

WOLBACHIA IN AEDES AFRICANUS: A SOURCE TO STUDY MICROBIAL COMPETITION IN MOSQUITO

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INTRODUCTION: *Wolbachia* is an obligate intracellular bacterium naturally found in about 60% of all arthropod's species (Hilgenboecker et al., 2008. FEMS Microbiology Letters, 281(2): 215-20). Its significance lies in its influence on host fitness (ability to survive and mate) and its ability, when specific strains are introduced into mosquitoes lacking *Wolbachia*, to decrease disease transmission by mosquitoes. These attributes of *Wolbachia* present a prospective vector control approach for diseases like dengue and other vector-borne illnesses. In either scenario, the outcome is a decline in viral transmission. Recently we have identified *Wolbachia* in the sylvatic African vector *Aedes africanus*, a mosquito vector widely distributed throughout sub-Saharan Africa, except Madagascar, where it acts as one of the important vectors of yellow fever (Smithburn et al., 1949. Ann Trop Med Parasitol, 43(1): 74-89), zika (Macnamara, 1954. Trans R Soc Trop Med Hyg, 48(2): 139-45) and chikungunya (Saluzzo et al., 1980. Bull Soc Pathol Exot Filiales, 73(4): 390-99). Here, for the first time, we have investigated the microbiota of *Ae. africanus* and the potential relationships and competition dynamics between *Wolbachia*, *Asaia*, and *Pantoea* symbionts.

MATERIALS AND METHODS: Microbiota analysis was performed on *Ae. africanus* mosquitoes collected in Cameroon in 2023. These specimens underwent morphological and molecular identification. The prevalence and quantity of *Wolbachia* were assessed using qPCR. Additionally, a cohort comprising both female and male mosquitoes was sacrificed to detect *Wolbachia* via fluorescence in situ hybridization (FISH). Microbiota composition was explored through 16S NGS analysis, focusing on the V3-V4 regions. Furthermore, a phylogenetic examination of the *Wolbachia* strain was conducted using multi-locus sequence typing (MLST) analysis.

RESULTS AND CONCLUSIONS: *Wolbachia* was found in nearly all the specimens examined, displaying varied quantities. The phylogenetic analysis via MLST revealed that this *Wolbachia* strain belonged to Supergroup B yet exhibited closer resemblance to *Wolbachia* strains observed in Lepidoptera and Hymenoptera rather than mosquitoes. FISH analysis demonstrated *Wolbachia* localization in both male and female reproductive organs. Microbiota analysis suggested a potential competition among *Wolbachia*, *Asaia*, and *Pantoea* symbionts, findings corroborated by qPCR. Genome sequencing of the three bacteria was conducted via shotgun analysis to facilitate a phylogenomic investigation and we are exploring metabolic pathways potentially influencing the dynamics of competition. Further comprehensive studies are underway to deepen our understanding of this competition phenomena. This kind of studies are relevant to determine phenomenon of microbial competition that may affect *Wolbachia*-based mosquitoes borne disease control.