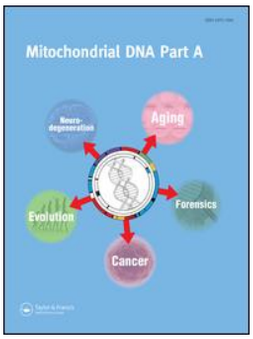

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of a cyprinid fish; *Metzia longinasus* (Teleostei, Cypriniformes)

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Abstract

The long polymerase chain reaction and primer walking method were applied for the sequencing of the complete mitochondrial genome sequence of a cyprinid species (*Metzia longinasus*) collected from the Hongshuihe River of the Pearl River drainage, Guangxi Province in China. It is 16,614 bp in length, containing 2 rRNA, 22 tRNA, 13 protein-coding genes and 1 control region generally found in most vertebrates. Most of the mitochondrial genes are encoded on the heavy strand except for eight tRNA and ND6 genes. The base composition of this genome was 31.9% A, 26.2%C, 26.2%T and 15.7%G, showing a lower level of G (15.7%) and a slighter AT bias (58.1%). This is the 2nd completely sequenced mitogenome from genus *Metzia*. The mtDNA sequence of *M. longinasus* shared 93% sequence similarity with that of *M. formosae* and it could contribute to a better solution of its phylogenetic position within cyprinid fishes based on the complete mitogenomic data.

Keywords

Cyprinidae, Cypriniformes, *Metzia longinasus*, mitogenome

History

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Metzia longinasus (Teleostei, Cypriniformes) is a newly discovered species from Hongshuihe River of the Pearl River drainage at Du'an County, Guangxi Province in China (Gan et al., 2009). Here, we obtained its complete mitochondrial genome based on the long PCR technique (Miya & Nishida, 1999) with the universal primers used in previous study (Wang et al., 2011). We annotated the genome sequence using DOGMA (Wyman et al., 2004; Austin, TX) and the GenBank accession number for the species is KF955011.

The length of the complete mitochondrial genome of *M. longinasus* is 16,614 bp and the gene order and structure are fairly similar to most other fishes (Huang et al., 2012; Peng et al., 2006). It is a circular molecule that consists of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and 1 control region (Table 1). The coding strands of these genes are also identical to other fishes: ND6 gene and eight tRNA genes (tRNA-Gln, Ala, Asn, Cys, Tyr, Ser, Glu and Pro) by L-strand and the others by H-strand.

Currently, there is only one complete mitogenome sequence data from the genus *Metiza* available for comparison (*M. formosae*; Lin et al., 2013). The total length of the mitogenome for the two species was identical. The initiation codon and stop codon of the 13 protein-coding genes in the two mitogenomes were also identical except for the incomplete stop codon of COIII which was ''T'' for *M. formosae*, while for *M. longinasus* it was ''TA''. As for the other genes, five protein-coding genes (ND2, COII, ND3, ND4 and cytb) were terminated with incomplete stop codon ''T'' or ''TA'' and the typical stop

Table 1. Characteristics of the mitochondrial genome of *Metzia longinasus*.

Gene/Element	From	To	Length (bp)	Codon Start	Codon Stop	Intergenic nucleotides*	Strand†
tRNA-Phe	1	69	69			–	H
12S rRNA	70	1027	958			0	H
tRNA-Val	1028	1099	72			4	H
16S rRNA	1104	2787	1684			0	H
tRNA-Leu (UUR)	2788	2863	76			1	H
ND1	2865	3839	975	ATG	TAA	4	H
tRNA-Ile	3844	3915	72			−2	H
tRNA-Gln	3914	3984	71			1	L
tRNA-Met	3986	4054	69			0	H
ND2	4055	5099	1047	ATG	T−−	0	H
tRNA-Trp	5100	5170	71			0	H
tRNA-Ala	5171	5240	70			1	L
tRNA-Asn	5242	5314	73			32	L
tRNA-Cys	5347	5414	68			1	L
tRNA-Tyr	5416	5486	71			1	L
COI	5488	7038	1551	GTG	TAA	0	H
tRNA-Ser (UCN)	7039	7109	71			3	L
tRNA-Asp	7113	7186	74			13	H
COII	7200	7890	693	ATG	T−−	0	H
tRNA-Lys	7891	7966	76			1	H
ATP8	7968	8132	165	ATG	TAG	−7	H
ATP6	8126	8809	684	ATG	TAA	−1	H
COIII	8809	9593	786	ATG	TA–	0	H
tRNA-Gly	9594	9665	72			0	H
ND3	9666	10,014	351	ATG	T−−	0	H
tRNA-Arg	10,015	10,084	70			0	H
ND4L	10,085	10,381	297	ATG	TAA	−7	H
ND4	10,375	11,756	1383	ATG	TA–	0	H
tRNA-His	11,757	11,825	69			0	H
tRNA-Ser (AGY)	11,826	11,894	69			1	H
tRNA-Leu (CUN)	11,896	11,968	73			0	H
ND5	11,969	13,804	1836	ATG	TAA	−4	H
ND6	13,801	14,322	522	ATG	TAA	0	L

(*continued*)

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Table 1. Continued

Gene/Element	From	To	Length (bp)	Codon Start	Codon Stop	Intergenic nucleotides*	Strand†
tRNA-Glu	14,323	14,391	69			4	L
cyt b	14,396	15,536	1143	ATG	T– –	0	H
tRNA-Thr	15,537	15,608	72			0	H
tRNA-Pro	15,609	15,677	69			0	L
D-loop	15,678	16,614	937			0	–

Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between adjacent genes.
†H: heavy strands; L: light strands.

codon ''TAA'' was used for ND1, COI, ATP6, ND4L, ND5, and ND6, while the ATP8 was terminated by ''TAG''. Six genes/segments (12S rRNA, 16S rRNA, tRNA-Ala, tRNA-Asp, tRNA-Pro and D-loop) are variant at length, while the remaining genes of the two species had the same sequence length. Meanwhile, MEGA5 (Tamura et al., 2011; Tempe, AZ) was used to analyze the variable sites between the two sequences. There were 1140 substitution sites between them with approximately 6.9% sequence divergence.

Based on the previous studies (Dai & Yang, 2003; Gaubert et al., 2009; Yue & Luo, 1996), the phylogenetic position of the genus *Metiza* was not well resolved. Furthermore, the monophyly of *Meztia* was also questioned by Shibukawa et al. (2012). Thus we expected that the complete mitochondrial genome sequence of *M. longinasus* could make some contributions towards the phylogeny reconstruction of *Metiza*.

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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.

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