

Complete mitogenomes of pangasiid catfishes and their phylogeny for taxonomic implications for Pangasiidae and the suborder Siluroidei

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Abstract

Although Pangasiidae (four genera: Pangasius, Pangasianodon, Helicophagus, and Pseudolais) is known to be a monophyletic family, the generic and phylogenetic relationships, as well as inter- and intrafamilial relationships of the catfish families in Siluroidei, are poorly resolved. In this study, we obtained complete mitogenomes from three catfish species of the Mekong River in Vietnam: *Pangasius mekongensis* (16,462 bp), *Pangasius krempfi* (16,475 bp), and *Pangasianodon hypophthalmus* (16,523 bp) and reconstructed a comprehensive phylogeny with 117 mitogenomes of 32 recognized siluriform families. The genomic features of the three mitogenomes were similar to those of previously reported pangasiids, including all regulatory elements, extended terminal associated sequences (ETAS), and conserved sequence blocks (CSBs) (CSB-1, CSB-2, CSB-3, and CSBs, A to F) in the control region. The phylogeny established Pangasiidae as monophyletic and a sister group of Austroglanididae. The [Pangasiidae + Austroglanididae] + [Ictaluridae + Cranoglanididae] + Ariidae] clade is a sister group to the “Big Africa” major clade of Siluriformes. Furthermore, both phylogenies constructed from the single barcodes (83 partial cox1 and 80 partial cytB, respectively) clearly resolved the Pangasiidae’s intrafamilial and intergeneric relationships. Pangasianodon was monophyletic and conclusively as a sister to the (Pangasius + Helicophagus + Pseudolais) group. *Pangasius mekongensis* was placed as a sister taxon to *P. pangasius* within the genus *Pangasius*, while *Pangasius sanitwongsei* was found to be related to and grouped with *Pangasianodon*. However, in the single-gene phylogenies, this species was assigned to the [Pangasius + Helicophagus + Pseudolais] group. The datasets in this study are useful for reappraising pangasiid taxonomy, as well as for siluriform catfish identification, DNA barcoding, systematics, phylogenetics, population genetics, and timeline and mode of diversification studies.

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