

# VIROME METAGENOMIC ANALYSIS OF CULEX MOSQUITOES FROM KENYA AND CHINA

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**T**raditionally, many blood feeding arthropods are known vectors of viruses that cause unprecedented global health concern. Mosquitoes are an integral part of these arthropod vectors. The advancement in next generation sequencing and bioinformatics has expanded our knowledge on the richness of viruses harbored by arthropods. In the present study, we applied a metagenomic approach to determine the intercontinental virome diversity of *Culex quinquefasciatus* and *Culex tritaeniorhynchus* in Kwale, Kenya and provinces of Hubei and Yunnan in China. Our results showed that viromes from the three locations were strikingly diverse and composed of 30 virus families specific to vertebrates, invertebrates, plants and protozoa as well as unclassified group of viruses. We found that both Kwale and Hubei viromes were dominated by vertebrate viruses in contrast to Yunnan that was dominated by insect-specific viruses. However, each virome was unique in terms of virus proportions partly influenced by type of ingested meals (blood, nectar, plant sap, environment substrates). The dominant vertebrate virus family in Kwale virome was *Papillomaviridae* (57%) while in Hubei, it was *Herpesviridae* (30%) and Yunnan had unclassified viruses group (27%). Given that insect-specific viruses occur naturally in their hosts, they should be the basis to define the viromes. For instance, in this study, the dominant insect-specific viruses in Kwale, Hubei and Yunnan were *Baculoviridae*, *Nimaviridae* and *Iflaviridae*, respectively. Our study is preliminary, but emerging theories that suggest manipulation of mosquito viromes could yield potential agents for control and prevention of pathogenic arboviruses and also the global emerging trends of mosquito-borne infectious diseases, it therefore warrants more studies to uncover the global patterns of composition and diversity of mosquito viromes

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