

TEN COMPLETE MITOCHONDRIAL GENOMES OF GYMNOCHARACINI (STETHAPRIONINAE, CHARACIFORMES)

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Abstract

Stethaprioninae is a subfamily of characiform fish that comprises small animals popularly known as tetras. Some species of the genus, such as *Astyanax*, share several common features that difficult their recognition, leading to efforts to identify diagnostic characteristics or molecular signatures for the group. In an attempt to contribute to these efforts, we are presenting eight new complete mitogenomes of species/cytotypes from Neotropical Ecozone belonging to the *Astyanax* and *Psalidodon* genus: *A. aeneus*, *A. altiparanae*, *P. fasciatus* (from two basins), *A. lacustris*, *P. rivularis* (two cytotypes) and *P. rioparanaibano*. Total genomic DNA was extracted from liver and heart samples of six species. The Whole Genome Sequencing from these species was performed in a Novaseq 6000. We assembled the mitogenomes from raw reads on Novoplasty v3.7 in a parallel cluster computer using the mitogenome of *P. paranae* from GenBank as seed. We annotated the obtained sequences on MitoAnnotator (MitoFish). In the Galaxy platform, we accessed the quality of raw reads (using FastQC) and filtered with Fastp tool. For broader comparisons, we also assembled the mitogenome of two species with raw reads available on European Nucleotide Archive: *P. fasciatus* from Upper Parana river basin and *A. aeneus* from Mexico. We perform comparative genomics analysis by BLAST comparison of all *Astyanax*/*Psalidodon* mitochondrial genomes against a reference (*P. paranae*) generated by Blast Ring Image Generator. Our results have shown that all mitogenomes content and gene order were identical, with 13 protein-coding genes (PCGs), 22 tRNA genes and two rRNA genes, following an expected order according to already described Characiformes mitogenomes. All PCGs and tRNAs are on the heavy chain, except the Nd6 gene and eight tRNAs. The length of mitochondrial sequence range from 16,626bp in *P. fasciatus* to 16,812bp in *P. rivularis*. The average length of D-loop was 1,061bp. Deepening the knowledge about the D-loop, can play a fundamental role in understanding the evolutionary history of the *Astyanax* and *Psalidodon* genera. In this work, we observed that the size variation between different *Astyanax*/*Psalidodon* mitogenomes occurs mainly due to the extension of the D-loop. In conclusion, our methodology used in the reconstruction of the mitochondrial genome proved to be satisfactory and able to access the length of this type of genome, plus the composition and nature of the D-loop, solving possible gaps in previous methodologies.

Funding:

Link to Video: