

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data set on the diversity and core members of bacterial community associated with two specialist fruit flies *Bactrocera melastomatos* and *B. umbrosa* (Insecta, Tephritidae)



Sze-Looi Song^{a,b,*}, Hoi-Sen Yong^c, Kah-Ooi Chua^{d,*}, Phaik-Eem Lim^b, Praphathip Eamsobhana^e

^a Institute for Advanced Studies, Universiti Malaya, Kuala Lumpur, Malaysia

^b Institute of Ocean and Earth Sciences, Universiti Malaya, Kuala Lumpur, Malaysia

^c Institute of Biological Sciences, Faculty of Science, Universiti Malaya, Kuala Lumpur, Malaysia

^d Centre for Research in Biotechnology for Agriculture, Universiti Malaya, Kuala Lumpur, Malaysia

^e Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand

ARTICLE INFO

Article history: Received 13 July 2022 Revised 1 October 2022 Accepted 2 November 2022 Available online 8 November 2022

Dataset link: Bioproject PRJNA528573 (Original data)

Keywords: Next generation sequencing Miseq Microbiome 165 rRNA gene Dacinae

ABSTRACT

Bactrocera melastomatos Drew & Hancock and Bactrocera umbrosa (Fabricius) are fruit flies of the subfamily Dacinae under the family Tephritidae [1]. B. melastomatos occurs in India (Andaman Island), Thailand, Peninsular Malaysia, Singapore, and Indonesia (Sumatra, Kalimantan, Java) [1] while B. umbrosa is distributed from southern Thailand and Malaysia to New Guinea and New Caledonia [2]. The adult male flies of B. melastomatos are attracted to Cue lure while the adult male flies of B. umbrosa are attracted to methyl eugenol [3]. Fruit flies of Bactrocera melastomatos infest Melastomataceae while those of B. umbrosa infest Moraceae. We compare the diversity of microbiota associated with the wild adult males of these two specialist fruit flies infesting different families of host plants. Targeted 16S rRNA gene (V3-V4 region) was sequenced using the Illumina MiSeq platform. Six bacterial phyla (Actinobacteria, Armatimonadetes, Bacteroidetes, Cyanobacteria/Melainabacteria group, Firmicutes, Proteobacteria) were detected at 97% similarity clustering and 0.001% abundance filtering. Four phyla (Actinobacteria, Bac-

* Corresponding authors.

E-mail addresses: szelooi@um.edu.my (S.-L. Song), kahooi@um.edu.my (K.-O. Chua).

https://doi.org/10.1016/j.dib.2022.108727

^{2352-3409/© 2022} Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/)