

of which were assigned correctly to species with *a posteriori* classification scores >90%. Our findings suggest that mtDNA and otolith morphometry provide accurate markers for discriminating among *Menticirrhus* species. These markers should assist researchers interested in species-level investigations of kingfish recruitment, age, growth, reproduction, predator/prey interactions and stage-specific habitat ecology.

---

Miya, Masaki<sup>1</sup>; Sado, Tetsuya<sup>1</sup>; Saitoh, Kenji<sup>2</sup>; Bart, Jr., Henry L.<sup>7</sup>; Doosey, Michael H.<sup>7</sup>; Doadrio, Ignacio<sup>8</sup>; Keivany, Yazdan<sup>4</sup>; Shrestha, Jiwan<sup>5</sup>; Zardoya, Rafael<sup>8</sup>; Nishida, Mutsumi<sup>6</sup>; Mayden, Richard L.<sup>3</sup>

### **Cypriniformes Tree of Life: Higher-level Relationships of the Cypriniformes (Actinopterygii: Ostariophysi) Inferred from 152 Whole Mitochondrial Genome Sequences**

<sup>1</sup>Natural History Museum and Institute, Chiba, Chiba 260-8682, Japan, <sup>2</sup>Tohoku National Fisheries Research Institute, Miyagi 985-0001, Japan, <sup>3</sup>Saint Louis University, MO 63103-2010, United States, <sup>4</sup>Isfahan University of Technology, Isfahan 84156, Iran, Islamic Republic of, <sup>5</sup>Nepal Academy of Science and Technology, Kathmandu, Nepal, <sup>6</sup>Ocean Research Institute, University of Tokyo, Tokyo 164-8639, Japan, <sup>7</sup>Tulane University, LA 70037, United States, <sup>8</sup>Museo Nacional de Ciencias Naturales, 28006 Madrid, Spain

Fishes of the order Cypriniformes are almost completely restricted to freshwaters and number over 3400 species placed in six families, each with poorly-defined subfamilies and/or tribes. In the previous mitogenomic study based on 59 whole mitogenome sequences (Saitoh et al. 2006), we confirmed monophyly of the Cypriniformes and found four major clades comprising Cyprinidae, Catostomidae, Gyrinocheilidae, and Balitoridae + Cobitidae (Psilorhynchidae not available), with the latter two loach families reciprocally paraphyletic. Interrelationships of these major clades, however, were ambiguous despite the longer nucleotide sequences used in the analyses. The present study represents the second step towards resolution of the higher-level relationships of the world's largest freshwater-fish clade based on more extensive taxon sampling from 146 cypriniforms (including two psilorhynchids). Unambiguously aligned, concatenated mitogenome sequences are divided into five partitions (1st, 2nd, and 3rd codon positions of the protein-coding genes, rRNA genes, and tRNA genes) and partitioned maximum likelihood and Bayesian analyses are conducted, with protein-coding genes being treated in three different manners (all positions included; 3rd codon positions converted into purine [R] and pyrimidine [Y] [= RY-coding]; 3rd codon positions excluded). We will demonstrate preliminary results from the analyses and discuss utility of the denser taxon sampling in resolving higher-level relationships.

---

Modra, Allyson<sup>1</sup>; Gutberlet, Ronald<sup>2</sup>; Evans, Jennafer<sup>1</sup>; Parkinson, Christopher<sup>1</sup>

### **Total Evidence and Taxonomic Completeness in the Phylogeny and Biogeography of *Bothrops*, *Bothriopsis*, and *Bothrocophias* (Serpentes: Viperidae: Crotalinae)**

<sup>1</sup>University of Central Florida, Orlando, FL, United States, <sup>2</sup>University of Texas at Tyler, Tyler, TX, United States

Total evidence phylogenetic analyses using morphological and DNA sequence data were conducted to infer evolutionary relationships of most species of South American pitviper genera *Bothrops*, *Bothriopsis* and *Bothrocophias*, and to explore