

## High Diversity of Bacterial Communities in Developmental Stages of *Bactrocera carambolae* (Insecta: Tephritidae) Revealed by Illumina MiSeq Sequencing of 16S rRNA Gene.

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### Abstract

*Bactrocera carambolae* is a highly polyphagous fruit pest of agricultural importance. This study reports the bacterial communities associated with the developmental stages of *B. carambolae*. The microbiota of the developmental stages were investigated by targeted 16S rRNA gene (V3-V4 region) sequencing using the Illumina MiSeq. At 97% similarity, there were 19 bacterial phyla and unassigned bacteria, comprising 39 classes, 86 orders, 159 families and 311 genera. The bacterial composition varied among the specimens of developmental stage and across developmental stages as well as exuviae. Four phyla of bacteria (with relative abundance of  $\geq 1\%$  in at least one specimen)-Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria-were recovered from the larva, pupa, adult stages and exuviae. Proteobacteria was the predominant phylum in all the developmental stages as well as the exuviae. Enterobacteriaceae (Proteobacteria) was the predominant family in the adult flies while the family [Weeksellaceae] (Bacteroidetes) was predominant in the larval and pupal stages. Among the genera occurring in more than one developmental stage of *B. carambolae*, *Erwinia* was more abundant in the larval stage, *Halomonas* more abundant in adult female, *Stenotrophomonas* more abundant in adult male, and *Chryseobacterium* more abundant in the larval and pupal stages. The results indicate transmission of bacteria OTUs from immatures to the newly emerged adults, and from exuviae to the environment.

PMID: 28642971 DOI: [10.1007/s00284-017-1287-x](https://doi.org/10.1007/s00284-017-1287-x)

