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Mitochondrial genome of the shorthead catfish (*Pelteobagrus eupogon*): structure, phylogeny, and intraspecific variation

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ABSTRACT. The complete 16,532-nucleotide sequence of the mitochondrial genome of the shorthead catfish (*Pelteobagrus eupogon*) was determined using the long and accurate polymerase chain reaction method, and compared with the mitochondrial genome sequences of 49 other catfish species belonging to the order Siluriformes. The locations of protein-coding genes and ribosomal ribonucleic acids (RNAs) were identified by comparison with known sequences of other catfishes, including *P. fulvidraco* and *P. nitidus*. The *P. eupogon* mitochondrial genome was composed of 13 protein-coding genes, two ribosomal RNAs, 22 transfer RNA genes, and a non-coding control region. The gene order was identical to that of other Siluriformes. Phylogenetic analyses based on mitochondrial 12S ribosomal RNA, 16S ribosomal RNA, and 13 protein-coding gene sequence data sets were carried out to further clarify the relative phylogenetic position of *P. eupogon*, and identify phylogenetic relationships among 24 families of Siluriformes. Phylogenetic analyses Randomized Axelerated Maximum Likelihood (RAxML) 8.0.X were congruent with a basal split of the order into Clupeiformes, Characiformes, Cypriniformes, and Siluriformes, and

supported a closer relationship of *P. eupogon* with Amblycipitidae than Siluridae. We therefore concluded that this species appears to be closely related to the Amblycipitidae. In the phylogenetic tree, the Amblycipitidae appeared as the most basal extant lineage within the Siluriformes, while the Bagridae appeared as the sister group of Cranoglanididae and Pangasiidae. The mitochondrial genome sequence of *P. eupogon* has been deposited in GenBank (accession No. KJ001784).

Key words: Intraspecific variation; Mitochondrial genome; Phylogeny; Shorthead catfish

INTRODUCTION

Mitochondrial DNA is commonly used in population and phylogenetic studies due to its maternal mode of inheritance and relatively low recombination rate (Curole and Kocher, 1999). The mitochondrial DNA (mtDNA) of most animals is a self-replicating, circular DNA molecule, approximately 16 kb long, that codes for 13 mitochondrial proteins, 22 mitochondrial tRNAs, and two mitochondrial specific ribosomal RNAs (12S and 16S rRNA). It also contains DNA regions that control its replication and transcription (control region). From an evolutionary viewpoint, mtDNAs are "small genomes" that co-evolve at their own rate within the organism in which they reside (Peng et al., 2006).

Catfishes (Siluriformes) are widely distributed across all continents of the globe. In China, Siluriformes are composed of 11 families (Chen, 1977), the most widely distributed of which is the Bagridae family that includes the shorthead catfish (*Pelteobagrus eupogon*). Many Bagridae species are economically important in China, and the genetic diversity of wild populations is crucial for artificial culture. However, wild populations of these species have rapidly declined in recent years due to overfishing, pollution, and human other disturbances. Therefore, it is important to assess the genetic diversity of wild populations, to understand the impact that such rapid declines in populations have had. With the recent improvement of molecular techniques, it has become comparatively easier to obtain complete sequences of mitochondrial genomes.

In this study, we analyzed the complete DNA sequence and structure of the mitochondrial genome of shorthead catfish from the Hokiang, a tributary of the Yangtze River. We also assessed phylogenetic relationships within the order Siluriformes in combination using the mitochondrial genomes of other fishes (Table 1). To date, five mitochondrial genomes from four species in the genus *Pelteobagrus* have been reported to GenBank, including two from *P. eupogon* (Table 1). Thus, genetic variation can be analyzed across different geographical populations. Our findings provide a strong basis for evaluating the genetic diversity of catfish species in natural populations.

MATERIAL AND METHODS

Fish samples and DNA extraction

A shorthead catfish (*P. eupogon*) specimen was collected from the Hokiang in Sichuan

Province, China, and identified from morphology as described previously (Wu, 1989). The nuclear and mitochondrial DNA as extracted from muscle tissues using a 3S Spin Genomic DNA Miniprep Kit (Shanghai, China) following the manufacturer's protocol.

Table 1. Mitochondrial genome information for fishes in Siluriformes and other related orders.

Species	GenBank ID	Source
Siluriformes		
Amphilius sp *NM-2010*	AP012002	Nakatani et al. (2011)
Amblydoras gonzalezi	AP012001	Nakatani et al. (2011)
Auchenoglanis occidentalis	AP012005	Nakatani et al. (2011)
Astroblepus sp *NM-2010*	AP012004	Nakatani et al. (2011)
Bunocephalus coracoideus	AP012006	Nakatani et al. (2011)
Chaca bankanensis	AP012008	Nakatani et al. (2011)
Centromochlus perugiae	AP012024	Nakatani et al. (2011)
Cetopsidium sp *NM-2010*	AP012007	Nakatani et al. (2011)
Chrysichthys sp *NM-2010*	AP012009	Nakatani et al. (2011)
Clarias sp *NM-2010*	AP012010	Nakatani et al. (2011)
Corydoras rabauti	AB054128	Saitoh et al. (2003)
Cranoglanis bouderius	AY898626	Peng et al. (2006)
Diplomystes nahuelbutaensis	AP012011	Nakatani et al. (2011)
Glyptothorax fokiensis	JQ917224	Zhou et al. (2012)
Hara jerdoni	AP012012	Nakatani et al. (2011)
Hemibagrus macropterus	JF834542	Zeng et al. (2012)
Helogenes marmoratus	AP012014	Nakatani et al. (2011)
Heteropneustes fossilis	AP012013	Nakatani et al. (2011)
Ictalurus punctatus	AF482987	Waldbieser et al. (2003)
Leiocassis crassilabris	JX867257	Liang et al. (2013)
Leiocassis longirostris	GU596454	Wang et al. (2011)
Liobagrus kingi	Kc193779	Jia et al. (2013a)
Liobagrus marginatoides	Kc473938	Jia et al. (2013b)
Liobagrus nigricauda	KC316116	Jia et al. (2013c)
Liobagrus obesus	DQ321752	Kartavtsev et al. (2007)
Liobagrus reinii	AP012015	Nakatani et al. (2011)
Malapterurus electricus	AP012016	Nakatani et al. (2011)
Pangasianodon gigas	AY762971	Jondeung et al. (2007)
Pangasius larnaudii	AP012018	Nakatani et al. (2011)
Pareutropius debauwi	AP012017	Nakatani et al. (2011)
Pelteobagrus eupogon	JQ734476	Wang et al. (2013)
Pelteobagrus eupogon	KJ001784	Wang et al. (this study)
Pelteobagrus fulvidraco	HM641815	Liang et al. (2012a)
Pelteobagrus nitidus	HM746659	Liang et al. (2012b)
Pelteobagrus vachellii	HM746660	Liang et al. (2011)
Pimelodus pictus	AP012019	Nakatani et al. (2011)
Plotosus japonicas	AP012020	Nakatani et al. (2011)
Pseudobagrus brevicaudatus	JX867256	Liang et al. (2014a)
Pseudobagrus brevicorpus	HM355585	Kim et al. (2011)
Pseudobagrus tokiensis	AB054127	Saitoh et al. (2003)
Pseudobagrus truncatus	JX867259	Liang et al. (2014b)
Pseudobagrus ussuriensis	KC188782	Wan et al. (2013)
Pterygoplichthys disjunctivus	AP012021	Nakatani et al. (2011)
Sciades seemanni	AP012003	Nakatani et al. (2011)
Silurus asotus	JX087351	Wang et al. (2015)
Silurus glanis	AM398425	Vittas et al. (2011)
Silurus lanzhouensis	JF895472	Wang et al. (2012)
Silurus meridionalis	JX087350	Wang et al. (2015)
Synodontis schoutedeni	AP012023	Nakatani et al. (2011)
Trichomycterus areolatus	AP012026	Nakatani et al. (2011)
Tetranematichthys quadrifilis	AP012025	Nakatani et al. (2011)
Outgroup		
Cypriniformes		
Crossostoma lacustre	M91245	Tzeng et al. (1992)
Clupeiformes		
Sardinops melanostictus	AB032554	Inoue et al. (2000)
Characiformes		
Phenacogrammus interruptus	AB054129	Saitoh et al. (2003)

PCR amplification and sequencing

A total of seven long and accurate polymerase chain reaction (LA-PCR) primer pairs were designed by primer premier 5.0 (Table 2), based on the complete mitochondrial genome of *P. fulvidraco* (GenBank ID HM641815). Two short fragments were amplified to link the long fragments based on their sequences.

Table 2. PCR primers for *Pelteobagrus eupogon* mtDNA amplification.

Forward	Sequence (5'-3')	Reverse	Sequence (5'-3')	Size (bp)
Phe-ND2 F	AATCAAAGCATAACACTG	Phe-ND2 R	GCTTATGAATGTGAGGGT	4100
ND1-Trp F	AAACTTCCTGCCCCTGAC	ND1-Trp R	GAATGCTCGCTGGCTTGA	2500
ND2-CO2 F	CAGCGAGCATTCATCTAC	ND2-CO2 R	GAACGGCTTCTACAACAA	2600
Ser-ND3 F	TTACCACCAAACTCACCA	Ser-ND3 R	GAAGAATCGTAGGGAAAA	2500
CO3-ND5 F	TGCCTGATATTGACACTT	CO3-ND5 R	GCAGACTTTCCAGTAGCG	3000
ND5-Cytb F	TCGGCTGAGAAGGAGTAGGA	ND5-Cytb R	TAGGGATGCGAGGGCTGT	2600
Cytb-12S F	CTACAAAGACATTCTAGGGTTC	Cytb-12S R	ATGGCTAAGCATAGTGGG	2000

Long and accurate PCR (LA-PCR) was carried out in 50 µL reactions containing 5 µL 10X LA PCR buffer II, 8 µL 1.5 mM mix dNTPs, 2 µL each primer at 10 µM, 0.5 U LA Taq polymerase (Takara, Dalian China), and approximately 50 ng template DNA. The thermal cycle profile was: pre-denaturation at 94°C for 4 min; 40 cycles of denaturation at 94°C for 60 s; annealing at 50°C for 60 s; extension at 72°C for 5 min; final extension at 72°C for 10 min. The PCR mixture for short fragments was the same as in LA-PCR, with the exception that the first extension time was changed to 1 min in the PCR program. PCR products were sent to Biosune Biotech Company (Beijing) for sequencing with primer walking.

Data analysis

DNA sequences were analyzed using the Sequencing Analysis software v 3.4.1 (Applied Biosystems, USA) and SeqMan v 5.05 (DNASTAR Inc., USA). The locations of protein-coding genes and rRNAs were identified by comparison with known sequences of other catfishes, including *P. fulvidraco* (GenBank ID: HM641815), (Liang et al., 2012a) and *P. nitidus* (GenBank ID: HM746659), (Liang et al., 2012b). Transfer RNA genes were identified by tRNA scan-SE 1.21 (Lowe and Eddy, 1997). Alignment of DNA sequences was performed using ClustalX version 1.81 (Thompson et al., 1997). Phylogenetic relationships were generated from the nucleotide sequences of the mitochondrial genes (including 12S and 16S rRNA genes), and the deduced amino acid sequences of each of the 13 complete mitochondrial protein-coding genes, using RAxML 8.0.X Inference (Stamatakis, 2006). The locations of the protein-coding genes and rRNAs were identified based on known sequences of other catfish species, including *P. fulvidraco* (GenBank ID HM641815) and *P. vachelli* (GenBank ID HM746660) (Liang et al., 2011). The DNA sequences of the 13 mitochondrial protein-coding genes used for analysis of *P. eupogon* are listed in Table 3.

RESULTS AND DISCUSSION

Structure of the mitochondrial genome

The complete mitochondrial genome of *P. eupogon*, with a total length of 16,532 bp,

was sequenced and deposited in GenBank (GenBank ID KJ001784). The gene order and gene-coding strands in *P. eupogon*:two rRNAs, 22 tRNAs, 13 protein-coding genes, and a control region (Table 3 and Figure 1), were identical to those of the Atlantic cod, Javeline goby, and Japanese flying fish (Johansen and Bakke, 1996; Nagase et al., 2005; Kim et al., 2011). The overall base composition of H-strand in *P. eupogon* was as follows: A, 30.3%; C, 28.7%; G, 16.0%; and T, 25.0%.

Table 3. Organization of the *Pelteobagrus eupogon* mitochondrial genome.

Gene	Abbreviation	Strand	Position	Size	Start codon	Stop codon
$tRNA^{Phe}$	F	H	1-72	72		
12S ribosomal RNA	12S	H	73-1026	953		
$tRNA^{Val}$	V	H	1027-1098	72		
16S ribosomal RNA	16S	H	1099-2776	1678		
$tRNA^{Leu}$	L	H	2777-2851	75		
NADH dehydrogenase subunit 1	ND1	H	2852-3826	975	ATG	TAA
$tRNA^{Ile}$	I	H	3831-3902	72		
$tRNA^{Gln}$	Q	L	3903-3973	71		
$tRNA^{Met}$	M	H	3973-4041	69		
NADH dehydrogenase subunit 2	ND2	H	4042-5088	1047	ATG	TAG
$tRNA^{Trp}$	W	H	5087-5157	71		
$tRNA^{Ala}$	A	L	5160-5228	69		
$tRNA^{Asn}$	N	L	5230-5302	73		
$tRNA^{Cys}$	C	L	5334-5400	66		
$tRNA^{Tyr}$	Y	L	5401-5471	71		
Cytochrome c oxidase subunit 1	COI	H	5473-7023	1551	GTG	TAA
$tRNA^{Ser}$	S	L	7024-7094	71		
$tRNA^{Asp}$	D	H	7099-7171	73		
Cytochrome c oxidase subunit 2	COII	H	7186-7876	691	ATG	T-
$tRNA^{Lys}$	K	H	7877-7950	74		
ATP synthase F0 subunit 8	ATP8	H	7952-8119	168	ATG	TAA
ATP synthase F0 subunit 6	ATP6	H	8110-8793	684	ATG	TAA
Cytochrome c oxidase subunit 3	COIII	H	8793-9576	784	ATG	T-
$tRNA^{Gly}$	G	H	9577-9650	74		
NADH dehydrogenase subunit 3	ND3	H	9651-10001	351	ATG	TAG
$tRNA^{Arg}$	R	H	10000-10070	71		
NADH dehydrogenase subunit 4L	ND4L	H	10071-10367	297	ATG	TAA
NADH dehydrogenase subunit 4	ND4	H	10361-11741	1381	ATG	T-
$tRNA^{His}$	H	H	11742-11811	70		
$tRNA^{Ser}$	S	H	11812-11882	71		
$tRNA^{Leu}$	L	H	11883-11955	73		
NADH	ND5	H	11956-13782	1827	ATG	TAA
NADH	ND6	L	13779-14294	516	ATG	TAA
$tRNA^{Glu}$	E	L	14295-14363	69		
Cytochrome	Cyt B	H	14366-15503	1138	ATG	T-
$tRNA^{Thr}$	T	H	15504-15576	73		
$tRNA^{Pro}$	P	L	15575-15644	70		
Displacement loop (control region)	D-loop	H	15645-16532	888		

The protein-coding genes in the *P. eupogon* mitochondrial genome utilize ATG as a start codon, except for COI that initiated with GTG (Table 3). These findings are similar to the dogfish, Chinese longsnout catfish, and Yellow River catfish (Delarbre et al., 1998; Wang et al., 2011; Wang et al., 2012), Nine open reading frames ended with TAA or TAG, and the remaining genes had an incomplete stop codon T (Table 3). In *P. eupogon*, overlaps were found in ATP8-ATP6 (10 bp) and ND4-ND4L (7 bp), which occurred on the same strand, and in ND5-ND6 (5 bp) located on different strands.

The mitochondrial genome of *P. eupogon* contained 22 tRNA genes, ranging from 66 to 75 bp in size. All tRNA genes, except for $tRNA^{Ser}$ (AGY), were predicted to display the typical cloverleaf secondary structure with normal base pairing. Among these tRNA genes, nine

were encoded on L-strand, and the remaining on H-strand. The 12S and 16S rRNA genes in *P. eupogon* had 953 and 1678 bp, respectively. 12S and 16S rRNA genes were located between the $tRNA^{Phe}$ and $tRNA^{Leu}$ genes and separated by the $tRNA^{Val}$ gene, as in *S. meridionalis* and *S. asotus* (Wang et al., 2015) (Figure 1).

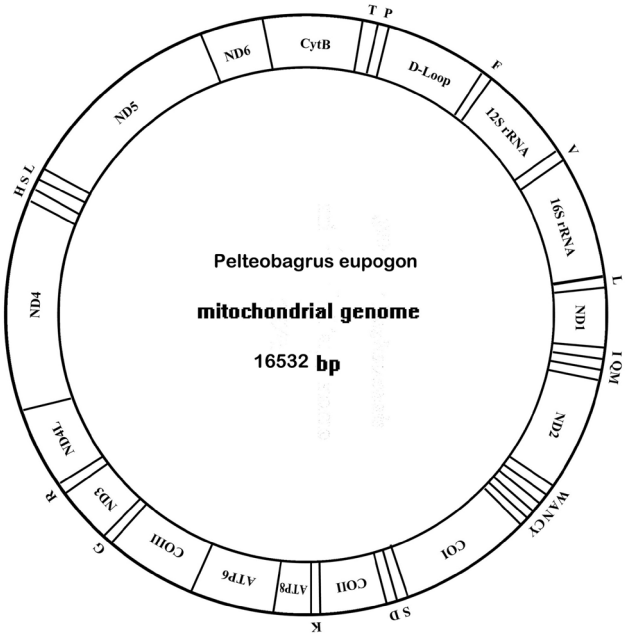

Figure 1. Gene organization of the *Pelteobagrus eupogon* mitochondrial genome. Gene names and abbreviations are listed in Table 3.

The major non-coding segment of the mitochondrial genome is the control region, which regulates replication and transcription (Inoue et al., 2000; Jondeung et al., 2007). The control region in *P. eupogon* was 888 bp long. Similar to other fish species (Kim et al., 2005; Xu et al., 2011), there are three candidates for promoters containing the TATA box conserved sequence block 5'-GTATATATACA-3' (CSB) domains that were found in the control region of P. eupogon: CSB-1 at the 5' end, and CSB-2 and CSB-3 at the 3' end (see annotation in GenBank ID KJ001784).

Phylogenetic analysis

Phylogenetic relationships of *P. eupogon* within the order Siluriformes are shown in Figure 2. Twelve species of catfish in the family Bagridae formed a distinct clade with high bootstrap values (100). This is consistent with the previously determined morphological classification of Bagridae, and its significant differentiation from other families within Siluriformes (Chen, 1977). As expected, the monophyly of Siluriformes, and the inclusion of *P. eupogon* within this order, were highly supported (bootstrap value of 100).

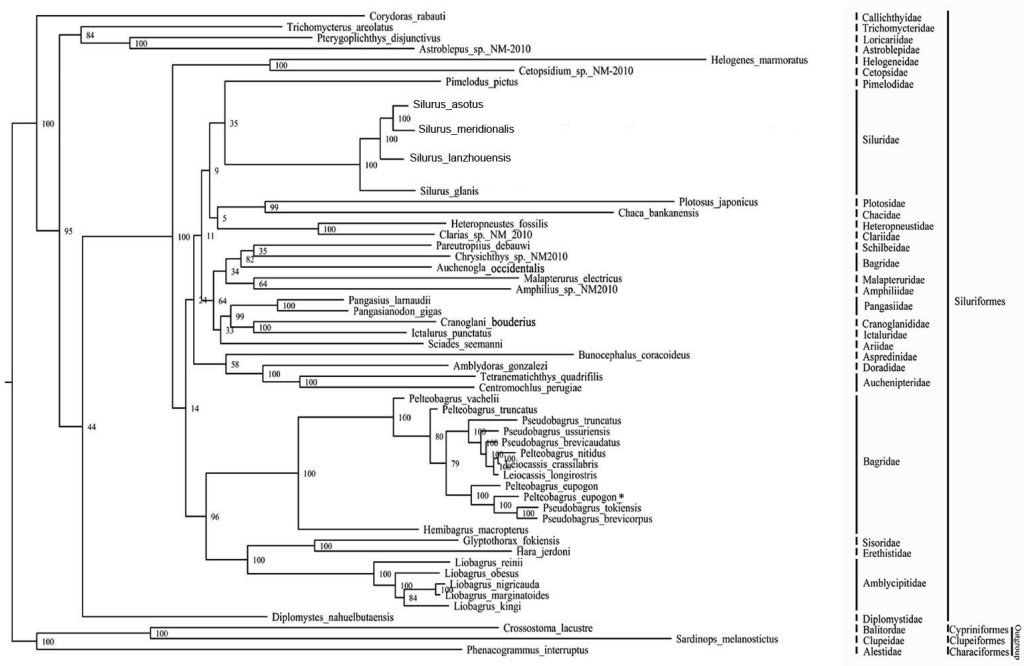

Figure 2. Phylogenetic relationships among Siluriformes as determined by RAxML. Majority rule consensus of maximum likelihood bootstrap measure trees from RAxML inference analysis based on rRNA and protein code data set under the GTR+I+G (General Time Reversible; I: invariable sites; G: gamma distribution) model is shown. Branch lengths are mean estimates. Asterisks indicate specimens used in the present study. Numbers in the nodes are from highest to lowest bootstrap value. The scale in the left lower corner indicates relative branch lengths.

The family of Bagridae and a sister group comprising Amblycipitidae, Sisoridae, and Erethistidae were strongly supported (bootstrap value of 96). These findings are consistent with the previously determined morphological classification that Bagridae is significantly differentiated from other families within Siluriformes. Bagridae was recovered with maximal support (bootstrap value of 100) as a sister group of Amblycipitidae. The Sisoridae and Erethistidae families were recovered as other sister groups. The Bagridae and Amblycipitidae families were closely related, however, *Chrysichthys* sp NM 2010 (Nakatani et al., 2011) and *Auchenoglanis occidentalis* are excluded from Bagridae.

In other branches, the Schilbeidae, Malapteruridae, Amphiliidae, Cranoglanididae, Pangasiidae, Ariidae, and Ictaluridae families formed a distinct group (bootstrap value of 100). Four catfish species in the family Siluridae formed a distinct clade with high bootstrap support (100), in agreement with the previously determined morphological classification, indicating that the family Siluridae is significantly differentiated from other families within Siluriformes. Siluridae was recovered with maximal support as a sister group of *Pimelodus pictus* (Pimelodidae), which is consistent with the previous report (Nakatani et al., 2011). The families of Plotosidae, Chacidae, Heteropneustidae, and Clariidae were also recovered as sister groups, however, these relationships were not as well supported (bootstrap value of 9).

Even though phylogenetic interrelationships of highly diversified families of the order Siluriformes are well studied at the molecular level, the main phylogenetic interrelationships

of families, such as Loricariidae, Trichomycteridae, Astroblepidae, and Callichthyidae, remain largely unresolved. *Corydoras rabauti* (Callichthyidae), which is assigned to the suborder Loricarioidei, was placed as a sister group to all other analyzed Siluriformes. The family Callichthyidae is an independent clade in the Siluriformes. The phylogenetic relationship of the Siluriformes families obtained in this study were similar to another study based on the entire mitochondrial genome, excluding the control region (Delarbre et al., 1998). At a higher taxonomic level, the monophyly of Otophysi (Cypriniformes, Gymnotiformes, Characiformes, and Siluriformes) was highly supported (bootstrap value of 100) by all methods of phylogenetic inference. We inferred therefore that Siluriformes originate from Characiformes. The monophyly of the different orders within Ostariophysi is well supported on morphological grounds.

Nucleotide variation

When the mitochondrial genome of *P. eupogon* obtained in the present study was compared with two others submitted to GenBank (Table 4), among the 16589 bp aligned sequences, 9.9% of the sites were variable. The rRNA genes showed 11.3% variable sites, and tRNAs were fairly conserved with 3.2% variable sites. Meanwhile, the control region was more variable at 15.4%. The percentages of variable sites in all 13 protein-coding genes ranged from 2.3% (COXII) to 19.1% (ND1), with an average of 10.1% (Table 4). The specimen of *P. eupogon* in this study was sampled from the Hokiang, the upstream branch of the Yangtze River in Sichuan Province (China), whereas the precise location of the specimen used for comparison was not available from GenBank (GenBank ID JQ733476). However, the intraspecific variation between the two specimens is considerable, and may even suggest that the two specimens are different species.

Table 4. Intraspecific variation of mitochondrial genomes of two *Pelteobagrus eupogon* individuals (GenBank ID KJ001784 and JQ734476).

	Length of aligned sequence	Number of variable sites	Percentage of variable sites (%)
All sites	16,589	1,640	9.9
tRNAs	1,570	51	3.2
rRNAs	2,647	298	11.3
Control region	928	143	15.4
Protein-coding genes	11,384	1,149	10.1
ND1	975	186	19.1
ND2	1,047	126	12.0
COX1	1,551	51	3.3
COX2	691	15	2.3
ATP8	168	5	2.9
ATP6	684	19	2.8
COX3I	784	75	9.6
ND3	351	17	4.8
ND4L	297	38	9.4
ND4	1,381	199	14.4
ND5	1,827	223	12.2
ND6	516	64	12.4
CytB	1,138	141	12.4

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REFERENCES

Chen XL (1977). A Review of the Chinese Siluridae. *Hydrobiol. Collected Papers* 197-216.

Curole JP and Kocher TD (1999). Mitogenomics: digging deeper with complete mitochondrial genomes. *Trends Ecol. Evol.* 14: 394-398. http://dx.doi.org/10.1016/S0169-5347(99)01660-2

Delarbre C, Spruyt N, Delmarre C, Gallut C, et al. (1998). The complete nucleotide sequence of the mitochondrial DNA of the dogfish, *Scyliorhinus canicula. Genetics* 150: 331-344.

Inoue JG, Masaki M, Katsumi T and Mutsumi N (2000). Complete mitochondrial DNA sequence of the Japanese sardine, *Sardinops melanostictus. Fish. Sci.* 66: 924-932. http://dx.doi.org/10.1046/j.1444-2906.2000.00148.x

Jia XY, Li YW, Wang DQ, Tian HW, et al. (2013a).The complete mitochondrial genome of *Liobagrus kingi* (Teleostei, Siluriformes: Amblycipitidae). *Mitochondr. DNA* 24: 323-325.

Jia XY, Li YW, Wang DQ, Tian HW, et al. (2013b).The mitogenome of *Liobagrus marginatoides* (Teleostei, Siluriformes:Amblycipitidae). *Mitochondr. DNA* 24: 645-647.

Jia XY, Li YW, Wang DQ, Li SH, et al. (2013c).The mitogenome of *Liobagrus nigricauda* (Teleostei, Siluriformes:Amblycipitidae). *Mitochondr. DNA* 24: 373-375.

Johansen S and Bakke I (1996). The complete mitochondrial DNA sequence of Atlantic cod (*Gadus morhua*): relevance to taxonomic studies among codfishes. *Mol. Mar. Biol. Biotechnol.* 5: 203-214.

Jondeung A, Sangthong P and Zardoya R (2007). The complete mitochondrial DNA sequence of the Mekong giant catfish (*Pangasianodon gigas*), and the phylogenetic relationships among Siluriformes. *Gene* 387: 49-57. http://dx.doi.org/10.1016/j.gene.2006.08.001

Kartavtsev YP, Jung SO, Lee YM, Byeon HK, et al. (2007).Complete mitochondrial genome of the bullhead torrent catfish, *Liobagrus obesus* (Siluriformes, Amblycipitidae): Genome description and phylogenetic considerations inferred from the Cyt b and 16S rRNA genes. *Gene* 396: 13-27.

Kim IC, Jung SO, Lee YM, Lee CJ, et al. (2005). The complete mitochondrial genome of the rayfish *Raja porosa* (Chondrichthyes, Rajidae). *DNA Seq.* 16: 187-194. http://dx.doi.org/10.1080/10425170500087975

Kim SK, Choi EH, Hong KB, Jang KH, et al. (2011). Complete mitochondrial genome of the Korean stumpy bullhead *Pseudobagrus brevicorpus* (Siluriformes, Bagridae). *Mitochondrial DNA* 22: 44-46. http://dx.doi.org/10.3109/19401736.2011.597388

Liang HW, Li L, Li Z, Zou GW, et al. (2011). Phylogenetic analysis of Silurus meridionalis based on the complete mitochondrial DNA sequence. *J. Northwest A & F Univ.* 39: 80-88.

Liang HW, Cao L, Li Z, Zou GW, et al. (2012a). Mitochondrial genome sequence of the shining catfish (*Pelteobagrus nitidus*). *Mitochondrial DNA* 23: 280-282. http://dx.doi.org/10.3109/19401736.2012.683185

Liang HW, Hu GF, Li Z, Zou GW, et al. (2012b). Mitochondrial DNA sequence of yellow catfish (*Pelteobagrus fulvidraco*). *Mitochondrial DNA* 23: 170-172. http://dx.doi.org/10.3109/19401736.2012.668899

Liang HW, Li Z and Zou W (2013). Complete mitochondrial DNA genome of *Leiocassis crassilabris* (Siluriformes: Bagridae). *Mitochondr. DNA* 24: 222-224.

Liang HW, Meng Y, Li Z, Zhang Y, et al. (2014a). Complete mitochondrial DNA genome of *Pseudobagrus brevicaudatus* (Siluriformes: Bagridae). *Mitochondr. DNA* 25: 179-180.

Liang HW, Meng Y, Li Z, Zhang Y, et al. (2014b). Complete mitochondrial DNA genome of *Pseudobagrus truncatus* (Siluriformes: Bagridae). *Mitochondr. DNA* 25: 179-180.

Lowe TM and Eddy SR (1997). tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25: 955-964. http://dx.doi.org/10.1093/nar/25.5.0955

Nagase M, Aimi T, Suginaka K, Kitamoto Y, et al. (2005). Complete mitochondrial DNA sequence of the Japanese flying fish *Cypselurus hiraii. Fish. Sci.* 71: 914-923. http://dx.doi.org/10.1111/j.1444-2906.2005.01045.x

Nakatani M, Miya M, Mabuchi K, Saitoh K, et al. (2011). Evolutionary history of Otophysi (Teleostei), a major clade of the modern freshwater fishes: Pangaean origin and Mesozoic radiation. *BMC Evol. Biol.* 11: 177. http://dx.doi.org/10.1186/1471-2148-11-177

Peng Z, Wang J and He S (2006). The complete mitochondrial genome of the helmet catfish *Cranoglanis bouderius* (Siluriformes: Cranoglanididae) and the phylogeny of otophysan fishes. *Gene* 376: 290-297. http://dx.doi.org/10.1016/j.gene.2006.04.014

Saitoh K, Miya M, Inoue JG, Ishquro NB, et al. (2003). Mitochondrial genomics of ostariophysan fishes: perspectives on phylogeny and biogeography. *J. Mol. Evol.* 56: 464–472.

Stamatakis A (2006). RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 22: 2688-2690. http://dx.doi.org/10.1093/bioinformatics/btl446

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, et al. (1997). The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res.* 25: 4876-4882. http://dx.doi.org/10.1093/nar/25.24.4876

Tzeng CS, Hui CF, Shen SC. (1992). The complete nucleotide sequence of the *Crossostoma lacustre* mitochondrial genome: conservation and variations among vertebrates. *Nucleic Acids Res.* 20: 4853–4858.

Vittas S, Drosopoulou E, Kappas I, Pantzartzi CN, et al. (2011). The mitochondrial genome of the European catfish *Silurus glanis* (Siluriformes, Siluridae). *J. Biol. Res.* 15: 25-35.

Waldbieser GC, Bilodeau AL and Nonneman DJ (2003). Complete sequence and characterization of the channel catfish mitochondrial genome. *DNA Seq.* 14: 265-277.

Wan Q, Tao G, Cheng Q, ChenY, et al. (2013). The complete mitochondrial genome sequence of *Pseudobagrus ussuriensis* (Siluriformes: Bagridae). *Mitochondr. DNA* 24: 333-335.

Wang J, Shen T, Ju J and Yang G (2011). The complete mitochondrial genome of the Chinese longsnout catfish *Leiocassis longirostris* (Siluriformes: Bagridae) and a time-calibrated phylogeny of ostariophysan fishes. *Mol. Biol. Rep.* 38: 2507-2516. http://dx.doi.org/10.1007/s11033-010-0388-4

Wang QR, Xu C, Xu CR and Wang RJ (2012). Mitochondrial genome structure of yellow river catfish (*Silurus lanzhouensis*) and phylogenetic analysis. *Acta Sci. Nat. Univ. Pekinensis.* 28: 376-380.

Wang XY, Cao L, Liang HW, Li Z, et al. (2013). Mitochondrial genome of the Shorthead catfish (*Pelteobagrus eupogon*). *Mitochondr. DNA* 24: 1-2.

Wang QR, Xu C, Xu CR and Wang RJ (2015). Complete mitochondrial genome of the Southern catfish (*Silurus meridionalis* Chen) and Chinese catfish (*S. asotus* Linnaeus): Structure, phylogeny, and intraspecific variation. *Genet. Mol. Res.* 14: 18198-18209. http://dx.doi.org/10.4238/2015.December.23.7

Wu L (1989). The Fishes of Guizhou Province. People's Publishing House of Guizhou, Guiyang.

Xu TJ, Cheng YZ, Sun YN, Shi G, et al. (2011). The complete mitochondrial genome of bighead croaker, *Collichthys niveatus* (Perciformes, Sciaenidae): structure of control region and phylogenetic considerations. *Mol. Biol. Rep.* 38: 4673-4685. http://dx.doi.org/10.1007/s11033-010-0602-4

Zeng Q, Ye H, Peng Z and Wang Z (2012). Mitochondrial genome of *Hemibagrus macropterus* (Teleostei, Siluriformes). *Mitochondr. DNA* 23: 355-357.

Zhou C, Wang D, Yu M and He S (2012). The complete mitochondrial genome of *Glyptothorax fukiensis fukiensis* (Teleostei, Siluriformes: Sisoridae). *Mitochondr. DNA* 23: 414-416.