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The first two mitochondrial genomes of the family Aphelinidae with novel gene orders and phylogenetic implications

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Abstract

Chalcidoidea is one of the most diverse group in Hymenoptera by possessing striking mitochondrial gene arrangement. By using next generation sequencing method, the first two nearly complete mitochondrial genomes in the family Aphelinidae (Insecta, Hymenoptera, Chalcidoidea) were obtained in this study. Almost all previously sequenced mitochondrial genome of Chalcidoidea species have a large inversion including six genes (*atp6-atp8-trnD-trnK-cox2-trnL2-cox1*) as compared with ancestral mitochondrial genome, but these two *Encarsia* mitochondrial genomes had a large inversion including nine genes (*nad3-trnG-atp6-atp8-trnD-trnK-cox2-trnL2-cox1*), which was only congruent with the species in the genus *Nasonia*. Moreover, we found that one shuffling changes (*trnD* and *trnK*) happened in the species *E. obtusiclava* but not in another species *E. formosa* within the same genus, of which such shuffling within the same genus at this region was only detected in *Polistors* within Insecta. Phylogenetic analysis displayed that different data matrix (13PCG+ 2 rRNA or 13 PCG) and inference methods (BI or ML) indicate the identical topology with high nodal supports that Aphelinidae formed a sister group with (Trichogrammatidae + Aganoidae) and the monophyly of Pteromalidae. Our results also indicated the validity of assembling and feasibility of next-generation technology to obtain the mitochondrial genomes of parasitic Hymenoptera.

Keywords: mitochondrial genome; phylogeny; Chalcidoidea

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