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

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To cite this article: Wenxian Hu, Zhigang Gao, Bin Kang & Jie Zhang (2015) Mitochondrial genome of Monotrete leiurus (Osteichthyes: Tetraodontidae), Mitochondrial DNA, 26:5, 793-794, DOI: 10.3109/19401736.2013.855757

To link to this article: http://dx.doi.org/10.3109/19401736.2013.855757

Published online: 10 Dec 2013.

Mitochondrial DNA

http://informahealthcare.com/mdn
ISSN: 1940-1736 (print), 1940-1744 (electronic)

Mitochondrial DNA, 2015; 26(5): 793–794
 DOI: 10.3109/19401736.2013.855757

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MITOGENOME ANNOUNCEMENT

Mitochondrial genome of *Monotrete leiurus* (Osteichthyes: Tetraodontidae)

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Abstract

Monotrete leiurus is the only freshwater puffer founded in Nala River, which is a tributary of the Langcang–Mekong River in China. The complete mitochondrial genome sequence of the *Monotrete leiurus* is 16,448 bp long and consists of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and 1 control region (CR). The base composition of the genome is 29% A, 23.8% T, 31.8% C and 15.4% G and this composition shows a bias for A + T. The mitochondrial genes from *Monotrete leiurus* are overlapped in a total of 34 bp at seven locations and interleaved with a total of 64 bp intergenic spacers at 13 locations. The results can not only help clarify the classification problem in sibling freshwater puffers, but also provide information for their protection in the future.

Keywords

Genome, mitochondrion, *Monotrete leiurus*

History

Received 25 September 2013
Accepted 29 September 2013
Published online 10 December 2013

The genus *Monotrete* belongs to the family of Tetraodontidae of the order Tetraodontiformes, which are a monophyletic group of teleosts comprising 19 families with approximately 400 species (Nelson, 1994; Santini & Tyler, 2003; Tyler & Santini, 2002). *Monotrete* species are distributed in the Mekong and Chao Phraya basins, and possibly in the Malay Peninsula and in Sumatra, Indonesia. *Monotrete leiurus* inhabits streams and medium- to large-sized rivers in upland and lowland areas with flowing or standing water in Southeast Asia (Kottelat & Widjanarti, 2005; Rainboth, 1996; Roberts, 1998; Taki, 1978). The fish is the only freshwater puffer founded in Nala River, which is a tributary of the Langcang–Mekong River in China. This distribution is also the most north limitation of the genus.

To date, the classification *M. leiurus* is amphibolous and difficult to grasp in real life (Li, 1976). The possibility of two or three species existing in the Rivers in Yunan, China requires further research (Chu & Chen, 1990). Moreover, habitat degradation and overexploitation have caused a sharp decline in the population of fish resources (Port et al., 2012). The quantity of *M. leiurus*, which has been a common species since the 1980s, significantly reduced (Chu & Chen, 1990). Thus, we present the complete mitochondrial genome of *M. leiurus*.

In this study, the complete mtDNA of *M. leiurus* was amplified by polymerase chain reaction (PCR) and sequenced by using 20 primers. Nucleotide sequences were deposited in GenBank (Accession number KF667490). The complete mitochondrial genome of *Monotrete leiurus* is 16,448 bp in length. It contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA) and 1 control region. Eleven of the 13 protein-coding genes require ATG as the start codon, while *CO1* and *ND6* utilize GTG and TCT, respectively. Five of the 13 protein-coding genes use TAA as stop codons. The *COI* stops with AGG, the *ND6* end with CAT. The *ND2*, *ATP6* and *CO3* end with TA-, the *CO2*, *ND3* and *ND4* end with T- - as an incomplete stop codon, which is presumably completed as TAA by post-transcriptional polyadenylation (Anderson et al., 1981). The 22 tRNA genes range in size from 74 bp in $tRNA^{Leu}$ to 64 bp in $tRNA^{cys}$. The 12S and 16S rRNA genes are 946 and 1675 bp, respectively, and are located between the $tRNA^{Phe}$ and $tRNA^{Leu}$ genes and separated by the $tRNA^{Val}$ gene. The control region is 821 bp long and lies between the $tRNA^{Pro}$ and $tRNA^{Phe}$ genes. Thirteen protein-coding genes for 3802 amino acids were identified. The longest gene is *ND5* with 1839 bp and the shortest is *ATP8* with only 168 bp. The nucleotide composition is 29% A, 31.8% C, 15.4% G and 23.8% T, and this composition shows a bias for A + T. The mitochondrial genes from *Monotrete leiurus* are overlapped in a total of 34 bp at seven locations and interleaved with a total of 64 bp intergenic spacers at 13 locations (Table 1).

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Table 1. Characteristics of the *M. leiurus* mitochondrial DNA genome.

Gene names	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
tRNA^{Phe}	H	1	68			68			
12S rRNA	H	69	1014			946			
tRNA^{Val}	H	1015	1085			71			
16S rRNA	H	1086	2760			1675			
tRNA^{Leu}	H	2761	2834			74			
ND1	H	2835	3809			975	324	ATG	TAA
tRNA^{Ile}	H	3813	3882	3		70			
tRNA^{Gln}	L	3882	3952		1	71			
tRNA^{Met}	H	3952	4020		1	69			
ND2	H	4021	5066			1046	348	ATG	TA-
tRNA^{Trp}	H	5067	5137			71			
tRNA^{Ala}	L	5140	5208	2		69			
tRNA^{Asn}	L	5210	5282	1		73			
tRNA^{Cys}	L	5316	5379	33		64			
tRNA^{Tyr}	H	5380	5449			70			
CO1	H	5451	7010	1		1560	519	GTG	AGG
tRNA^{Ser}	L	7002	7072		9	71			
tRNA^{Asp}	H	7076	7145	3		70			
CO2	H	7151	7841	5		691	230	ATG	T- -
tRNA^{Lys}	H	7842	7914			73			
ATP8	H	7916	8145	1		168	55	ATG	TAA
ATP6	H	8074	8756		10	683	227	ATG	TA-
CO3	H	8757	9541			785	261	ATG	TA-
tRNA^{Gly}	H	9542	9612			71			
ND3	H	9613	9961			349	116	ATG	T- -
tRNA^{Arg}	H	9962	10,030			69			
ND4L	H	10,032	10,328	1		297	98	ATG	TAA
ND4	H	10,322	11,702		7	1381	460	ATG	T- -
tRNA^{His}	H	11,703	11,770			68			
tRNA^{Ser}	H	11,772	11,838	1		67			
tRNA^{Leu}	H	11,845	11,917	6		73			
ND5	H	11,918	13,756			1839	612	ATG	TAA
ND6	L	13,752	14,273		5	522	174	TCT	CAT
tRNA^{Glu}	L	14,274	14,342			69			
Cyt b	H	14,346	15,482	3		1137	378	ATG	TAA
tRNA^{Thr}	H	15,487	15,558	4		72			
tRNA^{Pro}	L	15,558	15,627		1	70			
D-loop	H	15,628	16,448			821			

This genome is a valuable molecule to understand the differentiation time with sibling species and provides information for the research of conservation genetics of freshwater puffers.

Acknowledgements

The authors are grateful to Mr. Xin Huang and Miss Baojuan Yang and Liqian Ren for their help in the lab work and specimen preparation.

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 Program of the Chinese Academy of Sciences (No. KSCX2-EW-J-2) and the National Natural Science Foundation of China (U0936602).

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