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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Leiocassis crassilabris* (Teleostei, Siluriformes: Bagridae)

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Abstract

The *Leiocassis crassilabris* is an important economic fish in China, and is widely distributed in south China, e.g. Yangtze River, Pearl River, and Min River, so it is a good model to study population genetics and geological changes of these regions. In this study, the complete mitochondrial genome sequence of *L. crassilabris* has been obtained with PCR. The gene arrangement and composition *L. crassilabris* of mitochondrial genome sequence are similar to most of the other vertebrates', which contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a non-coding control region with the total length of 16,530 bp. Except for eight tRNA and ND6 genes, other genes are encoded on heavy-strand (H-strand). Similar to most other vertebrates, the bias of G and C have universality in different region (genes). The complete mitochondrial genome sequence of *L. crassilabris* would contribute to better understand population genetics, conservation, biogeography, evolution of this lineage.

Keywords

Bagridae, complete mitochondrial genome, *Leiocassis crassilabris*

History

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In this study, we have presented the complete mitochondrial genome of *Leiocassis crassilabris* (Teleostei, Siluriformes: Bagridae), with the GenBank accession number JKC768227. Twenty-two primarily primers were used to amplify contiguous, overlapping segments to obtain the complete mitochondrial genomes of *L. crassilabris* according to the reference (Zhou et al., 2011, Table S1). The PCR products were purified and then sequenced with the same primers as those for PCR. New middle primers will be design if entire target segments can not obtain by using the public primers. The DNA sequence was annotated by comparing with the complete mitochondrial genome of the helmet catfish, *Cranoglanis bouderius* (Siluriformes: Cranoglanididae) (Peng et al., 2006), the channel catfish *Ictalurus punctatus* (Siluriformes: Ictaluridae) (Waldbieser et al., 2003) and the southern catfish, *Silurus meridionalis* (Siluriformes: Siluridae) (Zhou et al., 2011). The statistic result of base composition of every region (gene) and codon position of the protein-coding genes were computed and implemented with the program Editseq in package Lesergene (http://www.dnastar.com/t-sub-products-lasergene-editseq.aspx) and MEGA 5.1 (Tamura et al., 2011). The conservative region of the complete mitochondrial genome of *L. crassilabris* was alignment and identified with the complete mitochondrial genome of *Cranoglanis bouderius*, *Ictalurus punctatus* and *Silurus meridionalis* with MEGA 5.1 (Tamura et al., 2011)

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The complete mitochondrial genome of *L. crassilabris* is about 16,530 bp in size with 22 tRNA genes, 13 protein-coding genes, 2 rRNA (ribosomal RNA) genes and a non-coding displacement loop (control region, Table 1). Most of the *L. crassilabris* mitochondrial genes are encoded on H-strand except for ND6 and eight tRNA genes (tRNA-Gln, Ala, Asn, Cys, Tyr, Ser, Glu and Pro, see Table 1) which were encoded on light-strand (L-strand). The arrangement and gene numbers are similar to the typical vertebrate mitochondrial genomes (e.g. Peng et al., 2006; Waldbieser et al., 2003; Zhou et al., 2011). Like most vertebrates, ATG is the very common start codon for most protein-coding genes except for COI which start with GTG. TAA is the typical stop codon in six protein-coding genes (COI, APT8, APT6, ND4L, ND5 and ND6) while TAG is the stop codon of ND1, ND2 and ND3. The other four genes (COII, COIII, ND4 and cytb) have the incomplete stop codons T which is presumably completed by polyadenylation of the RNA messager after cleavage (Nardi et al., 2001). There are 10 regions of gene overlap (ranging from 1 to 10 bp, e.g. the overlap between ATP8 and ATP6) and 13 intergenic spacer regions (ranging from 1 to 33 bp, e.g. the intergenic spacer regions $tRNA^{Cys}$ and $tRNA^{Asn}$ which was believed to be associated with the transition from RNA synthesis to DNA synthesis, Hixson et al., 1986, Table 1). The statistics results of base composition of different genes/regions are not shown (available from Zhou upon request). G bias is found in all genes, elements, and different statistics regions, especially in 2nd (11.58%) and 3rd (9.05%) codon of protein-coding genes and D-loop (14.68%), and the A + T is significiant higher than G + C in all genes/regions. This status was found in other fishes (Kartavtsev et al., 2007; Wang et al., 2008, 2011) and was believed to be a specific evolution of mitochondrial genome.

Table 1. The mtDNA organization of the of *L. crassilabris*.

Gene/element	Position	Space(+) overlap(−)	Length (bp)	Start codon	Stop codon	Strand
$tRNA^{Phe}$	1–70	0	70			H
12S rRNA	71–1032	0	962			H
$tRNA^{Val}$	1033–1103	0	71			H
16S rRNA	1103–2770	+1	1668			H
$tRNA^{Leu}$	2771–2844	0	74			H
ND1	2846–3820	+1	975	ATG	TAG	H
$tRNA^{Ile}$	3823–3894	+2	72			H
$tRNA^{Gln}$	3894–3963	−1	70			L
$tRNA^{Met}$	3964–4033	−1	70			H
ND2	4034–5080	0	1047	ATG	TAG	H
$tRNA^{Trp}$	5079–5149	−1	71			H
$tRNA^{Ala}$	5153–5220	+3	68			L
$tRNA^{Asn}$	5222–5294	+1	73			L
$tRNA^{Cys}$	5327–5393	+33	67			L
$tRNA^{Tyr}$	5396–5464	+2	69			L
COI	5466–7016	+1	1551	GTG	TAA	H
$tRNA^{Ser}$	7017–7086	0	70			L
$tRNA^{Asp}$	7091–7163	+4	73			H
COII	7178–7867	+10	691	ATG	T	H
$tRNA^{Lys}$	7868–7941	0	74			H
ATP8	7944–8111	+2	168	ATG	TAA	H
ATP6	8102–8785	−10	684	ATG	TAA	H
COIII	8785–9568	−1	784	ATG	T	H
$tRNA^{Gly}$	9569–9641	0	73			H
ND3	9642–9992	0	351	ATG	TAG	H
$tRNA^{Arg}$	9991–10,061	−1	71			H
ND4L	10,062–10,358	0	297	ATG	TAA	H
ND4	10,352–11,731	−7	1380	ATG	T	H
$tRNA^{His}$	11,732–11,801	0	70			H
$tRNA^{Ser}$	11,804–11,867	+2	64			H
$tRNA^{Leu}$	11,872–11,944	+4	73			H
ND5	11,945–13,771	0	1827	ATG	TAA	H
ND6	13,768–14,283	−4	516	ATG	TAA	L
$tRNA^{Glu}$	14,284–14,352	0	69			L
cytb	14,355–15,492	+2	1138	ATG	T	H
$tRNA^{Thr}$	15,493–15,565	0	73			H
$tRNA^{Pro}$	15,564–15,635	−1	72			L
D-loop	15,635–16,526	−1	892			

Abbreviations: ATP 6 and 8, ATPase subunits 6 and 8; bp, base pair(s); COI–III, cytochrome c oxidase subunits I–III; cyt b, cytochrome b; ND1–6, 4L, NADH dehydrogenase subunits 1–6, 4L; tRNA, transfer RNA; 12SrRNA and 16S rRNA, 12S and 16S ribosomal RNA; mtDNA, mitochondrial DNA

Leiocassis crassilabris is widely distribution in in south China, e.g. Yangtze river, Pearl River, and Min River and formed different geographical population (Chu et al., 1999). But to date, the study about *L. crassilabris* only involved in domestication and artificial propagation (Zhang et al., 1997; Wang et al., 2003), hematology (Chen et al., 2007) and basal biology (Wang et al., 1995; Chen et al., 2008, 2012). The complete mitochondrial DNA of *L. crassilabris* will contribute to study conservation, population genetics, biogeography and further use of this lineage

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Declaration of interest

The authors declare no conflict of interest. The authors alone are responsible for the content and writing of the paper. This work was supported by the grants from National Natural Science Foundation of China (31272290, 31090254 and U1036603) and Chinese Academy of Sciences (KSCX2-EW-Q-12).

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