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 x $10^{-4}$ 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 20th 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[1,*], J.M. Montgomery[2], I. Kimuli[3], J.J. Lutwama[4]

[1] *AMISOM, Mogadishu, Somalia*
[2] *Centers for Disease Control and Prevention-Kenya (CDC-K), Nairobi, Kenya*
[3] *Makerere University, Kampala, Uganda*
[4] *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 > $38^0$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 < $3.5x10^3$ cells) and 83% thrombocytopenic (platelet count < $100x10^3$ 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[1,*], J. Lutomiah[2], J. Mutisya[3], F. Mulwa[1], B. Orindi[1], Z. Ng'ang'a[4], R. Sang[1]

[1] *International Center for Insect Physiology and Ecology (ICIPE), Nairobi, Kenya*
[2] *Kenya Medical Research Institute (KEMRI), Nairobi, Kenya*
[3] *United States Army Medical Research Unit-Kenya (USAMRU-K), Nairobi, Kenya*
[4] *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.

**Methods & Materials**: *Ae. aegypti* eggs were collected from the two sites, hatched and reared to $F_1$ generation in a Biosafety level-2 insectary. Four-day old females were exposed to infectious, defibrinated sheep-blood mixed (1:1 ratio) with Dengue-2 virus isolated from Mandera-(5.08pfu/ml), using a membrane feeder. Fed mosquitoes were incubated under two sets of temperatures equivalent to the coastal-(29-31 °C) and Nairobi-(25-28 °C) region annual mean temperatures. In both experiments mosquitoes were monitored for up to 21days, and at 7day intervals, a third were randomly sampled, legs and abdomen separated. Abdomens were homogenized and virus quantified by plaque assay to determine midgut infection rates. Legs for mosquitoes with midgut infection were assayed for virus to determine dissemination rates. Results were compared using Chi-square/Fisher's exact test.

**Results**: A total of 1,117 female *Ae.aegypti* mosquitoes were tested. 87/517(16.8%; 95%CI: 13.7-20.3%) of Nairobi mosquitoes had infection. The proportion infected was significantly greater in high temperature (21.3%) than low temperature (12.0%; p = 0.0037). For Kilifi mosquitoes 54/600 (9%; 95%CI: 6.8-11.6%) were infected, this proportion also varied significantly with temperature (high = 11.6%, low = 6.8%; p = 0.0162). Among the infected mosquitoes, the proportion that had dissemination was significantly greater in Kilifi (40.7%; 95%CI: 27.6-55.0%) than Nairobi (10.3%; 95%CI: 4.8-18.7%; p < 0.0001).

**Conclusion**: There is significant difference in midgut infection rates under varying temperatures for both populations from the two geographical sites. Although it was observed that dissemination rates did not vary significantly with temperature in the two populations, the Kilifi population exhibited a high dissemination rates compared to the Nairobi population suggesting that the Kilifi population may be inherently more competent with a lower midgut barrier than the Nairobi population. These finding are important in understanding the distribution of re-emerging Infectious diseases in Africa.

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## Bacteriuria and urinary schistosomiasis in primary school children in rural communities in Enugu State, Nigeria, 2012

O. Ossai[1,*], S.A. Idris[2], G. Abonyi[3], D. Turkur[2], R. Dankoli[4], O. Ekwueme[5], D. Nwagbo[5], E. Ezeanolue[6], O. Nwanyanwu[7], C.C. Nwodo[8], P. Nguku[9], P. Nsubuga[10], D. Ogbuabor[5]

[1] *Nigerian Field Epidemiology and Laboratory Training Programme(NFELTP), Abuja, Abuja, Nigeria*
[2] *Ahmadu Bello University, Zaria, Nigeria*
[3] *Enugu State Ministry of Health, Enugu, Nigeria*
[4] *NFELTP, Abuja, Nigeria*
[5] *University of Nigeria, Enugu, Nigeria*
[6] *Las Vegas University, las Vegas, USA*
[7] *CDC, Nigeria, Abuja, Nigeria*
[8] *Nigerian Field Epidemiology and Laboratory Training Programme(NFELTP), Abuja, Nigeria*
[9] *FELTP, Abuja, FCT, Nigeria*
[10] *US Centers for Disease Control and Prevention, Atlanta, GA, USA*

**Background**: According to a study conducted in1989, Enugu State has an estimated urinary schistosomiasis prevalence of 79%. Recently, studies have implicated bacteriuria co-infection in bladder cancer. These bacteria accelerate the multi-stage process of bladder carcinogenesis. Knowledge about the prevalence of this co-infection is not available in Enugu and the information provided by the 1989 study is too old to be used for current decision making.

**Methods & Materials**: We carried out a cross-sectional survey of primary school children aged5-15years, who were randomly selected through a multi stage sampling method using guidelines recommended by WHO for schistosomiasis surveys. An interviewer administered questionnaire was used to collect data on demography, socioeconomic variables and clinical presentations. Urine samples were collected between 10.00am and 2.00pm. Each sample was divided into two: (A) for prevalence and intensity using syringe filtration technique and (B) for culture. Intensity was categorized as heavy (>50ova/10mls urine) and light (<50ova/10mls urine). Significant bacteriuria was bacteria count $\geq 10^5$ colony forming units/ml of urine.

**Results** Of the 842 pupils, 50.6% were females. The prevalence of urinary schistosomiasis was 34.1%. Infection rate was higher(52.8%) among 13-15 years(Prevalence Ratio {PR} = 2.45, 95% Confidence Interval{CI} 1.63-3.69).Heavy infections wad 62.7% and egg count/10mls urine ranged from 21-1138.Significant bacteriuria among pupils with urinary schistosomiasis was 53.7% compared to 3.6% in the uninfected(PR = 30.8,95% CI 18.91-52.09). The commonest implicated organism was *Escherchia.coli*.

**Conclusion** We found high prevalence of bacteriuria co-infection among children with urinary schistosomiasis in Enugu State. This underscores the need for concurrent antibiotics administration and follow-up to avert later complications.

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