Phylogenetic and taxonomic relationships of the Polypedates leucomystax complex (Amphibia)

Abstract

We investigated the phylogenetic and taxonomic relationships and estimated the history of species diversification and biogeography in the Asian rhacophorid genus Polypedates, focusing on the Polypedates leucomystax complex, whose members are notoriously difficult to classify. We first estimated phylogenetic relationships within the complex using 2005-bp sequences of the mitochondrial 12S rRNA, tRNA val and 16S rRNA genes with maximum parsimony, maximum likelihood (ML) and Bayesian methods of inference. Polypedates exhibits well-supported monophyly, with distinct clades for P. otilophus, P. colletti, P. maculatus and the P. leucomystax complex, consisting of P. macrotis, and the Malay (Polypedates sp. from Malay Peninsula), North China (P. braueri), South China (Polypedates cf. mutus 1), Indochina (P. megacephalus), Sunda (P. leucomystax) and Laos (Polypedates cf. mutus 2) clades. In a subsequent phylogenetic analysis of 4696-bp sequences of the nuclear brain-derived neurotrophic factor (BDNF), sodium/calcium exchanger 1 (NCX), POMC, Rag-1, Rhod and Tyr genes using Bayesian methods of inference, all of these clades were recovered. Some clades of the P. leucomystax complex occur sympatrically and show high genetic diversity or morphological and acoustic differences. Similar tendencies were observed between some allopatric clades. Therefore, we consider each of these groups to be distinct specifically. We also estimated absolute divergence times within the genus using Bayesian methods. Divergence in Polypedates began with the divergence of a primarily South Asian Clade from the common ancestor of secondarily South-East Asia P. maculatus and South-East Asian members. The divergence between the latter occurred much later. The P. leucomystax complex diverged in the Pliocene, much later than other congeners, and seems to have been greatly affected by human-related dispersal after the Pleistocene.