



Article

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Bleeker was right: Revision of the genus *Cyclocheilichthys* (Bleeker 1859) and resurrection of the genus *Anematischthys* (Bleeker 1859), based on morphological and molecular data of Southeast Asian Cyprininae (Teleostei, Cypriniformes)

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Abstract

The taxonomy within the order Cypriniformes is subject to frequent changes, thanks to the results coming from recent molecular phylogenies that help understand the Cypriniformes tree of life previously established through morphological characters. In this paper, we focus on species belonging to the Cyprininae – the largest sub-family among Cypriniformes – and we present both morphological and phylogenetic arguments to revise the taxonomy of the genus *Cyclocheilichthys*. For morphological investigations, we characterized external traits as well as the postcranial skeleton and the neurocranium. For molecular phylogenies, we used four markers, both mitochondrial and nuclear, to establish a phylogenetic tree. We studied four species currently assigned to the genus *Cyclocheilichthys* as well as the species *Cosmochilus harmandi* and *Puntioplites falcifer* and we show that the genus *Cyclocheilichthys* is non-monophyletic as *Cyclocheilichthys enoplos* is closer to *C. harmandi* and *P. falcifer* than *Cyclocheilichthys armatus*, *Cyclocheilichthys apogon* and *Cyclocheilichthys repasson*. Finally, we revise the genus *Cyclocheilichthys* and we propose to split this genus into two genera: genus *Cyclocheilichthys* with the species *Cyclocheilichthys enoplos* and genus *Anematischthys* with species *Anematischthys armatus*, *Anematischthys apogon* and *Anematischthys repasson*.

Key words: Cypriniformes, taxonomy, morphology, molecular phylogeny, *Cyclocheilichthys*

Introduction

Cypriniformes constitutes the largest order of freshwater fishes encompassing more than 3,000 extant species (Nelson 2006). The taxonomy of Cypriniformes has been the subject of a long debate since the 19th century; see Howes (1991) for a review. Recently, molecular phylogenies have brought much information on phylogenetic relationships among Cypriniformes (Saitoh *et al.* 2006, Mayden *et al.* 2009), but there are still many unresolved nodes in the Cypriniformes tree of life. The subfamily Cyprininae is the largest subfamily among Cypriniformes, with around 1,300 living species distributed within 110 genera (Yang *et al.* 2010). Although some classifications based on morphological characters (Howes 1991, Rainboth 1996) have been later validated by molecular phylogenies (Wang *et al.* 2007, Li *et al.* 2008, Yang *et al.* 2010), some clades like Semiploti and Osteobramae (according to Rainboth 1996) still lack solid confirmation by molecular studies. Recently published molecular investigations have shown that most species included in these two clades form a monophyletic group (Yang *et al.* 2010), with the exception of *Onychostoma*. This latter genus was moved into the Semiploti by Rainboth (1996), but recent molecular studies grouped *Onychostoma* together with *Schizothorax*, *Gymnocypris*, and *Spinibarbus* (Wang *et al.* 2007, Li *et al.* 2008, Yang *et al.* 2010) into a clade corresponding to Schizothoracin and Onychostoma-Cyprinion lineages by Howes (1991). A problem is that molecular studies dealing with the phylogeny of Cyprininae have poorly sampled species belonging to the sub-tribes Semiploti and Osteobramae (according to