



Mitochondrial DNA

The Journal of DNA Mapping, Sequencing, and Analysis

ISSN: 1940-1736 (Print) 1940-1744 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn20>

Complete mitochondrial genome of *Acrossocheilus stenotaeniatus* (Osteichthyes: Cyprinidae)

Chunying Yuan, Aihong Chai, Qingman Cui, Enqi Ye & Jie Zhang

To cite this article: Chunying Yuan, Aihong Chai, Qingman Cui, Enqi Ye & Jie Zhang (2014): Complete mitochondrial genome of *Acrossocheilus stenotaeniatus* (Osteichthyes: Cyprinidae), Mitochondrial DNA

To link to this article: <http://dx.doi.org/10.3109/19401736.2014.933325>



Published online: 10 Sep 2014.



Submit your article to this journal [↗](#)



Article views: 8



View related articles [↗](#)



View Crossmark data [↗](#)

Full Terms & Conditions of access and use can be found at
<http://www.tandfonline.com/action/journalInformation?journalCode=imdn20>

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of *Acrossocheilus stenotaeniatus* (Osteichthyes: Cyprinidae)

Chunying Yuan¹, Aihong Chai^{1,2}, Qingman Cui¹, Enqi Ye², and Jie Zhang²

¹College of Marine Science & Engineering, Tianjin University of Science & Technology, Tianjin, P.R. China and ²Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, P.R. China

Abstract

Acrossocheilus stenotaeniatus (Cypriniformes, Cyprinidae) is a barred cyprinid fish that inhabits the flowing freshwaters in China. The complete mitochondrial genome sequence of *A. stenotaeniatus* is 16,594 bp in length and comprises 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region. The base composition of the genome is 31.22% A, 24.70% T, 28.02% C, and 16.07% G, which shows considerable bias to A + T (55.91%). Results of this study provide important DNA molecular data for further phylogenetic analysis and resource management not only for congeneric species but also for higher taxa of Cyprinid fish.

Keywords

Acrossocheilus stenotaeniatus, genome, mitochondrial

History

Received 3 June 2014
Accepted 7 June 2014
Published online 10 September 2014

Acrossocheilus comprises 24 valid species that are distributed in China, Vietnam, and Laos (FishBase: <http://www.fishbase.org/Nomenclature/ScientificNameSearchList.php?>). Among the 24 species, 18 are found in China, of which 16 are endemic. Therefore, the biodiversity and endemism of *Acrossocheilus* are high in China, comprising three-quarters of the extant species worldwide. *Acrossocheilus stenotaeniatus* is a barred cyprinid fish that inhabits the flowing freshwaters and mainly found in Pearl River and Hainan Island, South China (Yue et al., 2000). Many investigations focused on the taxonomy and morphology of *Acrossocheilus*, but only a few on the taxonomy and phylogeny of *A. stenotaeniatus* (Wang et al., 2010; Yuan et al., 2006, 2012).

Therefore, this study presents the complete mitochondrial genome of *A. stenotaeniatus*.

The complete mtDNA of *A. stenotaeniatus* was initially amplified and sequenced by polymerase chain reaction with 27 primer pairs. Nucleotide sequences were deposited in GenBank (Accession Number KJ909660). The specimen was deposited in the Institute of Zoology, Chinese Academy of Sciences. The complete mtDNA of *A. stenotaeniatus* is a closed circular molecule with a genome length of 16,594 bp. It comprises 13 protein-coding genes, 22 tRNA, 2 rRNA genes (12S rRNA and 16S rRNA), and 1 control region.

Table 1. Characteristics of the *A. stenotaeniatus* mitochondrial DNA genome.

Gene names	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Sizes (bp)	No. of the codons	Start codon	Stop codon
<i>tRNA^{Phe}</i>	H	1	69			69			
<i>12S rRNA</i>	H	70	1028			959			
<i>tRNA^{Val}</i>	H	1029	1100			72			
<i>16S rRNA</i>	H	1101	2782			1682			
<i>tRNA^{Leu}</i>	H	2783	2858			76			
<i>ND1</i>	H	2860	3834	1		975	324	ATG	TAA
<i>tRNA^{Ile}</i>	H	3839	3910	4		72			
<i>tRNA^{Gln}</i>	L	3909	3979		2	71			
<i>tRNA^{Met}</i>	H	3982	4050	2		69			
<i>ND2</i>	H	4051	5059			1009	336	ATG	T--
<i>tRNA^{Trp}</i>	H	5096	5166	36		71			
<i>tRNA^{Ala}</i>	L	5169	5237	2		69			
<i>tRNA^{Asn}</i>	L	5239	5311	1		73			
<i>tRNA^{Cys}</i>	L	5345	5411	33		67			
<i>tRNA^{Tyr}</i>	L	5411	5481		1	71			

(continued)

Table 1. Continued

Gene names	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Sizes (bp)	No. of the codons	Start codon	Stop codon
<i>COI</i>	H	5483	7033	1		1551	516	GTG	TAA
<i>tRNA^{Ser}</i>	L	7034	7104			71			
<i>tRNA^{Asp}</i>	H	7106	7177	1		72			
<i>CO2</i>	H	7192	7882	14		691	230	ATG	T--
<i>tRNA^{Lys}</i>	H	7883	7958			76			
<i>ATP8</i>	H	7960	8124	1		165	54	ATG	TAG
<i>ATP6</i>	H	8118	8801		7	684	227	ATG	TAA
<i>CO3</i>	H	8801	9585		1	785	261	ATG	TA-
<i>tRNA^{Gly}</i>	H	9586	9657			72			
<i>ND3</i>	H	9658	10,006			349	116	GTG	T--
<i>tRNA^{Arg}</i>	H	10,008	10,077	1		70			
<i>ND4L</i>	H	10,078	10,374			297	98	ATG	TAA
<i>ND4</i>	H	10,368	11,748		7	1381	460	ATG	T--
<i>tRNA^{His}</i>	H	11,749	11,817			69			
<i>tRNA^{Ser}</i>	H	11,818	11,886			69			
<i>tRNA^{Leu}</i>	H	11,888	11,960	1		73			
<i>ND5</i>	H	11,961	13,784			1824	607	ATG	TAA
<i>ND6</i>	L	13,781	14,302		4	522	173	TTA	CAT
<i>tRNA^{Glu}</i>	L	14,303	14,371			69			
<i>Cyt b</i>	H	14,378	15,518	6		1141	380	ATG	T--
<i>tRNA^{Thr}</i>	H	15,519	15,590			72			
<i>tRNA^{Pro}</i>	L	15,590	15,659		1	70			
D-loop	H	15,662	16,594	2		933			

Of the 13 protein-coding genes, 10 started with ATG; *COI* and *ND3* started with GTG and *ND6* with TTA. Five protein-coding genes ended with TAA; *ATP8* and *ND6* end with TAG and CAT, respectively. *CO3* ends with TA-, and *ND2*, *CO2*, *ND3*, *ND4*, and *Cyt b* ended with T-- as an incomplete stop codon. The 22 tRNA genes exhibit lengths from 67 bp in *tRNA^{Cys}* to 76 bp in *tRNA^{Lys}* and *tRNA^{Leu}*. The 12S and 16S rRNA genes were 959 and 1682 bp long, respectively. These genes were located between *tRNA^{Phe}* and *tRNA^{Leu}*, and separated by *tRNA^{Val}*. The control region was 933 bp long and lies between *tRNA^{Pro}* and *tRNA^{Phe}*. *ND5* was the longest gene with 1824 bp. The shortest gene was *ATP8* with only 165 bp. A total of 13 protein-coding genes for 3782 amino acids were identified. The nucleotide composition was 31.22% A, 24.70% T, 28.02% C, and 16.07% G. This composition shows considerable bias to A + T, which is 55.91%. The mitochondrial genes from *A. stenotaeniatus* were overlapped in 23 bp at seven locations and interleaved in 106 bp intergenic spacers at 15 locations (Table 1).

MtDNA is a biomarker used to determine the phylogenetic relationships among individuals, populations, and even species (Irwin et al., 1991; Perdices et al., 2005; Zhao et al., 2005). We expect this study to provide important DNA molecular data for further phylogenetic analysis and resource management not only for congeneric species but also for higher taxa of cyprinid fish.

Acknowledgements

The authors are grateful to Mr. Hongsheng Guo and Miss Haiting Zhang for their help in the lab work and specimen preparation.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing style of this article. This study was funded by the National Natural Science Foundation of China (30970321; 31272287).

References

- Irwin DM, Kocher TD, Wilson AC. (1991). Evolution of the cytochrome *b* gene of mammals. *J Mol Evol* 32:128–44.
- Perdices A, Sayanda D, Coelho MM. (2005). Mitochondrial diversity of *Opsariichthys bidens* (Teleostei, Cyprinidae) in three Chinese drainages. *Mol Phylogenet Evol* 37:920–7.
- Wang Li, Wang Xuzhen, He Shunping. (2010). Phylogenetic relationships of seven barred species of *Acrossocheilus* based on sequences of the mitochondrial DNA ND4 gene, with doubt on the taxonomic status of *Acrossocheilus hemispinus*. *Acta Hydrobiol Sin* 34: 1218–22.
- Yuan LY, Wu ZQ, Zhang E. (2006). *Acrossocheilus spinifer*, a new species of barred cyprinid fish from south China (Pisces: Teleostei). *J Fish Biol* 68:163–73.
- Yuan Leyang, Chan Bosco pui lok, Zhang E. (2012). *Acrossocheilus longipinnis* (Wu 1939), a senior synonym of *Acrossocheilus stenotaeniatus* Chu & Cui 1989 from the Pearl River basin (Teleostei: Cyprinidae). *Zootaxa* 3586:160–72.
- Yue Peiqi, Shan Xianghong, Lin Renduan, Chu Xinluo. (2000). Fauna Sinica: Ostichthyes, Cypriniformes (III). Beijing, China: Science Press (In Chinese).
- Zhao K, Li JB, Yang GS, Duan ZY, He SP, Chen YY. (2005). Molecular phylogenetics of *Gymnocypris* (Teleostei: Cyprinidae) in Lake Qinghai and adjacent drainages. *Chin Sci Bull* 50:1325–33.