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