

AMONG GENERA: A PHYLOGENETIC INFERENCE WITH MITOGENOMES OF NINE SPECIES OF STETHAPRIONINAE (CHARACIDAE, CHARACIFORMES)

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Abstract

The Stethaprioninae is a species-rich subfamily that comprises small freshwater fishes with wide distribution in the Neotropical Ecozone. Most of the diversity of the group comes from *Astyanax*, a polyphyletic and high diverse genus with around 170 species. But with great diversity comes numerous taxonomic problems and even with wide studies with the group, many phylogenetic relationships remain unsolved. Given this scenario, we aimed to provide a better understanding of the relationships among the three genera through a mitogenomic phylogenetic inference. To achieve this goal, we sampled a total of 12 mitogenomes from four species of *Astyanax*, four of *Psalidodon*, one from *Deuterodon* giton and one from *Brycon nattereri*, which we assigned as an outgroup. We removed all rRNA, tRNA and the control region D-loop, leaving only the 13 protein-coding genes (PCGs) which we aligned one by one using the ClustalW algorithm. Then, we calculated the pairwise distances and conducted a Maximum Likelihood (ML) analysis with bootstrap as branch support value on MEGA X. Next, we concatenated the alignment on SequenceMatrix to partitioned and attribute the best evolutionary nucleotide model for each gene with Partition Finder 2.1. Ultimately, we performed the Bayesian Inference (BI) on MrBayes 3.2.7 with 4 independent Markov chains, with 10 million generations which 25% of them were discarded at the end of the analyses and used Tracer 1.7 software to verify the effective sample size (ESS) and strand convergence. We obtained phylograms from ML and BI analysis that show strong correlations with the genetic distance, with solid bootstrap and posterior probabilities in most of the branches, respectively. Showing a consistent clade subdivided in 2 monophyletic groups: *Psalidodon* and *Astyanax*, with *Deuterodon* as sister group of them. The topologies obtained leads to similar conclusions seen in previous works with *Astyanax*, reinforcing the *Psalidodon* status and the early divergence of the *Deuterodon* from the other genera. Hereby, we conclude that mitogenomes poses as a great tool to the phylogenetic inference among genera.

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Link to Video: