

MITOGENOME ANNOUNCEMENT

Mitochondrial genome of *Acrossocheilus parallens* (Osteichthyes: Cyprinidae)

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Abstract

Genus *Acrossocheilus* includes approximately 24 valid species, 19 of which are endemic to China. The complete mitogenome of *A. parallens* is 16,588 bp long and includes 13 protein-coding genes, 22 tRNA genes (ranging from 67 bp in *tRNA^{Cys}* to 76 bp in *tRNA^{Leu}* and *tRNA^{Lys}*), 2 rRNA genes (955 bp in 12S rRNA and 1675 bp in 16S rRNA), and 1 control region (CR). Only *ND6* and other eight tRNA genes are encoded on the L-strand while most of these genes are located in the H-strand. Resolving taxonomic uncertainties and defining evolutionary divergence in this genus are important contributions to cladogenesis in cyprinid fishes in East Asia.

Keywords

Acrossocheilus parallens, genome, mitochondrion

History

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Acrossocheilus, a genus of small-sized freshwater fishes belonging to Barbinae, Cyprinidae, is distributed throughout southeast China with an extension to Vietnam and Laos (Chen, 1991; Kottelat, 2001a,b; Nichols, 1931; Yue et al., 2000; Zheng, 1989). This genus includes approximately 24 valid species, 19 of which are endemic to China (Fishbase). All species of this genus are highly rheophilic and usually inhabit mountain streams or upper reaches of rivers. The *Acrossocheilus* species can partially or completely share habitats, thereby showing typical sympatry. The striation pattern (vertical bar and longitudinal stripes) of the body, the type of dorsal spine (smooth or serrated posteriorly), and the morphology of the mouthpart are the main diagnostic characteristics (Chen, 1991; Yue et al., 2000). However, aside from sexual

dimorphism, considerable variations in such characteristics can also be found if fishes are from different stocks or at different developmental stages. Although taxonomists have exerted considerable effort to study *Acrossocheilus*, several extremely elusive questions remain in terms of species identification (Yuan & Zhang, 2010a,b). Thus, the combination of DNA barcodes and key morphological characteristics is necessary for the precise identification of *Acrossocheilus*.

In this study, we used 13 primer pairs to acquire the mitogenome of *A. parallens* via polymerase chain reaction. The complete mitogenome of *A. parallens* is 16,588 bp (Accession Number KP257293) long and includes 13 protein-coding genes, 22 tRNA genes, two rRNA genes (12S rRNA and 16S rRNA), and

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

Gene names	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Sizes (bp)	No. of the codons	Start condon	Stop condon
<i>tRNA^{Phe}</i>	H	1	69			69			
<i>12S rRNA</i>	H	70	1024			955			
<i>tRNA^{Val}</i>	H	1025	1096			72			
<i>16S rRNA</i>	H	1097	2771			1675			
<i>tRNA^{Leu}</i>	H	2772	2847			76			
<i>ND1</i>	H	2849	3823	1		975	324	ATG	TAA
<i>tRNA^{Ile}</i>	H	3828	3899	4		72			
<i>tRNA^{Gln}</i>	L	3898	3968		2	71			
<i>tRNA^{Met}</i>	H	3971	4039	2		69			
<i>ND2</i>	H	4040	5084			1045	348	ATG	T--
<i>tRNA^{Trp}</i>	H	5085	5155			71			
<i>tRNA^{Ala}</i>	L	5158	5226	2		69			

(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>tRNA^{Asn}</i>	L	5228	5300	1		73			
<i>tRNA^{Cys}</i>	L	5333	5399	2		67			
<i>tRNA^{Tyr}</i>	L	5399	5469		1	71			
<i>CO1</i>	H	5471	7021	1		1551	516	GTG	TAA
<i>tRNA^{Ser}</i>	L	7022	7092			71			
<i>tRNA^{Asp}</i>	H	7096	7167	3		72			
<i>CO2</i>	H	7182	7872	14		691	230	ATG	T--
<i>tRNA^{Lys}</i>	H	7873	7948			76			
<i>ATP8</i>	H	7950	8114	1		165	54	ATG	TAG
<i>ATP6</i>	H	8108	8791		7	684	227	ATG	TAA
<i>CO3</i>	H	8791	9575		1	785	261	ATG	TA-
<i>tRNA^{Gly}</i>	H	9576	9647			72			
<i>ND3</i>	H	9648	9996			349	116	ATG	T--
<i>tRNA^{Arg}</i>	H	9997	10,066			70			
<i>ND4L</i>	H	10,067	10,363			297	98	ATG	TAA
<i>ND4</i>	H	10,357	11,737		7	1381	460	ATG	T--
<i>tRNA^{His}</i>	H	11,738	11,806			69			
<i>tRNA^{Ser}</i>	H	11,807	11,875			69			
<i>tRNA^{Leu}</i>	H	11,877	11,949	1		73			
<i>ND5</i>	H	11,950	13,773			1824	607	ATG	TAA
<i>ND6</i>	L	13,770	14,291		4	522	173	TTA	CAT
<i>tRNA^{Glu}</i>	L	14,292	14,360			69			
<i>Cyt b</i>	H	14,367	15,507	6		1141	380	ATG	T--
<i>tRNA^{Thr}</i>	H	15,508	15,579			72			
<i>tRNA^{Pro}</i>	L	15,579	15,648		1	70			
D-loop	H	15,648	16,588		1	941			

I control region (CR) (Table 1). Only *ND6* and other eight tRNA genes are encoded on the L-strand while most of these genes are located in the H-strand.

Eleven of the 13 protein-coding genes start with the ATG codon, whereas *ND6* and *COX1* start with TAA and GTG, respectively. *ND1*, *COX1*, *ATP6*, *ND4L*, and *ND5* end with TAA; *ATP8* with TAG; *ND6* with CAT; *ND2*, *COX2*, *ND3*, *ND4*, and *Cytb* with T (incomplete stop codon); and *COX3* with TA (incomplete stop codon). These 22 tRNA genes have lengths ranging from 67 bp (*tRNA^{Cys}*) to 76 bp (*tRNA^{Leu}* and *tRNA^{Lys}*). The 12S rRNA and 16S rRNA genes are located between *tRNA^{Phe}* and *tRNA^{Leu}* and are separated by *tRNA^{Val}*. The 12S rRNA and 16S rRNA genes are 955 and 1675 bp long, respectively. The control region is 941 bp long and is located between *tRNA^{Pro}* and *tRNA^{Phe}*.

The genetic distance between *Acrossocheilus parallens* and *A. hemispinus* is particularly near (2.44% in *CO1*, 2.97% in *Cytb*, 2.61% in D-loop, and 3.35% in *ND2*). However, the former is morphologically different from the latter and has a more extensive distribution in south China. Resolving taxonomic uncertainties and defining evolutionary divergence in the genus *Acrossocheilus* are important contributions to cladogenesis in cyprinid fishes in East Asia.

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Declaration of interest

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