



Full Length Article

Complete mitochondrial genome of *Dacus conopsoides* (Insecta: Tephritidae) with tRNA gene duplication and molecular phylogeny of Dacini tribe

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ARTICLE INFO

Keywords:

Dacus conopsoides
Gene duplication
Mitogenome

ABSTRACT

To date there is only a single report on the complete mitochondrial genome of the *Dacus* fruit flies. We report here the whole mitogenome of *Dacus conopsoides* with first report of tRNA gene duplication in tephritid fruit flies determined using next-generation sequencing and discuss the molecular phylogeny of Dacini tribe. It had a total length of 15,852 bp, comprising 13 protein coding genes, 2 rRNA genes, 23 tRNA genes, and a non-coding region (A + T-rich control region). The 65-bp *trnF* gene was duplicated, and the 68-bp *trnE* gene was partially duplicated resulting in a 31-bp pseudogene. The cloverleaf structure for *trnN*, *trnH*, and *trnF* lacked the TΨC-loop, while *trnS* lacked the D-stem. The start codons for the protein coding genes included 6 ATG, 3 ATC, 2 ATA, and 1 each of ATT and TCG. Seven PCGs had TAA stop codon, two had TAG and four had incomplete T stop codon. Molecular phylogeny based on 15 mt-genes (13 PCGs + 2 rRNA genes) and 30 taxa of Tephritidae indicated *D. conopsoides* forming a monophyletic sister group with *D. longicornis* supported by high bootstrap value. The lineage containing also the monophyletic genus *Zeugodacus*. The Dacini and Ceratitidini tribes of the subfamily Dacinae were monophyletic but the subfamilies Dacinae and Trypetinae were paraphyletic. A broader taxa sampling of the Tephritidae is needed to better elucidate the phylogenetics and systematics of the tribes and subfamilies of tephritid fruit flies.

Introduction

Tephritid fruit flies of the genus *Dacus* Fabricius are distributed in the Afrotropical and Indo-Australian regions. They are represented by some 274 species worldwide, with 81 species in Asia-Pacific and 193 species (Doorenweerd et al., 2018), or 194 species in Africa (Hancock, 2009, 2010). Of the 274 species, 19 species have been documented as pest species (Carroll et al., 2002).

Most of the *Dacus* species with known record are attracted to the male attractant Cue lure, e.g. 55 species are attracted to Cue lure, two species to methyl eugenol (IAEA, 2013) and one species (*D. vertebratus*) is attracted to vert lure (White and Elson-Harris, 1992). The larvae of *Dacus* species feed on the fruits of Apocynaceae (including Asclepiadaceae), Cucurbitaceae and Passifloraceae (White and Elson-Harris, 1992; Leblanc et al., 2012; Virgilio et al., 2009).

The molecular phylogeny of 32 species of African *Dacus* has been

studied based on two mitochondrial (*cox1*, *rnl*) and one nuclear (*per*) gene fragments (Virgilio et al., 2009). This study indicates that Apocynaceae feeders form a monophyletic group which is sister to the monophyletic group comprising the Cucurbitaceae and Passifloraceae feeders.

Despite the large number of species, to date, there is only a single report on the complete mitochondrial genome (mitogenome) of *Dacus* fruit fly–*D. longicornis* (Jiang et al., 2016a). We report here the whole mitogenome of *D. conopsoides* de Meijere with first report of tRNA gene duplication in tephritid fruit flies determined using next-generation sequencing and discuss the molecular phylogeny of Dacini fruit flies. Compared to partial individual genes, mitogenome provides more gene contents for phylogenetic and systematics analyses.

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<https://doi.org/10.1016/j.jape.2019.07.013>

Received 23 May 2019; Received in revised form 17 July 2019; Accepted 20 July 2019

Available online 23 July 2019

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