

Next-generation sequencing yields the complete mitochondrial genome of *Pterygoplichthys pardalis* (Loricariidae; Siluriformes)

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ABSTRACT

In this study, we report the complete mitochondrial genome of *Pterygoplichthys pardalis* has derived by next-generation sequencing. The complete mitochondrial genome of *P. pardalis* contains 16,425 bp encompassing 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and one control region (D-loop). The base composition is A 31.79%, C 26.89%, G 14.63%, and T 26.69%, and its gene arrangement is consistent with mitochondrial genomes derived from other representatives of Loricariidae. A phylogenetic tree of 24 Loricariidae species constructed based on the 13 coding genes shows that *P. pardalis* is clustered with other *Pterygoplichthys* genus. It suggests that the molecular classification results confirm its external morphological characteristics. These results have reference value for the further study of phylogenetic relationship, taxonomic classification, and phylogeography of Loricariidae.

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Catfish; Loricarioidei; mitogenome; molecular data; phylogeny

Pterygoplichthys pardalis (Castelnau, 1855) is an neotropical sucker mouth armored catfish, that is extremely exported as ornamental aquarium fish to many other countries and often released becoming an invasive species (Nico et al. 2009; Ebenstein et al. 2015; Lujan et al. 2015; Kumar et al. 2018). Due to its strong survival ability and rapid spread, it has caused damage to the local ecological environment (Nico et al. 2009; German et al. 2010; Jumawan et al. 2010; Lujan et al. 2015; Nurubhasha et al. 2019). As a relatively well known representative species in Loricariidae, *P. pardalis* has long been the subject of intense interest among ecological biologists (Hoover et al. 2004; Chaichana and Jongphadungkiet 2012). However, its complete mitochondrial genome was not known until now.

To sequence, assemble, and annotate the complete mitogenome of *P. pardalis*, one individual was acquired from the Chinese breeding base in Xi'an city (108°41'E, 33°85'N) and deposited at the lab of Institute of Basic Translational Medicine, Xi'an Medical University under the voucher number 20190815PP01. The species identification was determined from the sequence of the molecular data and multiple morphological features, such as the characteristics of head (radiate pattern of light lines) and body (hexagonal leopard patches) (Rao and Sunchu 2017). Genomic DNA of *P. pardalis* was extracted from muscle tissue using Qiagen Blood & Cell Culture DNA Mini Kit. Then, the short paired-end library was constructed by Illumina protocol and sequenced with HiSeq X-Ten PE150 platform. MitoZ software was applied to

assemble the mitogenome with default parameters (Meng et al. 2019). The mitochondrial genes were predicted and annotated using the MITOS Web Server (Bernt et al. 2013) and tRNAscan-SE Search Server (Chan and Lowe 2019). Finally, the assembly and annotation results of the complete mitochondrial genome of *P. pardalis* were made publicly accessible (GenBank accession number: MW401674).

The whole mitogenome sequence of *P. pardalis* has 16,425 bp in length, containing 13 protein-coding genes, 22 tRNA genes, two rRNA genes, and one control region (D-loop). The base content and gene arrangement were similar to other species of teleosts (Jiang et al. 2017, 2018; Li et al. 2019; Liu et al. 2019a, 2019b). Almost all the protein-coding genes were encoded by H-strand except *ND6* and eight tRNAs (Gln, Ala, Asn, Cys, Tyr, Ser, Glu, Pro) genes which are located on the L-strand. In addition, 12 protein-coding genes start with the start codon ATG, while *COX1* use GTG as the start codon. For the stop codon, six protein-coding genes (*ATP6*, *ATP8*, *COX1*, *ND1*, *ND4L*, *ND5*) end with TAA, only *ND2* and *ND6* ends with TAG, and *COX2*, *COX3*, *CYTB*, *ND3*, and *ND4* ends with T. The base compositions are A 31.79%, C 26.89%, G 14.63%, T 26.69%, and AT and GC contents are 58.48% and 41.52% with a significant AT bias, respectively. The 13 protein coding genes are 11,385 bp, accounting for 69.31% of the whole mitogenome, which encodes 3795 amino acids in total. The predicted lengths of 12S rRNA located between tRNA^{Phe} and tRNA^{Val} and 16S rRNA located between tRNA^{Val} and tRNA^{Leu} are 955 bp and 1686 bp,

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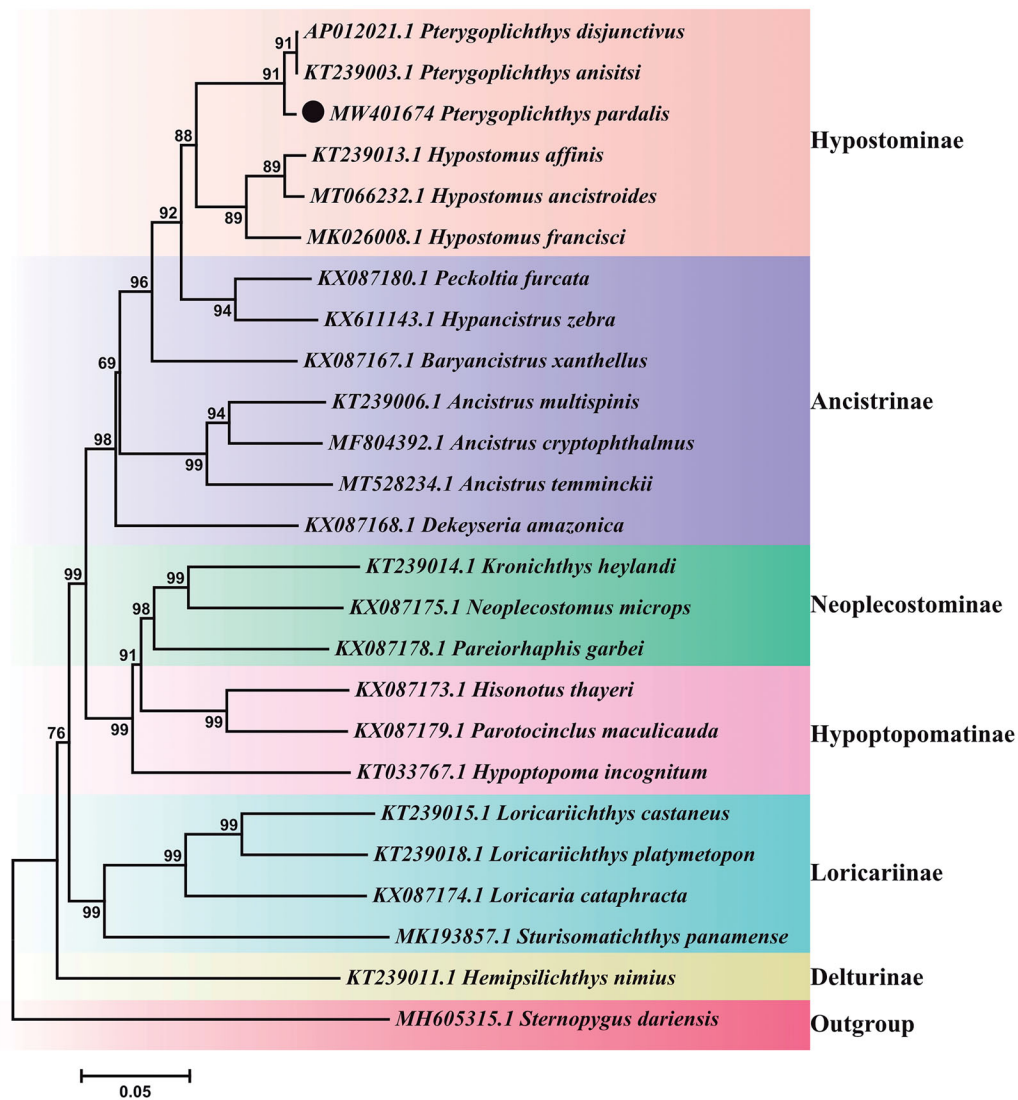


Figure 1. Neighbor-joining tree of 24 Loricariidae and one outgroup (*Sternopygus dariensis*) species based on the 13 protein-coding genes. The number at each node is the bootstrap probability. The number before the species name is the GenBank accession number. The dark spot indicates the species in this study.

respectively. The control region located between tRNA^{Pro} and tRNA^{Phe} is 786 bp.

To phylogenetically infer the position of *P. pardalis* within Loricariidae with available mitogenomes, the sequence alignments were performed by ClustalW (Thompson et al. 1994) in BioEdit software (Hall 1999) and the phylogenetic tree was constructed in Mega7 by the neighbor-joining (NJ) method with 10,000 bootstraps (Kumar et al. 2016). The phylogenetic relationship of *P. pardalis* and other 23 Loricariidae species (from six different subfamilies) were analyzed based on the 13 protein-coding genes with *Sternopygus dariensis* Meek & Hildebrand 1916 (Gymnotiformes) as the outgroup. The result shows that *P. pardalis* is clustered with other *Pterygoplichthys* genus. Our result confirms that the identification based on morphological features corroborates with the molecular analysis (Figure 1). We expect that these results would provide valuable reference data for other studies.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data that support the findings of this study are openly available in NCBI at <https://www.ncbi.nlm.nih.gov/>, reference number [MW401674], or available from the corresponding author.

References

- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsche G, Pütz J, Middendorf M, Stadler PF. 2013. Mitos: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69(2): 313–319.
- Chaichana R, Jongphadungkiet S. 2012. Assessment of the invasive catfish *Pterygoplichthys pardalis* (Castelnau, 1855) in Thailand: ecological impacts and biological control alternatives. *Trop Zool.* 25(4):173–182.

- Chan PP, Lowe TM. 2019. Trnscan-se: searching for trna genes in genomic sequences. *Methods Mol Biol.* 1962:1–14.
- Ebenstein D, Calderon C, Troncoso OP, Torres FG. 2015. Characterization of dermal plates from armored catfish *Pterygoplichthys pardalis* reveals sandwich-like nanocomposite structure. *J Mech Behav Biomed Mater.* 45:175–182.
- German DP, Neuberger DT, Callahan MN, Lizardo NR, Evans DH. 2010. Feast to famine: the effects of food quality and quantity on the gut structure and function of a detritivorous catfish (Teleostei: Loricariidae). *Comp Biochem Physiol A Mol Integr Physiol.* 155(3): 281–293.
- Hall TA. 1999. Bioedit: a user-friendly biological sequence alignment editor and analysis program for windows 95/98/nt. *Nucleic Acids Symp Ser.* 41:95–98.
- Hoover JJ, Killgore KJ, Cofrancesco AF. 2004. Suckermouth catfishes: threats to aquatic ecosystems of the United States? *ANSRP Bull.* 4:1–9.
- Jiang H, Gong L, Liu L, Liu B, Lü Z. 2017. The complete mitochondrial genome of *Sardinella lemuru* (Clupeinae, Clupeidae, Clupeoidei) and phylogenetic studies of Clupeoidei. *Mitochondrial DNA Part B.* 3(1): 50–52.
- Jiang H, Lü Z, Liu L, Liu B, Gong L. 2018. The complete mitochondrial genome of *Thryssa hamiltonii* (Engraulinae, Engraulidae, Clupeoidei) and phylogenetic studies of Clupeoidei. *Mitochondrial DNA Part B.* 3(1):110–111.
- Jumawan J, Salunga T, Catap E. 2010. Lipid peroxidation and patterns of cadmium and lead accumulation in the vital organs of the Suckermouth armored catfish *Pterygoplichthys* Gill, 1858 from Marikina River, Philippines. *J Appl Sci Environ Sanit.* 5:375–390.
- Kumar B, Schofield P, Raj S, Satheesh S. 2018. Salinity tolerance of non-native suckermouth armoured catfish (Loricariidae: *Pterygoplichthys* sp.) from Kerala, India. *Manage Biol Invas.* 9(1):49–57.
- Kumar S, Stecher G, Tamura K. 2016. Mega7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol.* 33(7): 1870–1874.
- Li C, Chen K, Qian Z, Zeng B, Song P, Jiang Z. 2019. The complete mitochondrial genome of *Acrossocheilus yunnanensis* (Teleostei: Cypriniformes: Cyprinidae) and its phylogenetic position. *Mitochondrial DNA Part B.* 4(2):4061–4062.
- Liu Q, Liu Y, Xiao T, Xu B. 2019a. Complete mitochondrial genome of *Corydoras panda* (Teleostei, Siluriformes, Callichthyidae, Corydoradinae). *Mitochondrial DNA Part B.* 4(2):2878–2879.
- Liu Q, Liu Y, Xiao T, Xu B. 2019b. Next-generation sequencing yields the complete mitochondrial genome of *Corydoras sterbai* (Teleostei, Siluriformes, Callichthyidae, Corydoradinae). *Mitochondrial DNA Part B.* 4(2):2880–2881.
- Lujan NK, Armbruster JW, Lovejoy NR, López-Fernández H. 2015. Multilocus molecular phylogeny of the suckermouth armored catfishes (Siluriformes: Loricariidae) with a focus on subfamily Hypostominae. *Mol Phylogenet Evol.* 82(Part A):269–288.
- Meng G, Li Y, Yang C, Liu S. 2019. Mitoz: a toolkit for animal mitochondrial genome assembly, annotation and visualization. *Nucleic Acids Res.* 47(11):e63.
- Nico L, Jelks H, Tuten T. 2009. Non-native suckermouth armored catfishes in Florida: description of nest borrows and burrow colonies with assessment of shoreline conditions. *ANSRP Bull.* 9:1–30.
- Nurubhasha R, Sampath Kumar NS, Thirumalasetti SK, Simhachalam G, Dirisala VR. 2019. Extraction and characterization of collagen from the skin of *Pterygoplichthys pardalis* and its potential application in food industries. *Food Sci Biotechnol.* 28(6):1811–1817.
- Rao KR, Sunchu V. 2017. A report on *Pterygoplichthys pardalis* Amazon sailfin suckermouth Catfishes in Freshwater tanks at Telangana state, India. *Int J Fish Aquat Stud.* 5(2):249–254.
- Thompson JD, Higgins DG, Gibson TJ. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 22(22):4673–4680.