

Despite the widespread distribution of ZIKV, the genetic relationships among the circulating viral strains remain poorly understood. Therefore, we undertook a study on phylogeny and phylodynamics ZIKV in Africa and Asia.

**Methods & Materials:** We investigated 37 ZIKV isolates from 1968 to 2002 obtained from Senegal, Ivory Coast, Burkina Faso, Central African Republic and Malaysia, to evaluate the viral spread and its molecular epidemiology. Phylogenetic reconstructions and datation were performed while recombination while viral population migrations were investigated.

**Results:** Phylogenetic analysis of the 3 partial gene (E, NS5 and NS5/3'NC) showed two distinct ZIKV clusters circulate in Africa and a third lineage formed by the Micronesia and Malaysia strains. Besides, analysis of full length genome sequence reveal 5 potential recombinants isolates in Senegal and Ivory Cost. The 3 gene regions sequences evolved at a average rate of  $7.74 \times 10^{-4}$  nucleotide substitutions per site per year with a most recent common ancestor of all ZIKV samples around 325 years ago. The migration rates showed a considerable movement of the virus from Senegal to Ivory Cost and the other countries include in this study.

**Conclusion:** Our results suggested at least two independent introductions of ZIKV during the 20<sup>th</sup> century in West Africa and, apparently that viral lineages were not restricted by mosquito vector species. Moreover, we present evidence that ZIKV possibly undergone recombination in nature and that a loss of the N154 glycosylation site in the envelope was a possible adaptive response to the *Aedes dalzieli* vector.

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### Dengue fever outbreak in Mogadishu, Somalia 2011: Co-circulation of three dengue virus serotypes

H. Kyobe Bosa<sup>1,\*</sup>, J.M. Montgomery<sup>2</sup>, I. Kimuli<sup>3</sup>, J.J. Lutwama<sup>4</sup>

<sup>1</sup> AMISOM, Mogadishu, Somalia

<sup>2</sup> Centers for Disease Control and Prevention-Kenya (CDC-K), Nairobi, Kenya

<sup>3</sup> Makerere University, Kampala, Uganda

<sup>4</sup> Uganda Virus Research Institute, Entebbe, Uganda

**Background:** In June 2011 an acute febrile illness (AFI) outbreak, with three deaths, was reported among African Union Mission in Somalia (AMISOM) peacekeepers in Mogadishu. All were negative for malaria by blood smear. An initial set of samples (n = 122) were sent to CDC-Kenya/Kenyan Medical Research Institute (CDC/KEMRI) laboratories to test for various viral hemorrhagic fevers by RT-PCR. A majority (82%) were positive for dengue virus (DENV).

**Methods & Materials:** CDC-Kenya and CDC-Uganda subsequently supported AMISOM to implement an enhanced hospital-based dengue fever surveillance system in two military hospitals in Mogadishu. Case defiantion: all patients with axillary temperature > 38°C

**Results:** During June–August 2011, 134 (94%) of 143 blood samples from AFI cases were tested by RT-PCR and MAC-ELISA. Of these, 62% were positive for DENV by RT-PCR, 18% (n=24) had a positive sole anti-DENV MAC-ELISA and 20% had a negative RT-PCR and MAC-ELISA. All specimens had negative malaria smear or RDT. Infections of DENV-1, DENV-2, DENV-3 and co-infections of DENV-1/2 and DENV-2/3 sero-types were identified in 37%, 7%, 25%, 1% and 25%, respectively. Of the confirmed cases (n = 107; 75%), median age was 32 years (range 20–49), majority (96%) were male and 60% were hospitalized (median length of stay = 3.5 days). Of the hospitalized patients, 87% had leucopenia (WBC < 3.5x10<sup>3</sup> cells) and 83% thrombocytopenic (platelet count < 100x10<sup>3</sup> cells).

Except for a high proportion of hemorrhagic manifestations (n = 14, 13%), frequency of other clinical findings (fever, headache, joint pains, vomiting and body pains) (≥60%) was consistent as with other settings.

**Conclusion:** Co-circulation of multiple dengue sero-types and possible repeated secondary heterotypic dengue infections may be responsible for a high proportion of severe forms of dengue, including death. The extent of severe dengue infection, co-circulation of three dengue serotypes and co-infection with multiple dengue sero-types has not been previously documented in African. Despite the limited scope of this study given the hospital-based design it appears the intensity of dengue fever transmission, severity of dengue in this setting appears under-reported especially in the civilian population.

Given the frequent rotations of peacekeepers from Somalia, the potential of dengue viruses' importation to many African countries where the vectors exist is real.

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### The vector competence of *Ae. aegypti* mosquito populations from Kilifi and Nairobi for dengue-2 virus and the effect of temperature

E. Chepkorir<sup>1,\*</sup>, J. Lutomiah<sup>2</sup>, J. Mutisya<sup>3</sup>, F. Mulwa<sup>1</sup>, B. Orindi<sup>1</sup>, Z. Ng'ang'a<sup>4</sup>, R. Sang<sup>1</sup>

<sup>1</sup> International Center for Insect Physiology and Ecology (ICIPE), Nairobi, Kenya

<sup>2</sup> Kenya Medical Research Institute (KEMRI), Nairobi, Kenya

<sup>3</sup> United States Army Medical Research Unit-Kenya (USAMRU-K), Nairobi, Kenya

<sup>4</sup> Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

**Background:** Dengue virus principally transmitted by *Aedes aegypti* mosquitoes, is a re-emerging infection in Kenya causing major outbreaks in parts of Northern Kenya since 2011 and Coastal regions in 2013. Since these outbreaks started, no cases have been reported in Nairobi despite the level of human movement among these cities. In addition to the vector population/strains, temperature is one of the most important environmental factor affecting biological processes of mosquitoes, including their interactions with viruses.

