cases. Although PUUV is identified as the main infectious agent, little is known about the genetic variability of PUUV in the RT.
Methods & Materials: Materials and methods: Total RNA was extracted from 49 HFRS blood samples diagnosed in RT during 2015 and 2016 outbreak. RNA was used for RT-PCR analysis of the PUUV S-segment RNA. PCR products were sequenced using ABI Prism® 3730XL DNA Analyzer (ABI, USA) and analyzed using LaserGene software packet (DNASTAR, USA).
Results: Results: Phylogenetic tree analysis revealed high similarity (99.4 %) between PUUV S-segment RNA isolated during 2015-2016 period. Also, PUUV RNA from 11 cases collected during 2015 outbreak clustered together with the Finish lineage with 93.0-100.0% identity. The remaining 14 PUUV RNA S-segment sequences closely resembled that of Russian lineage with 91.0-96.0% identity. Interestingly, 23 out of total 24 samples collected during the 2016 outbreak clustered with Finish lineage (93.6-99.4% identity) and only one sample clustered with Russian lineage (92.0-93.6 % identity). The proportion of FIN lineage strains found in HFRS patients far exceeds the share of this lineage strains detected in populations of their native host (bank voles) in RT. Therefore, PUUV strains of the FIN lineage might be more virulent for human than the RUS lineage strains.
Conclusion: Conclusion: This data suggest the co-circulation of two PUUV lineages FIN and RUS in the patients diagnosed with HFRS in Tatarstan.

08.011

Incentives that Influence Low Income Filipinos with Tuberculosis Symptoms to Change Health-
seeking Behaviour: a Randomized Controlled Trial

S. Lee[1], L. Lau[2], K. Lim[3], D. Cole[4]; [1]International Care Ministries, Research, Manila/PH, [2]University of Toronto, Dalla Lana School of Public, Markham, ONTARIO/CA, [3]International Care Ministries, Manila/PH, [4]University of Toronto, Dalla Lana School of Public Health, Toronto, ON/CA

Purpose: Philippines has one of the highest TB prevalence rate gloablly. However, despite the high prevalence of TB and awareness of common TB symptoms, Filipinos in low socio-economic status often fail to get tested for TB. Nevertheless, early case detection among the vulnerable population is crucial in curbing the rising TB incidence rate. We hope to understand if incentives are effective in promoting TB testing through a randomised controlled trial (RCT).

Methods & Materials: This study was carried out as part of the International Care Ministries (ICM)'s, a non-profit organization in the Philippines, TB active case finding (ACF) and health education program. Communities were randomly divided into 4 different RCT groups that were given: nothing (control); rice packages; transportation cost; rice packages and transportation cost. Participants were screened for TB symptoms during the second week of the program and those with symptoms were given a referral card and asked to visit the closest health facility for testing. Incentives were distributed when TB suspects were given a referral. Those who successfully completed testing were given the same incentive again (according to their RCT group). All data were collected by ICM staff and data analysis was conducted using R.

Results: From May to September, 2018, a total of 21,345 participants were screened for TB symptoms. Of these, 369 were referred to the closest healthcare facility for testing. 179 of those referred tested for TB and 6 were confirmed to have TB. Participants who received both incentives, rice packages and transportation subsidy, were most likely to get tested for TB (65%). They were followed by the group that received transportation money; rice packages; and the control group (58%, 41%, 27% respectively).

Conclusion: In a remote, resource limited setting where TB suspects face financial and geographical restrictions, financial assistance for transportation could change health-seeking behaviour. Providing incentives have been criticized in the past for being ineffective but in our study, both food and cash assistance intervention groups showed significant change. To increase case detection, public health policy makers should consider subsidizing transportation cost for those living in poverty in the Philippines.

08.012

Measles among Healthcare Workers during the Ongoing 2017-2018 Epidemic in Greece

H. Maltezou[1], X. Dedoukou[2], A. Mentis[3], M. Theodoridou[4], T. Georgakopoulou[5]; [1]Hellenic Center for Disease Control and Prevention , Department for Interventions in Healthcare Facilities , Athens/GR, [2]HCDCP, Athens/GR, [3]Hellenic Pasteur Institute , Athens/GR, [4]University of Athens , Athens/GR, [5]Hellenic Center for Disease Control and Prevention, Epidemiological Surveillance and Intervention, Athens/GR

Purpose: Starting in May 2017, Greece experiences a measles epidemic within the frame of the large measles epidemic in Europe. The aim of our study was to describe the measles notified cases among healthcare workers (HCWs) in this country.

Methods & Materials: Data were retrieved from the national database of notified measles cases. Cases were classified in accordancw with the European Union definitions.

Results: From 2017 through May 3, 2018 117 measles cases among HCWs were notified, accounting for 4.2% of all (2747) notified measles cases in Greece. The notification rate is 1429 cases per 1,000,000 HCWs (5.6-fold increase compared with the general population). HCWs with measles had a mean age of 38.1 years (range:20-55 years). Most (91.4%) HCWs worked in a hospital. Physicians accounted for most cases followed by nurses [n=45 (38.5%) and 34 (29.1%), respectively]. Sixty-seven (57.2%) HCWs were hospitalized. Measles-associated complications (mainly pneumonia/pneumonitis and/or hepatitis) occurred in 36 (30.8%) HCWs, which is more than two-fold compared with the general population. Three (2.6%) HCWs were admitted in an intensive care unit and were intubated. None died. Of 99 HCWs with a known vaccination status, 59 (59.6%) were unvaccinated, 30 (30.3%) were incompletely vaccinated, six (6.1%) were completely vaccinated, while four (4.0%) had received an unknown number of doses.

Conclusion: Our study confirms that HCWs constitute a high-risk group for acquisition of measles and manifestation of serious illness. Modifications in the routine vaccination program against measles the past two decades may have resulted in the suboptimal vaccination coverage in young HCWs. Protection of HCWs against measles through a two-dose vaccination regimen is imperative. Mandatory vaccination of HCWs against measles should be considered, particularly in the context of an ongoing community epidemic.

08.013

Significant range expansion of Lloviu rirus in Europe: Re-emergence in 2016, Hungary

G. Kemenesi[1], S. Boldogh[2], T. Görföl[3], S. Bücs[4], P. Estók[5], I. Budinski[6], M. W Carroll[7], K. Kurucz[1], B. Zana[1], F. Földes[1], F. Jakab[1]; [1]University of Pécs, Szentágothai Research Centre, Virological Research Group, Pécs/HU, [2]Aggtelek National Park, Directorate, Jósvafő/HU, [3]Hungarian Natural History Museum, Department of Zoology, Budapest/HU, [4]Centre for Bat Research & Conservation, Cluj/RO, [5]Eszterházy Károly College, Department of Zoology, Eger/HU, [6]University of Belgrade, Department of Genetic Research, Institute for Biological Research "Siniša Stanković", Belgrade/RS, [7]Public Health England, Porton Down/UK

Purpose: The discovery of Lloviu virus (LLOV) in *Miniopterus schreibersii* bat samples from Spain, 2003 dramatically changed our understanding of the genetic diversity, geographic distribution, and host preference of filoviruses. However, the ecology of LLOV is largely unclear mainly due to the lack of reports following the first report of LLOV. In our study, we try to solve the open questions regarding LLOV genetics and ecology, based on a continuous screening of a selected *M. schreibersii* colony, proved to be positive for LLOV during a mortality event in 2016.

Methods & Materials: We established a countrywide surveillance system in Hungary for the early detection of *M. schreibersii* dye-offs in 2012 in collaboration with conservation bilogists and chiropterologists. In each case, carcasses were collected as soon as possible and transported to the laboratory in liquid nitrogen. Multiple events were examined during the past few years with viral metagenomic analyses and LLOV-specific TaqMan-based real-time PCR screening.

Results: In 2016, we detected LLOV virus RNA in tissue samples of a *M. schreibersii* individual. Partial sequences of the nucleoprotein and the RNA-dependent RNA-polymerase gene suggests a close genetic relatedness with the original isolate in Spain. Following this event, several additional mortalities were registered to date in the same habitat with the same gross pathology of hemorrhagic symptoms, but no other positives were verified with PCR method, possibly because of the bad conditioned carcasses. In 2018, we started a monthly sampling activity, after the maternity period, in order to examine the seroprevalence, and other related factors of the virus in this cave.

Conclusion: Here we present the current results of our survey programme, showing the relation of the Hungarian isolate to the original Spanish virus from 2003. A major goal of our presentation is to call attention to this pathogen, possibly affecting the stability of *M. schreibersii* colonies across Europe, representing a paramount concern for conservation biology. We discuss the possible factors leading to the dispersal of the virus in Europe and the possible transmission routes between bats to be examined in future studies and we also summarize current knowledge about the virus.

_____

10.001

Investigation Of Serological Cross-Reactivity Within The Alphavirus Genus Using IFA Biochip
              Mosaics

E. Lattwein, M. Janku, K. Bohm, S. Lederer, K. Fechner; EUROIMMUN AG, Institute for
Experimental Immunology, Lübeck/DE

Purpose: The alphavirus genus comprises several human pathogens, e.g. chikungunya virus
(CHIKV), Ross River virus (RRV) and Eastern equine encephalitis virus (EEEV). Depending on the
antigenic relatedness cross-reactivity in serological assays is commonly observed. Due to overlapping
geographical distribution and similar clinical pictures a serological differentiation is desirable.
Methods & Materials: Human serum or plasma samples from different geographical areas and
precharacterised for IgG and IgM antibodies against various alphaviruses were investigated with
multiplex indirect immunofluorescence assays. The method is based on a mosaic of up to nine
biochips which carry infected or transfected cell lines each expressing antigens of another alphavirus.
The samples were tested for the presence of specific IgG and IgM antibodies and endpoint titers were
determined for every virus in parallel.
Results: Investigation of samples from patients with different alphavirus infections led to a significant
amount of cross-reactivities on IFA biochip mosaics, especially regarding IgG antibodies. Using
parallel endpoint titration it was possible to determine the causative alphavirus in the vast majority of
samples. For example, investigating samples from RRV infected patients, 93% and 11% reacted
positive on CHIKV infected cells regarding IgG and IgM antibodies, respectively. Regarding samples
from Barmah-Forest virus (BFV) infected patients, 28% and 3% were positive on CHIKV for IgG and
IgM, respectively. By comparison of the endpoint titers for the respective viruses resulting from the
same incubation on a biochip mosaic, 88% of RRV IgG samples and all IgM samples showed an at
least ten times higher titer on the RRV biochip than on the CHIKV biochip. Regarding BFV patients,
all samples showed at least ten times higher titers for BFV than for CHIKV in both IgG and IgM
investigation.
Conclusion: Cross-reactivity of IgG and IgM antibodies plays an important role in serological
diagnostics of alphavirus infections. Parallel investigation of a sample using different alphavirus
antigens in a biochip mosaic can identify the causative virus in most of the cases, depending on the
antigenic relatedness of the viruses.

10.002

Flavivirus serocomplex cross-reactive immunity is protective by activating heterologous memory CD4 T cells

W. Saron[1], A. Rathore[2], T. Lim[1], E. E. Ooi[1], J. Low[3], S. Abraham[2], **A. L. St. John**[1]; [1]Duke-NUS Medical School, Programme in Emerging Infectious Diseases, Singapore/SG, [2]Duke University, Pathology, Durham/US, [3]Singapore General Hospital, Infectious Diseases, Singapore/SG

Purpose: How prior immunity influences immune memory recall and protection against related flaviviruses is largely unknown; yet encounter with multiple flaviviruses in a lifetime is increasingly likely. Here, we aimed to determine whether serocomplex cross-reactive immunity is detrimental during vaccination or if it can prime for protective immune responses.

Methods & Materials: Using sequential challenges with dengue (DENV), Yellow Fever (YFV) and Japanese encephalitis (JEV) viruses, we induced cross-reactive cellular and humoral immunity amongst flaviviruses from differing serocomplexes in mice. After memory formation, mice were re-challenged with a virus from a heterologous serocomplex. Cross-reactive antibody responses were assessed by neutralization tests and ELISAs to measure antibody binding and avidity. Flow cytometry and ex vivo assays were used to identify cross-activated T cells, including T follicular helper cells. Cross-activation of human T effector memory cells in JEV-vaccinated donors was measured in response to DENV, YFV, and Zika virus.

Results: Antibodies against JEV enhanced DENV replication; however, JEV immunity was protective *in vivo*during secondary DENV1 infection, promoting rapid gains in antibody avidity. Mechanistically, JEV-immunity activated effector memory T cells, which developed a T follicular helper cell phenotype in draining lymph nodes upon secondary DENV1 infection. We identified cross-reactive epitopes that promote recall from a pool of flavivirus serocomplex cross-reactive memory CD4 T cells and confirmed that a similar serocomplex-cross-reactive immunity occurs in humans.

Conclusion: These results show that sequential immunizations for flaviviruses sharing CD4 epitopes should promote protection during a subsequent heterologous infection.

10.003

Evaluation of a candidate WHO International Standard for Zika antibody as a vaccine reference reagent

S. Kempster[1], C. Ham[1], J. Hall[1], D. Ferguson[1], N. Berry[1], G. Mattiuzzo[2], M. Page[2], N. Almond[1];
[1]NIBSC, Virology, Potters Bar/UK, [2]National Institute for Biological Standards and Control (NIBSC), Potters Bar/UK

Purpose: We investigated whether a candidate material could be established as a serological vaccine reference reagent. NIBSC works with the WHO to produce 95% of the International Standards for biological medicines and as part of a programme to produce an International Standard for anti-Zika antibodies.
The development of safe effective and affordable vaccines against emerging pathogens is hindered by the lack of serological vaccine reference reagents. Where there is evidence that convalescent sera/plasma protect against reinfection, these materials facilitate all stages of vaccine development by harmonising data from assays performed in different places or at different times.
These reagents are particularly valuable for vaccine development of Priority Emerging Pathogens as the high bio-containment and bio-security issues arising from working with these pathogens limit efficacy challenge studies to relatively few facilities and serological reference reagent with a known titre of protective immunity provides an invaluable benchmark allowing immunogenicity studies.
Methods & Materials: Anti-zika plasma (NIBSC: 16/320-14 – convalescent plasma) was administered to cynomolgus macaques (n=4) intraperitoneally 24 hours prior to challenge with Zika virus (PRVABC59) by the sub-cutaneous route. Plasma and serum were collected at daily / weekly intervals to establish viremia by qRT-PCR and anti-zika IgG and IgM by ELISA and neutralising antibody by *in vitro* neutralisation of homologous virus.
Results: All animals were protected against detectable infection when administered anti-zika antibody 24 hours prior to challenge when compared to controls. The human IgG was detectable in serum from animals administered 16/320-14 at time of challenge and was almost undetectable 42 days post-challenge. No *de novo* antibodies e.g. IgM responses were detected. Control animals showed IgM responses after challenge followed by IgG increases 42 days post challenge. There was a significant correlation between the NS-1 ELISA and neutralisation titre (r=0.3494, p=0.0161).
Conclusion: The anti-Zika reference material alone is sufficient to confer protection *in vivo*. This study sets a paradigm to produce serological vaccine reference reagents for other Priority Emerging Pathogens such as Lassa Fever and NIPAH virus that require BSL 4 containment. Vaccine reference reagents will enable the efficacy of candidate vaccines to be compared.

10.004

Endemicity of Zika Virus in Indonesia: Serological Evidence in Pediatric Population

R. T. Sasmono[1], R. Dhenni[1], B. Yohan[1], P. Pronyk[2], S. R. Hadinegoro[3], E. J. Soepardi[4], C. Ma'roef[1], H. Satari[3], H. Menzies[5], W. Hawley[5], A. Powers[6], R. Rosenberg[6], K. S. Myint[1], A. Soebandrio[1]; [1]Eijkman Institute for Molecular Biology, Jakarta/ID, [2]UNICEF Indonesia, Jakarta/ID, [3]Faculty of Medicine, Universitas Indonesia, Jakarta/ID, [4]Ministry of Health, Jakarta/ID, [5]Centers for Disease Control and Prevention, Atlanta/US, [6]Centers for Disease Control and Prevention, Fort Collins/US

Purpose: Zika virus (ZIKV) has been reported in Indonesia for decades and the recent ZIKV isolation in 2014 provides evidence of its active circulation. Although detected, details on ZIKV prevalence and distribution across Indonesian archipelago are unknown. The study was aimed to understand the prevalence and geographic distribution of ZIKV based on serological evidence in pediatric urban population in Indonesia.

Methods & Materials: Sera from healthy 1-4 year-old children were collected from 30 study sites distributed across 14 provinces in Indonesia in 2014. ZIKV neutralizing antibodies were measured using ZIKV and dengue virus (DENV) combo Plaque Reduction Neutralization Test (PRNT). All specimens were subjected to two tiers of testing. First, serum suppressed the formation of ZIKV plaque-forming units by ≥ 90% (PRNT90) were considered to be potentially positive for neutralizing antibody specific to ZIKV. Specimens positive in the first tier were subjected to a second PRNT90 in which the serum was further tested against ZIKV alongside all four DENV in a single assay. Specimens positive for ZIKV neutralizing antibody without any detectable levels of DENV antibodies were classified as ZIKV seropositive, as were results where ZIKV titers were ≥4-fold higher than DENV antibodies. Specimens were categorized as flavivirus seropositive when ZIKV antibodies were present but at titers <4-fold greater than for DENVs.

Results: PRNT90 screening of 662 sera detected possible ZIKV antibody in 73 (11.0%) samples. Of these, 72 samples undergo ZIKV and DENV combo PRNT testing. Of these, 60 (83.3%) were classified as ZIKV seropositive and the remaining 12 (16.7%) as flavivirus seropositive. Eleven of 14 provinces contributed ZIKV positive specimens, ranging from 4.5% of specimens from North Sumatra, Banten, and East Kalimantan to more than 18% of specimens from Central Java. Overall ZIKV seroprevalence in the 1-4 year-old cohort was 9.1 %.

Conclusion: We have conducted ZIKV serological screening on samples collected from children in representative areas in Indonesia and revealed the seroprevalence of ZIKV in most regions. The data provide evidence of widespread recent transmission and endemicity of ZIKV in the country. This knowledge provides clues for understanding future patterns of Zika virus transmission in non-endemic areas.

10.005

Development And Validation Of Microarray-Based Serological Assay For Crimean-Congo Hemorrhagic Fever (CCF) And Determination Of The Prevalence Of CCFV In Guinea

O. Stukolova[1], I. Goptar[1], L. Karan[1], E. Kotenev[2], A. Sudina[1], M. Polugalova[1], A. Kulichenko[3], M. Y. Boiro[4], G. Shipulin[1]; [1]Central Research Institute of Epidemiology, Molecular diagnostics and epidemiology, Moscow/RU, [2]Stavropol anti-plague Institute, laboratory of natural focal infections, Stavrapol/RU, [3]Stavropol anti-plague Institute, Stavropol anti-plague Institute, Stavrapol/RU, [4]4 Institute of Applied Biology in Guinea, 4 Institute of Applied Biology in Guinea, Kindia, Kindia/GN

Purpose: CCF is an arboviral disease characterized by fever, severe intoxication and hemorrhagic syndrome with high mortality. CCFV is spread in many countries of Europe, Africa and Asia, including the South of the Russian Federation and Guinea. Here we aimed to develop and evaluate the recombinant protein-based microarray for detection of IgM/IgG to CCFV antigens.

Methods & Materials: The microarray includes recombinant proteins NP, it's antigenic fragment NPsh, 3 glycoprotein G1 antigenic fragments and one of protein L. The microarray development was conducted using sera collected in the endemic region of Russia from 20 patients (40 samples in total), in which CCFV RNA was determined using the «AmpliSensCCFV-FL» kit (CRIE, Russia), and 100 samples of healthy controls. IgM/IgG levels were measured using ELISA kit (Bioservice, Russia) and developed microarray. The seroprevalence of CCFV infection in humans in Guinea, was determined in serum samples from Guinean healthy population (200 in total).

Results: According to data obtained while testing of healthy controls samples, the presence of IgG/IgM to one of G1 or L fragment leads to negative result of analysis, to two of G1 fragments – to equivocal result and to NP and/or one G1 and L fragments together – to positive result. Thus the specificity of microarray was determined to be 98%. When specified interpretation criteria and only serums obtained on day 4-7 of the disease are used, the clinical diagnosis could be confirmed by the combination of IgG and IgM detection in 17/20 cases (16/20 for ELISA), and for paired serum samples - in 20/20 cases (both methods). The advantage of microarray is determination of IgM/IgG separately but in one well due to usage of Cy3/Cy5-labeled specific antibodies.

From 200 Guinean samples IgM to CCFV antigens were found in 2 sera (1%), IgG – in 14 sera (7%). This data consistent with data obtained for neighbor countries.

Conclusion: We showed that developed microarray is highly sensitive and specific diagnostic mean. The results shown that approximately 8% of the study population in Guinea, have a history of CCFV infection. As far the study is the first case of determination of prevalence of CCFV in humans in Guinea.

10.006

Baseline Data On The Bionomics Of *Aedes Aegypti* To Support Dengue Control Strategies In Burkina Faso

A. Badolo[1], A. Sombie[1], P. Pignatelli[2], F. Yaméogo[1], A. Sanon[1], W. D. Wangrawa[1], A. Sanon[1], H. Kanuka[3], D. Weetman[2], P. J. McCall[2]; [1]University Ouaga 1 JKZ, Entomology, Ouagadougou/BF, [2]Liverpool School of Tropical Medicine, Vector Biology, Liverpool/UK, [3]The Jikei University School of Medicine, Department of Tropical Medicine, Tokyo/JP

Purpose: In the last two years Burkina Faso has experienced dengue outbreaks resulting in 2,600 cases and 21 deaths in 2016, and 14,944 cases, 30 deaths in 2017. Lack of preparation and of updated information on Aedes populations hinders responses to the first outbreaks of dengue. We carried out a three-month surveillance study to collect baseline data on Aedes populations including characterization of breeding sites, susceptibility to insecticides, and resting and feeding behaviors in urban, periurban and rural localities in or near Ouagadougou the capital city.

Methods & Materials: Vacuum aspirators were used to collect indoor and outdoor resting mosquitoes. Potential breeding sites were sampled for immature stages. Mosquitoes were morphologically identified as *A. a aegypti*, *A. a formosus* or intermediate. WHO and CDC susceptibility tests were used to assess *A. aegypti* susceptibility to commonly-used insecticides at the larval and adult stages. PCR detection methods were applied to identify the bloodmeal origin and qPCR to investigate candidate mutations and gene expression that might underlie resistance to insecticides.

Results: Morphological identification showed that classical diagnostics did not consistently separate *A. aegypti/formosus* with many intermediates found. We recorded an increasing density from urban to rural locality consistent with the abundance and productivity of breeding sites. *A. aegypti* exhibited more outdoor than indoor biting and, although mixed human-animal blood meals were detected, a strong preference for human hosts was evident. Adults exhibited a higher level of resistance to pyrethroids in the urban area, supported by higher frequencies of the 1534C and 1016I target site mutations and an overall elevated expression of candidate P450 detoxification genes. Both adults and larvae remain susceptible to organophosphates.

Conclusion: The results provide baseline data on *A. aegypti* bionomics in Ouagadougou and its neighborhood that can be used to support the response to outbreaks of dengue and other *A. aegypti*-transmitted arboviruses in Burkina Faso. The results provide an updated evidence base, essential to establish a locally-informed strategy for vector control.

10.007

Investigation Of The Public Health Event In The Cafunfu Town, Lunda-Norte, December 2017

D. Pode[1], M. Nsuka[2], A. Cruz[2], M. Pambasage[2], R. Alfredo[2], B. Felix[3], J. Pires[4]; [1]National School of Public Health , Luanda/AO, [2]National School of Public Health, Luanda/AO, [3]Ministry of Health / National School of Public Health, Luanda/AO, [4]CDC, Luanda/AO

Purpose: On November 22th, 2017, the people from Cafunfu municipality in Lunda-Norte Province, alerted through the media, "the occurrence of unidentified disease, manifested mainly by high fevers, among other symptoms". After verification of the alert, a multidisciplinary outbreak investigation team was sent to the town in December to investigate this public health event.

Methods & Materials: In order to investigate the etiology of this public health event, 370 febrile children were randomly selected for testing with rapid diagnostic tests (RDT) for malaria. Further, 25 RDT for dengue and chikunguya were performed. In order to evaluate the factors associated with the disease, a 1:2 age-matched case-control study was conducted in the neighborhoods of Elevação and Bala bala. The target population were children under 15 years old. The sample size was calculated using the EPI Info Calculator: 60 cases and 120 controls were recruited. Significance level was set at p<0.05 for all hypothesis tests.

Results: The RDT positivity rate was 70% for malaria. Of the 60 cases analyzed, 39 (65%) were male; 34 (57%)> 5 years, 36 (60%) lived in Bala bala .The epidemic curve was typical of vector-borne disease and revealed the occurrence of underreporting with the arrival of the external teams and the beginning of the outbreak investigation.

Logistic regression identified the following associated factors for contracting malaria: having an open dump close to home, OR of 11.3 [4.54-28.32] (p<0.001); not sleeping under mosquito net, OR = 16.3 [6.23-42.49] (p<0.001).

Conclusion: The upsurge in malaria cases was the trigger for the rumor that circulated through the media by the population of Cafunfo. Control measures taken included: distribution of LLITNs; vector control strategies, improved case management. It was further recommended that local health authorities strengthen the epidemiological surveillance system, improve basic sanitation, maintain vector control strategies and develop risk communication strategies.

10.008

Severe Malaria in Canada 2014-2017: Report from the Canadian Malaria Network.

A. McCarthy[1], S. Carson[2], P. Ampaw[3], S. Sarfo[3], J. Geduld[4]; [1]University of Ottawa, Medicine, Ottawa, ONTARIO/CA, [2]Ottawa Hospital Research Institute , Medicine , Ottawa/CA, [3]Ottawa Health Research Institute, Medicine, Ottawa/CA, [4]Public Health Agency of Canada, Office of Border and Travel Health, Ottawa/CA

Purpose: Imported malaria is the principle, preventable life-threatening infection among Canadians travelling abroad. The Canadian Malaria Network (CMN) supplies information and parenteral malaria therapies to healthcare providers treating severe and complicated malaria. The CMN data gathers surveillance information on these cases.

Methods & Materials: Data on the characteristics, risk factors, and clinical outcomes of severe malaria cases in Canada from January 2014 to December 2017 were analyzed.

Results: There were 367 malaria cases treated with parenteral therapy (artesunate or quinine) over four years; 344 received intravenous artesunate (IVAS) alone; 18 received only quinine; and 5 received both drugs. The mean age of cases was 33.4 years; the mean age of the 103 children was 7.6 years. Most (67.5%; 248) presented in Ontario and Quebec. Although the majority of cases (212; 58%) were Canadian residents only 19% (69) were Canadian born. Most (54%; 198) were born in Africa and Africa was the region of exposure in 76% (279) of cases. Reason for travel was to visit friends and relatives (VFR) in 43% (161) and migration in 20% (72).; children accounted for 22% of all VFR travellers and 71% of all recent migrants. 10% (38) of cases reported using malaria chemoprophylaxis, yet only 4% (15) reported adherence.

Conclusion: The need for parenteral therapy in Canada has markedly increased over the last few years, there were 293 cases between 2001-2013. The vast majority of cases are reported from Ontario and Quebec and occur among travellers to and from Africa. The overall use and appropriateness of pre-travel advice and chemoprophylaxis remains low. Most cases result from patient delays in recognizing symptoms and seeking appropriate medical attention.

Data from the Canadian Malaria Network provides insight into the characteristics of imported severe and complicated malaria infections in Canada. Improved understanding of this population can help target risk reduction strategies and interventions to limit personal susceptibility and healthcare treatment delays.

10.009

Gestational And Congenital Toxoplasmosis - The Clinicial Findings In A Teaching Hospital

M. R. Nogueira[1], L. Spegiorin[2], D. Barbosa[3], S. Caron[4], F. H. A. Murata[5], V. L. Pereira-Chioccola[6], L. de Mattos[7], **C. C. Brandão de Mattos**[8]; [1]Faculdade de Medicina de São José do Rio Preto, Molecular Biology, São José do Rio Preto/BR, [2]Faculdade de Medicina de São José do Rio Preto, Ginecology and Obstetrics, Sao Jose do Rio Preto/BR, [3]Faculdade de Medicina de São José do Rio Preto, Pediatrics, São José do Rio Preto/BR, [4]Secretaria Municipal de Saúde, São José do Rio Preto/BR, [5]Faculdade de Medicina de São José do Rio Preto - FAMERP, Molecular Biology, São Jose do Rio Preto, SÃO PAULO/BR, [6]Instituto Adolfo Lutz, Parasitology Service, São Paulo, SÃO PAULO/BR, [7]Faculdade de Medicina de São José do Rio Preto, Molecular Biology, Sao Jose do Rio Preto/BR, [8]Faculdade de Medicina de São José do Rio Preto , Molecular Biology, São José do Rio Preto, SÃO PAULO/BR

Purpose: Toxoplasmosis is a cosmopolitan zoonosis caused by the intracellular parasite *Toxoplasma gondii,* usually asymptomatic, in pregnant women may lead to fetuses threat of miscarriage or disabilities. There is no official coutrywide protocol describing laboratory and clinical protocols to be used in prenatal and postnatal care. Here we describe the clinical findings in pregnant women's with clinical suspicion of gestacional toxoplasmosis and as well as in their newborns until their first 18 months of life.

Methods & Materials: A retrospective study was conducted and 49 medical records of pregnant women who received prenatal monitoring at the High-Risk Pregnancy Clinic of the Base Hospital of Regional School of Medicine Foundation (FUNFARME) in 2009 to 2013 were evaluated according to: gestational age, recommended treatment, obstetrical ultrasounds, clinical and laboratory diagnosis, which included IgM and IgG serologies and amniotic fluid PCRs. 39 records of their potencially infected newborns were screened observing: neurological, visual and otologic development and exams, prematurity and recommended treatment.

Results: The average age of the 49 pregnant women was 23,6 ±6,3 (min: 13; max: 39; median: 23); 22,4% (n=11) were primigravidae and 42,8% (n=21) multigravidae.; 75,5% (n=37) of the pregnants presented positive serology; 46,9% (n=23) underwent amniocentesis, 20,4% (n=10) had a positive amniotic fluid PCR and 8,16% (n=4) fetal ultrasound scans showed changes (shortened long bones, retrocorionic hematoma, retroamniotic hematoma and hyperechogenic intracardiac focus). Their recommended treatment included spiramycin or the triple scheme (sulfadiazine, pyrimethamine and folinic acid). Among the babies were presented: positive IgM serology (2,5% with n=1), or positive blood PCR (7,69% with n=3) or suspicion and signs of clinical changes (17,94% with n=7) as cerebral calcifications, schizencephaly, seizures, chorioretinal alterations and prematurity. Although only 17,94% (n=7) of the children underwent treatment for congenital toxoplasmosis, based on the triple scheme, not necessarily those with clinical features.

Conclusion: The gestational toxoplasmosis is occurring in multigravidae more than in primigravidae. The amount of positive amniotic fluid PCRs confirm a reasonable number of fetal infection, confirming congenital toxoplasmosis; however, the number of children underwent the treatment was very low.

10.010

The Pathogenesis Of Genetically Diverse Strains Of Crimean-Congo Hemorrhagic Fever Virus In The Cynomolgus Macaque Model

D. Smith[1], **C. J. Shoemaker**[2], A. Garrison[1], K. M. Ricks[2], O. Flusin[2], M. Voorhees[2], J. Zelko[1], A. Kimmel[1], J. Koehler[2], J. Golden[1], W. Pratt[1], C. Fitzpatrick[1], J. Shamblin[1], F. Rossi[1], R. Schoepp[2], C. Schmaljohn[3]; [1]USAMRIID, Virology, Frederick/US, [2]USAMRIID, Diagnostic Systems Division, Frederick/US, [3]USAMRIID, Headquarters Division, Frederick/US

Purpose: Crimean-Congo hemorrhagic fever virus (CCHFV) is a tick-borne virus with a wide geographical distribution, which includes Africa, the Balkans, the Middle East, Russia and western Asia. As a result of its wide dissemination, there is a considerable amount of genetic diversity amongst different CCHFV strains. Infection with CCHFV can cause a severe, often fatal, human disease characterized by fever and hemorrhage. No licensed vaccines or therapeutics currently exist to treat infection with CCHFV. The development of a non-human primate (NHP) model that recapitulates human disease would significantly benefit development efforts for medical countermeasures to CCHFV. In a recent study by another group, cynomolgus macaques were infected intravenously with a European isolate of CCHFV and the animals experienced a severe, sometimes lethal, disease state. We expanded upon this initial study using the same intravenous NHP model to compare disease progression with the previous European isolate versus another contemporary isolate of central Asian origin.

Methods & Materials: Two groups of cynomolgus macaques were infected intravenously with either the European isolate (Kosova Hoti) or the Asian isolate (Afg09-2990). Animals were then monitored with real-time temperature telemetry and regularly assessed across a range of clincial criteria. Serological collection was performed on a daily basis during acute phase, and a range of viremic, hematological, blood chemistry, and immunological assays were performed.

Results: While we achieved a robust disease state for both challenge groups, our CCHFV disease model was not as severe as the initial study reported by Haddock, et al. Interestingly, despite its higher initial viremic load, Afg09-2990 appeared to resolve more quickly than Kosova Hoti with regard to both fever and clinical score criteria. Aside from this, both virus strains caused largely analogous disease states, which reflected many symptoms seen in human disease.

Conclusion: In this comparative study, we found that European and Asian CCHFV strains caused very similar disease profiles in cynomolgus macaques. This strongly suggests that future medical countermeasures can be tested in this NHP model for multiple CCHFV strains. In addition, the differences we observed in the severity of our disease model relative to that previously reported suggests that further model optimization may be desirable.

10.011

The First Ever Nipah Virus Outbreak And The Best Possible Response By a Tiny State Of India.

S. Ariyari[1], N. Vijayan[2], R. Sadanandan[3]; [1]Directorate of Health Services-Kerala, Public Health , Trivandrum/IN, [2]State Mission Directorate , NHM Kerala, Trivandrum/IN, [3]Directorate of Health Services , Public Health Surveillance , Trivandrum/IN

Purpose: To present a success model of outbreak response by a tiny state in India, well known globally for its excellent health and development indices.

Methods & Materials: In April 2018, a 23 yr old male, admitted with Acute Encephalitis, in a Government Medical School died without any laboratory conclusion. After 15 days, three persons from same family, reported to a private tertiary care centre with similar illness, tests confirmed Nipah Virus infection, the first in the state. The State Surveillance Unit notified, an emergency response launched within the next 24 hours. Outbreak response components include:Activation of ncident command center, Epidemiological investigation,Notification to Govt of India, isolation and treatment of symptomatics in designated centers with infection control processes, intensive contact tracking, disseminating information to community, regulation of social media, equipping health workforce, ensuring essential medicines and supportive logistics like personal protective gears, safe burial practices, food and livelihood support along with psychosocial counselling to affected families. With strong political commitment and precise response, the outbreak was brought under control within 10 days of confirmation of first case.

Results: Epidemiological investigation by multidisciplinary rapid response team confirmed the index case,the first death, which went un noticed. Source of infection identified as possible exposure to a small forest having fruit bats in large numbers, in which the presence of Nipah virus was subsequently confirmed. person to person transmission on close contact with respiratory secretions was confirmed as mode of spread. Intensive surveillance and contact tracking identified 324 close contacts, and subjected to labortory test. 18 cases confirmed as per standard guidelines, of which 16 died in subsequent days. (CFR 88.8%). Three hospitals were identified as the possible points of infection transmission. 3000+ persons were tracked for 21 days to rule out NiV infection.Last case reported on 26.5.18 and outbreak closed on 7.7.18, after intensified surveillance for 42 days. Two survivors are being monitored for any long term consequences.

Conclusion: The first ever Nipah virus outbreak reported from Kerala state was responded with clinical precision,aided by strong political commitment,excellent adminsitrative back up and profound community participation.

10.012

Safety and Immunogenicity of a mRNA-based Chikungunya Vaccine in a Phase 1 Dose-Ranging Trial

C. Shaw[1], L. Panther[2], **A. August**[3], T. Zaks[4], I. Smolenov[5], S. Bart[6], M. Watson[7]; [1]Moderna, Cambridge/US, [2]Moderna, Clinical Development and Research, Cambridge/US, [3]Moderna, Cambridge, MA/US, [4]Moderna, Chief Medical Officer, Cambridge/US, [5]Seqirus , Therapeutic Area Head, Seasonal Vaccines, Cambridge/US, [6]Optimal Research, Chief Scientific Officer, Rockville/US, [7]Modernatx, Cambridge/US

Purpose: *Purpose:* Despite the public health impact and threat of Chikungunya virus, a globally re-emerging mosquito-borne alphavirus, there are currently no effective therapeutic or preventative options available. This phase 1 study investigates the safety and immunogenicity of a mRNA-based chikungunya vaccine.

Methods & Materials: *Methods and Materials:* We are conducting a phase 1, first-in-human, randomized, placebo-controlled, dose-ranging study to evaluate the safety and immunogenicity of mRNA-1388 (VAL-181388), a mRNA-based vaccine for chikungunya, in healthy adults aged 18-49 years in a non-endemic region in the United States. Subjects are assigned to one of three dose level cohorts, 25 µg, 50 µg or 100 µg, each randomized 3:1 active to placebo. Intramuscular injections are administered on weeks 0 and 4, and subjects are followed for 1 year after the last injection. The primary endpoint is to assess safety of the vaccine. The secondary endpoint is to assess immunogenicity by measuring chikungunya-specific neutralizing and binding antibody titers.

Results: *Results:* A total of 60 participants were assigned to receive 25 µg (n=15), 50 µg (n=15), or 100 µg (n=15) of mRNA-1388, or placebo (n=15). The study is fully enrolled and an interim analysis of safety and immunogenicity has been conducted on data through 1 month after the second vaccination. The vaccine was well-tolerated at all dose levels. Immunogenicity was assessed on the primary Intent-to-Treat dataset. A dose-dependent increase in neutralizing and binding antibody titers was observed, with a substantial boost after the second vaccination, and an associated 100% seroconversion for all subjects administered 100 µg of mRNA-1388.

Conclusion: *Conclusions:* The mRNA-based chikungunya vaccine is safe, well-tolerated, and immunogenic, and therefore a promising vaccine candidate worthy of further development.

10.013

Antibody Response In Borrelia Miyamotoi Infection Studied By Protein Microarray

O. Stukolova[1], J. Koetsveld[2], N. Kolyasnikova[3], D. Sarksyan[3], M. Toporkova[3], L. Karan[3], A. Dolgova[3], M. Markelov[3], J. Hovius[2], G. Shipulin[3], A. Platonov[4]; [1]CRIE, Molecular diagnostics and epidemiology, Moscow/RU, [2]University of Amsterdam, Academic Medical Center, Amsterdam/NL, [3]Central Research Institute of Epidemiology, Molecular diagnostics and epidemiology, Moscow/RU, [4]Central Research Institute of Epidemiology, laboratory of natural focal infections, Moscow/RU

Purpose: During *Borrelia miyamotoi* disease (BMD) patients produce antibodies to glycerophosphodiester-phosphodiesterase (GlpQ) and to highly antigenic surface variable major proteins (Vmps). Individual *B.miyamotoi* spirochetes expresses presumably one VMP, but *in vivo* "switching" between Vmps may occur, as observed in animal models of *B. miyamotoi*.

Methods & Materials: We here studied IgM and IgG antibody responses by producing a plane protein microarray containing GlpQ and four Vmps: variable small protein (Vsp) 1, variable large protein (Vlp) 15/16 (Delta subfamily), Vlp5 (Gamma subfamily), Vlp18 (Alpha subfamily). This selection of Vmps represents all subfamilies of *B.miyamotoi* Vmps and these specific VMPs were selected based on expression in *B.miyamotoi* strains HT31 or LB-2001. In addition our microarray contains 14 antigenic variants of 8 *B.burgdorferi sensu lato* proteins. We tested 219 sera from 50 PCR-confirmed Russian BMD patients. Samples were drawn between hospital admission and one year after disease. In addition, we tested 70 sera from 70 healthy blood donors

Results: Antibodies to GlpQ were detected in 46/50 BMD cases and 50/50 BMD patients produced antibodies to at least one Vmp: IgM and/or IgG antibodies to Vlp15/16, Vsp1, Vlp5 and Vlp18 were detected in 34, 22, 13, and 11 patients, respectively. Interestingly, antibodies to two different Vmps were detected in blood of 13 patients, antibodies to 3 or 4 Vmps – in blood of 4 and 3 patients, respectively.

IgM antibodies peaked approximately 13 days after onset disease and decreased one year after; IgG antibodies reached a plateau at day 40 that remained year after.

Conclusion: Serial measurement of anti-GlpQ and anti-Vmp antibodies provided the possibility to diagnose BMD with 99% specificity and 92% sensitivity. Since about 40% of patients responded to two of more Vmps, this suggests antigen switching and immune evasion in BMD.

Session 15 (Oral Presentations)
Bugs and Drugs: Bacterial Infections and Antimicrobial Resistance
Sunday, November 11, 2018
16:30 – 18:00hrs

_____

15.001

El Nino Southern Oscillation Predicts Vibriosis Risk in the United States

R. Ling[1], C. Logar-Henderson[1], **D. Fisman**[2]; [1]University of Toronto, Dalla Lana School of Public Health, Toronto/CA, [2]University of Toronto, Toronto/CA

Purpose: While epidemics of diarrhea caused by toxigenic strains of *Vibrio cholerae* are of global public health concern, non-toxigenic strains of *V. cholerae* and non-cholera *Vibrio* (NCV) species are also important causes of human disease, including foodborne illness, skin and soft tissue infection, and sepsis. These bacteria are abundant in ocean waters, and climate change (and associated ocean warming) could lead to increased incidence of NCV infection.

Methods & Materials: We obtained United States monthly national vibriosis case counts by digitizing annual reports from the U.S. Cholera and Other *Vibrio* Illness Surveillance (COVIS) surveillance system from 1999 to 2014. Monthly population denominators were derived from census data. Oceanic conditions for the Pacific and North Atlantic Ocean, respectively, were modeled based on the Multivariate El Nino Index (MEI) and the North Atlantic Oscillation Index (NAO). The irregular nature of fluctuations in MEI, and the similarity of El Nino-like conditions to projected future climatic change conditions, have led to its use as a natural experimental exposure that may predict future climate change effects. We constructed distributed nonlinear lag models that estimated integrated risk of vibriosis based on integrated effects of lagged oceanic conditions over a 12 month period.

Results: Poisson models of temporal trend demonstrated significant seasonal oscillation (P-value for Fast Fourier Transform component < 0.001) and an 8% annual increase in disease risk (annual IRR 1.079, 95% CI 1.074-1.084). Distributed nonlinear lag models showed a strong association with El Nino-like Pacific Ocean conditions over the subsequent 12 months (RR associated with MEI = 3, 1.708, 95% CI 1.285-2.272) but not North Atlantic Conditions (RR associated with NAO = 3, 0.879, 95% CI 0.581-1.330).

Conclusion: While the lack in geographic specificity of cases in this national dataset limits our ability to identify oceanic effects on vibriosis risk with precision, we find that the past 15 years have witnessed a marked increase in vibriosis risk in the United States. This trend is explained at least in part by oceanic conditions that anticipate those that will be accentuated by global climate change.

15.002

An Outbreak of Necrotising Enterocolitis of Unknown Aetiology in Newborns Admitted to a Neonatal Unit in Gauteng Province, March – June 2018

A. M. Shonhiwa[1], L. Shuping[2], G. Feller[2], M. C. M. Mabotja[1], E. Ho[3], N. Makiwane[3], D. Lawrence[3], L. Nair[3], R. Chomba[4], S. Khumalo[5], K. McCarthy[1], G. Ntshoe[1], V. Essel[1], N. Govender[2], J. Fredericks[3]; [1]National Institute for Communicable Diseases, Division of Public Health Surveillance and Response, Outbreak Response Unit, Johannesburg/ZA, [2]National Institute for Communicable Diseases, Centre for Healthcare Associated Infections, Antimicrobial Resistance and Mycoses, Johannesburg/ZA, [3]University of the Witwatersrand, Department of Paediatrics & Child Health, Johannesburg/ZA, [4]National Health Laboratory Service, University of the Witwatersrand, Department of Clinical Microbiology and Infectious Diseases, Johannesburg/ZA, [5]Gauteng Department of Health, Environmental Health Directorate, Johannesburg/ZA

Purpose: A cluster of necrotising enterocolitis (NEC) cases among newborns admitted to neonatal ward at a Gauteng Province hospital was reported to the National Institute for Communicable Diseases on 4/4/2018. An investigation was conducted to determine the possible cause/source of the outbreak and implement prevention and control measures and make recommendation for prevention of future outbreaks in this setting

Methods & Materials: A cross-sectional study was conducted to describe the clinical, epidemiological and environmental characteristics and determine possible source/cause of the outbreak among newborns admitted to a neonatal ward in March to June 2018. Blood cultures (Bacterial/fungal blood stream infections), bacterial (*Salmonella*, *Shigella* and *Campylobacter* and enterohemorrhagic *Escherichia coli* species) stool cultures and real-time polymerase chain reaction for enteric viruses (rotavirus, astrovirus, sapovirus, norovirus and adenovirus) was carried out.

Results: A total of 37 cases, including 35 (95%) premature and two (5%) full-term babies were reported. Of the 37; eight (22%) died, 20 (54%) discharged, three (8%) transferred to other hospitals, six (16%) were still admitted. Twenty-one (57%) had stage IIA disease, nine (24%) stage IIB, three (8%) stage IIIA and four (11%) stage IIIB. Children aged <1 month accounted for 89% (n=33) of the cases. Eleven (30%) cases were fed breast milk, 10 (27%) were formula fed and 12 (32%) were on mixed feeding, while feeding type was unknown in four cases (11%). Blood cultures were performed in 33 cases (89%); no bacterial/fungal growth in 16 cases (48%), various pathogens were isolated in 16 cases (48%). Stool samples were tested in 17 cases (46%), none of the enteric pathogens tested for were isolated. *Bacillus* cereus and *Streptococcus* species were isolated in different brands of prepared and unprepared formula milk.

Conclusion: Although the aetiology and source of the outbreak has not been established, the isolation of *B*. cereus and *Streptococcus* species in formula milk is concerning. However, these findings should be interpreted with caution as toxin production tests were not done, *B*. cereus and *Streptococcus* species were not tested for in stools and the investigations are ongoing. Strengthening and strict adherence to infection prevention and control practices are recommended to prevent horizontal spread of potential pathogens.

15.003

Foodborne Outbreak Of An Acute Streptococcal Pharyngitis In A Portuguese Air Force Training
Center

J. S. M. Pita, T. Santiago, M. Monteiro; Portuguese Air Force, Health Department, Lisbon/PT

Purpose: On July 19th 2017, a sudden onset of several cases of pharyngitis took place at the Centro de Formação Militar e Técnica da Força Aérea (CFMTFA) - Air Force Military and Technical Training Center, in Ota, Alenquer, Portugal. The diagnosis of Group A Streptococcus pharyngitis (GAS) was soon established. The aim of this presentation is to describe the procedures used in the investigation of a streptococcal outbreak and to alert for the relevance of the foodborne transmission of GAS.
Methods & Materials: Diagnosis was confirmed by Clearview ® rapid test. All symptomatic cases were treated with a single intramuscular administration of Penicillin G benzathine 1.200.000 U and sent to mandatory convalescence at home. Due to the sudden presentation of several cases initial food dissemination was suspected. General hygiene measures were reinforced, especially regarding food handling. At-risk groups were screened with the rapid test and positive individuals were prophylactically treated. An epidemiological survey was carried out by the Health Department of the Portuguese Air Force.
Results: A total of 110 cases with a clinical compatible with GAS tonsillitis were recorded, with an overall attack rate of 16.03%. According to the epidemiological survey, the salad served in the 17th of July at lunch was significantly associated with the symptomatic students, showing an odds ratio of 1.75 (95% confidence interval 1.05-2.82, p=0.024). All bacteriological samples were negative, however it was not possible to analyze the sample with the associated risk. The epidemiological curve reveals two incidence peaks of onset of symptomatology, a first peak on July 19 and another peak 6/7 days later.
Conclusion: The epidemiological report suggests that food dissemination of GAS in the salad served at lunch on July 17th might have been the initial transmission via, followed by secondary interpersonal airborn transmission. Containment of the outbreak depended on the speed of diagnosis, therapy administration, reinforce of individual hygiene and food safety measures. These are critical measures when food manipulation is concerned. Although a streptococcal pharyngitis is typically airborne transmitted, it's important for all health personnel be aware that the foodborne transmission of GAS exists and it's relevant.

15.004

Silent antibiotic resistance genes: A threat to antimicrobial therapy

D. Vk[1], S. Srikumar[2], S. Shetty[3], S. van Nguyen[2], I. Karunasagar[3], S. Fanning[2]; [1]Nitte University Centre for Science Education and Research, Mangaluru, KARNATAKA/IN, [2]University College Dublin, Food Safety and zoonoses, Dublin/IE, [3]Nitte University Centre for Science Education and Research, NUCSER, Mangaluru/IN

Purpose: Bacterial resistance to drugs is an increasing threat to the human community. In recent times the resistance of Gram negative bacteria to several classes of drug such as beta lactams, fluoroquinolones, aminoglycosides and colistin is gaining importance as it is involved in severe health complications in humans. In addition, many reports suggest the presence of silent antibiotic resistance genes with varying level of expression could also pose a severe threat to the public health.
Methods & Materials: An *E. coli* isolate (MU2) phenotypically sensitive to quinolone/fluoroquinolone harboring *qnrB* resistance gene was selected in this study. To identify the silent nature of this resistance gene, plasmid sequencing was carried out. The growth kinetics of the isolate was determined and different stages were designated as Early Exponential Phase, Mid Exponential Phase (MEP), Late Exponential Phase, Early Stationary Phase and Late Stationary Phase. MU2 was subjected to various gut conditions such as bile shock, H_2O_2 shock, anaerobic shock and NaCl shock at MEP. Further, *TaqMan* probe real time PCR was carried out to check the variations in the expression of *qnrB* in *in vitro* gut conditions.
Results: We have earlier identified a plasmid-borne silent chloramphenicol resistance gene (*catA1*) in phenotypically sensitive *Salmonella* Weltevreden and the reason for its unexpressive nature was found to be the deletion of the promoter region. Further a fluoroquinolone sensitive *E. coli* isolated from UTI infection with a MIC of 0.047mcg/ml for ciprofloxacin and 3mcg/ml for nalidixic acid found to harbor a silent plasmid mediated quinolone resistance gene (*qnrB*). The promoter region and the gene itself was intact. The plasmid sequencing revealed the presence of prophage.
Conclusion: The reversible nature of the silent antibiotic resistance gene can cause the emergence of fully antibiotic resistance revertants in the gut upon antibiotic challenge. Further, their presence in conjugative plasmid increases the risk of being transmitted to a susceptible strain and converting it to a resistant pathogen. However, in the present study, various *in vitro* gut shocks could not influence *qnrB* expression suggests that the mere presence of PMQR gene will not always confer fluoroquinolone resistance in bacterial pathogens.

15.005

Sharing Of Antimicrobial Resistance Genes Among Animals, Humans, And The Environment In Nepal: A One Health Case Study

C. Young[1], D. Kharmacharya[2], M. Bista[2], A. Sharma[2], T. Goldstein[3], S. J. Anthony[4], W. Smith[5], J. Mazet[6], C. Johnson[7]; [1]University of California, Davis, One Health Institute, Davis, CALIFORNIA/US, [2]Center for Molecular Diseases, Nepal, Kathmandu/NP, [3]University of California - Davis, Davis, CA/US, [4]Columbia University, Center for Infection and Immunity, MSPH, New York, NY/US, [5]UC Davis, Davis/US, [6]UC Davis, Davis, CA/US, [7]UC Davis, One Health Institute, Davis/US

Purpose: Widespread antimicrobial use and the subsequent emergence and spread of antimicrobial resistance (AMR) is a pressing global health issue. High rates of AMR have been reported globally, and new antimicrobial resistance genes (ARGs) are being discovered at an unprecedented pace (1,2). The growing problem of resistance is especially important in low- and middle-income countries, both from human and veterinary health perspectives. Evidence is mounting that AMR is transmitted between animals, humans, and the environment through complex transmission routes (3,4). Therefore, a one health lens is needed to understand AMR transmission at the human-animal-environment interface and inform public policy (5). We investigated ARGs at an urban informal settlement study site with intensifying backyard livestock production in Nepal. Fieldwork was designed to examine sharing of ARGs among environmental, animal, and human samples within a community.
Methods & Materials: We sampled concurrently in time at an informal settlement in southeastern Kathmandu along the Manohara river, including humans (n=88), chickens (n=47), ducks (n=35), swine (n=11), and water (n=17) clustered by household, as well as rodents (n=8) and shrews (n=12) near dwellings. Real-time qualitative PCR was performed using the QIAGEN Antibiotic Resistance Genes array to screen for 88 different ARGs from 16 resistance classes.
Results: Seventy out of 88 ARGs were detected, with ARGs found in all but 12 samples (7 rodent, 5 water samples). The highest prevalence of ARGs were detected in ducks. Sharing of the same ARG among different species was widespread, and ARG prevalence varied markedly by species and sample type. Overall, *ermB*, *tetA*, *mefA*, and *tetB* were most commonly detected; antibiotics associated with these ARGs are widely used in Nepal (6).
Conclusion: This investigation characterized antimicrobial resistance sharing among humans and between human, animal, and environmental niches in Kathmandu, Nepal to aid in determining possible pathways for spread of ARGs within and between different reservoirs. The one health concurrent sampling study design presented here provides an overarching screening tool on which to base further efforts to elucidate transmission routes, characterize ARG bacterial reservoirs, and inform policy for promoting good stewardship and combating the spread of resistance among and between animals, humans, and the environment.

15.006

Molecular Surveillance for Drug Resistant Plasmodium falciparum Imported to Ontario

R. Kariyawasam[1], E. Shao[2], R. Lau[3], A. Showler[4], F. Ralevski[3], **A. K. Boggild**[5]; [1]University of Toronto, Institute of Medical Science, Toronto/CA, [2]Western University, Toronto/CA, [3]Public Health Ontario, Public Health Ontario Laboratories, Toronto/CA, [4]Georgetown University, Washington/US, [5]University of Toronto, Department of Medicine, Toronto, ON/CA

Purpose: *Plasmodium falciparum* can lead to rapid and fatal malaria in humans. Single nucleotide polymorphisms (SNPs) at several loci have been correlated to *P. falciparum* drug resistance. We examined the prevalence of molecular markers of resistance in *P. falciparum* imported to Ontario during three time periods over 10 years.

Methods & Materials: Biobanked isolates of *P. falciparum* detected in whole blood at the Public Health Ontario Laboratory between 2008-2009, 2013-2014, and 2017-2018 were screened for resistance SNPs at the following gene targets by pyrosequencing: PfATPase6 (*atpase6*), chloroquine resistance transporter *(pfcrt),* cytochrome b *(cytb),* dihydrofolate reductase-thymidylate synthase *(dhfr),* dihydropteroate synthetase *(dhps),* and multidrug resistance protein *(mdr1)*. Isolates were also screened for mutations of the kelch13 propeller region (*kelch13*) by Sanger sequencing. Mutation prevalence was calculated and compared across time periods.

Results: Two-hundred, twenty-three unique isolates of *P. falciparum* were identified from 2008-2009 (n=75), 2013-2014 (n=79) and 2017-2018 (n=69). Of 223 isolates, 126 had a documented travel history, with most (88%) imported from sub-Saharan Africa. Significant decreases in mutant genotypes from 2008-09 to 2013-14 for *mdr1* N86Y ($p<0.001$), D1246Y ($p=0.007$), *pfcrt* K76T ($p=0.032$) were observed. Similarly, significant decreases in mutant allelic frequencies were observed from 2013-14 to 2017-18 for *mdr1* N1042D ($p=0.0065$); and *cytB* Y268NSC ($p=0.0038$) and *mdr1* N86Y ($p=0.003$) across the three time frames. Significant increases in mutant allelic frequencies for *pfcrt* C72S ($p=0.027$); *dhfr* A16V ($p=0.01$), C50R ($p=0.04$); *dhps* K540E ($p<0.001$), A581G ($p<0.001$), A613S ($p<0.001$), and *mdr1* N1042D ($p<0.001$) were observed between 2008-09 and 2013-14. A significant increase in mutant allelic frequencies for *atpase6* was observed from 2013-14 and 2017-18 ($p <0.0001$). *Kelch13* mutations were not identified in any isolate between 2008-09 and 2013-14, including the 4 imported from southeast Asia.

Conclusion: Mutant genotypes for several molecular markers of drug resistance were highly prevalent among *P. falciparum* isolates imported to Ontario, especially mutations in *dhfr* conferring resistance to proguanil. Our observation of minor genotypes confirms the heterogeneous nature of infection, which may lead to differential drug resistance levels and therapeutic failure. *Atpase6* has shown significantly increases in mutant allelic frequencies associated with artemisinin resistance and warrants sustained surveillance.

15.007

Prevalence and Antimicrobial Resistance of Escherichia coli and Salmonella spp. Isolated from Poultry Drinking Water and Cloacal Swab Compared of Two Regions in Thailand

L. D. Lawwyne[1], C. Ruenghiran[2], S. Viriyarampa[3], S. Chumsing[3], **P. Tulayakul**[2]; [1]Faculty of Veterinary Medicine, Kasetsart University, ○Bio-Veterinary Science (InterRisk Program), Bangkok/TH, [2]Kasetsart University, Faculty of Veterinary Medicine, Bangkok/TH, [3]Faculty of Veterinary Medicine, Kasetsart University, Veterinary Public Health, Bangkok/TH

Purpose: A study was conducted to determine the prevalence as well as the antimicrobial susceptibility of Escherichia coli and Salmonella spp. from poultry drinking water and cloacal swab.
Methods & Materials: Water sample was analyzed to check water quality of poultry farm and laboratory method was used to confirm *E coli* and *Salmonella* spp. Isolates were tested to antimicrobial susceptibility testing using VetMIC and MICs are determining for Ampicillin, amxocillin, clavulanic acid, piperacin, cefalexin, cefovecin, cefpodoxime, ceftiofur, amikacin, gentamacin, tobramycin, imipenem, trimethoprim/sulfamethoxazole, chloramphenicol, enrofloxacin, marbofloxacin, polymyxin B, tetracycline, nitrofurantoin and rifampicin.
Results: The water samples from region 1 and 7 showed within acceptable level and it is suitable for poultry. None of the samples from water and cloacal swab were positive for *Salmonella* spp. *E coli* were found 10.7% in the water sample of 2018 and 7.14% from 2017. Cloacal swab sample showed 100% positive results. The highest rate of resistance was against ampicillin (100%), +amoxicillin (100%), tetracycline (100%), enrofloxacin (50%), marbofloxacin (50%), chloramphenicol (40%) and trimethoprim/sulfonamide (33%). Low levels of resistances were against gentamacin (20%), piperacin (20%), clavulanic acid (10%), cefalexin (10%), cefovecin (10%) and cefpodoxime (10%).
Conclusion: The antimicrobial profile showed that *E coli* isolates from both areas are highly resistant to ampicillin, amoxicillin and tetracycline. Multiple resistances were observed in all *E coli* isolates and long term monitoring must be carried on.

15.008

Staphylococcus aureus Nasal and Intestinal Carriage by Free-Ranging Red Deer: Evidence of Human, Domestic and Wild Animal Lineages

C. Luzzago[1], S. Lauzi[1], R. Ehricht[2], S. Monecke[2], T. Trogu[3], L. Pedrotti[4], P. Lanfranchi[1], R. Piccinini[1];
[1]University of Milano, Department of Veterinary Medicine, Milan/IT, [2]Abbott (Alere Technologies GmbH), InfectoGnostics Research Campus, Jena/DE, [3]Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Brescia/IT, [4]Parco Nazionale dello Stelvio, Bormio/IT

Purpose: Habitat loss and fragmentation, caused by human activities, can trigger interactions among humans, domestic and wild animals, creating opportunities for the transmission of infectious agents. In Stelvio National Park (SNP, Central Italian Alps, Lombardy sector), the increase of the red deer population, associated with an intense browsing impact and cross transmission of pathogens with livestock, imposed the activation of a culling plan. Moreover, culled deer from SNP entered the human food chain with 37.3 tons of meat in 2011-16.
This study evaluates the prevalence and genetic characteristics of *Staphylococcus aureus* isolates from nasal cavities and rectal tracts in red deer culled in SNP in January and February 2017.
Methods & Materials: Both nasal swabs and feces or rectal swabs, collected from 75 red deer, were incubated in Mueller-Hinton broth with 6.5% NaCl and seeded on Baird-Parker with rabbit plasma fibrinogen. *S. aureus* was confirmed by amplification of the *nuc* gene. One isolate per collection site from simultaneous nasal and intestinal carriers was characterized using a *S. aureus*-specific DNA microarray, which detects over 333 genes and alleles.
Results: A *S. aureus* prevalence of 90.67 % (95% CI: 81.97-95.41) and 26.67 % (95% CI:17.98-37.63) was detected in nasal and intestinal site respectively. All intestinal carriers (n=20) had also a nasal colonization. Clonal complex (CC) 425, known to be widespread in ruminants, was the most prevalent lineage (68.29%). Notably, 67.86 % of CC425 strains carried the leukocidin genes *lukM/lukF-P83*, which are not typical of this lineage. Further lineages identified included some that are also known to infect humans and/or livestock (CC7, CC9, CC350, CC707) and some (CC2328, CC2671) that are so rare that no epidemiological information is available. All isolates were negative for methicillin resistance genes, but human lineages harbored penicillin resistance genes and one isolate also *ermA* gene.
Conclusion: A high prevalence of *S. aureus* carriers has been observed among free-ranging red deer during the cold season in the Alps. Red deer *S. aureus* population mainly comprised lineages known to occur in domestic and wild ruminants. Sporadic overlaps with human and other animal lineages were observed.

_____

17.001

The Role Of Entry-Screening Procedures In The Identification Of Multidrug-Resistant *Mycobacterium Tuberculosis* Cluster Cases Amongst Patients Arriving In Europe From The Horn Of Africa, 2016-17.

P. Helbling[1], S. Kröger[2], W. Haas[2], S. Brusin[3], D. Cirillo[4], R. Groenheit[5], J.-P. Guthmann[6], H. Soini[7], **G. Pfaff**[8], D. Hendrickx[9], M. van der Werf[3]; [1]Federal Office of Public Health, Berne/CH, [2]Robert Koch Institute, Berlin/DE, [3]European Centre for Disease Prevention and Control, Solna/SE, [4]IRCCS San Raffaele Scientific Institute, Milan/IT, [5]Public Health Agency of Sweden, Solna/SE, [6]Santé Publique France, Paris/FR, [7]National Institute for Health and Welfare, Helsinki/FI, [8]Baden-Wuerttemberg State Health Office, Stuttgart/DE, [9]State Public Health Office of Baden-Württemberg, Stuttgart/DE

Purpose: A cluster of 36 multidrug-resistant tuberculosis (MDR-TB) cases among migrants was identified in 2016-17 in eight European countries. We aimed to determine in how far country migrant entry TB screening procedures contributed to the identification of cluster cases to inform public health policy.

Methods & Materials: We conducted a survey amongst countries known to be affected by the MDR-TB cluster to describe their migrant entry TB screening procedure, to identify the screening status (screened vs not-screened) of cluster cases, and to document the occasion of their diagnosis. Where cluster cases were not identified at screening, we sought to clarify why.

Results: Six of eight countries responded. Entry TB screening procedures varied by country. Screening information was received for 32 out of 36 cluster cases (89%). A total of twenty-seven cases (84%; age range 15 to 25 years) had been screened, all either in Germany (19) or Switzerland (8), where screening is mandatory. Cluster cases in France (1), Italy (2) and Finland (1) did not undergo entry screening. A cluster case in Sweden was diagnosed before entry screening. Amongst screened cases, 13 (48%) were diagnosed as a result of the screening, 12 (44%) later, when they became symptomatic, and 2 (7%) as part of contact tracing investigations. Unscreened cluster cases (5) were diagnosed when TB symptoms developed and medical care was sought.

Conclusion: Systematic entry screening programmes, where mandatory, contributed to MDR-TB cluster case identification for migrants with active disease. Essential, however, is ensuring barrier-free access to host-country health systems after arrival and ensuring health care workers' awareness of TB in persons from countries with a high incidence.

17.002

Traveller Sentinels for Global Surveillance of Malaria Drug Resistance and Diagnostic Test Evasion

C. Prosser[1], W. Meyer[2], J. Ellis[3], R. Lee[4]; [1]University of Sydney, Sydney Medical School, Sydney/AU, [2]University of Sydney, Westmead Institute for Medical Research, Sydney/AU, [3]University of Technology Sydney, School of Life Sciences, Sydney/AU, [4]Westmead Hospital, Centre for Infectious Diseases and Microbiology Laboratory Services, ICPMR , Westmead/AU

Purpose: Emerging drug resistance in *Plasmodium falciparum* imperils malaria control and elimination. Recently, resistance to the frontline therapy drug artemisinin, and combination therapy partner drugs, is accelerating throughout South East Asia. Molecular surveillance of genetic markers is a valuable tool to inform policy and forestall widespread drug resistance, however many regions are underrepresented in molecular studies. This project aimed to investigate imported malaria cases from travellers, immigrants, and refugees entering Australia to report on genotypes from neglected regions under selection.

Methods & Materials: Malaria diagnostic samples from the NSW Parasitology Reference Laboratory (n=397) were screened for known molecular markers of drug resistance including *pfKelch13* mutations underlying artemisinin resistance. The cohort was also screened for the presence of exons 1 and 2 for both *pfHRP2* and *pfHRP3* (deletion resulting in false negative results with rapid diagnostic tests). This cohort captured many endemic regions with limited ongoing surveillance – notably South Sudan and southern districts of Thailand. Epidemiologically relevant deidentified patient data associated with each case allowed patient profiling for trend analysis and increased the utility of molecular results.

Results: Propeller domain *pfKelch13* mutations were observed, including the C580**Y** mutation most strongly associated with artemisinin resistance. C580**Y** was found in an indigenous lineage of *P. falciparum* originating from Papua New Guinea, where resistance-associated kelch mutations were previously unreported. C580**Y** mutations were additionally observed (n=10/91) in Southern districts of Thailand, where treatment failure has been reported for the first time in 2018 (extending the known South East Asian artemisinin resistance perimeter).

Conclusion: The surveillance results demonstrate the utility of screening travellers as sentinels to report much needed molecular data for areas underrepresented in global surveillance of emerging malaria drug resistance and diagnostic test evasion.

17.003

The Potential for International Dissemination of Emerging Viral Pathogens

J. M. Read[1], D. Cummings[2]; [1]Lancaster University, Lancaster Medical School, Lancaster/UK, [2]University of Florida, Emerging Pathogens Institute, Gainesville/US

Purpose: Global pandemic preparedness requires an understanding of the risk of international spread following the emergence of a novel pathogen. Here we ask: what is the risk that international dissemination of human cases may already have occurred at the point human-to-human transmission of a novel pathogen is identified? We illustrate general findings by considering the emergence of human-adapted avian influenza A(H7N9) in China.

Methods & Materials: Using A(H7N9) case information published by the World Health Organization (WHO), we analysed factors associated with the time interval between onset of symptoms and WHO reporting, using time-to-event (survival) models. We constructed a stochastic epidemic model with realistic disease characteristics to estimate the risk of international dispersion of cases at the point the epidemic is identified. International travel patterns were parameterised using contemporary aviation industry passenger information.

Results: The median delay between symptom onset and WHO reporting was 14 days (mean 19.2 days) and ranged between 2 and 86 days; delays were significantly associated with the age, sex and province of cases, and with epidemic wave. Provinces with historically high A(H7N9) incidence are generally regions with a high level of departing domestic and international airline traffic. Taiwan, Thailand, South Korea, and Japan were found to have the highest probability ($p>0.05$) of having already imported cases when emergence is identified within China. The high volume of domestic travel related to Chinese New Year significantly increases the potential for within-China dissemination. Shorter incubation periods and higher R_0 cause cases to accumulate faster, which may translate to earlier detection of an emergence event.

Conclusion: Due to high levels of internal travel and the strong global connectivity of China, at the point a human-adapted epidemic is recognized to be underway, simulations suggest epidemics sufficiently large to represent a risk of international spread are possible by the time human-to-human transmission is recognized in an emergence scenario. The rapid detection and reporting of human-to-human transmission are important factors in containing a pandemic at source.

17.004

Outbreak DIY: A new tool for public communication about infectious disease and One Health

S. Sholts[1], A. Chang[2]; [1]Smithsonian Institution, Anthropology, Washington DC/US, [2]Smithsonian Institution, Office of Exhibits, Washington/US

Purpose: A free, customizable version of the Smithsonian exhibit *Outbreak: Epidemics in a Connected World* can help communities to raise awareness and understanding about public health issues.

Methods & Materials: *Outbreak: Epidemics in a Connected World* is an exhibition created by the Smithsonian's National Museum of Natural History (NMNH) that examines zoonotic emerging infectious diseases (EIDS) and our increasing pandemic risks in the 21st century. An adaptable and customizable Do-It-Yourself version of the NMNH exhibition, *Outbreak DIY*, was created and made freely available in May 2018. *Outbreak DIY* was designed to be easily installed in any type of location, such as hospitals, libraries, train stations, coffee shops, community centers, offices, and schools. Each interested venue is provided with digital design files for 16 pre-designed Exhibit Panels that each address one topic from the NMNH exhibition, such as "One World, One Health", "Vaccination Equals Prevention", and "Fighting Fear". These Exhibit Panels are available in a bilingual format that pairs American English with Arabic, Chinese (Simplified or Traditional), French, Spanish, or Thai. Venues are welcome to create additional translations and/or customize panels with two Panel Templates to serve their needs. Panels can be printed and fabricated in different sizes and materials, such as full-size posters on foam board or corrugated plastic, free-standing display banners, letter-size papers, or digital displays or projections. A multilingual selection of videos and interactive games and a variety of 3D printable models from the NMNH exhibition are also available. In addition, venues are provided with a Resource Guide that includes materials for promoting their exhibition, programming ideas for public events and activities, and suggestions and resources for training exhibition volunteers and staff.

Results: By June 2018, more than 50 venues in over 30 countries requested materials for *Outbreak DIY* exhibitions. Venue types include universities, museums, embassies, and libraries, and many expressed interest in customizing their exhibitions with Panel Templates.

Conclusion: *Outbreak DIY* is a desirable and versatile tool for community engagement with messages about EIDs and One Health. Its multilingual and customizable content have the potential to serve the global public on a scale unprecedented for a museum exhibition.

17.005

An Epidemic of Tariffs? Infectious Disease and Global Trade in an Era of Change

A. M. Kimball; Chatham House, Global Health Security, London/US

Purpose: Purpose: To examine the current state of trade related embargoes and regimes and how they affect or are impacted by outbreaks of infectious diseases.

Methods & Materials: Methods & Materials: Based on notifications to the World Trade Organization of urgent measures related to health concerns four historical case studies were reviewed: BSE (2000), Cholera in Lake Victoria (1998-2002), Cholera in Peru (1991) and Ebola (2014-2015). Subsequent notifications are also systematically reviewed. These observations are then placed in the context of IHR implementation and the shifting paradigms of the global multilateral trade regime.

Results: Results: 1) Health is the major justification provided for urgent measures trade disruption by WTO member countries 2) .Historically trade disruption is the major indirect cost of epidemics of infectious diseases 3) "Regionalization" as a national strategy by embargoed countries has mitigated costs of infections declared within nations. 4) In the era of IHR implementation the system remains vulnerable to non tariff trade restriction due to infectious disease outbreaks. This vulnerability may increase in this era of bilateral tariff restrictions.

Conclusion: Conclusion: As the global multilateral trading system enters a period of unprecedented challenge through "security" related tariffs and reciprocal tariffs on goods, the potential costs of outbreaks require careful consideration to assure population health into the future

17.006

Risk Communication of Zoonotic Spillover: Initial Lessons from a Satellite-Based Forecasting Platform

S. Malloy[1], E. Root[2], K. McAfee[1], E. Newton[1], D. Abernathy[1], A. Sauer[1], A. Steen[1], J. Horack[3];
[1]Battelle Center for Science, Engineering and Public Policy, Columbus/US, [2]The Ohio State University, Epidemiology, Columbus/US, [3]The Ohio State University, College of Engineering, Columbus/US

Purpose: While drivers of zoonotic spillover of emerging infectious diseases have been identified, few tools have been developed to understand how risk of spillover is precipitated by human activity in real time. We expand on recent efforts to develop a satellite-based forecasting platform for zoonotic spillover by describing implementation efforts through a user-driven design process. The pilot platform uses a spatial reduction approach to identify high-risk changes at the human-ecosystem interface in near real-time, and generates alerts for a target audience of surveillance practitioners and policymakers interested in directing prevention and mitigation resources with more precision.

Methods & Materials: We describe the implementation analysis for a prototype application that generates near real-time assessments of generalizable zoonotic spillover risk. Alerts of rapid change are generated at a spatial resolution of 30 meters and a temporal resolution of one week; further analysis with high spatial and hyperspectral imagery improves spatial resolution by one order of magnitude and characterizes disturbance type with high confidence. Through informal interviews and surveys with individuals identified as potential users, we implement an iterative design process to move from beta testing to a proposed final user interface design. Survey results and initial interviews informed a focus group following beta testing, which was used to enhance design features through an interactive group discussion which included simulating the use of the prototype.

Results: The iterative design process demonstrates that users are interested in clearly defined, actionable information, and benefit from contextual analysis in addition to statistical outputs alone. It is useful to delineate the algorithmic steps that lead to an alert, and furthermore to highlight at which point an alert is the product of human analysis and is no longer an automated process. Unfamiliarity with remote sensing techniques must be addressed through clear user-interface design features that interpret outputs for the public health community.

Conclusion: Near real-time assessment of the primary known drivers of zoonotic spillover can improve the spatial and temporal resolution of EID surveillance and can contribute to a proactive risk reduction strategy, but automated alerts must be provided with a clear preliminary interpretation for users to feel this information is actionable.

17.007

Development Of A Sustainable Diagnostic Toolbox For Serosurveillance Of West African Infectious
Diseases

K. M. Ricks[1], J. Koehler[2], C. Shoemaker[2], M. Voorhees[2], R. Schoepp[2]; [1]USAMRIID, Diagnostics Systems, Frederick, MARYLAND/US, [2]USAMRIID, Frederick/US

Purpose: The spread of infectious disease continues to present a challenge for modern global public health initiatives, as was evidenced by the recent Ebola outbreak in West Africa. In order to understand emerging and re-emerging pathogens and risk of exposure, overseas laboratories need access to sustainable and reliable immunodiagnostic assays.

Methods & Materials: We designed a multiplexed immunoassay centered on coupling recombinant proteins and/or virus-like particles to magnetic beads to detect IgM and IgG in a serum sample for EBOV, LASV, MARV, CCHFV, RVFV, alphaviruses, and flaviviruses. This flexible, immunoassay system, based on the MAGPIX® platform, improves sensitivity by up to 2-logs and has faster sample-to-answer time over traditional methods. Assays were developed and validated with animal models and human samples of known etiology. Nigerian human sera, through an acute febrile illness (AFI) study collaboration with the Joint West Africa Research Group (JWARG), were then screened with these assays to determine disease prevalence.

Results: Greater than 50% IgG prevalence for alphaviruses and flaviviruses was observed, which is expected as it is known these families of viruses circulate in these regions. Less than 10% IgG prevalence rates were observed for MARV, EBOV, LASV, and RVFV. Notably, we observed greater than 50% CCHFV IgG prevalence rate in samples tested.

Conclusion: Understanding the seroprevalence of emerging infectious diseases can give us a window into the risk of potential outbreaks. In the future, we will continue to screen AFI samples in Nigeria, Ghana, and Liberia in collaboration with JWARG. We also aim to extend surveillance to East African countries—Uganda and Kenya. Additionally, we hope to utilize these assays to screen acute sera for IgM and antigen prevalence. By developing a sustainable diagnostic program and transitioning these capabilities to our in-country collaborators, we have the best chance at rapidly responding to emerging infectious diseases and ultimately avoiding another widespread outbreak.

17.008

A Role for EpiCore with International NGOs: the Experience of MSF Spain (2018)

J. Mantero[1], M. J. Sagrado[2], R. Gutierrez[2], M. Libel[1], N. Divi[1], J. F. Saint-Sauveur[2], M. Smolinski[1];
[1]Ending Pandemics, San Francisco/US, [2]Doctors without Borders (MSF) - Spain, Medical Department, Barcelona/ES

Purpose: Epicore is a network of over 2,200 volunteer health professionals from 145 countries supporting the verification of public health events identified from informal sources. Volunteers operate as "Responders" and share their knowledge about events described in requests for information (RFI) sent by "Requesters" through a secure web-based platform. Originally designed to engage only ProMED as a requester, EpiCore has now expanded to allow multiple organizations to send RFIs on the platform, most recently engaging Médecins Sans Frontières Spain (MSF-E). We have reviewed Epicore RFIs created in 2018 to understand the potential value to NGOs in terms of operational implications within their activity.

Methods & Materials: We performed an analysis of EpiCore RFIs sent during January-June 2018 with a special focus on the ones that highlight the value EpiCore potentially provides to NGOs.

Results: Three selected RFIs that highlight valuable information provided to MSF-E via EpiCore are described here. The first RFI referred to rumors on several meningitis cases in Imatong (South Sudan, March): cases were confirmed within 1 hour by members that provided additional details quoting local health authorities. The second RFI was sent for verification purposes as well and followed rumors about suspected hemorrhagic fever cases in Manafwa (Uganda, May): suspect of Ebola was discarded within 12 hours by members quoting local health authorities and the event was described as a cluster of severe malaria complicated by blackwater fever syndrome (BWF). The third RFI was sent for monitoring purposes in relation to an ongoing concerning measles situation (Venezuela, May): the network provided epidemiological updates from 6 countries in the Region using official data. All the information collected in these cases was shared by MSF-E within the organization for risk assessment purposes.

Conclusion: EpiCore has enabled MSF-E to collect relevant information about public health events of concern. It has shown potential as a tool for such NGOs enabling first hand information gathering during preliminary stages of events and when information sources are limited. Further studies are needed to assess contribution to timely management of response activities.

17.009

How Culture Collections can Assist Responses to Emerging Diseases

K. Buttigieg, S. Alexander, J. Russell; Public Health England, Porton Down/UK

Purpose: Making relevant strains of emerging infectious diseases available to the research community

Methods & Materials: Culture Collections operated by Public Health England is a not-for-profit organisation that obtains, curates, authenticates and supplies strains of bacteria, viruses, fungi, and cell lines to researchers all over the world. The National Collection of Pathogenic Viruses (NCPV) and the National Collection of Type Cultures (NCTC) work with specialists in various fields who have isolated emerging or outbreak strains to accession these into the Collections free of charge. NCPV and NCTC bank, authenticate and viability test every batch of virus or bacteria produced, before listing them in an online catalogue and distributing them to genuine researchers at cost. Extracted nucleic acid is also available for genomic analysis or to researchers without access to containment laboratories.

Results: Five of the six viruses requiring handling at BSL2-3 that were identified by the World Health Organisation as most likely to cause severe outbreaks, are available from NCPV. The remaining viruses, requiring BSL-4 facilities, are either also available directly from NCPV or from our collaborators. For the first few months of the Zika virus outbreak, NCPV was the only publically available source of Zika virus. NCPV was also the exclusive source of the first Zika virus strain with extensive genome sequence data isolated from a semen sample.

Conclusion: Field epidemiologists, healthcare workers and researchers responding to outbreaks should deposit isolates of circulating strains into the Culture Collections, to facilitate the international response in understanding pathogenesis and developing novel interventions.

17.010

Improving Community Resilience through the Development of an Epidemic Risk and Priority
       Framework

K. Arslantas, F. Hierink, A. Teng, F. Lammers, C. Meijerink, B. Veneman; The Netherlands Red
Cross, 510 Data Team, Den Haag/NL

Purpose: Epidemics rank among the most costly and destructive of natural hazards.In the past few
years outbreaks such as Ebola, Zika, MERS and SARS demonstrated the limited preparedness to
respond swiftly and appropriate. This highlight the need to develop more proactive instead of reactive
policies Existing frameworks for epidemic response are either disease specific, category specific or
nonspecific national models, but so far no model exist that combine all elements. The aim of this
study is to create a holistic framework for early warning system for disease outbreaks by identifying
the risk factors of epidemics at an early stage. This framework can guide towards evidence based
decision making and prioritization.

Methods & Materials: INFORM is used as base for the new conceptual framework, as it is
recognized by various humanitarian organizations, and shown to be holistic. Literature reviews were
conducted to specify the framework specifically for and identify risk factors/indicators of epidemics.
The framework is tested by statistical modelling using data from the Philippines as a case study. The
model uses existing open data and compares it to the local dengue incidence in the Philippines. The
statistical methodology follows the steps to develop a composite indicator according to the 10-step
guideline by OECD.

Results: The results of the first analyses show an association between all dimensions and dengue
risk in the Philippines. However, when comparing the dimensions; infectious hazard and exposure,
vulnerability, and lack of coping capacity, especially the categories behavior and socio-economic risk
factors tend to contribute to dengue risk in provinces within the Philippines. Lack of coping capacity
contributes to a lesser extent to dengue risk. Further analyses are needed to study the relation.

Conclusion: The initial results are positive and suggest that further development of a holistic
framework is promising. However, it is currently only in the assessment phase for Dengue in the
Philippines. Next phases of the study need to determine the applicability to other infectious diseases
and the transferability to other countries and how it can be adapted to ensure a holistic framework.
Continuous revision and evaluation of the chosen indicators will be necessary to make the framework
more robust.

17.011

Technology Volunteerism - the Red Cross' Approach to Developing a Digital Community Based Surveillance Tool for Early Detection of Diseases with Epidemic Potential

A. Kongelf[1], R. M. Bushby[2], S. Gejibo[2], G. Kaur[3], T. Tingberg[4]; [1]Norwegian Red Cross, International department, Oslo/NO, [2]Norwegian Red Cross, International Programmes and Preparedness, Oslo/NO, [3]Norwegian Red Cross, International Programmes and Preparedness, Nairobi/KE, [4]Norwegian Red Cross, International department , Oslo/NO

Purpose: The Red Cross/Red Crescent Movement is currently developing a cutting-edge community based surveillance (CBS) platform in partnership with volunteers from the Norwegian tech community. CBS enables volunteers in communities at risk of epidemic-prone disease outbreaks to communicate health risks in real-time, thereby closing the surveillance gap. Real-time risk monitoring at the community level provides early detection, enabling an early response. The Red Cross' innovative technology, therefore, has the potential to detect and stop outbreaks, ultimately reducing morbidity and mortality.

Methods & Materials: The project uses a novel two-fold volunteer model; volunteers in Norway build the platform software, while volunteers in-country operationalise the tool to report on health risks using SMS. This volunteer model allows for data collection, analysis and software programming to take place in conjointly, therefore providing an opportunity for the CBS platform to adapt to needs of unique operational contexts.

Results: To date, 122 tech volunteers have contributed to the open source software development, with over 2000 additions made to the code. An initial version, launched in May 2018, is currently being piloted by the Somali Red Crescent Society, where 75 volunteers are monitoring and reporting on the diarrhoeal cases through SMS. Their reporting is registered and analysed real-time, informing early action, while user experiences feed directly into platform development.

Conclusion: By closing the surveillance gap and enabling communities outside of traditional public health surveillance mechanisms to alert of potential outbreaks in real time, CBS could provide the means for early detection and early response. Simultaneous implementation and software creation provides an opportunity to build a contextually suitable platform, which is adapted to provide a simple and reliable means for early detection and warning of outbreaks. This ensures that health responses happen earlier. In 2019, the CBS platform will be made available to additional National Societies and in emergency contexts. This will be yet an opportunity to respond rapidly and accurately to outbreaks whilst simultaneously shaping technological developments.

17.012

Surveillance of laboratory exposure to human pathogens and toxins in Canada

F. Tanguay, M. Heisz; Public Health Agency of Canada, Ottawa/CA

Purpose: Mandatory laboratory incident reporting involving Risk Group 2, 3, and 4 human pathogens and toxins is an integral component under the purview of the *Human Pathogens and Toxins Act* (HPTA) in Canada since December 1st, 2015.

Methods & Materials: Standardized data collection for exposure and non-exposure laboratory incidents through an online electronic reporting system allows for early response to laboratory incidents to ensure root causes are correctly identified, corrective actions are sufficient and appropriate to mitigate immediate risks and prevent future reoccurrence.

Results: Since the launch of the laboratory incidents surveillance system in 2015, 278 notifications have been received. Forty percent (n=112) of these reports were linked to exposure incidents that led to a total of 314 people exposed and 13 laboratory acquired infections (9 suspected and 4 confirmed). Compared to their respective shares of licences, the number of incidents is higher in the academic (30.4%) and hospital (34.8%) sectors and lower in the private industry/business sector (19.6%). Most incidents involved pathogens classified at a risk group 2 level (63.9%). However, 26 incidents (26.8%) involved security sensitive biological agents which are a subset of human pathogens and toxins that have been determined to pose an increased biosecurity risk due to their potential for use as a biological weapons.

Sharps-related incidents and procedure breaches were the most common incidents leading to an exposure. In 31 incidents, inadvertent possession (i.e., isolation of an unexpected biological agent during routine work) played a role. Possible improvements to standard operating procedures were cited as an area for improvement in 81.9% of incidents.

Conclusion: Data collected through this online laboratory incident surveillance system serve to inform evidence-based decision-making regarding biosafety and biosecurity. The ability to detect trends and potential patterns of concern near real time allows for immediate response to and communication with those who need to know through alerts, advisories, and reports, as well as enhanced policies and guidelines for biosafety and biosecurity. As stakeholders become more accustomed to reporting, the accuracy and timeliness of reporting will increase. This ultimately will benefit the culture of biosafety as well as public health in Canada.

17.013

Big Brother is Watching - Using Digital Disease Surveillance Tools for Near Real-Time Forecasting

S. Bhatia[1], M. Carrion[2], E. Cohn[3], A. Cori[1], P. Nouvellet[4], B. Lassmann[2], L. Madoff[2], J. Brownstein[5];
[1]Imperial College London, Department of Infectious Disease Epidemiology, London/UK, [2]ISID, Brookline, MA/US, [3]Boston Children's Hospital, Boston/US, [4]Imperial College London, MRC Centre for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, London/UK, [5]Childrens Hospital, Boston, MA/US

Purpose: In our increasingly interconnected world, it is crucial to understand the risk of an outbreak originating in one country/region and spreading to the rest of the world. Digital disease surveillance tools such as ProMed, HealthMap etc. can serve as important early warning systems as well as complement field surveillance data during an ongoing outbreak. While there are a number of systems that carry out digital disease surveillance, there is as yet a lack of tools that can compile and analyse the generated data to produce easily understood actionable reports.
The purpose of our work is to design and implement a flexible statistical model that uses different streams of data such as disease surveillance data, mobility data etc. for short-term incidence trend forecasting.
Methods & Materials: This is a modelling study making use of publicly available data. For incidence trends, we use data from ProMED and HealthMap. Other sources of data are Heathsites.io for information on health facilities and GADM for national and international administrative boundaries. The model will be made available as a R package as well as through a website for use by non-technical stakeholders.
Results: We will showcase the use of our model through the analysis of data from the 2014 West African Ebola Epidemic. We show that using only data obtained through digital surveillance (ProMED and HealthMap), we are able to forecast short term incidence trajectory that is consistent with that obtained using field surveillance data.
We will also highlight an example of disaggregating aggregated data to obtain incidence information at a fine spatial scale. This could be particularly important in instances where information at sub-national levels is lacking or incomplete.
Conclusion: Our work makes two key contributions:
 a) We provide a realistic appraisal of the strengths and limitations of data collected through digital surveillance in incidence forecasting.
  b) We infer incidence trends at finer spatial scales from aggregated data. Our work provided an example of the way in which data from digital surveillance systems can complement the data collected from traditional public health infrastructure.