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Complete mitochondrial genomes of two Oriental dobsonflies, *Neoneuromus tonkinensis* (van der Weele) and *Nevromus exterior* (Navás) (Megaloptera: Corydalidae), and phylogenetic implications of Corydalinae

YUNLAN JIANG¹, YAJUN ZHOU¹, YIRAN WANG¹, LU YUE¹, YAN YAN¹,
MENGQING WANG² & XINGYUE LIU^{1,3}

¹Department of Entomology, China Agricultural University, Beijing 100193, China

²Key Laboratory of Integrated Pest Management in Crops, Ministry of Agriculture, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, 100081, China

³Corresponding author. E-mail: xingyue_liu@yahoo.com

Abstract

The complete mitochondrial (mt) genomes of two Oriental endemic dobsonfly species, *Neoneuromus tonkinensis* (van der Weele) and *Nevromus exterior* (Navás), were determined and analyzed, which represent the first mt genomes of the genera *Neoneuromus* van der Weele, 1909 and *Nevromus* Rambur, 1842. The mt genome of *N. tonkinensis* is a typical circular DNA of 15776 bp with A+T content being 76.3%, while that of *N. exterior* is 15763 bp with A+T content being 77.5%. Both mt genomes are composed of 37 genes with an ancestral gene arrangement of the insect mt genome. Eleven of the 13 protein coding genes (PCGs) start with codon ATT and ATG, except for *cox1* and *nad1* respectively having ATC and ATA as the start codons in the mt genome of *N. tonkinensis*. Complete termination codons TAG and TAA were found in nine PCGs, while the remaining four genes are supposed to end with a single T. Most tRNAs are folded into the typical clover-leaf structure except for the *trnS1* whose dihydrouridine arm is a simple loop. The secondary structure of *rrnL* consists of five structural domains and 50 helices, while the *rrnS* includes three domains and 34 helices. In the phylogenomic analysis, both Bayesian inference (BI) and maximum likelihood (ML) approaches, based on sequence data of all 13 PCGs and two rRNA genes of the mt genomes, suggested that *Neoneuromus* and *Nevromus* form a monophyletic group, which is the sister group of the lineage including *Corydalus* and *Acanthacorydalis* but not the sister group of *Acanthacorydalis* van der Weele, 1907 as previously reported based on morphological data.

Key word: Corydalinae, *Neoneuromus*, *Nevromus*, mitochondrial genome, phylogeny

Introduction

Corydalinae (dobsonfly) is one of the subfamilies of the megalopteran family Corydalidae. Adult dobsonflies are characterized by the head with well-developed postocular plane (usually bearing a pair of postocular spines), and by the male genitalia having callus cerci not fused with ectoprocts and having a pair of well-developed ninth gonostyli, while the dobsonfly larvae can be easily distinguished by the presence of ventral abdominal tufts as a respiratory structure for adaptation of aquatic habitats (Glorioso 1981; Yang & Liu 2010). Currently, there are ca. 160 dobsonfly species sorted into nine genera which are vicariously distributed in America, eastern and southern Asia, and southern Africa (Yang & Liu 2010). *Neoneuromus* van der Weele, 1909 and *Nevromus* Rambur, 1842 are Oriental endemic genera of Corydalinae respectively including nine and six valid described species (Yang & Liu 2010; Liu *et al.* 2012). Adults of these two genera are relatively large-sized with acute postocular spines and the male genitalia are characterized by the male ninth tergum medially not separated anteriorly with an ovoid internal fossa and by the male ninth sternum which is attenuate and much narrower than ninth tergum (Liu & Yang 2004; Liu *et al.* 2012). Previous phylogenetic studies on the intergeneric phylogeny of Corydalinae using morphological data suggested that *Neoneuromus* and *Nevromus* are sister groups (Glorioso 1981; Penny 1993; Contreras-Ramos 1998, 2011). However, the position of these two genera in Corydalinae has not been resolved. *Neoneuromus* +