



# Comparative analysis of the complete mitochondrial genomes of three *Zeugodacus* species (Insecta: Tephritidae: Dacinae) and their phylogenetic relationships with other congeners

Hoi-Sen Yong<sup>1</sup>, Sze-Looi Song<sup>2,3</sup>, Kah-Ooi Chua<sup>4</sup>, Yvonne Jing Mei Liew<sup>5,6</sup>, I. Wayan Suana<sup>7</sup>, Phaik-Eem Lim<sup>3</sup>, Kok-Gan Chan<sup>1</sup>, Praphathip Eamsobhana<sup>8</sup>

<sup>1</sup> Institute of Biological Sciences, Faculty of Science, Universiti Malaya, 50603 Kuala Lumpur, Malaysia; <http://orcid.org/0000-0002-9832-8826>

<sup>2</sup> Institute for Advanced Studies, Universiti Malaya, 50603 Kuala Lumpur, Malaysia; <https://orcid.org/0000-0002-1188-9728>

<sup>3</sup> Institute of Ocean and Earth Sciences, Universiti Malaya, 50603 Kuala Lumpur, Malaysia

<sup>4</sup> Centre for Research in Biotechnology for Agriculture, Universiti Malaya, 50603 Kuala Lumpur, Malaysia

<sup>5</sup> University of Malaya Centre for Proteomics Research, Universiti Malaya, 50603 Kuala Lumpur, Malaysia

<sup>6</sup> Deputy Vice Chancellor's Office (Research and Innovation), Universiti Malaya, 50603 Kuala Lumpur, Malaysia

<sup>7</sup> Faculty of Science and Mathematics, Mataram University, Mataram, Indonesia

<sup>8</sup> Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand

<https://zoobank.org/82B390E6-748D-4F44-98FC-4A04DC9076B9>

Corresponding authors: Sze-Looi Song ([szelooi@um.edu.my](mailto:szelooi@um.edu.my)), Kah-Ooi Chua ([kahooi@um.edu.my](mailto:kahooi@um.edu.my))

**Received** 16 April 2023

**Accepted** 24 July 2023

**Published** 8 September 2023

**Academic Editors** Marianna Simões, Monika Eberhard

**Citation:** Yong H-S, Song S-L, Chua K-O, Liew YJM, Suana IW, Lim P-E, Chan K-G, Eamsobhana P (2023) Comparative analysis of the complete mitochondrial genomes of three *Zeugodacus* species (Insecta: Tephritidae: Dacinae) and their phylogenetic relationships with other congeners. *Arthropod Systematics & Phylogeny* 81: 747–759. <https://doi.org/10.3897/asp.81.e105025>

## Abstract

The complete mitogenomes of fruit flies *Zeugodacus* (*Javadacus*) *calumniatus*, *Z. (Javadacus) heinrichi* and *Z. (Sinodacus) hochii* have similar gene order and contain 37 genes and a non-coding region. They share an identical start codon for the respective protein-coding genes (PCGs), an identical TAA stop codon for 11 PCGs, TAG for *cob*, and an incomplete T stop codon for *nad5*. The cloverleaf structure of most of the tRNAs is similar in the three *Zeugodacus* species. Phylogenetic analyses reveal *Z. (Parasinodacus) cilifer* to be external to two main clades: (A) monophyletic subgenus *Zeugodacus*; and (B) subgenera *Javadacus* and *Sinodacus*. The present results indicate that the taxonomic status of some taxa needs clarification. *Z. calumniatus* is genetically very similar to *Z. tau* and is not congruent with its current placement in the *munda* complex. *Z. mukiae* NC\_067083 is genetically very similar to *Z. scutellaris*, but differs significantly from *Z. mukiae* MG683384 of the *arisanicus* (*arisanica*) complex. On the other hand, *Z. proprediaphorus* is genetically distinct from and not a synonym of *Z. diaphorus*. *Z. caudatus* sensu stricto from Indonesia forms a sister lineage with *Z. diversus*, instead of with the Malaysian and Chinese taxa of *Z. caudatus* sensu lato. A notable incongruence is the sister lineage of *Z. (Sinodacus) hochii* and *Z. (Javadacus) heinrichi* among other taxa of subgenus *Javadacus*. A more extensive taxon sampling, particularly the subgenus *Sinodacus* (and other subgenera), is needed to clarify/resolve their subgenus status.

## Keywords

Fruit fly, mitogenomics, phylogeny, systematics, *Zeugodacus* subgenera