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Molecular systematics of western North American cyprinids (Cypriniformes: Cyprinidae)

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Abstract

The phylogenetic or evolutionary relationships of species of Cypriniformes, as well as their classification, is in an era of flux. For the first time ever, the Order, and constituent Families are being examined for relationships within a phylogenetic context. Relevant findings as to sister-group relationships are largely being inferred from analyses of both mitochondrial and nuclear DNA sequences. Like the vast majority of Cypriniformes, due to an overall lack of any phylogenetic investigation of these fishes since Hennig's transformation of the discipline, changes in hypotheses of relationships and a natural classification of the species should not be of surprise to anyone. Basically, for most taxa no properly supported phylogenetic hypothesis has ever been done; and this includes relationships with reasonable taxon and character sampling of even families and subfamilies. As such, like others, many western North American cyprinid genera have had a controversial taxonomic and systematic history.

Our effort to better understand the evolutionary history of this artificial geographic grouping of species (Western) surveyed taxa and characters broadly. We analyzed 127 taxa (71 species) from 36 genera, including representative taxa from all 22 western genera hypothesized to form the Western Clade *sensu* Coburn and Cavender (1992). Our evaluation also included additional sampling from a heterogeneous array of species from the western genera *Algansea*, *Gila*, *Lepidomeda*, *Ptychocheilus* and *Siphateles*. Resulting phylogenetic inferences, based on one mitochondrial and three nuclear genes (mtDNA: *cytb*; nDNA: *Rag1*, *Rhod*, *S7*), consistently resolved a well-supported Western Clade, but one inclusive of *Chrosomus erythrogaster*. This taxon, always formed the sister group to the extant species of *Gila* plus 10 other western genera. Our Western Clade is qualitatively different from that of prior studies and does not include the genera *Agosia*, *Algansea*, *Iotichthys*, *Lepidomeda*, *Meda*, *Mylocheilus*, *Plagopterus*, *Pogonichthys*, *Rhinichthys*, *Tiaroga* or *Yuriria*. All of these taxa were, however, included in Coburn and Cavender's (1992) Western Clade. Our broader-scale survey and increased character sampling were always resolved these latter taxa within one of two different major clades: the OPM Clade (*sensu* Mayden 1989) and the Creek Chub—Plagopterin Clade (*sensu* Simons *et al.* 2003). Our hypothesized Western Clade places *Orthodon* sister to a Western Chub-Pikeminnow Clade also inclusive of *Acrocheilus*, *Eremichthys*, *Gila*, *Hesperoleucus*, *Lavinia*, *Moapa*, *Mylopharodon*, *Ptychocheilus*, *Relictus* and *Siphateles*. The latter taxa have traditionally been recognized at the generic level, simply on the basis of their morphological distinctiveness and not on the basis of a phylogenetic evaluation of relationships. Composition of our Western Chub-Pikeminnow Clade also reveals genetic divergences between species of some genera (*Gila*, *Ptychocheilus*, *Siphateles*) comparable to genetic divergences documented between genera within the Western Clade. Relationships for these 10 genera also highlight taxonomic inconsistencies relative to recent phylogenetic analysis and, in some cases, are in need of focused attention using morphology or additional molecular data to test relationships that will eventually establish a stable classification. Some of these genera are clearly unnatural relative to other genera and their classification or ranking is an obligatory change in modern science of phylogenetics.

Key words: Western Clade, Phoxinins, sequence analyses, *Gila* lineage, controversial taxonomy