



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 *Hemisalanx brachyrostralis* (Osteichthyes: Salangidae)

Jie Zhang, Mei Ding, Jiwei Qi, Haiping Chen & Baowei Zhang

To cite this article: Jie Zhang, Mei Ding, Jiwei Qi, Haiping Chen & Baowei Zhang (2014): Complete mitochondrial genome of *Hemisalanx brachyrostralis* (Osteichthyes: Salangidae), Mitochondrial DNA

To link to this article: <http://dx.doi.org/10.3109/19401736.2014.919465>



Published online: 03 Jun 2014.



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



Article views: 13



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 *Hemisalanx brachyrostralis* (Osteichthyes: Salangidae)Jie Zhang¹, Mei Ding^{1,2}, Jiwei Qi³, Haiping Chen⁴, and Baowei Zhang²¹Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, ²School of Life Science, Anhui University, Hefei, China, ³College of Life Science, Capital Normal University, Beijing, China, and ⁴Fisheries Bureau of Tai Hu County, Anhui, China**Abstract**

Hemisalanx brachyrostralis belonging to the family Salangidae is endemic to the Yangtze River. This species has been listed on the Chinese Red List because of the serious decrease in its resources. In this study, we analyzed the complete mtDNA (16588 bp long) of *H. brachyrostralis*. Overall base composition of the genome is 25.1% A, 25.4% T, 18.7% G, and 30.8% C. The complete mtDNA contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA), and 1 control region. Apart from the *ND6* gene and nine tRNA genes encoded on the L-strand, most of the genes are on the H-strand. *H. brachyrostralis* has the lowest genetic diversity among the Salangid species, so further studies on conservation genetics must be conducted.

KeywordsGenome, *Hemisalanx brachyrostralis*, mitochondrion**History**

Received 14 April 2014

Accepted 26 April 2014

Published online 3 June 2014

The Salangidae family comprises six genera and approximately 17 species (Nelson, 2006; Zhang et al., 2007a), which inhabit both freshwater and marine areas in Eastern Asia; the species of this family are essential components of Chinese historical fisheries (Nelson, 2006; Zhu, 1985). *Hemisalanx brachyrostralis* is endemic to the Yangtze River and highly vulnerable to environmental changes and habitat degradation (Wang, 2005; Zhang et al., 2007b). This species has been listed on the Chinese Red List because of the serious decrease in its resources (Zhang, 2008). Mitochondrial DNA is a maternally-inherited circular genome that serves important functions in metabolism and population genetics (Boore, 1999). However, little is known about the complete mitochondrial genome of *H. brachyrostralis* in GenBank.

In this study, the complete mtDNA of *H. brachyrostralis* was amplified by polymerase chain reaction with 13 primer pairs. The complete mtDNA sequence of *H. brachyrostralis* (16,588 bp long; Accession Number KJ645979) has 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA), and

1 control region (Table 1). Apart from the *ND6* gene and nine tRNA genes encoded on the L-strand, most genes are on the H-strand.

Eleven of 13 protein-coding genes begin with ATG codon, whereas *ND2* and *COX1* begin with CGC and GTG, respectively. *ND1*, *COX1*, *ATP8*, and *ND4L* end with TAA; *ND2*, *COX2*, *ND3*, *ND4*, and *Cyt b* with T (incomplete stop codon); *ATP6* and *COX3* with TA (incomplete stop codon); *ND5* with AGA; and *ND6* with TAG. The 22 tRNA genes have lengths ranging from 66 bp (*tRNA^{Cys}*) to 76 bp (*tRNA^{Lys}*). The 12S rRNA and 16S rRNA genes are 945 and 1717 bp long, respectively. These genes are located between *tRNA^{Phe}* and *tRNA^{Leu}*, and are separated by *tRNA^{Val}*. The control region is 900 bp long and located between *tRNA^{Pro}* and *tRNA^{Phe}*.

H. brachyrostralis has the lowest genetic diversity among the salangid species (Si, 2012; Zhao et al., 2008, 2010). Therefore, further studies on conservation genetics must be conducted. We hope that our study can help conserve the genetic resources of this endangered species.

Table 1. Characteristics of the *H. brachyrostralis* mitochondrial 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	CGC	T--
<i>tRNA^{Trp}</i>	H	5118	5189			72			
<i>tRNA^{Ala}</i>	L	5191	5259	1		69			
<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		1553	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	7975			76			
<i>ATP8</i>	H	7977	8144	1		168	55	ATG	TAA
<i>ATP6</i>	H	8135	8817		10	683	227	ATG	TA-
<i>COX3</i>	H	8818	9602			785	261	ATG	TA-
<i>tRNA^{Gly}</i>	H	9603	9673			71			
<i>ND3</i>	H	9674	10,022			349	116	ATG	T--
<i>tRNA^{Arg}</i>	H	10,023	10,092			70			
<i>ND4L</i>	H	10,093	10,389			297	98	ATG	TAA
<i>ND4</i>	H	10,383	11,763		7	1381	460	ATG	T--
<i>tRNA^{His}</i>	H	11,764	11,832			69			
<i>tRNA^{Ser}</i>	H	11,833	11,901			69			
<i>tRNA^{Leu}</i>	H	11,903	11,975	1		73			
<i>ND5</i>	H	11,976	13,815			1841	612	ATG	AGA
<i>ND6</i>	L	13,811	14,332		5	522	173	ATG	TAG
<i>tRNA^{Glu}</i>	L	14,333	14,402			70			
<i>Cyt b</i>	H	14,406	15,546	3		1141	380	ATG	T--
<i>tRNA^{Thr}</i>	H	15,547	15,618			72			
<i>tRNA^{Pro}</i>	L	15,619	15,688			70			
D-loop	H	15,689	16,588			900			

Acknowledgements

This paper has benefited from the help of Hui Wang, Ling Ding, Tao Pan, and Aihong Chai. We show our sincerely gratitude for their kindly assistance.

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).

References

- Boore JL. (1999). Animal mitochondrial genomes. *Nucleic Acids Res* 27: 1767–80.
- Nelson JS. (2006). *Fishes of the world*. 4th ed. New York: John Wiley and Sons, Inc.
- Si SL, Zhang Q, Huang Y, Ma B, Yue XL. (2012). Genetic diversity of *Salanx curvieri* in South China inferred from mtDNA cytb sequences. *Mar Fisheries* 34:1–6.
- Wang ZS, Lu C, Xu CR, Lei GC. (2005). Impact of river-lake isolation on the spatial distribution pattern of *Hemisalanx brachyrostralis*. *Biodiv Sci* 13:407–15.
- Zhang J, Li M, Xu MQ, Takita T, Wei FW. (2007a). Molecular phylogeny of icefish Salangidae based on complete mtDNA cytochrome *b* sequences, with comments on estuarine fish evolution. *Biol J Linn Soc* 91:325–40.
- Zhang J, Wei FW, Li M, Xu MQ. (2007b). Threatened fishes of the world: *Hemisalanx prognathus* (Regan, 1908) (Salangidae). *Environ Biol Fish* 78:209–10.
- Zhang J. (2008). Biodiversity of Chinese icefishes (Salangidea) and their diversity conservation. *Bull Biol* 43:4–6 (in Chinese).
- Zhao L, Zhang J, Liu ZJ, Funk SM, Wei FW, Xu MQ, Li M. (2008). Complex population genetic and demographic history of the Salangid, *Neosalanx taihuensis*, based on cytochrome *b* sequences. *BMC Evol Biol* 8:201. [Online] Available at: <http://www.biomedcentral.com/1471-2148/8/201> (Accessed 14 July 2008).
- Zhao L, Zhang J, Liu ZJ, Xu MQ, Li M. (2010). Population genetic structure and demographic history of *Neosalanx jordani* based on cytochrome *b* sequences. *Biodiv Sci* 18:251–61.
- Zhu CD. (1985). A preliminary study on growth and feeding habits of icefish in Taihu Lake. *J Fish China* 9:275–87 (in Chinese).