

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the *Rhodeus shitaiensis* (Teleostei, Cypriniformes, Acheilognathidae)

Fan Li¹, Kwang-Tsao Shao², Yeong-Shin Lin³, and Chia-Hao Chang^{2,3}

¹Institute of Biodiversity Science, Ministry of Education Key Laboratory for Biodiversity Science and Ecological Engineering, Fudan University, Shanghai, China, ²Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, and ³Department of Biological Science and Technology, National Chiao Tung University, Hsinchu, Taiwan

Abstract

The complete mitochondrial genome of the *Rhodeus shitaiensis* was determined by using a PCR-based method. The total length of mitochondrial DNA of this bitterling is 16,774 bp and includes 13 protein-coding genes, 2 ribosomal RNA, 22 transfer RNA genes, 1 replication origin region and 1 control region. The mitochondrial gene arrangement of the *R. shitaiensis* is also matching the one observed in the most vertebrate creatures. Base composition of the genome is A (28.7%), T (26.5%), C (27.4%) and G (17.4%) with an A + T rich hallmark as that of other vertebrate mitochondrial genomes.

Keywords

Bitterling, complete mitochondrial genome, *Rhodeus shitaiensis*

History

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Bitterling fishes feature the unique symbiosis with the freshwater unionid mussels, and distribute in East Asia and Europe. They belong to the subfamily Acheilognathinae in Cyprinidae and include three genera, *Acheilognathus*, *Rhodes* and *Tanakia* (Arai & Akai, 1988). The genus *Rhodes* includes about 18 species/subspecies, and *Rhodes shitaiensis* is the latest one reported from China (Li & Arai, 2010). In type locality, *R. shitaiensis* was only found in riffle areas. Compared with the other Chinese *Rhodes* species, *R. shitaiensis* has a narrow range of distribution.

In this study we sequenced the complete mitochondrial genome of the *R. shitaiensis* (GenBank accession number KF176560). The specimen was collected from its type locality, Qiupu River, Anhui Province. The total DNA was extracted from

a piece of fin tissue using a Quick Gene DNA tissue Kit S (Fujifilm, Tokyo, Japan). The mitochondrial genome was amplified with primers that were designed on the basis of the conserved regions of the mitochondrial genomes of *R. ocellatus kurumeus* (AB070205), *R. suigensis* (NC_013709) and *R. uyekii* (NC_007885).

The *R. shitaiensis* had a similar mitochondrial genome structure to that of the most Cyprinidae, such as *Aphyocypris kikuchii*, *A. moltrechti* and *Rasbora steineri*, (Chang et al., 2012; Jang-Liaw et al., 2012a,b). The *R. shitaiensis* had 16,774 bp in its complete mitochondrial genome which consisted of 2 *rRNA* genes, 22 *tRNA* genes, 13 protein-coding genes, 1 replication origin region (*O_L*) and 1 control region (*D-loop*) (Table 1).

Table 1. Mitochondrial genome of the *R. shitaiensis*.

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>tRNA^{Phe}</i>	1	68	68			–	H
<i>12S rRNA</i>	69	1023	955			0	H
<i>tRNA^{Val}</i>	1025	1096	72			1	H
<i>16S rRNA</i>	1097	2774	1678			0	H
<i>tRNA^{Leu(UUR)}</i>	2775	2850	76			0	H
<i>ND1</i>	2851	3825	975	ATG	TAA	0	H
<i>tRNA^{Ile}</i>	3830	3901	72			4	H
<i>tRNA^{Gln}</i>	3900	3970	71			–2	L
<i>tRNA^{Met}</i>	3972	4041	70			1	H
<i>ND2</i>	4042	5088	1047	ATG	TAG	0	H
<i>tRNA^{Trp}</i>	5087	5157	71			–2	H
<i>tRNA^{Ala}</i>	5159	5227	69			1	L

(continued)

Table 1. Continued

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>tRNA</i> ^{Asn}	5229	5301	73			1	L
<i>O_L</i>	5302	5333	32			0	–
<i>tRNA</i> ^{Cys}	5334	5402	69			0	L
<i>tRNA</i> ^{Tyr}	5403	5472	70			0	L
<i>COI</i>	5474	7024	1551	GTG	TAA	1	H
<i>tRNA</i> ^{Ser(UCN)}	7025	7095	71			0	L
<i>tRNA</i> ^{Asp}	7097	7165	69			1	H
<i>COII</i>	7175	7865	691	ATG	T–	9	H
<i>tRNA</i> ^{Lys}	7866	7941	76			0	H
<i>ATP8</i>	7943	8107	165	ATG	TAA	1	H
<i>ATP6</i>	8101	8784	684	ATG	TAA	–7	H
<i>COIII</i>	8784	9567	784	ATG	T–	–1	H
<i>tRNA</i> ^{Gly}	9568	9638	71			0	H
<i>ND3</i>	9639	9989	351	ATG	ATG	0	H
<i>tRNA</i> ^{Arg}	9988	10,057	70			–2	H
<i>ND4L</i>	10,278	10,574	297	ATG	TAA	220	H
<i>ND4</i>	10,568	11,950	1383	ATG	TAG	–7	H
<i>tRNA</i> ^{His}	11,950	12,018	69			–1	H
<i>tRNA</i> ^{Ser(AGY)}	12,019	12,085	67			0	H
<i>tRNA</i> ^{Leu(CUN)}	12,087	12,159	73			1	H
<i>ND5</i>	12,160	13,995	1836	GTG	TAG	0	H
<i>ND6</i>	13,992	14,516	525	ATG	TAA	–4	L
<i>tRNA</i> ^{Glu}	14,517	14,585	69			0	L
<i>Cytb</i>	14,591	15,731	1141	ATG	T–	5	H
<i>tRNA</i> ^{Thr}	15,732	15,804	73			0	H
<i>tRNA</i> ^{Pro}	15,804	15,873	70			–1	L
D-loop	15,874	16,774	901			0	–

*Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between contiguous genes.

†H and L, respectively, denote heavy and light strands.

The positions of RNA genes were predicted by the MITOS (Bernt et al., 2012) and the locations of protein-coding genes were identified by comparing with the homologous genes of other *Rhodeus* fishes. The overall base composition of the entire genome was as follows: A (28.7%), T (26.5%), C (27.4%) and G (17.4%), which demonstrated a A+T (55.2%) rich feature. Among the mitochondrial protein-coding genes, the *ND5* was the longest (1836 bp), while the *ATP8* was the shortest (165 bp). The usage of the start codon was mainly ATG in the most of mitochondrial protein coding genes besides the *COI* and *ND5* genes employing the GTG; the usage of the stop one was either complete or incomplete. The Control region was 901 bp in size and had no repeats inspected by the program “TANDEM REPEATS FINDER (Benson, 1999)”.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

References

- Arai R, Akai Y. (1988). *Acheilognathus melanogaster*, a senior synonym of *A. morioka*, with a revision of the genera of the subfamily Acheilognathinae (Cypriniformes, Cyprinidae). Bull Natn Sci Mus Tokyo (A) 14:199–213.
- Benson G. (1999). Tandem repeats finder: A program to analyze DNA sequences. Nucl Acids Res 27:573–80.
- Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritsch G, Putz J, et al. (2012). MITOS: Improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. [Epub ahead of print]. doi: 10.1016/j.ympev.2012.08.023.
- Chang C-H, Tsai C-L, Jang-Liaw N-H. (2012). Complete mitochondrial genome of the Chinese rasbora *Rasbora steineri* (Teleostei, Cyprinidae). Mitochondr DNA 24:183–5.
- Li F, Arai R. (2010). *Rhodeus shिताiensis*, a new bitterling from China (Teleostei: Cyprinidae). Ichthyol Explor Freshwaters 21:303–12.
- Jang-Liaw N-H, Tsai C-L, Watanabe K. (2012a). Complete mitochondrial genome of the Kikuchi's minnow *Aphyocypris kikuchii* (Teleostei, Cyprinidae). Mitochondr DNA 24:11–13.
- Jang-Liaw N-H, Tsai C-L, Chang C-H, Watanabe K. (2012b). Complete mitochondrial genome of the Moltrecht's minnow, *Aphyocypris moltrechti* (Teleostei, Cyprinidae), in comparison with *A. kikuchii*. Mitochondr DNA 24:117–19.