MASTER THESIS

„Virus diversity in mosquitos“

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Virus diversity in mosquitos

Alina Domdey studied in the Elite Graduate Program “Global Change Ecology” at the University of Bayreuth. In her master thesis, she examined global data on mosquito-associated viruses, data gaps, factors influencing virus species richness, and its modeling.

Mosquito-associated viruses as a global challenge

Approximately 70% of human pathogens originate in animals, and over 90% of viruses transmitted by arthropods are spread by mosquitoes. In the wake of climate change and globalization, mosquito-borne diseases are increasingly coming into focus as both pathogens and their vectors spread to new regions.

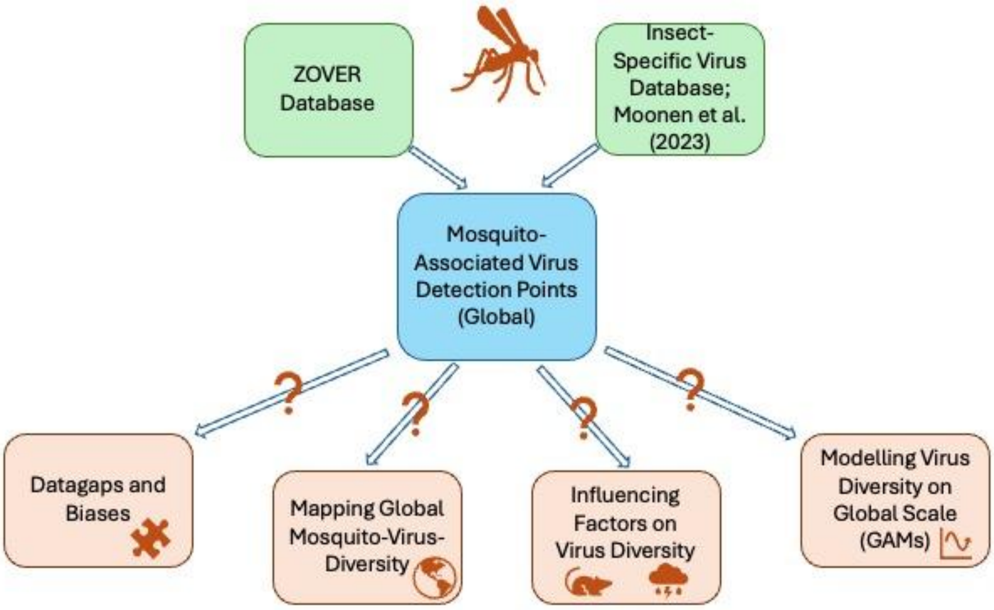
The global diversity of mosquito-associated viruses (MAVs) has not yet been sufficiently researched. While mosquito-borne viruses (MBVs) can infect both insects and vertebrates, mosquito-specific viruses are limited to mosquitoes. Nevertheless, the latter also pose potential health risks and benefits. On the one hand, they are considered possible precursors of MBVs and could become pathogenic to vertebrates through mutation or host jump; on the other hand, they can influence the transmission of other MBVs or even enter into symbiotic relationships with their hosts.

For these reasons, a comprehensive understanding of the diversity of mosquito-associated viruses, including those that cannot currently be transmitted to vertebrates or humans, is essential.

Large data gaps and hotspots of species richness of mosquito-associated viruses identified

In Bayreuth, the Department of Biogeography is conducting intensive research on mosquito-related topics, such as the spread of the Asian tiger mosquito and West Nile virus. In her master's thesis, Alina Domdey provides an overview of the global diversity patterns of mosquito-associated viruses and investigates potential correlations with bioclimatic factors and host diversity. To this end, she uses publicly available data on virus detections from the ZOVER database and an insect-specific virus database by Moonen et al. (2023) to map the global species diversity of MAVs. In doing so, she identified significant geographical data gaps and distortions in data availability.

Bioclimatic variables and host species diversity were analyzed as factors influencing MAV diversity. In addition, generalized additive models could be used to predict global MAV species diversity in regions with data gaps and to identify hotspot areas. The study emphasizes the need for standardized research on mosquito viruses in identified hotspots to better understand the factors influencing MAV diversity and the associated risks and benefits for human health.



Graphical summary of the central research questions and approaches of the master's thesis entitled “Global, spatial analysis of mosquito-associated virus diversity and its potential drivers” at the Chair of Biogeography at the University of Bayreuth, Elite Graduate Program “Global Change Ecology” by Alina Domdey.

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