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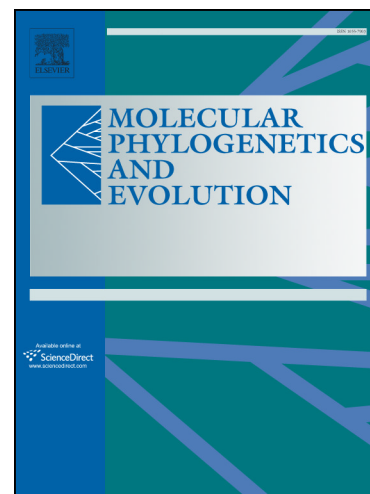
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A tangle of forms and phylogeny: extensive morphological homoplasy and molecular clock heterogeneity in *Bonnetina* and related tarantulas

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Abstract

Tarantula spider systematics has long been considered problematic. Species diagnosis and phylogenetic hypotheses have historically relied on morphological features, which are known to be relatively conserved and/or highly homoplastic across the family. Morphology-based attempts to clarify the phylogeny of the highly diverse New World Theraphosinae, have only been moderately successful, and the time-frame of tarantulas' evolution is nearly *terra incognita*. Here we present a molecular phylogenetic analysis of the Theraphosinae genus *Bonnetina* and related lineages, employing one mitochondrial (COI) and five nuclear (ITS1, EF1G, MID1IP1, MRPL44, and I3568) loci. We also perform ancestral state reconstruction of a newly formulated morphological data matrix. Our analysis includes 47 species placed in 17 genera and other undetermined lineages. We obtained well resolved and supported topologies. COI and EF1G substitution rates were much lower than the values generally accepted for mygalomorph evolution, with substantial rate heterogeneity among lineages. The origin of Theraphosinae was dated during the Late Cretaceous, followed by rapid diversification into the three recently proposed Theraphosinae tribes. North and Central American Hapalopini (including *Bonnetina*) form a monophyletic group that likely originated during the Oligocene to a dispersing ancestor from the then isolated South America. A clade that includes all but one *Bonnetina* species is estimated to have originated in the early Miocene and is the sister group of two morphologically

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