Welcome to Atlanta!

“I wish I could clone myself in order to attend all talks…”

“Genetically modified mosquitoes – fascinating!”

“One session and I’m already amazed”

“ASTMH is a good place to rock”

“Go vector biologists!”

“Brilliant presentations; great camaraderie”

“Plasmodium Rocks!”

“Amore science!”

“Worms rule!”

“I traveled 26,000 miles to attend the Annual Meeting”

“#TropMed15 fascinating time! Here’s to #TropMed16”

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Supplement to
The American Journal of Tropical Medicine and Hygiene
were fever (92%), fatigue (85.7%) and anorexia (75.3%). The lethality rate was 82.9% and 55.8% for less 5 and 6-16 age groups respectively. age less than 5 and hospitalization less than 7 days were associated with death.

Conclusion: We observed that the risk of getting the Ebola disease was significantly lower in children under 5 years. In contrast, the fatality rate was a higher rate in the same group (82.9%).

143

HEPATITIS E SEROPREVALENCE AMONG BLOOD DONORS IN RWANDA

Fred Mugabo 1, Walker Timothy 2, Theogene Twagirumugabe 3, Swaibu Gatara 4, Fredrick Kateera 1

1University of Rwanda, Huye, Rwanda, 2Rwanda Biomedical Center, Kigali, Rwanda

Hepatitis E Virus is mainly transmitted by the fecal-oral route but other routes have been reported. It usually causes self limited disease but can cause fulminant hepatitis in pregnant women. The prevalence of hepatitis E viral infection among Rwandan adults has not been reported previously. We aimed to determine the seroprevalence of Hepatitis E Virus among adult Rwandans, its relationship with pork consumption and other risk factors. A cross-sectional survey was conducted between November and December, 2014 on 309 blood donors in Rwanda. A subsequent nested case-control study assessed exposures in seropositive cases and seronegative controls. Hepatitis E Virus testing was performed by detection of anti Hepatitis E Virus IgG antibodies. Demographic data and information about risk factors for Hepatitis E Virus infection were recorded. The average age was 30.6 years with a male to female ratio of 4:1. 54% were farmers. The overall Hepatitis E Virus seroprevalence was 13.3%. Rates of anti- Hepatitis E Virus positivity were lower in the Eastern Province and Kigali city than the Southern Province (p=0.01 and p=0.003, respectively). An association was found between pork consumption and Hepatitis E Virus seropositivity (p=0.04). The rate of pork consumption positively correlated with the rate of anti-HEV seropositivity (p=0.01). The analysis did not show an association between Hepatitis E Virus seropositivity and the source of drinking water, status of drinking water, exposure to animals or exposure activity. Therefore Hepatitis E Virus seroprevalence among blood donors in Rwanda is high. Anti-Hepatitis E Virus IgG seropositivity is likely associated with pork consumption and may be more prevalent in some regions of Rwanda.

144

SINU VIRUS, A NOVEL ORTHOMYXOVIRUS RELATED TO MEMBERS OF THE THOGOTOVIRUS GENUS, ISOLATED FROM MOSQUITOES IN COLOMBIA

Maria Angélica Contreras Gutierrez 1,2, Marcio Roberto Nunes 2, Hilda Guzman 1, Sandra I. Uribe 1, Richard O. Hoyos 1, Juan Carlos Gallego Gomez 2, Sandro Patroca da Silva 2, Jadson Ferreira Cardoso 2, Vsevolod Popov 3, Nikos Vasilakis 3, Robert B. Tesh 3

1Programa de Estudio y Control de Enfermedades Tropicales (PECET), Universidad de Antioquia. Grupo de Investigación en Sistemática Molecular (GSM), Universidad Nacional de Colombia, Medellin, Colombia, 2Center for Technological Innovation, Evandro Chagas Institute, Ministry of Health, Ananindeua, Pará, Brazil, 3Department of Pathology, University of Texas Medical Branch, Galveston, TX, United States, 4Grupo de Investigación en Sistemática Molecular (GSM), Escuela de Biociencias, Universidad Nacional de Colombia, Medellin, Colombia, 5Grupo de Investigación en Enfermedades Tropicales y Resistencia Bacteriana, Universidad del Sinú, Montería, Colombia, 6Molecular and Translational Medicine Group, Medical Research Institute, Faculty of Medicine, Universidad de Antioquia, Medellín, Colombia

During the past decade, many novel insect-specific viruses have been isolated from characterized in mosquitoes and phlebotomine sandflies. These insect-specific viruses are widely distributed geographically and represent a number of different virus taxa, including Togaviridae, Flaviviridae, Bunyaviridae, Rhabdoviridae, Reoviridae and Birnaviridae. Here we report a novel insect-specific orthomyxovirus, designated CoB 38d, isolated in C6/36 cells from mosquitoes collected northwestern Colombia. Genome sequencing of CoB38d revealed the presence of a hexa-segmented RNA virus (Segments 1 to 6). Genetic analysis of each RNA segment demonstrated the presence of six distinct ORFs encoding for the following genes: PBS (Segment 1), PA1 (Segment 2), PA2 subunit (Segment 3), envelope glycoprotein gene (Segment 4), Nucleoprotein (Segment 5), and Membrane gene (Segment 6). Multiple sequence alignment, using all RNA segments of CoB 38d, revealed low nucleotide and amino acid identity (<50%) with all other members of the Orthomyxoviridae family. Phylogenetic analysis using the polymerase subunit 1 (PB1) amino acid sequences showed that the isolate is most closely related to members of the Thogotovirus genus. Based on the geographic origin of the isolate and phylogenetic analyses, we propose the name of Sinu virus (SINU) and show that it is a new member of the family Orthomyxoviridae, and possibly a new genus within the family.

145

PREDICTING THE GEOGRAPHIC SPREAD OF THE 2014-2016 WEST AFRICA EBOLA VIRUS DISEASE OUTBREAK

Moritz U. Kraemer 1, Nick Golding 1, Donal Bisanzio 1, Samir Bhatt 1, David M. Pigott 1, Nuno R. Faria 1, Oliver G. Pybus 1, David L. Smith 1, Andrew J. Tatem 2, Simon I. Hay 1, Robert C. Reiner, Jr. 4

1University of Oxford, Oxford, United Kingdom, 2University of Melbourne; University of Oxford, Oxford, United Kingdom, 3University of Southampton, Southampton, United Kingdom, 4Indiana University, Indiana, IN, United States

Between 2013 and 2016 West Africa experienced the most geographically extensive outbreak of Ebola virus disease (EVD) recorded to date. It affected all districts in Sierra Leone and Liberia and most of Guinea, resulting in more than 11,301 deaths among 28,603 reported cases. The outbreak spread from its origin in Meliandou, Guinea by movements of infected individuals across the region. Understanding how human mobility influenced the transmission dynamics of this epidemic is important in planning responses to future outbreaks. Using empirical data on human mobility, we model the effect of human movement on the geographic diffusion of the outbreak, as well as on the dynamics of the growth and decline phases of the epidemic within and between each country’s districts, to identify areas that were the main exporters and importers of disease transmission. We identify considerable spatio-temporal heterogeneity in transmission that is driven by human mobility both locally and between regions. We show that by incorporating a range of different human mobility models we improve predictions of both spatial spread and the prediction of the epidemic’s trajectory. These results provide a robust approach to predicting the geographic spread of future outbreaks. Such models are crucial information for surveillance and control strategies both in preparation for, and in response to, future contagious disease outbreaks.