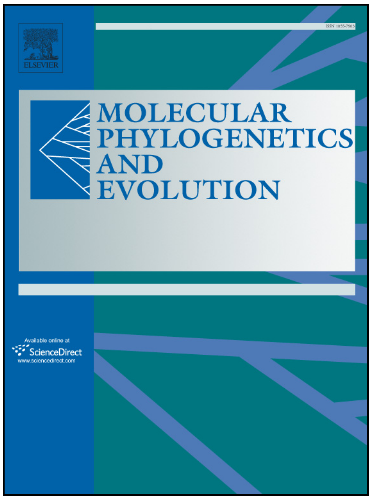

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Phylogeny of the monarch flycatchers reveals extensive paraphyly and novel relationships within a major Australo-Pacific radiation

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Abstract

Monarch flycatchers are a major component of Australo-Pacific and Wallacean avifaunas. To date, the family has received incomplete attention by molecular systematists who focused on subclades with minimal character and/or taxon sampling. As a result, Monarchidae taxonomy is still out-of-date, and biogeographic reconstructions have been based on poorly-resolved phylogenies, limiting their interpretation. Here, we produced a comprehensive, molecular phylogeny of the Monarchidae inferred from mitochondrial and nuclear loci using both concatenated and multilocus coalescent frameworks. We sampled 92% of the 99 recognized monarchid biological species and included deeper sampling within several phylogenetic species complexes, including *Monarcha castaneiventris*, *Symposiachrus barbatus*, and *Terpsiphone rufiventer. Melampitta* is identified as sister to the monarch flycatchers, which themselves comprise four major lineages. The first lineage is composed of *Terpsiphone* and allies, the second lineage is *Grallina*, the third is *Arses* and *Myiagra*, and the fourth lineage comprises a diverse assemblage of genera including the “core monarchs” and the most geographically isolated groups like *Chasiempis* (Hawaii) and *Pomarea* (eastern Polynesia). Gene tree discordance was evident in *Myiagra*, which has implications for basal lineages in the genus (e.g., *M. azureocapilla*, *M. hebetior*, and *M. alecto*). Numerous genera within the core monarchs are paraphyletic, including *Mayrornis* and *Pomarea*, whereas the validity of others such as *Metabolus* are questionable. We recognize polytypic taxa as multiple species, including *Lamprolia victoriae* and *Myiagra azureocapilla*. In general, the topology of species complexes included short internodes that were not well resolved, owing to their rapid diversification across island archipelagos. *Terpsiphone rufiventer* comprises multiple lineages, including a heretofore-unappreciated West African lineage, but relationships within these rapid radiations will require extensive genomic sampling for further resolution. This study establishes a new benchmark for Monarchidae systematics and it provides an excellent framework for future work on biogeography and character evolution in a diverse Australo-Papuan radiation.

Keywords