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Diversity of midgut bacteria in larvae and females of *Aedes aegypti* and *Aedes albopictus* from Gampaha District, Sri Lanka

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Abstract

Background: The midgut microbiota of mosquitoes maintain basal immune activity and immune priming. In recent years, scientists have focused on the use of microbial communities for vector control interventions. In the present study, the midgut bacteria of larvae and adults of *Aedes aegypti* and *Ae. albopictus* were assessed using both field-collected and laboratory-reared mosquitoes from Sri Lanka.

Methods: Adults and larvae of *Ae. aegypti* and *Ae. albopictus* were collected from three selected areas in Gampaha Medical Officer of Health area, Gampaha District, Western Province, Sri Lanka. Bacterial colonies isolated from mosquito midgut dissections were identified by PCR amplification and sequencing of partial *16S rRNA* gene fragments.

Results: Adults and larvae of *Ae. aegypti* and *Ae. albopictus* harbored 25 bacterial species. *Bacillus endophyticus* and *Pantoea dispersa* were found more frequently in field-collected *Ae. aegypti* and *Ae. albopictus* adults, respectively. The midgut bacteria of *Ae. aegypti* and *Ae. albopictus* adults ($\chi^2 = 556.167$, $df = 72$, $P < 0.001$) and larvae ($\chi^2 = 633.11$, $df = 66$, $P < 0.001$) were significantly different. There was a significant difference among the bacterial communities between field-collected adults ($\chi^2 = 48.974$, $df = 10$, $P < 0.001$) and larvae ($\chi^2 = 84.981$, $df = 10$, $P < 0.001$). *Lysinibacillus sphaericus* was a common species in adults and larvae of laboratory-reared *Ae. aegypti*. Only *P. dispersa* occurred in the field-collected adults of *Ae. aegypti* and *Ae. albopictus*. Species belonging to genera *Terribacillus*, *Lysinibacillus*, *Agromyces* and *Kocuria* were recorded from *Aedes* mosquitoes, in accordance with previously reported results.

Conclusions: This study generated a comprehensive database on the culturable bacterial community found in the midgut of field-collected (*Ae. aegypti* and *Ae. albopictus*) and laboratory-reared (*Ae. aegypti*) mosquito larvae and adults from Sri Lanka. Data confirm that the midgut bacterial diversity in the studied mosquitoes varies according to species, developmental stage and strain (field vs laboratory).

Keywords: Midgut, Bacteria, Diversity, *16S rRNA* gene, Mosquitoes, *Aedes*

Background

Mosquitoes have received more attention than other arthropod vectors because of their ability to transmit many pathogens causing significant diseases, including malaria, dengue, zika and chikungunya. The increasing

incidence of dengue virus (DENV) and other arboviruses worldwide is a major public health concern [1]. *Aedes aegypti* and *Aedes albopictus* are highly anthropophilic species that are responsible for the transmission of DENV and other arboviruses [2, 3].

Conventional mosquito control measures have many downsides, such as the development of insecticide resistance, which have led to efforts to develop novel strategies needed for an integrated vector management (IVM) approach [4]. These efforts have resulted in the

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