

Molecular Phylogeny of Syngnathiformes Fishes

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The previous morphology-based taxonomic frameworks within the family Sygnathidae had emphasized the significance of the male brood pouch and reproductive biology in defining the group. However, several different hypotheses had been proposed by different investigators. This study have been carried out to determine the phylogenetic relationships among 19 species belonging to the order Syngnathiformes with three Gasterosteiformes species as outgroup taxa by using the mitochondrial cytochrome *b* and Rag2 nuclear DNA sequences. Phylogenetic analyses based on neighbor-joining distance, maximum parsimony, minimum evolution and maximum likelihood method strongly supported that the family Sygnathidae, the suborder Syngnathoidei and the order Syngnathiformes were all monophyletic group. Much of previous morphological analyses were supported by our molecular data, but some deep relationships were not clearly resolved with regard to members of the suborder Aulostomoidei.

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