



# Complete mitochondrial genome of *Bactrocera ritsemai* (Insecta: Tephritidae) and phylogenetic relationship with its congeners and related tephritid taxa

Sze-Looi Song<sup>a,\*</sup>, Hoi-Sen Yong<sup>b</sup>, I. Wayan Suana<sup>c</sup>, Phaik-Eem Lim<sup>a</sup>

<sup>a</sup> Institute of Ocean and Earth Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia

<sup>b</sup> Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia

<sup>c</sup> Faculty of Science and Mathematics, Mataram University, Mataram, Indonesia

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## ABSTRACT

*Bactrocera ritsemai* is a dacine fruit fly found in Indonesia. We report here the complete mitogenome of this fruit fly from Lombok, Indonesia determined by Illumina MiSeq sequencing and its phylogenetic relationship with its congeners and related tephritid taxa. The whole mitogenome of *B. ritsemai* had a total length of 15,927 bp, comprising 37 genes – 13 protein-coding genes (PCGs), 2 ribosomal ribonucleic acid (rRNA) and 22 transfer ribonucleic acid (tRNA) genes – and a control region (D-loop). Of the PCGs, 6 (*atp6*, *cob*, *cox2*, *cox3*, *nad4*, *nad4l*) had ATG start codon, 4 (*nad2*, *nad3*, *nad5*, *nad6*) had ATT, and one each had ATA (*nad1*), GTG (*atp8*) and TCG (*cox1*). Seven PCGs (*atp6*, *atp8*, *cox2*, *cox3*, *nad2*, *nad4l*, *nad6*) had TAA stop codon, 3 (*cob*, *nad3*, *nad4*) had TAG, and 3 had incomplete stop codon (*cox1* – TA; *nad1*, *nad5* – T). The TΨC-loop of tRNA was absent in *trnF* while *trnS1* lacked the DHU-loop. Phylogenetic analysis based on 15 mt-genes (13 PCGs + 2 rRNA genes) indicated *B. ritsemai* forming a sister group with *B. umbrosa* and the subgenus *Bactrocera* was monophyletic. The genera *Bactrocera* and *Zeugodacus* were monophyletic while the subfamilies Dacinae and Tephritinae were paraphyletic. A broader taxa sampling of the Tephritidae is needed to better elucidate the phylogenetics and systematics of the tribes and subfamilies of tephritid fruit flies.

## Introduction

Fruit flies of the genus *Bactrocera* are of economic importance in agriculture (White and Elson-Harris, 1992). They are represented by some 651 described species (Vargas et al., 2015). Seventy-three species have been documented as economically important in the Pacific Region and many are highly polyphagous (Vargas et al., 2015).

The genus *Bactrocera* is represented by some 218 species in Southeast Asia, of which 89% are endemic to the region (Drew, 2004). Among them, *B. ritsemai* (Wayenbergh), a member of the subgenus *Bactrocera*, is found only in Indonesia (Java, Lombok and Sulawesi) (Drew and Romig, 2013; Hardy, 1983). The male is attracted to Cue lure. There is no known record of its host plant (Drew and Romig, 2013).

To date, the complete mitochondrial genomes (mitogenomes) of nine species of the subgenus *Bactrocera* – *B. arecae*, *B. carambolae*, *B. correcta*, *B. dorsalis* (including the conspecific taxa *B. invadens*, *B. papayae* and *B. philippinensis*), *B. latifrons*, *B. melastomatos*, *B. tryoni*, *B. umbrosa*, and *B. zonata* – are available in GenBank. However, there is no report on the complete mitogenome of *B. ritsemai* and its phylogenetic

relationship with other taxa of the subgenus *Bactrocera* as well as its congeners of other subgenera and related tephritid taxa. In this study, we compared the gene synteny of *B. ritsemai* with other congeners and generated a robust 15-mt genes phylogeny using the complete mitogenome gene sequences. Compared to partial individual genes, mitogenomes provide more gene contents for systematics and phylogenetic analyses.

## Materials and methods

### Ethics statement

*B. ritsemai* is an insect pest. It is not endangered or protected by law. No permits are required to study this fruit fly.

### Specimen collection

Male fruit flies of *B. ritsemai* were collected by H.-S. Yong and I. Wayan Suana in Karandangan Forest, Lombok, Indonesia on 6 November 2015 by means of Cue lure according to the method of Yong

\* Corresponding author.

E-mail address: [szelooi@um.edu.my](mailto:szelooi@um.edu.my) (S.-L. Song).