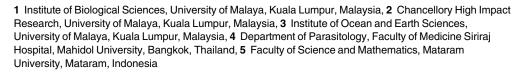




Complete Mitochondrial Genome of Three *Bactrocera* Fruit Flies of Subgenus *Bactrocera* (Diptera: Tephritidae) and Their Phylogenetic Implications

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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.