

O1002 Mosquitos are mixing vessels for interspecies viral microbiome

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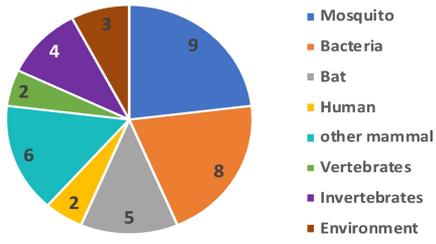
Background: Infectious viral pathogens such as Dengue virus are highly adapted to their arthropod vector. Nevertheless, mosquitos do carry also other mosquito- specific viruses, allowing genetic recombination of diverse viruses that turns mosquitos into potential virologic mixing vessels. Advances in NGS have expanded our knowledge on the richness of viruses harbored by arthropods. Yet, little is known about the actual composition and sources of the mosquito virome as in most of previously conducted studies only 1-5% of metagenomic reads were of viral origin.

Materials/methods: In this study, we tested a pool of *Aedes aegypti* mosquitos from a tropical region (Barbados) and compared their virome profile to pools of *Culex spp.* mosquitos from the same and from a distinctively other habitat (Austria) by applying our previously developed virus purification and enrichment protocol (VIPEP), combined to a metagenomic NGS based approach. Bioinformatic sequence analysis was done on nucleotide and protein level with subsequent molecular validation by specific qPCR assays.

Results: Throughout all 4 mosquito pools, an average of 70% of reads matched viral database sequences of 111 virus taxa from 18 phylogenetic families with nucleotide sequence similarities from 64% - 99%. We detected a great diversity of viruses infecting human, animal and plant hosts as well as marginally described viruses previously found in environmental samples only. Viral species of the families of *Genomoviridae*, *Circoviridae* and *Microviridae* were among the most abundant.

Conclusions: We traced back the sources of the mosquito virome by individual phylogenetic sequence analysis, identifying four big reservoirs of viral infection and colonization of mosquitos: (i) known mosquito specific viruses (ii) viruses of animals or humans that mosquitos feed on (iii) viruses isolated from feces of animals, feeding on mosquitos (iv) environmental viruses colonizing mosquito surfaces. Beside sequences with high similarity to database entries we also report several novel sequences with low identity rates to conserved viral marker genes. This study characterizes the virome of field caught *Aedes aegypti* and *Culex spp.* mosquitos at unseen sensitivity, contributing to a better understanding of arbovirus evolution that may act as prediction tool for human disease epidemics at early stage.

***Aedes aegypti* virome α diversity;
annotated host species**



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