

RESEARCH ARTICLE

# Complete Mitochondrial Genome of Three *Bactrocera* Fruit Flies of Subgenus *Bactrocera* (Diptera: Tephritidae) and Their Phylogenetic Implications

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**Data Availability Statement:** The whole mitochondrial genome sequences are available in GenBank database (accession number: *Bactrocera latifrons* KT881556; *Bactrocera melastomatos* KT881557; and *Bactrocera umbrosa* KT881558).

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## Abstract

*Bactrocera latifrons* is a serious pest of solanaceous fruits and *Bactrocera umbrosa* is a pest of Artocarpus fruits, while *Bactrocera melastomatos* infests the fruit of Melastomataceae. They are members of the subgenus *Bactrocera*. We report here the complete mitochondrial genome of these fruit flies determined by next-generation sequencing and their phylogeny with other taxa of the subgenus *Bactrocera*. The whole mitogenomes of these three species possessed 37 genes namely, 13 protein-coding genes (PCGs), 2 rRNA and 22 tRNA genes. The mitogenome of *B. latifrons* (15,977 bp) was longer than those of *B. melastomatos* (15,954 bp) and *B. umbrosa* (15,898 bp). This difference can be attributed to the size of the intergenic spacers (283 bp in *B. latifrons*, 261 bp in *B. melastomatos*, and 211 bp in *B. umbrosa*). Most of the PCGs in the three species have an identical start codon, except for *atp8* (adenosine triphosphate synthase protein 8), which had an ATG instead of GTG in *B. umbrosa*, whilst the *nad3* (NADH dehydrogenase subunit 3) and *nad6* (NADH dehydrogenase subunit 6) genes were characterized by an ATC instead of ATT in *B. melastomatos*. The three species had identical stop codon for the respective PCGs. In *B. latifrons* and *B. melastomatos*, the TΨC (thymidine-pseudouridine-cytidine)-loop was absent in *trnF* (phenylalanine) and DHU (dihydrouracil)-loop was absent in *trnS1* (serine S1). In *B. umbrosa*, *trnN* (asparagine), *trnC* (cysteine) and *trnF* lacked the TΨC-loop, while *trnS1* lacked the DHU-stem. Molecular phylogeny based on 13 PCGs was in general concordant with 15 mitochondrial genes (13 PCGs and 2 rRNA genes), with *B. latifrons* and *B. umbrosa* forming a sister group basal to the other species of the subgenus *Bactrocera* which was monophyletic. The whole mitogenomes will serve as a useful dataset for studying the genetics, systematics and phylogenetic relationships of the many species of *Bactrocera* genus in particular, and tephritid fruit flies in general.