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## Complete mitochondrial genomes of *Bactrocera* (*Bulladacus*) *cinnabaria* and *B*. (*Bactrocera*) *propinqua* (Diptera: Tephritidae) and their phylogenetic relationships with other congeners

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## Abstract

*Bactrocera* (*Bulladacus*) *cinnabaria* and *B*. (*Bactrocera*) *propinqua* are tephritid fruit flies of the subfamily Dacinae, tribe Dacini. The whole mitogenomes of these two species (first report for the subgenus *Bulladacus*) possess 37 genes (13 protein-coding genes – PCGs, 2 rRNA and 22 tRNA genes). The mitogenome of *B. cinnabaria* (15,225 bp) is shorter than that of *B. propinqua* (15,927 bp), mainly due to the smaller size of the control region and intergenic spacers in *B. cinnabaria*. Molecular phylogeny based on mitochondrial genes (mt-genes) reveals two clades of the genus *Bactrocera*: one comprising the subgenus *Bactrocera* and the other comprising the subgenera *Bulladacus*, *Daculus*, *Tetradacus* and unassigned *Bactrocera* sp. '*yunnanensis*'. The subgenera represented by two or more taxa are monophyletic. *B.* (*Bulladacus*) *cinnabaria* forms a sister group with the subgenus *Daculus* (*B. oleae* and *B. biguttula*). *B. propinqua* forms a sister group with *B. ritsemai* and *B. limbifera* in a subclade containing also *B. umbrosa*, *B. curvifera* and *B. molucensis* of the monophyletic subgenus *Bactrocera*. The present study supports the synonymy of *B. ruiliensis* with *B. thailandica*. It also shows a high genetic similarity between (a) *B. melastomatos* and *B. rubigina*, (b) *B. papayae* and *B. philippinensis*, (c) *B. dorsalis* and *B. invadens*, (d) *B. tryoni* and *B. neohumeralis*, and (e) *B. cheni* and *B. tuberculata*; and *B. cheni* is distinct from and not a synonym of *B. tsuneonis* or *B. lombokensis*.

## Keywords

Bactrocera subgenera; Dacinae; Fruit flies; Mitogenomes; Molecular phylogeny

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