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Phylogenetic Relationships of the Genus *Homatula* (Cypriniformes: Nemacheilidae), with Special Reference to the Biogeographic History around the Yunnan-Guizhou Plateau

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Abstract

Species of the nemacheilid genus *Homatula* are endemic to the Yunnan-Guizhou Plateau of China. Herein we provide phylogenetic inferences of species relationships based on complete sequences of the mitochondrial *cytochrome b* gene (*cyt b*) and partial sequences of the nuclear *recombination activation* gene (RAG 1). Both gene trees (and the concatenated data set) support the recognition of five clades in the genus. These analyses also support the hypothesis that two of the lineages resolved represent undescribed species awaiting formal description, and, further, that two previously recognized species are junior synonyms; both are genetically indistinguishable from other previously recognized species. Divergence times of the major clades in *Homatula* are inferred to be Late Pliocene and the Early Pleistocene, and are correlated with the massive geological events associated with the uplift of the Qinghai-Tibetan Plateau occurring at these times. The reconstruction of drainage histories suggests that the fish faunas of the Nu and Lancang rivers are basal relative to other riverine faunas in the region, and that the Nanpan and the Jinsha rivers share a more recent history than with any other river systems included in our study.

Key words: molecular phylogeny, biogeography, molecular divergence times, Yunnan-Guizhou Plateau

Introduction

Many researchers have argued that biogeographic analyses of extant freshwater fish species can be used to reconstruct historical linkages within and between regional geographical areas and reveal aspects of the underlying diversification processes of biotic evolution (Wiley & Mayden 1985; Mayden 1987). Proposed mechanisms have included dispersal, large- or small-scale vicariance, population divergence through isolation, and genetic drift (Wiley & Mayden 1985; Mayden 1987). Given that freshwater fishes are confined to the lentic and lotic freshwater systems, it has been suggested that their history of evolution and the mechanisms underlying their diversification is probably more easily deciphered than for many other groups (Mayden 1988). Considerable discussion has occurred on the differentiation between divergences via dispersal versus vicariance, but the fact remains that dispersion of primary freshwater fishes depends on the formation of direct connections between drainages (Bermingham & Martin 1998; Lundberg 1993). In recent years our understanding of diversification has been enhanced through phylogenetic inferences coupled with robust estimates of phyletic divergence times. This new approach of combining data sources can provide tremendous insight into our understanding of both the patterns and the underlying the causes of the historical diversification of lineages (Castoe *et al.* 2009).

The Yunnan-Guizhou Plateau is situated at the southeastern fringes of the Qinghai-Tibetan Plateau, shaping the terrace gradient from the Qinghai-Tibetan Plateau to the southeastern flood plain. The Yunnan-Guizhou Plateau is a key area in investigating biotic and environmental responses of species to the geological and geographical