

Phylogenetic relationships of Ansonia from Southeast Asia inferred from mitochondrial DNA sequences: Systematic and biogeographic implications (Anura: Bufonidae)

Abstract

We investigated the phylogenetic relationships and estimated the history of species diversification and biogeography in the bufonid genus *Ansonia* from Southeast Asia, a unique organism with tadpoles adapted to life in strong currents chiefly in montane regions and also in lowland rainforests. We estimated phylogenetic relationships among 32 named and unnamed taxa using 2461 bp sequences of the mitochondrial 12S rRNA, tRNA^{Val}, and 16S rRNA genes with equally-weighted parsimony, maximum likelihood, and Bayesian methods of inference. Monophyletic clades of Southeast Asian members of the genus *Ansonia* are well-supported, allowing for the interpretation of general biogeographic conclusions. The genus is divided into two major clades. One of these contains two reciprocally monophyletic subclades, one from the Malay Peninsula and Thailand and the other from Borneo. The other major clade primarily consists of Bornean taxa but also includes a monophyletic group of two Philippine species and a single peninsular Malaysian species. We estimated absolute divergence times using Bayesian methods with external calibration points to reconstruct the relative timing of faunal exchange between the major landmasses of Southeast Asia.