

## **CHARACTERIZATION OF MOSQUITOES FOR RHABDOVIRUSES IN ARUA AND KASESE DISTRICTS IN UGANDA**

### **Abstract**

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Mosquitoes are vectors of a number of undescribed viruses that are likely to affect human and animal populations. This study investigated mosquito species composition and diversity in selected villages of Arua and Kasese districts. It also assessed for the presence of Rhabdoviruses and other viral genomes using metagenomic next generation sequencing (NGS). Mosquito collections were done using ovitraps, larvae search and Centers for Disease Control (CDC) light traps baited with solid Carbon dioxide. Identified mosquitoes were pooled according to species, sex and place of origin. Data was recorded by Excel and used to calculate species richness, composition, diversity and abundance. Viral RNA was extracted, processed and screened for rhabdoviruses using next generation sequencing (NGS). Data analysis was performed using scripts and pipelines found on the server in /home2/HCV2/Uganda/Scripts.

Mosquito species richness was higher in Kasese (74 species, n=13,446) than Arua (62 species, n=9009) district although it did not differ significantly across the sampling units (Kruskal Wallis test,  $X^2=0.97$ ,  $df=3$ ,  $p > 0.05$ ). However, species diversity was significantly higher in Arua than Kasese district ( $p < 0.05$ , Mann Whitney U test). More than 30% of the species documented in the study had been previously documented as potential vectors for human and animal viruses. During the study we also identified *Culex litwakae* a species which had been reported only once in Uganda during studies conducted in Ogwapoke of Kitgum district in Northern Uganda.

A total of 1487 mosquitoes combined into 96 complimentary DNA pools when sequenced on an illumina platform revealed eighty-seven (87) viruses from 33 virus genera and 21 families in both districts. 7/21 (33%) of the virus families (*Rhabdoviridae*, *Flaviviridae*, *Orthomyxoviridae*, *Nairoviridae*, *Peribunyaviridae*, *Phenuiviridae* and *Togaviridae*) carry viruses associated with disease in humans and other animal hosts. Other virus families detected included *Mesoniviridae*, *Xinmoviridae*, *Phasmaviridae*, *Iflaviridae*, *Nudiviridae*, *Reoviridae*, *Retroviridae*, *Iridoviridae*, *Piconarviridae*, *Parvoviridae*, *Permutetraviridae*, *Qinviridae*, *Alphatetraviridae* and *Nodaviridae* majority of which were insect specific virus families. Fourteen virus contigs had open reading frames highly divergent from the already described viruses and reached the criteria for novel viruses.

#### **Conclusion**

To our knowledge, this was the first documented account of mosquito species in Adumi of Arua and the human settled communities close to Queen Elizabeth National Park of Kasese district in Uganda. The presence of high mosquito species diversity including rare mosquito species suggests the presence of suitable habitats for diverse mosquito proliferation. Majority of the viruses detected in this study were species described for the first time, with unknown potential to cause disease. The diversity of virus species in mosquitoes from Uganda, a hotspot for emerging arboviruses, has been only partially characterized. This study illustrate the scale of richness of mosquitoes and viruses in the region and the need to further characterise the virome in mosquitoes, especially those with a propensity to feed from human and animal hosts in larger studies.