Complete mitochondrial genome of Orthetrum dragonflies and molecular phylogeny of Odonata

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ABSTRACT

Dragonflies of the genus Orthetrum are members of the anisopteran family Libellulidae. To date, there are no reports on the phylogeny of Orthetrum dragonflies based on the complete mitochondrial genome (mitogenome). There is only a single entry of a nearly complete mitogenome for O. melania. We report here the complete mitogenome of O. chrysis, O. glaucum, O. sabina and O. testaceum and their phylogenetic relationships with other taxa of Libellulidae as well as Epiophlebiidae, Anisoptera and Zygoptera. The whole mitogenomes of these four species possessed 37 genes (13 protein-coding genes – PCGs, 2 rRNA and 22 tRNA genes) and a non-coding region. Molecular phylogeny based on 13 PCGs was concordant with 15 mitochondrial genes (13 PCGs and 2 rRNA genes). The Libellulidae (Anisoptera) was monophyletic with two lineages: (Orthetrum) + (Brachythe mis + Hydrobasileus). It formed a sister group with Corduliidae. The Zygoptera was monophyletic with three lineages: (Calopterygidae) + (Euphaeidae + Pseudolestidae) + (Coenagrionidae + Platycnemididae). The enigmatic Epiophlebia superstes (Epiophlebiidae) forms a sister group with Zygoptera. The complete mitogenome is useful for determining the higher-level phylogenetic relationships of Odonata.

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1. Introduction

Dragonflies of the genus Orthetrum (Newman, 1833) are members of the anisopteran family Libellulidae. Fifty-nine species are currently recorded in the World Odonata List (Schorr and Paulson, 2015). The number of species will increase with the documentation of additional cryptic species (Yong et al., 2014). Of the genus Orthetrum, two species complexes have been well resolved: (1) O. japonicum species complex comprising O. japonicum and O. internum (Futahashi, 2011; Karube et al., 2012); and (2) O. triangulare species complex comprising O. triangulare and O. melania (Sasamoto and Futahashi, 2013). Recently two