



Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Mitochondrial genome of the *Salanx cuvieri* (Osteichthyes: Salangidae)Mei Ding^{1,2}, Zhongming Wang³, Jiwei Qi⁴, Baowei Zhang¹, and Jie Zhang²¹School of Life Science, Anhui University, Hefei, China, ²Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, ³Marine Fisheries Research Institute of Zhejiang, Zhoushan, China, and ⁴College of Life Science, Capital Normal University, Beijing, China**Abstract**

Salanx cuvieri, a salangid species endemic to China, is mainly distributed in the coastal waters in South China. In this study, we have studied the complete mitochondrial genome of the *S. cuvieri*. The results show that the complete mtDNA of *S. cuvieri* is 16,588 bp in length, which contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA), and 1 control region (CR). The base composition of the genome is 25.3% A, 24% T, 18.2% G, and 32.1% C. Most of the genes are existed in the H-strand, except for the *ND6* and other 9 tRNA genes which are encoded on L-strand. A recent study on *S. cuvieri* has revealed that significant genetic differentiations are found among populations inhabiting different estuaries, so our result can contribute to the preservation of this endangered species.

KeywordsGenome, mitochondrion, *Salanx cuvieri***History**

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The Salangidae family of the superorder Protacanthopterygii and order Osmeriformes contains six genera and approximately 17 species; the species of this family are endemic to eastern Asia (Nelson, 2006; Zhang et al., 2007a). Salangids, which exhibit annualism, are neotenic or padomorphic fish with cylindrical and elongated bodies (Zhang et al., 2013).

Salanx cuvieri, a salangid species endemic to China, is mainly distributed in the coastal waters in South China (Cheng & Zheng, 1987). *S. cuvieri* has been traditionally exploited in China because of its high commercial value (Zhang, 2008). Similar to other *Salanx* species, *S. cuvieri* is highly sensitive to overfishing, habitat degradation, and environmental changes; the population of this species has rapidly decreased (Dou & Chen, 1993; Zhang et al., 2007b).

In this study, 13 primer pairs were used to acquire the mitogenome of *S. cuvieri* by polymerase chain reaction. The complete mtDNA of *S. cuvieri* is 16,588 bp long (Accession Number KJ645978) and contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA), and 1 control region (CR) (Table 1). Most of these genes are located in the H-strand; only *ND6* and other nine tRNA genes are encoded on the L-strand.

Twelve of the 13 protein-coding genes begin with ATG, whereas *COX1* begins with GTG. *ND1*, *COX1*, *ATP8*, and *ND4L* end with TAA; *ND5* with AGA; *ND6* with TAG; *ND2*, *COX2*, *ND3*, *ND4*, and *Cytb* with T (incomplete stop codon); and *ATP6* and *COX3* with TA (incomplete stop codon). The 22 tRNA genes were distributed around or between the

Table 1. Characteristics of the *S. cuvieri* mitochondrial DNA genome.

Gene name	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
<i>tRNA^{phe}</i>	H	1	68			68			
<i>12s rRNA</i>	H	69	1013			945			
<i>tRNA^{val}</i>	H	1014	1084			71			
<i>16s rRNA</i>	H	1085	2801			1717			
<i>tRNA^{Leu}</i>	H	2802	2875			74			
<i>ND1</i>	H	2876	3850			975	324	ATG	TAA
<i>tRNA^{Ile}</i>	H	3853	3924	2		72			
<i>tRNA^{Gln}</i>	L	3924	3994		1	71			
<i>tRNA^{Met}</i>	H	3994	4062		1	69			
<i>ND2</i>	H	4067	5117	4		1051	350	ATG	T--
<i>tRNA^{Trp}</i>	H	5118	5189			72			
<i>tRNA^{Ala}</i>	L	5191	5259	1		69			

(continued)

Table 1. Continued

Gene name	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
<i>tRNA^{Asn}</i>	L	5261	5333	1		73			
<i>tRNA^{Cys}</i>	L	5361	5426	27		66			
<i>tRNA^{Tyr}</i>	L	5427	5494			68			
<i>COX1</i>	H	5496	7046	1		1551	516	GTG	TAA
<i>tRNA^{Ser}</i>	L	7047	7117			71			
<i>tRNA^{Asp}</i>	H	7122	7194	4		73			
<i>COX2</i>	H	7209	7899	14		691	230	ATG	T--
<i>tRNA^{Lys}</i>	H	7900	7974			75			
<i>ATP8</i>	H	7976	8143	1		168	55	ATG	TAA
<i>ATP6</i>	H	8134	8816		10	683	227	ATG	TA-
<i>COX3</i>	H	8817	9601			785	261	ATG	TA-
<i>tRNA^{Gly}</i>	H	9602	9672			71			
<i>ND3</i>	H	9673	10,021			349	116	ATG	T--
<i>tRNA^{Arg}</i>	H	10,022	10,091			70			
<i>ND4L</i>	H	10,092	10,388			297	98	ATG	TAA
<i>ND4</i>	H	10,382	11,762		7	1381	460	ATG	T--
<i>tRNA^{His}</i>	H	11,763	11,831			69			
<i>tRNA^{Ser}</i>	H	11,832	11,900			69			
<i>tRNA^{Leu}</i>	H	11,902	11,974	1		73			
<i>ND5</i>	H	11,975	13,813			1839	612	ATG	AGA
<i>ND6</i>	L	13,810	14,330		5	521	173	ATG	TAG
<i>tRNA^{Glu}</i>	L	14,331	14,400			70			
<i>CYTB</i>	H	14,404	15,544	3		1141	380	ATG	T--
<i>tRNA^{Thr}</i>	H	15,545	15,616			72			
<i>tRNA^{Pro}</i>	L	15,617	15,686			70			
<i>D-loop</i>	H	15,692	16,588	6		897			

13 protein-coding genes. These genes have lengths ranging from 66 bp in *tRNA^{Cys}* to 75 bp in *tRNA^{Lys}*. The 12S rRNA and 16S rRNA genes are 945 and 1717 bp long, respectively. These genes were located between *tRNA^{Phe}* and *tRNA^{Leu}*, and were further separated by *tRNA^{Val}*. The CR of the *S. cuvieri* mitochondrial DNA is 897 bp long and lies between *tRNA^{Pro}* and *tRNA^{Phe}*.

A recent study on *S. cuvieri* has revealed that significant genetic differentiations are found among populations inhabiting different estuaries (Cortey et al., 2004; Si et al., 2012). Mitochondrial DNA evolves more rapidly than nuclear DNA (Brown et al., 1979). It can serve as a powerful tool for studies on population structure and conservation genetics (Moritz et al., 1987). We hope our result can contribute to the preservation of this endangered species.

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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 Knowledge Innovation Project of the Chinese Academy of Sciences (KSCX2-EW-J-2).

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