



## Mitochondrial DNA

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# Mitochondrial genome of *Onychostoma macrolepis* (Osteichthyes: Cyprinidae)

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## MITOGENOME ANNOUNCEMENT

**Mitochondrial genome of *Onychostoma macrolepis* (Osteichthyes: Cyprinidae)**Aihong Chai<sup>1,2</sup>, Jie Zhang<sup>2</sup>, Qingman Cui<sup>1</sup>, and Chunying Yuan<sup>1</sup><sup>1</sup>College of Marine Science & Engineering, Tianjin University of Science & Technology, Tianjin, PR China and <sup>2</sup>Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, PR China**Abstract**

*Onychostoma macrolepis*, which belongs to the genus *Onychostoma* (Cypriniformes, Cyprinidae), is a benthopelagic fish that inhabits the flowing freshwaters in China. The complete mitochondrial genome sequence of *O. macrolepis* is 16,595 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 31.29% A, 24.53% T, 27.97% C, and 16.21% G, showing considerable bias toward an A+T preference as 55.82%. The results can provide a basic database for analyzing the phylogenetic relationship and conservation genetics in the genus *Onychostoma*.

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The cyprinid genus *Onychostoma* comprises 21 valid species, which are distributed in China and Southeast Asia (FishBase). Of the 21 species, 15 inhabit China, of which 10 are endemic to China. Therefore, the biodiversity and endemism of *Onychostoma* are very high in China, comprising at least two-third the extant species in the world. *Onychostoma macrolepis*, is a benthopelagic fish and is mainly found in Jialing River (upper Yangtze River), the headstream of Huai River, Wei River, Hai River, and the Yellow River (Yue et al., 2000), which define the northern limitation of the distribution of this genus. *O. macrolepis* has been listed as a National Second-class Protected Animal by the List of Aquatic Wild Animal Protection in China (Chen, 2007). Considering its distribution pattern, the phylogeny of the *Onychostoma* species should be studied using molecular approaches.

In the present study, we amplified the complete mtDNA of *O. macrolepis* by polymerase chain reaction (PCR) with 31 pairs of primers. Nucleotide sequences were deposited in GenBank (Accession number KF999680). The complete mtDNA of *O. macrolepis* was a closed circular molecule with a genome size of 16,595 bp, comprising 13 protein-coding genes, 22 tRNA

genes, 2 rRNA genes (12S rRNA and 16S rRNA) and 1 control region. Ten of the 13 protein-coding genes required ATG as the start codon, whereas *CO1* and *ND5* required GTG, and *ND6* required TTA. Five protein-coding genes used TAA as stop codons. *ATP8* and *ND6* stop codons include TAG and CAT, respectively. *CO3* ends with TA–, and *ND2*, *CO2*, *ND3*, *ND4*, and *Cytb* end with T– as an incomplete stop codon. The 22 tRNA genes range in size from 67 bp in *tRNA<sup>Cys</sup>* to 76 bp in *tRNA<sup>Lys</sup>* and *tRNA<sup>Leu</sup>*. The 12S and 16S rRNA genes were 956 and 1676 bp, respectively, and were located between the *tRNA<sup>Phe</sup>* and *tRNA<sup>Leu</sup>* genes and separated by the *tRNA<sup>Val</sup>* gene. The control region was 939 bp and lay between the *tRNA<sup>Pro</sup>* and *tRNA<sup>Phe</sup>* genes. *ND5* is the longest gene with 1836 bp, and the shortest is *ATP8* with only 165 bp. Thirteen protein-coding genes for 3797 amino acids were identified.

The nucleotide composition was 31.29% A, 24.53% T, 27.97% C, and 16.21% G, showing considerable bias toward an A+T preference as 55.82%. The mitochondrial genes from *O. macrolepis* were overlapped in a total of 36 bp at nine locations and interleaved in a total of 77 bp intergenic spacers at 11 locations (Table 1).

Table 1. Characteristics of the *O. macrolepis* 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<sup>Phe</sup></i>	H	1	69			69			
<i>12S rRNA</i>	H	70	1025			956			
<i>tRNA<sup>Val</sup></i>	H	1026	1097			72			

(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>12S rRNA</i>	H	1098	2773			1676			
<i>tRNA<sup>Leu</sup></i>	H	2773	2848		1	76			
<i>ND1</i>	H	2849	3823			975	324	ATG	TAA
<i>tRNA<sup>Ile</sup></i>	H	3832	3903	8		72			
<i>tRNA<sup>Gln</sup></i>	L	3902	3972		2	71			
<i>tRNA<sup>Met</sup></i>	H	3976	4044	3		69			
<i>ND2</i>	H	4045	5089			1045	348	ATG	T--
<i>tRNA<sup>Trp</sup></i>	H	5090	5159			70			
<i>tRNA<sup>Ala</sup></i>	L	5163	5231	3		69			
<i>tRNA<sup>Asn</sup></i>	L	5233	5305	1		73			
<i>tRNA<sup>Cys</sup></i>	L	5341	5407	35		67			
<i>tRNA<sup>Tyr</sup></i>	L	5407	5477		1	71			
<i>CO1</i>	H	5479	7029	1		1551	516	GTG	TAA
<i>tRNA<sup>Ser</sup></i>	L	7030	7100			71			
<i>tRNA<sup>Asp</sup></i>	H	7106	7175	5		70			
<i>CO2</i>	H	7190	7880	14		691	230	ATG	T--
<i>tRNA<sup>Lys</sup></i>	H	7881	7956			76			
<i>ATP8</i>	H	7958	8122	1		165	54	ATG	TAG
<i>ATP6</i>	H	8116	8799		7	684	227	ATG	TAA
<i>CO3</i>	H	8799	9583		1	785	261	ATG	TA-
<i>tRNA<sup>Gly</sup></i>	H	9584	9655			72			
<i>ND3</i>	H	9656	10,004			349	116	ATG	T--
<i>tRNA<sup>Arg</sup></i>	H	10,005	10,074			70			
<i>ND4L</i>	H	10,075	10,371			297	98	ATG	TAA
<i>ND4</i>	H	10,365	11,745		7	1381	460	ATG	T--
<i>tRNA<sup>His</sup></i>	H	11,746	11,814			69			
<i>tRNA<sup>Ser</sup></i>	H	11,815	11,883			69			
<i>tRNA<sup>Leu</sup></i>	H	11,885	11,957	1		73			
<i>ND5</i>	H	11,949	13,784		9	1836	610	GTG	TAA
<i>ND6</i>	L	13,778	14,299		7	522	173	TTA	CAT
<i>tRNA<sup>Glu</sup></i>	L	14,300	14,368			69			
<i>Cyt b</i>	H	14,374	15,514	5		1141	380	ATG	T--
<i>tRNA<sup>Thr</sup></i>	H	15,515	15,586			72			
<i>tRNA<sup>Pro</sup></i>	L	15,586	15,656		1	71			
D-loop	H	15,657	16,595			939			

The genetic distance of *O. macrolepis*, *O. barbatum* and *O. lini* is particularly less (0.021–0.024 in *CO1*, 0.029–0.039 in *Cytb*, and 0.030–0.046 in *ND2*). These species either share common habitats in the Yangtze River or in the Pearl River. The evolutionary rate of the mitochondrion in cyprinid fishes is estimated to be 1% (Brito et al., 1997; Li et al., 2009; Wang et al., 2004; Zhao et al., 2005). Therefore, the last glacial maximum (18 kyr ago) may potentially be a key geomorphological driver for range expansion toward the north and for cladogenesis in the genus *Onychostoma*.

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### 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).

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