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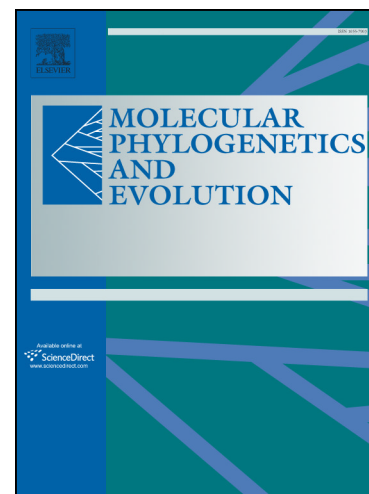
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**A multilocus phylogeny of the genus *Sarcohyla* (Anura: Hylidae), and an investigation of species boundaries using statistical species delimitation**

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**ABSTRACT**

The genus *Sarcohyla* is composed by 24 species endemic to México. Despite the large number of phylogenetic studies focusing on the family Hylidae, the relationships among the species of *Sarcohyla* are still poorly known, and the scarce numbers of specimens and tissue samples available for some of the species has hampered an appropriate phylogenetic analysis. We present the most comprehensive molecular phylogenetic study of *Sarcohyla* to date. We included 17 species of the genus *Sarcohyla* using data from two mitochondrial (*ND1* and *12S*) and three nuclear genes (*Rag-1*, *Rhod*, and *POMc*). We performed phylogenetic analyses using Bayesian inference, and the absence of conflicts with strong support between the separate gene trees indicates that incomplete lineage sorting and/or introgressive hybridization are negligible. A coalescent-based species-tree analysis of the four independent loci (three nuclear genes + mtDNA) mostly supports the same species-level relationships as the analysis of the concatenated data. By including new samples from additional species and localities, we find that: (1) the widely distributed species *S. bistrincta* is a complex of at least three species, (2) another undescribed species exists in the group, (3) the species *S. ephemera* is not valid and it corresponds to a junior synonym of *S. calthula*. In addition, we conducted marginal

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