

TITLE: MICROBIOME PROFILE FROM WILD YELLOW FEVER MOSQUITOES USING SHOTGUN APPROACH

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ABSTRACT:

Mosquitoes belonging to genus *Sabethes* are wild vectors of an important disease: yellow fever, which one after decades of control re-emerged in a major outbreak at the end of 2016 calling researchers' attention to the wild cycle once this can be the starting point for an urban cycle; this, because, if unprotected people (without vaccine) enter the forest, they can contract the virus and take it to the city, where *Aedes aegypti* acts as a vector. Therefore, it is a disease that deserves double surveillance. Because of *Sabethes* medical importance and limited amount of information about their role in yellow fever transmission, we decided to briefly describe their microbiome, mainly because we know that the presence of some bacteria can directly influence the ability of mosquitoes to transmit viruses, and not just that, but the diversity of bacteria and viruses present in these insects can affect their reproductive life, nutritional profile and even longevity. In this study, we extracted total DNA from four species: *S. bipartipes*, *S. cyaneus*, *S. quasicyaneus* and *S. tarsopus* (pool) and sequenced on NextSeq platform (Illumina); after sequencing, the present genomes were assembled in their entirety by SPAdes and then mined against a plasmid and virus database downloaded from the NCBI, and then contigs were visualized in MEGAN. We observed a large variety of species in the phylogenetic tree, and some important bacteria such as *Serratia marcescens*, which has pathogenic behavior, causing hospital (sepsis) and urinary infections, and that has been studied in other mosquitoes such as *Anopheles* since it seems to be involved in the mosquito's competence for the *Plasmodium* spp. transmission; and because of it, researchers are working to try to use this bacterium as biological control of malaria. We also found another important bacterium, *Listeria monocytogenes*, which can cause meningitis in humans, and has been isolated from mammals, birds, fish and insects, and which has long been known to be transmitted mechanically by the mutuca, which is an insect of the same order as the *Sabethes*. We also found *Acanthamoeba polyphaga mimivirus*, which is a giant virus that seems to play some role in the cause of pneumonia in humans. The presence of these pathogens does not necessarily mean that they can be transmitted by the *Sabethes*, but they can be used in biological control in a near future.

Keywords: microbiome, *Sabethes*, yellow fever.

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