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Phylogeny of suckers (Teleostei: Cypriniformes: Catostomidae): further evidence of relationships provided by the single-copy nuclear gene IRBP2

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Abstract

The order Cypriniformes and family Catostomidae, the Holarctic suckers, have received considerable phylogenetic attention in recent years. These studies have provided contrasting phylogenies and classifications to historical, morphology-based phylogenetic and prephylogenetic hypotheses of relationships of species and the naturalness of hypothesized genera, tribes, and subfamilies. To date, nearly all molecular work on catostomids has been done using DNA sequence variation of mitochondrial genes. In this study, we add to our previous investigations to identify single-copy nuclear gene markers for diploid and polyploid cypriniforms, and to expand sequences of nuclear IRBP2 gene to 1,933 bp for 23 catostomid species. This effort expands our previous studies using only partial sequences of 849 bp. The extended gene fragment consists of nearly the complete gene across exon1 to exon 4 and is used in two analyses to infer phylogenetic relationships of the currently, or formerly, recognized genera, tribes, and subfamilies. One analysis includes 23 ingroup species for which the larger fragment of IRBP2 could be obtained; these taxa were also included in a second analysis of 67 samples of 52 species for the shorter fragment. As is typical of other nuclear genes examined to date for cypriniform species, variation in IRBP2 provided strong nodal support for some supra-specific groupings and species relationships. The two analyses revealed slightly different relationships, yet are largely consistent with one another. The resulting tree from variation in the shorter fragment for 52 species is somewhat inferior to the tree derived using the extended fragment in that not as many nodes were resolved, and few have strong support. Relationships from the latter analysis are, however, consistent with inferred relationships that are more robustly supported in the smaller taxon analysis using the larger fragment, lending credence to the use of more complete sequence data of genes in phylogenetic analyses. The current classification of the family (e.g., Nelson 2006) is not fully supported herein. The Ictiobinae is monophyletic, but some ambiguity exists as to relationship of this group relative to Cycleptinae and Myxocyprininae, as well as the need to recognize the latter two subfamilies. Catostominae is monophyletic. *Catostomus* is clearly not monophyletic; unnaturalness of the genus is supported herein as well as in multiple, consistently repeated and highly supported studies resolving *Deltistes*, *Chasmistes*, and *Xyrauchen* within *Catostomus*. We herein synonymize the former three genera into the latter genus; their recognition as distinct genera has been based on historical methods of classification based strictly on “distinctiveness” or anagenesis of each lineage alone and not phylogenetic relationships relative to species of *Catostomus*. The monophyly of *Erimyzonini* is strongly supported within the analysis of the longer sequence data set. The monophyly of *Thoburniini* is ambiguous, but *Moxostomatini*, including “*Scartomyzon*,” is monophyletic in both analyses. The proposed recognition of *Scartomyzon* as a monophyletic group separate from *Moxostoma* is again falsified but with evidence from the nuclear gene IRBP2.

Key words: interphotoreceptor retinoid-binding protein gene; IRBP2, molecular systematics; polyploidy; gene duplication

Introduction

Catostomidae, Holarctic suckers, is recognized as a monophyletic group in analyses using either morphological and molecular characters, and is one of several families from the world's largest clade of freshwater fishes—the Cypriniformes. Catostomids are closely related to the clade containing three species of algae eaters (Gyrinocheilidae) plus the diverse lineage of loaches (Cobitidae and other related families). These three lineages form a major, large and diverse lineage that has been reclassified in the Superfamily Cobitoidea (Nelson 2006; Saitoh *et al.* 2006;