Molecular phylogenetic reconstruction of the endemic Asian salamander family Hynobiidae (Amphibia, Caudata)

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Abstract

The salamander family Hynobiidae contains over 50 species and has been the subject of a number of molecular phylogenetic investigations aimed at reconstructing branches across the entire family. In general, studies using the greatest amount of sequence data have used reduced taxon sampling, while the study with the greatest taxon sampling has used a limited sequence data set. Here, we provide insights into the phylogenetic history of the Hynobiidae using both dense taxon sampling and a large mitochondrial DNA sequence data set. We report exclusive new mitochondrial DNA data of 2566 aligned bases (with 151 excluded sites, of included sites 1157 are variable with 957 parsimony informative). This is sampled from two genic regions encoding a 12S–16S region (the 3' end of 12S rRNA, tRNAVal, and the 5' end of 16S rRNA), and a ND2–COI region (ND2, tRNATrp, tRNAAla, tRNAAsn, the origin for light strand replication—OL, tRNACys, tRNTyr, and the 5' end of COI). Analyses using parsimony, Bayesian, and maximum likelihood optimality criteria produce similar phylogenetic trees, with discordant branches generally receiving low levels of branch support. Monophyly of the Hynobiidae is strongly supported across all analyses, as is the sister relationship and deep divergence between the genus Onychodactylus with all remaining hynobiids. Within this latter grouping our phylogenetic results identify six clades that are relatively divergent from one another, but for which there is minimal support for their phylogenetic placement. This includes the genus Batrachuperus, the genus Hynobius, the genus Pachyhynobius, the genus Salamandrella, a clade containing the genera Ranodon and Paradactylodon, and a clade containing the genera Liua and Pseudohynobius. This latter clade receives low bootstrap support in the parsimony analysis, but is consistent across all three analytical methods. Our results also clarify a number of well-supported relationships within the larger Batrachuperus and Hynobius clades. While the relationships identified in this study do much to clarify the phylogenetic history of the Hynobiidae, the poor resolution among major hynobiid clades, and the contrast of mtDNA-derived relationships with recent phylogenetic results from a small number of nuclear genes, highlights the need for continued phylogenetic study with larger numbers of nuclear loci.

Key words:

Introduction

The salamander family Hynobiidae is comprised of a diverse assemblage of over 50 species distributed entirely within continental Asia and adjacent islands. Subsets of this family have been the focus of numerous allozyme and mitochondrial DNA-based evolutionary investigations (Fu et al., 2001; Matsui et al., 1992, 2000, 2001, 2004, 2006; Matsui, Nishikawa, et al., 2007; Matsui, Tominaga, et al., 2007; Nishikawa et al., 2005; Nishikawa et al., 2001, 2007; Tominaga et al., 2003, 2005, 2006; Zeng et al., 2006). Three different studies have investigated phylogenetic relationships on a broader scale within the Hynobiidae. Zhang et al. (2006) analyzed complete mitochondrial DNA genome data (>14,000 aligned nucleotides) from 16 hynobid taxa representing major groups within the family and a cryptobranchid outgroup (Andrias davidianus).