

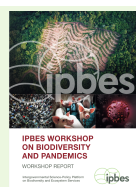
Diversity Components in Mosquito-borne Diseases in the Face of Climate Change



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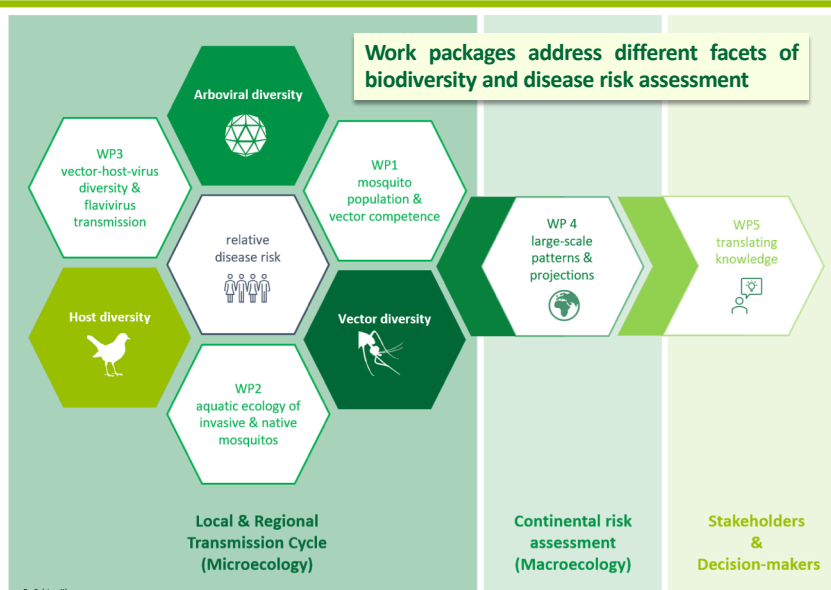
Context Mosquito-borne pathogens such as chikungunya virus and West Nile virus are an increasing threat within veterinary and public health in Europe. Emerging and re-emerging transmission patterns are influenced by global transport, long-distance travel and environmental and climatic changes, while vaccination and pharmaceutical treatment is either not available or very limited. The role of biodiversity on disease transmission is becoming evident as far as introduced invasive species and habitat degradation are concerned. However, very little is known about its attenuating or promoting effects on the chain of infection – from arboviruses and mosquitoes to infected humans or animals. **Drawing on expertise and data from the medical, natural and social sciences, DiMoC will provide insights into the effects of biodiversity in the transmission of mosquito-borne zoonotic diseases and inform health, environmental and development policy to prevent and mitigate outbreaks.**

Research Plan DiMoC contributes to better understand the effects of biodiversity in mosquito-borne pathogen transmission. Through the analysis of different **organisational** (hosts, insects, viruses, human population), **spatial** (continental, regional, local, organism) and **temporal scales** (current conditions, future projections). This will be done through an integrated series of **empirical studies** (laboratory and field experiments) and **model developments**.



Workshop Report on Biodiversity and Pandemics

DiMoC partners contributed as co-authors and reviewers.



Native **mosquitos** (*Culex pipiens*), tiger mosquitos (*Aedes albopictus*) and Asian bush mosquitos (*Aedes japonicus*) will be captured at selected sites in Belgium, Germany and Italy. They will be studied to understand the effects of **local microhabitat diversity** on the **interspecific interactions** which affect the diversity and abundance of the native and invasive mosquitoes.



Salivation assays of mosquitoes will be used to determine the differences in the **vector competence** for West Nile, chikungunya and Japanese encephalitis viruses. Using molecular methods, **vertebrate blood-meals** in mosquitoes will be used to identify the differences in host assemblages within and between studied sites.



The impact of **host, vector, and virus diversity along a gradient of human-presence and land use** (urban, rural natural) on West Nile Virus transmission risk will be assessed: **mosquito captures (from Mexico, France and Germany)** will be used to determine mosquito abundance, richness and diversity.



Modelling techniques compare different large-scale patterns of virus, mosquito, and host diversity, taking into account the landscape diversity, climatic factors and prevailing socio-economic conditions. **Uncertainty in future trends** of risks in pathogen transmission can be quantified by comparing climate scenarios and models including landscape and societal diversity.



Ongoing **consultations** with **authorities, institutions and associations** which are competent for the monitoring and control of mosquitoes, and the management of mosquito-borne diseases in Belgium, France, Germany and Mexico. A **guidebook and policy briefs** will be produced, **translating project results** into practice-oriented conclusions for the management of both biodiversity and mosquito-borne disease risk.

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