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## Microbiota and potential opportunistic pathogens associated with male and female fruit flies of Malaysian *Bactrocera carambolae* (Insecta: Tephritidae)



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ABSTRACT

Bactrocera carambolae Drew & Hancock is an agricultural pest that causes considerable damage to various fruit crops in Southeast Asia and South America. We report here the bacterial communities associated with fieldcaught male and female adult flies from University Malaya campus. The microbiota was determined by targeted 16S rRNA gene (V3-V4 region) sequencing using the Illumina MiSeq. At 97% similarity, four bacterial phyla (with relative abundance of  $\geq 1\%$  in at least one specimen) – Bacteroidetes, Firmicutes, Proteobacteria, and Tenericutes - were recovered from the adult flies. Proteobacteria was the predominant phylum in all the samples, with the female flies (86.81  $\pm$  6.57%) having higher mean relative abundance than the male flies (71.57  $\pm$  18.37%). The Firmicutes was more abundant in the male flies (14.47  $\pm$  17.30%) than female flies (0.69  $\pm$  1.25%). There were in total seven classes, nine orders, 13 families, 23 genera, and 31 putative species. Thirteen genera had higher mean relative abundance in male flies, and nine in female flies. Klebsiella was the predominant genus in female flies, while Desulfovibrio was more abundant in some male flies. The mean relative abundances of the putative species Orbus sasakiae and Enterococcus moraviensis were significantly higher in male than female flies, while female flies had significantly higher mean relative abundance for Escherichia fergusonii and Klebsiella variicola. Alpha diversity indices indicated that the bacterial diversity varied within and between male and female flies, and the mean bacterial diversity was significantly higher in male flies. The differences in bacterial diversity and relative abundance may be reasonably attributed to stochastic processes, in part to environmental factors such as food resources and habitats. It is significant that several putative bacterial species recovered in the present study have not been reported in Bactrocera fruit flies. Sixteen of the 31 detected putative bacterial species are potential opportunistic pathogens of medical/public health importance.

## 1. Introduction

The carambola fruit fly *Bactrocera carambolae* Drew & Hancock is a member of the *B. dorsalis* species complex (Drew & Hancock, 1994). It is one of the most severe pests of economic importance in the Pacific Region (Vargas et al., 2015) and Suriname (van Sauers-Muller, 2005). It is highly polyphagous, infesting many plant families (Yong, 1994; Allwood et al., 1999; Malavasi et al., 2013; Lemos et al., 2014; Marchioro, 2016).

*B. carambolae* is native to Southeast Asia (Vietnam to Indonesia) and India (Andaman Island) but has been introduced into South America (Drew & Hancock, 1994; van Sauers-Muller, 2005; Malavasi et al., 2013; Lemos et al., 2014; Vargas et al., 2015; Marchioro, 2016). It is listed as a quarantine insect pest (version 2017–09) by the European and Mediterranean Plant Protection Organization (EPPO, 2017). To date, the microbiota associated with *B. carambolae* has been reported for the developmental stages recovered from the host fruit *Averrhoa carambola* L. (family Oxalidaceae) (Yong et al., 2017a) and field-caught adult male flies (Yong et al., 2017b). The microbiota reports on the different life stages of *B. carambolae* indicate transmission of bacteria from the immatures to the newly emerged adults, and from the exuviae to the environment (Yong et al., 2017a). There is however no study on the microbiota of field-caught adult female flies, and therefore differential diversity and abundance of the associated microbiota in male and female flies. Studies on the field caught adult flies will also contribute to our knowledge on the transmission modes of the associated microbiota. Male *B. carambolae* flies are attracted to methyl eugenol while the female flies are not. Many plants possess methyl eugenol or eugenol that attract the male flies and would therefore cause them to pick up environmental microbes on these plants (Shelly, 2010).

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