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Diversity of midgut symbiotic bacteria in *Aedes* mosquito genera: A meta-analysis

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The gut bacterial composition of mosquitos has the capability of altering mosquito pathogen transmission through numerous mechanisms, which is useful in novel transmission control strategies. Therefore, understanding the diversity of gut bacteria in different mosquito genera is highly important. The present analysis was carried out to evaluate the variations in gut-bacteria in field-caught *Aedes* adult mosquitos from different geographical locations. A literature survey was conducted to identify quantitative data related to the midgut bacterial abundance in *Aedes*, using standard search terms and keywords. The collected data were arranged at the bacterial class level and were subjected to a square-root transformation. A resemblance matrix was constructed based on the Bray-Curtis resemblance. Cluster analysis followed by the Analysis of Similarities (ANOSIM) and Distance based Redundancy Analysis (dbRDA) were used for data analysis. Gut bacterial abundance from six different countries; Netherlands, USA, Sri Lanka, India, Brazil, and Panama, were used in the study. A total of 12 bacterial classes, were recorded and bacterial classes of Alphaproteobacteria and Gammaproteobacteria accounted for the highest abundance in *Aedes* mosquitoes from most of the countries. Interestingly, *Aedes* mosquitoes from Brazil, India and Sri Lanka, did not report the abundance of Alphaproteobacteria in their gut contents. Based on the Bray-Curtis similarity-based cluster analysis, four major clusters were identified at a similarity level of 48.9%, based on the overall abundance of bacterial classes. *Aedes* mosquitoes of Sri Lanka and India formed one cluster, sharing a similarity of 81.6%, while Brazil and Panama formed another cluster. Meanwhile, *Aedes* mosquitoes from Netherland and USA formed two separate clusters. The statistical significance of aforementioned clustering status was further verified by the Analysis of Similarities (ANOSIM), which reported a Global R value of 0.96. The clustering status suggested by the cluster analysis was further verified by the findings of the dbRDA. As indicated by the loadings of the dbRDA axes, the abundance of Gammaproteobacteria and Bacilli bacterial classes were found to be responsible for the similarity between gut bacterial diversity in *Aedes* mosquitoes from India and Sri Lanka. Further studies on the gut-microbial diversity of *Aedes* mosquitoes are recommended to support the implementation of novel vector control strategies in Sri Lanka.

Keywords: *Aedes*, Diversity, Gut-microbes, Geographical, Similarity