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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of *Mugilogobius chulae* (Perciformes: Gobiidae)

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Abstract

In this paper, the complete mitogenome sequence of *Mugilogobius chulae* is reported. The circular mitochondrial DNA of *M. chulae* is 16,489 bp in length, containing 13 protein-coding genes, 22 *tRNAs*, 2 *rRNAs* and 2 non-coding regions (control region and origin of light-strand replication). The overall base composition of *M. chulae* is 27.8% A, 27.1% T, 16.8% G, 28.3% C. This genome reported here provides a resource for studies on taxonomy and genetics of *M. chulae* and closely related species.

Keywords

Complete mitogenome, gobiidae, *mugilogobius chulae*

History

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The *Mugilogobius chulae* is a small egg-lying marine teleost, which is mainly distributed in Western Pacific Rim. Because of the features of morphology, reproduction and development (Li et al., 2012), *M. chulae* is more suitable as a laboratory animal, the closed colony of *M. chulae* has been established, and used in environment monitoring of ocean (Li et al., 2013). However, the genetic background of the *M. chulae is* incomprehensive. Regarding the genomic information of the *M. chulae*, only 12 sequences can be obtained in public database (http://www.ncbi.nlm.nih.gov/). The complete mitochondrial genome of *M. chulae* will be useful for further studies on molecular identification and phylogenetic relationships within this genus.

In this study, we amplified the complete mitochondrial DNA of *M. chulae* (GeneBank accession NO. KP144793) using the polymerase chain reaction (PCR) method. The *M. chulae* was collected from the closed colony kept in the laboratory. Total genomic DNA was extracted from the tail fin with the HiPure Tissue DNA Mini Kit (UMagen, Guangzhou, China). Primers were designed on the basis of the mitogenome sequence of *Mugilogobius abei* (GenBank Accession No. NC_023353.1) (Huang et al., 2013). PCR was performed in a total volume of 50 μL.The PCR products were sequenced using the ABI 3730 DNA Analyzer (Applied Biosystems, Foster, CA). DNA sequences were analyzed using the software Vector NTI 11.5 (http://www.lifetechnologies.com). The tRNA genes were scanned by tRNAscan-SE 1.21 (Lowe & Eddy, 1997).

The gene organization of mitogenome of *M. chulae* is similar to most other fishes (Hwang et al., 2014; Kim et al., 2014;

Table 1. Characteristics of the mitochondrial genome of *Mugilogobius chulae*.

Gene	Position	Size(bp)	Codon		Anticondon	Strand	Intergenetic nucleotides
			Start	Stop			
$tRNA^{Phe}$	1–68	68			GAA	H	0
12S rRNA	69–1021	953				H	0
$tRNA^{Val}$	1022–1092	71			TAC	H	0
16S rRNA	1093–2768	1676				H	0
$tRNA^{Leu1(UAA)}$	2769–2842	74			TAA	H	0
ND1	2843–3817	975	ATG	TAA		H	1
$tRNA^{Ile}$	3819–3888	70			GAT	H	−1
$tRNA^{Gln}$	3888–3958	71			TTG	L	−1
$tRNA^{Met}$	3958–4026	69			CAT	H	0
ND2	4027–5073	1047	ATG	TAA		H	−1
$tRNA^{Trp}$	5073–5143	71			TCA	H	2
$tRNA^{Ala}$	5146–5214	69			TGC	L	1
$tRNA^{Asn}$	5216–5288	73			GTT	L	0
Rep origin(OL)	5289–5323	35				–	0

(*continued*)

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Table 1. Continued.

Gene	Position	Size(bp)	Codon		Anticondon	Strand	Intergenetic nucleotides
			Start	Stop			
$tRNA^{Cys}$	5324–5388	65			GCA	L	0
$tRNA^{Tyr}$	5389–5455	67			GTA	L	1
COXI	5457–7010	1554	GTG	TAA		H	0
$tRNA^{Ser1(UGA)}$	7011–7081	71			TGA	L	3
$tRNA^{Asp}$	7085–7156	72			TAA	H	2
COXII	7159–7849	691	ATG	T		H	0
$tRNA^{Lys}$	7850–7924	75			TTT	H	1
ATP8	7926–8090	165	ATG	TAA		H	−7
ATP6	8084–8767	684	ATG	TAA		H	−1
COXIII	8767–9551	785	ATG	TA		H	−1
$tRNA^{Gly}$	9551–9622	72			TCC	H	0
ND3	9623–9973	351	ATG	TAG		H	−2
$tRNA^{Arg}$	9972–10,040	69			TCG	H	0
ND4L	10,041–10,337	297	ATG	TAA		H	−7
ND4	10,331–11,716	1386	ATG	AGG		H	−5
$tRNA^{His}$	11,712–11,780	69			GTG	H	0
$tRNA^{Ser2(GCU)}$	11,781–11,851	71			GCT	H	0
$tRNA^{Leu2(UAG)}$	11,852–11,924	73			TAG	H	0
ND5	11,925–13,763	1839	ATG	TAA		H	−4
ND6	13,760–14,284	522	ATG	TAA		L	0
$tRNA^{Glu}$	14,282–14,350	69			TTC	L	4
CYTB	14,355–15,495	1141	ATG	T		H	0
$tRNA^{Thr}$	15,496–15,567	72			TGT	H	4
$tRNA^{Pro}$	15,572–15,642	71			TGG	L	0
D-loop(CR)	15,643–16,489	847				–	0

Liang et al., 2014; Qiao et al., 2014). The complete mitogenome of *M. chulae* is 16,489 bp, including 13 protein-coding genes, 22 tRNAs, 2 rRNAs and 2 non-coding regions: control region (D-loop) and origin of light-strand replication (O_L) (Table 1). Except for the eight *tRNA* ($tRNA^{Gln}$, $tRNA^{Ala}$, $tRNA^{Asn}$, $tRNA^{Cys}$, $tRNA^{Tyr}$, $tRNA^{Ser1}$, $tRNA^{Glu}$ and $tRNA^{Pro}$) and *ND6* genes are encoded on the L-strand, all other mitochondrial genes are encoded on the H-strand. The overall nucleotide composition of *M. chulae* is 27.8% A, 27.1% T, 16.8% G, 28.3% C with a higher AT content of 54.9%, which is similar to *M. abei* (54.7%) in the Gobiidae family. The homology of *M. chulae* to the sequence of *M. abei* is 87.7% in the nucleotide. All 13 protein-coding genes start with ATG except *COXI* which starts with GTG (Table 1). Most of the protein-coding genes(10 of 13 genes) end with TAA, TAG and AGG, the other three genes (*COXII COXIII*, and *CYTB*) have T or TA incomplete stop condon, which is very typical in many other gobioid fishs (Huang et al., 2014; Chen et al., 2014; Quan et al., 2014; Zhang et al., 2014). Four overlapping sequences among the 13 protein-coding genes were found: *ATP8* overlaps with *ATP6* for 7 bp, *ATP6* overlaps with *COXIII* for 1 bp, *ND4L* overlaps with *ND4* for 7 bp and *ND5* overlaps with *ND6* for 4 bp. The 12S and 16 S rRNA genes are located between $tRNA^{Phe}$ and $tRNA^{Leu}$ genes and separated by $tRNA^{Val}$ gene. *Mugilogobius chulae* contains two non-coding regions: the control region (D-loop) is 847 bp in length, which is located between $tRNA^{Pro}$ and $tRNA^{Phe}$ genes; another small non-coding region, which is a 35 bp fragment and the origin of light-strand replication (O_L), is located between the $tRNA^{Asn}$ and $tRNA^{Cys}$ genes.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was supported by the Strategic Cooperation Project by Guangdong Province and China Academy of Sciences (Grant No. 2011B090300099) and National Science and Technology Support Program of China (Grant No. 2013BAK11B02).

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