

Culture-Dependent Characterization of the Midgut Microbiota from Three Field-Caught *Aedes aegypti* Populations

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Aedes aegypti is of considerable medical importance as a vector of dengue and yellow fever. Microorganisms play important and often essential roles in the growth and development of many insect species. Microorganisms associated to the insect may have an important role for human infectious diseases epidemiology. Once a key role bacterium is discovered, it may be modified in order to affect the insect development and, consequently, the disease transmission. The objective of this work was to identify and characterize the gut microbiota of *Ae. aegypti* collected in Campos dos Goytacazes, Recife and Manaus in order to verify common microbiota among these mosquito populations. The midgut from newly emerged *Ae. aegypti* was dissected under aseptic conditions, homogenized and plated on BHI medium. Microbial isolates were identified by sequencing of 16S rDNA. The culturable bacteria were identified as *Enterobacter*, *Pantoea*, *Pseudomonas*, *Chryseobacterium*, *Margalefia*, *Serratia*, *Aeromonas*, *Staphylococcus*, *Swine*, *Achromobacter*, and *Delftia*. All bacteria isolated from Campos dos Goytacazes population belonged to the Enterobacteriaceae family while a most diverse bacterial flora was observed in the population from Manaus. The genera *Chryseobacterium* e *Enterobacter* were isolated from Campos dos Goytacazes and Manaus populations while the *Staphylococcus* genus was found to be associated with Manaus and Recife populations. Therefore, the results of this study indicate that different mosquito species harbor common representatives of the microbiota that may be the potential candidates for genetic manipulation to express anti-viral molecules in the mosquito gut.

Key Words: *Aedes aegypti*, microbiota, midgut

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