



Molecular phylogenetic and dating analysis of pierid butterfly species using complete mitochondrial genomes

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ABSTRACT. Pieridae is a butterfly family whose evolutionary history is poorly understood. Due to the difficulties in identifying morphological synapomorphies within the group and the scarcity of the fossil records, only a few studies on higher phylogeny of Pieridae have been reported to date. In this study, we describe the complete mitochondrial genomes of four pierid butterfly species (*Aporia martineti*, *Aporia hippia*, *Aporia bieti*, and *Mesapia peloria*), in order to better characterize the pierid butterfly mitogenomes and perform the phylogenetic analyses using all available mitogenomic sequence data (13PCGs, rRNAs, and tRNAs) from the 18 pierid butterfly species comprising the three main subfamilies (Dismorphiinae, Coliadiinae and Pierinae). Our analysis shows that the four new mitogenomes share similar features

with other known pierid mitogenomes in gene order and organization. Phylogenetic analyses by maximum likelihood and Bayesian inference show that the pierid higher-level relationship is: Dismorphiinae + (Coliadinae + Pierinae), which corroborates the results of some previous molecular and morphological studies. However, we found that the *Hebomoia* and *Anthocharis* make a sister group, supporting the traditional tribe Anthocharidini; in addition, the *Mesapia peloria* was shown to be clustered within the *Aporia* group, suggesting that the genus *Mesapia* should be reduced to the taxonomic status of subgenus. Our molecular dating analysis indicates that the family Pieridae began to diverge during the Late Cretaceous about 92 million years ago (mya), while the subfamily Pierinae diverged from the Coliadinae at about 86 mya (Late Cretaceous).

Key words: Mitogenomes; Pieridae; Phylogeny; Divergence time