



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

DAVID W. WEISROCK^{1,6}, J. ROBERT MACEY^{2,3}, MASAFUMI MATSUI⁴, DANIEL G. MULCAHY⁵,
& THEODORE J. PAPENFUSS³

¹Department of Biology, University of Kentucky, 101 Thomas Hunt Morgan Building, Lexington, KY, 40506-0225

²Genomics, Department of Biology, Merritt College, 1250 Campus Drive, Oakland, CA 94619

³Museum of Vertebrate Zoology, 3101 Valley Life Science Building, University of California, Berkeley, CA 94720

⁴Graduate School of Human and Environmental Studies, Kyoto University, Kyoto 606-8501, Japan

⁵Smithsonian Institution, National Museum of Natural History, 4210 Silver Hill Rd., MRC 534, Suitland, MD 20746

⁶Corresponding author. E-mail: dweis2@uky.edu; Phone: 859-257-2249; FAX: 859-257-1717

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, tRNA^{Val}, and the 5' end of 16S rRNA), and a ND2–COI region (ND2, tRNA^{Tyr}, tRNA^{Ala}, tRNA^{Asn}, the origin for light strand replication—O_L, tRNA^{Cys}, tRNA^{Tyr}, 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 hynobiid taxa representing major groups within the family and a cryptobranchid outgroup (*Andrias davidianus*).