

RESEARCH ARTICLE

Complete mitochondrial genome of *Zeugodacus tau* (Insecta: Tephritidae) and differentiation of *Z. tau* species complex by mitochondrial cytochrome *c* oxidase subunit I gene

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Abstract

The tephritid fruit fly *Zeugodacus tau* (Walker) is a polyphagous fruit pest of economic importance in Asia. Studies based on genetic markers indicate that it forms a species complex. We report here (1) the complete mitogenome of *Z. tau* from Malaysia and comparison with that of China as well as the mitogenome of other congeners, and (2) the relationship of *Z. tau* taxa from different geographical regions based on sequences of cytochrome *c* oxidase subunit I gene. The complete mitogenome of *Z. tau* had a total length of 15631 bp for the Malaysian specimen (ZT3) and 15835 bp for the China specimen (ZT1), with similar gene order comprising 37 genes (13 protein-coding genes—PCGs, 2 rRNA genes, and 22 tRNA genes) and a non-coding A + T-rich control region (D-loop). Based on 13 PCGs and 15 mt-genes, *Z. tau* NC_027290 (China) and *Z. tau* ZT1 (China) formed a sister group in the lineage containing also *Z. tau* ZT3 (Malaysia). Phylogenetic analysis based on partial sequences of *cox1* gene indicates that the taxa from China, Japan, Laos, Malaysia, Bangladesh, India, Sri Lanka, and *Z. tau* sp. A from Thailand belong to *Z. tau* sensu stricto. A complete *cox1* gene (or 13 PCGs or 15 mt-genes) instead of partial sequence is more appropriate for determining phylogenetic relationship.

Introduction

Zeugodacus tau (Walker) is the most common tephritid fruit fly species of the genus *Zeugodacus* found in Southeast Asia [1]. It is among the economically important species belonging to the Dacinae subfamily, occurring from Pakistan to Philippines and south to Indonesia [2]. It is a polyphagous fruit pest, infesting host fruits of the families Anacardiaceae, Cucurbitaceae, Elaeocarpaceae, Moraceae, Myrtaceae, Oxalidaceae, Rutaceae, Sapotaceae, and Solanaceae [3–7]. The adult male flies are attracted to Cue lure.

Studies based on cytogenetics, partial sequences of mitochondrial cytochrome *c* oxidase subunit I (*cox1*) gene and allozymes have revealed that *Z. tau* (previously referred to as