

ABSTRACT

Arthropod-borne viruses (Arboviruses) transmitted by mosquito vectors are a menace to public health because they cause emerging or re-emerging infectious disease in humans. The (re)-emergence of arboviral diseases is mainly due to worldwide spreading of their main vectors, the mosquitoes *Aedes aegypti* and *Aedes albopictus*. The understanding of the co-evolutionary processes between viruses and their vectors is important to provide novel venues for vector control, which to date is the primary way to prevent arboviral transmissions to humans.

Arboviruses, which are non-retroviral RNA viruses, form episomal viral DNA fragments following infection of mosquitoes, a process that is mediated by retrotransposon-derived reverse transcriptase. Additionally, sequences derived from non-retroviral RNA viruses have been found integrated into mosquito genomes.

In this experimental thesis, I used a bioinformatic approach to analyze the presence, abundance, distribution and transcriptional activity of integrations from 425 viruses, including 133 arboviruses, across the currently available 22 mosquito genome sequences. The number and origin of viral integrations differed between mosquito species from the same regions. I detected ~10-fold more viral integrations in the arboviral vectors *Ae. aegypti* and *Ae. albopictus* than in any other tested species and integrations were mainly from Flaviviruses and Rhabdoviruses. This suggests that integrations are mediated by viral-host lineage-specific interactions. Moreover, viral integrations of the *Ae. aegypti* and *Ae. albopictus* genomes are enriched within piRNA clusters and produce primary piRNAs of antisense orientation with respect to infecting viral genomes. Overall, these results support the conclusion that integrations of viral sequences in *Aedes* species is a more common process than previously thought and may be an additional virus control strategy mediated by an expanded and functionally-evolved piRNA pathway.