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Phylogenetic placements of the barbin genera *Discherodontus*, *Chagunius*, and *Hypselobarbus* in the subfamily Cyprininae (Teleostei: Cypriniformes) and their relationships with other barbins

LEI YANG¹, M. VINCENT HIRT², TETSUYA SADO³, M. ARUNACHALAM⁴, RAJA MANICKAM⁴, KEVIN L. TANG⁵, ANDREW M. SIMONS⁶, HSIN-HUI WU¹, RICHARD L. MAYDEN¹ & MASAKI MIYA³

¹Department of Biology, Saint Louis University, 3507 Laclede Ave. St. Louis, MO 63103, USA. E-mails: leiyangslu@gmail.com (LY), hwu5@slu.edu (HW), cypriniformes@gmail.com (RLM)

²Graduate Program in Ecology, Evolution, and Behavior, University of Minnesota, St. Paul, MN 55108, USA. E-mail: hirt0021@umn.edu

³Department of Zoology, Natural History Museum and Institute, Chiba, 955-2 Aoba-cho, Chuo-ku, Chiba 260-8682, Japan. E-mails: zacco_evolangs@yahoo.co.jp (TS), miya@chiba-muse.or.jp (MM)

⁴Sri Paramakalyani Centre for Environmental Sciences, Manonmaniam Sundaranar University, Alwarkurichi - 627 412, Tamil Nadu, India. E-mails: arunacm@gmail.com (MA), wetlandraja@gmail.com (RM)

⁵Department of Biology, University of Michigan-Flint, 303 E. Kearsley St. Flint, MI 48502. E-mail: ktang@umflint.edu

⁶Department of Fisheries, Wildlife, and Conservation Biology and Bell Museum of Natural History, University of Minnesota, St. Paul, MN 55108, USA. E-mail: asimons@umn.edu

Abstract

The barbin genera *Discherodontus* Rainboth 1989, *Chagunius* Smith 1938 and *Hypselobarbus* Bleeker 1860 are distributed in Southeast and South Asia and are among the least studied taxa of the order Cypriniformes. Few morphological studies have been conducted on these genera and only a very limited number of morphological characters were employed to hypothesize or infer their monophyly, inter-relationships, and relationships with other barbins. The main aim of this study is to examine the monophyly of these three genera and propose hypothesis of relationship among these taxa and other barbins based on a molecular phylogeny of the subfamily Cyprininae. A total of 106 cypriniform species were sampled, including 64 species and 31 genera of barbins collected from Eurasia and Africa. Partitioned maximum likelihood analysis was performed using DNA sequences derived from five mitochondrial genes (5601 bp): cytochrome *c* oxidase subunit I (COI), cytochrome *b* (Cyt *b*), 16S ribosomal RNA (16S), NADH dehydrogenase subunits 4 (ND4) and subunits 5 (ND5). The resulting phylogeny demonstrates that, under current taxon sampling, *Discherodontus*, *Chagunius*, and *Hypselobarbus* are all monophyletic genera. Together they do not form a monophyletic group, as hypothesized in previous studies, but are instead part of three distinct and unrelated clades. *Discherodontus* constitutes the basal lineage of a clade formed by Southeast Asian barbins (e.g. *Poropuntius*, *Hypsibarbus*, *Balantiocheilos*); *Chagunius* is basal to a clade formed mainly by *Puntius* and allies (although this relationship was only weakly supported); *Hypselobarbus* and *Barbus carnaticus* formed a clade sister to a clade including *Tor*, *Neolissochilus*, *Labeobarbus*, and *Varicorhinus*. Homoplasy and shared plesiomorphy of some hypothesized important morphological characters employed in previous studies that led researchers to hypothesize earlier relationships are discussed.

Key words: homoplasy; mitochondrial; molecular; morphology; phylogeny

Introduction

With over 60 genera and 800 species, barbin fishes (e.g. *Barbus*, *Puntius*) have achieved great diversity in Eurasia and Africa. Historically, these taxa were thought to be members of the cypriniforme subfamily Cyprininae, a group that lack synapomorphic characters. Some recent molecular studies (e.g. Chen & Mayden 2009; Mayden & Chen 2010) have demonstrated that the Cyprininae is monophyletic and sister to the family Psilorhynchidae, rendering the current classification of subfamilies and families in the superorder Cyprinoidea of Cypriniformes somewhat chaotic. However, we continue to refer the target species to the Cyprininae, a group with which they consistently align with in molecular studies and the subfamily to which they have historically been allocated.