



## The Cypriniformes Tree of Confusion

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In a recent paper, Mooi & Gill (2010) raised various issues related to recent developments in molecular systematic ichthyology that they found alarming. They went so far as to call this a “crisis in fish systematics.” They criticised the trend that alternative trees for the placement of a taxon in question are not critically discussed and the reason for the divergent positions is not adequately evaluated. They raise the important question “On what basis is one topology to be preferred over the other?”

This is a decisive question if we look at the issue of conflicting topologies in molecular systematics in a group of fishes, the teleost order Cypriniformes, for which a large number of molecular analyses have been published in the last 4 years. With more than 3700 species, cypriniforms dominate the freshwaters in North America, Africa, and Eurasia (Nelson 2006). This huge diversity has so far prevented an attempt to resolve their phylogenetic relationships down to subfamily or lower systematic levels. Nevertheless, a few convincing phylogenetic hypotheses based on morphological characters have been available for the main clades of cypriniforms since the 1980s (Siebert 1987; Sawada 1982).

Cypriniform systematics thus led the life of a sleeping beauty until it started to be woken up by establishing the zebra danio, *Danio rerio* (Hamilton 1822), as THE vertebrate model species for developmental genetic work (see the “zebrafish issue” of the journal *Development* in 1996). Suddenly moved into the limelight of modern biological science, cypriniforms and cypriniform systematics and taxonomy attracted a growing interest from various disciplines in ichthyology, but especially from molecular systematists (e.g. Meyer et al. 1993, 1995; Zardoya et al. 1996).

### Molecular onslaught on the Cypriniformes Tree of Life

In 2005, the Cypriniformes Tree of Life (CToL) project funded by the National Science Foundation (NSF) pledged to fill the huge gap in our knowledge of cypriniform phylogenetic relationships by generating “an array of nuclear and mitochondrial sequences as well as a diverse suite of internal and external morphological characters for a targeted group of 1,000 species,” which then would be used to “2. Reconstruct relationships of ca. 350 genera and species using entire mitochondrial sequences, nDNA, and a suite of morphological characters.” and “3. Reconstruct relationships of 1,000 species using three mitochondrial genes and four nuclear genes and a suite of morphological characters.” (<http://bio.slu.edu/mayden/cypriniformes/objectives.html>, accessed 15.06.2010). CToL participants have since produced a number of molecular systematic papers on the relationships of cypriniform clades (e.g. Saitoh et al. 2006; Mayden et al. 2007, 2008; He et al. 2008; Chen et al. 2008; Chen et al. 2009; Conway et al. 2008, 2009; Chen & Mayden 2009; Tang et al. 2010; Mayden & Chen 2010; Yang & Mayden, 2010; Yang et al., 2010), although the pledged morphology based studies do not seem to have produced any published results yet. Research groups not associated with CToL have also added additional molecular phylogenetic analyses of cypriniforms and their various subgroups (Šlechtová et al. 2006, 2007, 2008; Bohlen & Šlechtová 2009; Rüber et al. 2007; Fang et al. 2009), so that we should at least expect to have a clearer picture of cypriniform intrarelationships based on molecular data.