

# Differentiating sibling species of *Zeugodacus caudatus* (Insecta: Tephritidae) by complete mitochondrial genome

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**Abstract** *Zeugodacus caudatus* is a pest of pumpkin flowers. It has a Palearctic and Oriental distribution. We report here the complete mitochondrial genome of the Malaysian and Indonesian samples of *Z. caudatus* determined by next-generation sequencing of genomic DNA and determine their taxonomic status as sibling species and phylogeny with other taxa of the genus *Zeugodacus*. The whole mitogenome of both samples possessed 37 genes (13 protein-coding genes—PCGs, 2 rRNA and 22 tRNA genes) and a control region. The mitogenome of the Indonesian sample (15,885 bp) was longer than that of the Malaysian sample (15,866 bp). In both samples, TΨC-loop was absent in *trnF* and DHU-loop was absent in *trnS1*. Molecular phylogeny based on 13 PCGs was concordant with 15 mitochondrial genes (13 PCGs and 2 rRNA genes),

with the two samples of *Z. caudatus* forming a sister group and the genus *Zeugodacus* was monophyletic. The Malaysian and Indonesian samples of *Z. caudatus* have a genetic distance of  $p = 7.8\%$  based on 13 PCGs and  $p = 7.0\%$  based on 15 mitochondrial genes, indicating status of sibling species. They are proposed to be accorded specific status as members of a species complex.

**Keywords** *Zeugodacus caudatus* · Indonesia · Malaysia · Mitogenome · Sibling species

## Introduction

Fruit flies of the genus *Bactrocera* are of great economic and agriculture importance because of damage caused to commercial fruits and vegetables (White and Elson-Harris 1992). Seventy-three species in the Pacific Region have been listed as destructive or potential pests (Vargas et al. 2015). *Zeugodacus caudatus* (Fabricius) is among these economically important species. It is a pest of commercial

Accession Code: The whole mitochondrial genome sequence of the Malaysian and Indonesian samples of *Z. caudatus* are available in GenBank database (accession number: KT625491 and KT625492).

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