

SESSION 9: Emerging and Re-emerging Viruses

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Organizer : Dr. Joel Montgomery

Chair: Dr. Joel Montgomery

ORAL PRESENTATIONS

1. Investigation of potential circulation of Hantavirus among Kenyan wild rodents and the implications for public health and zoonoses monitoring

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Abstract

Background: Hantaviruses (Family Bunyaviridae) have been associated with the human disease Hantavirus pulmonary syndrome (HPS). This virus has been documented to be transmitted to humans through rodent (Family Murinae) feces and urine. Evidence of Hantavirus across Africa remains quite scanty, although serological evidence has been published in several countries, including Kenya. To date, two Hantaviruses have been isolated from wild a rodent and a shrew in Guinea, Sangassou virus (*Hylomiscua stella*) and Tanganya virus (*Crocidura thersae*) respectively. Presence and epidemiology of these viruses across East Africa remain largely unknown.

Materials and Methods: From May 2008 through June 2010, rodents and mammals were trapped across a broad geographic range within Kenya, selected based on varying ecological and climatic conditions, thereby increasing rodent species diversity in the sample population. Total nucleic acid was extracted from lungs

of necropsized rodents and reverse transcription Polymerase Chain Reaction used to amplify S and L segment of the Bunyaviridae family genome.

Results: A total of 392 rodents and small animals consisting of 18 different species of rodents and shrews were trapped. Six samples generated a 494bp fragment with primers designed to amplify the S segment coding for nucleocapsid protein, depictive of Bunyavirus presence. Two of these samples were isolated from shrews (*Crocidura* species) and four from *Mastomys* species trapped in semi arid areas of Marigat (Rift valley) and Garissa (North Eastern) Kenya respectively. High throughput pyrosequencing and bioinformatic analysis was conducted on the six suspected positive samples to characterize the nature, genetic similarity and identity of the PCR positive samples. One sample from a *Mastomys* mouse caught in Marigat on 28 May 2008 showed 99% homology with Dugbe virus (Genus *Nairovirus*) isolates ArD44313 and IbAr1792.

2. Kenya bats as reservoirs of lyssaviruses

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Abstract

A survey of bats for lyssaviruses has been performed in Kenya during 2006-2011. Over 3000 bats of at least 28 species were sampled from 26 locations across the southern part of the country. Representatives of different phylogenetic lineages of Lagos bat virus (LBV) were isolated from fruit bats. Seroprevalence to

LBV was documented in fruit bats at all locations where they were present, and varied from 25 to 60%. A new lyssavirus, named Shimoni bat virus (SHIBV), was isolated from an insectivorous bat, *Hipposideros commersoni*. In addition, serologic evidence of circulation of another lyssavirus, related to the West Caucasian bat virus (WCBV), was detected in

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insectivorous bats from the *Miniopterus* genus at all roosts where these bats were sampled, and varied between 17 and 26%. After the infection of a Dutch tourist with Duvenhage virus (DUVV) during 2007 (the exposure occurred from a small bat in Tsavo West National Park), efforts were directed to identify the potential reservoir host of DUVV in Kenya. To date, only a few serum samples from *Miniopterus* spp. bats demonstrated weak reactivity to DUVV, except one serum, which neutralized DUVV with a titer of 1:1000. The absence of adequate surveillance does not allow proper assessment of the significance of bat lyssaviruses for public health in Kenya at this time.

However, in prior experimental studies in animals, including non-human primates, these viruses caused typical rabies (i.e. acute progressive encephalitis with a fatal outcome). As an additional concern, such antigenically divergent lyssaviruses as LBV, SHIBV and WCBV, are not covered by the conventional rabies biologics. This is not the case for DUVV, but the circumstances of the infection of the Dutch tourist demonstrate the need for appropriate health communications and education, and a better understanding of lyssavirus ecology related to prevention and control.

3. Dengue in Africa: is it important?

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Abstract

Dengue is recognized as a major public health in tropical and subtropical areas of Asia, the Americas, Caribbean and Oceania. However, the disease is only infrequently reported from Africa though the mosquito vector for dengue virus (DENV) transmission, *Aedes aegypti* is present in most countries. Dengue has been reported from travelers returning to Europe and the US from Africa, limited studies have indentified all four

dengue serotypes among persons with dengue fever, and several studies have found serologic evidence of previous DENV infection. A recent outbreak of dengue among peacekeeping forces in Mogadishu has highlighted the presence of DENV in the region, the susceptibility of persons traveling to at-risk areas, and the need for awareness about the disease, including dengue diagnostic testing and clinical case management.