

## Mitochondrial DNA Part B Resources

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MITOGENOME ANNOUNCEMENT



## The complete mitochondrial genome sequence of *Astyanax paranae* (Teleostei: characiformes)

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### ABSTRACT

Complete mitochondrial genome of the characiform fish *Astyanax paranae* was characterized in the present study. The whole mitogenome was 16,707 bp long and consisted of 13 protein-coding genes, 22 tRNAs, 2 rRNAs genes, a control region and origin of light-strand replication. The gene order is similar to those of the congeneric blind cavefish *A. mexicanus*. The nucleotide content of *A. paranae* mitogenome was 29.5% for A, 27.6% for T, 15.8% for G, 27.1% for C. Nucleotide identity between *A. paranae* and *A. mexicanus* across all the 37 genic regions ranged from 74.9% (ND2) to 90.3% (COX3).

### ARTICLE HISTORY

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### KEYWORDS

Characidae; mitochondrial DNA; mtDNA; next generation sequencing

*Astyanax* is a specious characiform fish genus with a wide distribution throughout the Neotropical drainages, occurring from southern United States to central Argentina (Ornelas-García et al. 2008). This group is currently composed of 154 valid species (Eschmeyer 2015), but it does not represent a monophyletic entity, as evidenced by morphological and molecular characters (Javonillo et al. 2010; Mirande 2010; Oliveira et al. 2011). Additionally, the phylogenetic relationships in this group still remain confused due to the existence of 'species complexes', e.g. *A. scabripinnis*, *A. altiparanae* and *A. fasciatus* (Moreira-Filho & Bertollo 1991; Artoni et al. 2006; Castro et al. 2015) and putative cryptic species (Pansonato-Alves et al. 2013). Here we provided the complete mitochondrial genome of *A. paranae*, a species belonging to the *A. scabripinnis* complex. This is the second mitogenome available for the *Astyanax* genus after the *A. mexicanus* mitogenome.

The *A. paranae* specimen was collected at the Capivara river (22°53'57"S 48°23'11"W), Botucatu, São Paulo, Brazil. The specimen was identified and deposited in the fish collection of the Laboratório de Biologia e Genética de Peixes de Botucatu, São Paulo, Brazil, under the code LBP19572. Total genomic DNA from liver was extracted using a tissue kit (Macherey-Nagel, Düren, Germany), including a step of RNA removal with RNase A (Invitrogen, Waltham, MA). Genomic DNA sequencing was performed at Life Sciences Core Facility (LaCTAD) of Universidade Estadual de Campinas (UNICAMP) using Illumina HiSeq2000 platform (2×101bp paired-end) (Illumina, San Diego, CA). The whole-genome sequencing generated 140,184,276 reads, from which 369,366 were used to assemble the mitogenome of *A. paranae*. The NGS reads obtained from Illumina Sequencing were assembled using

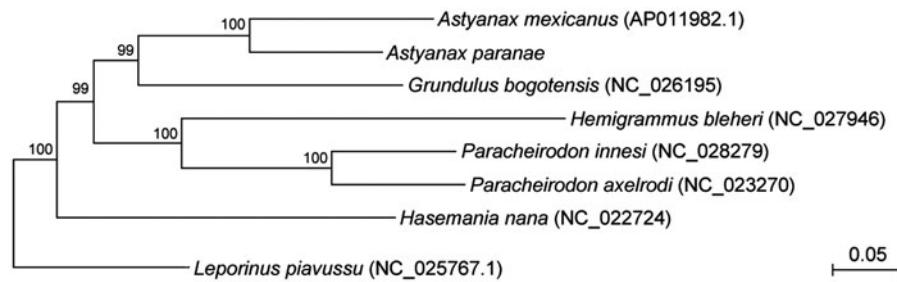
two methods. First, the MITObim mitogenome assembler (Hahn et al. 2013) was used taking the sequence of the almost complete *Astyanax mexicanus* mitogenome as a reference (accession number AP011982.1). We run MITObim with the two-step protocol performing an initial mapping with MIRA software (Chevreux et al. 2004) using the default parameters. An assembly with the 'de novo assembly' option and with the 'reference-based genome assembly' option was performed as well. We generated a consensus sequence of the resulting contigs. The assembly was completed by selecting homologous reads pairs to 200bp sequences adjacent to the low-quality regions of the consensus sequence with custom script ([https://github.com/fjruizruano/ngs-protocols/blob/master/mapping\\_blat\\_gs.py](https://github.com/fjruizruano/ngs-protocols/blob/master/mapping_blat_gs.py)) and assembling them using the CAP3 software (Huang & Madan 1999) with default parameters. For annotation procedures, we compared the assembled mitogenome of *A. paranae* to the annotated mitogenome of *A. mexicanus* using Geneious Pro v8.1.5 software created by Biomatters (<http://www.geneious.com/>). To validate, the results were compared to those obtained using the MitoAnnotator software (Iwasaki et al. 2013). The final mitogenome of *A. paranae* was deposited in GenBank under the accession number KX609386.

The complete mitochondrial genome of *A. paranae* has 16,707bp and is composed by 13 PCGs, 22 transfer tRNAs, 2 ribosomal RNAs, a control region (D-loop) and origin of light-strand replication ( $O_L$ ). The gene order follows the typical arrangement of vertebrates and the organization of the protein-coding genes (PCGs) of *A. paranae* mitogenome is very similar to the *A. mexicanus*. The A + T content in the *A. paranae* mitogenome is 57.1%, and its overall base composition is 29.5% for A, 27.6% for T, 15.8% for G, 27.1% for C. Most of the

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**Figure 1.** Maximum likelihood tree showing the phylogenetic relationships between the *A. paranae* mitogenome and all mitogenomes available for Characidae species, using as external group Anostomidae species.

genes were encoded on the H-strand, except for tRNA-Gly, tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Tyr, tRNA-Ser, ND6, tRNA-Glu and tRNA-Pro. The putative  $O_L$  is composed by 33 bp (from 5334 to 5366 nucleotide) between tRNA-Asn and tRNA-CysA. The putative control region (D-loop) has 1032 bp (from 15,676 to 16,707) between tRNA-Pro and tRNA-Phe.

In addition, we studied the phylogenetic relationships between the *A. paranae* mitogenome and all mitogenomes available for Characidae species, using as external group Anostomidae species. The 13 protein-coding genes were extracted and aligned with the Muscle algorithm (Edgar 2004) implemented in the Geneious software. We used the resulting alignment to build a maximum likelihood tree using PhyML (Guindon et al. 2010) with a GTR+I+G model and 1000 bootstrap replicates. In the phylogenetic analysis all nodes were strongly supported and the closer species with *A. paranae* was *A. mexicanus* as expected (Figure 1).

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## Disclosure statement

All authors declare that they have no conflicting interests.

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## References

- Artoni RF, Shibatta OA, Gross MC, Schneider CH, Almeida MC, Vicari R, Bertollo LAC. 2006. *Astyanax aff. fasciatus* Cuvier, 1819 (Teleostei; Characidae): evidences of a species complex in the upper Rio Tibagi basin (Paraná, Brazil). *Neotrop Ichthyol.* 4:1997–2002.
- Castro PC, Moura MO, Moreira-Filho O, Shibatta OA, Santos MH, Nogaroto V, Vicari RM, de Almeida MC, Artoni RF. 2015. Diversity of the *Astyanax scabripinnis* species complex (Teleostei, Characidae) in the Atlantic forest, Brazil: species limits and evolutionary inferences. *Rev Fish Biol Fisher.* 25:231–244.
- Chevreaux B, Pfisterer T, Drescher B, Driesel AJ, Müller WE, Wetter T, Suhai S. 2004. Using the miraEST assembler for reliable and automated mRNA transcript assembly and SNP detection in sequenced ESTs. *Genome Res.* 14:1147–1159.
- Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 32:1792–1797.
- Eschmeyer WN. 2015. Catalog of Fishes. California Academy of Sciences, electronic version. Available from: <http://www.calacademy.org/scientists/projects/catalog-of-fishes> [last accessed December 15, 2015]
- Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst Biol.* 59:307–321.
- Hahn C, Bachmann L, Chevreaux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. *Nucleic Acids Res.* 41:e129.
- Huang X, Madan A. 1999. CAP3: a DNA sequence assembly program. *Genome Res.* 9:868–877.
- Iwasaki W, Fukunaga T, Isagozawa R, Yamada K, Maeda Y, Satoh TP, Sado T, Mabuchi K, Takeshima H, Miya M, Nishida M. 2013. MitoFish and MitoAnnotator: a mitochondrial genome database of fish with an accurate and automatic annotation pipeline. *Mol Biol Evol.* 11:2531–2540.
- Javonillo R, Malabarba LR, Weitzman SH, Burns JR. 2010. Relationships among major lineages of characid fishes (Teleostei: Ostariophysi: Characiformes) based on molecular sequence data. *Mol Phylogenet Evol.* 54:498–511.
- Mirande JM. 2010. Phylogeny of the family Characidae (Teleostei: Characiformes): from characters to taxonomy. *Neotrop Ichthyol.* 8:385–568.
- Moreira-Filho O, Bertollo LCA. 1991. *Astyanax scabripinnis* (Pisces, Characidae). A species complex. *Brazil J Genet.* 14:331–357.
- Oliveira C, Avelino G, Abe K, Mariguela T, Benine R, Ortí G, Vari RP, Corrêa e Castro RM. 2011. Phylogenetic relationships within the speciose family Characidae (Teleostei: Ostariophysi: Characiformes) based on multilocus analysis and extensive ingroup sampling. *BMC Evol Biol.* 11:275.
- Ornelas-García CP, Domínguez-Domínguez O, Doadrio I. 2008. Evolutionary history of the fish genus *Astyanax* Baird & Girard (1854) (Actinopterygii, Characidae) in Mesoamerica reveals multiple morphological homoplasies. *BMC Evol Biol.* 8:340.
- Pansonato-Alves JC, Hilsdorf AWS, Utsunomia R, Silva DMZA, Oliveira C, Foresti F. 2013. Chromosomal mapping of repetitive DNA and cytochrome C oxidase I sequence analysis reveal differentiation among sympatric samples of *Astyanax fasciatus* (Characiformes, Characidae). *Cytogenet Genome Res.* 141:133–142.