MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Freshwater Catfish *Rita rita* (Siluriformes, Bagridae)

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Abstract

Complete mitochondrial genome of Catfish, *Rita rita*, was isolated by LA PCR (TakaRa LAtaq, Dalian, China); and sequenced by Sanger's method to obtain the complete mitochondrial genome, which is listed critically endangered and red listed species. The complete mitogenome was 16,475 bp in length and contains 13 typical vertebrate protein-coding genes, 2 rRNA and 22 tRNA genes. The whole genome base composition was estimated to be 33.40% A, 27.41% C, 14.25% G and 24.92% T. The complete mitochondrial genome of catfish, *Rita rita* provides the basis for genetic breeding and conservation studies.

Freshwater Catfish Rita (*Rita rita* H.1822), belongs to family Bagridae and genus Rita. This fish was found in abundant quantity about two decades ago in Afghanistan, Pakistan, India, Nepal, Bangladesh and Mayanmar (Tripathi, 1996). It is an important commercial fish due to its meat taste (Anonymous, 2000; Dubey, 1994; Khan et al., 1988; Lal & Dwevedi, 1969; Rahman 2005). However, it has become critically endangered and red listed. Recently, genetic diversity of *Rita rita* had been reduced significantly due to decreasing population size (IUCN, 2000, 2012, 2013; Mishra et al., 2009). Considering its economic importance and population reduction, it is necessary to protect this species by developing genetic techniques. Mitochondrial DNA is a useful molecular marker for population genetic and phylogenetic studies for its fast evolutionary rate (Peng et al., 2006). Hence, mitochondria genome of this important fish will be a helpful tool to protect this indigenous species and increase its genetic resources. The *Rita rita* was sampled from Indus River Sindh, Pakistan, on July 25, 2012. Total DNA was isolated by Qiagen (Valencia, CA) DNeasy Blood and Tissue kit Mitogenome was amplified in two large overlapping fragments by long PCR (TakaRa LAtaq, Dalian, China), using the specific primers designed by previously reported two genes of *Rita rita* (GenBank accession numbers: EU490921.1; FJ459396.1). The complete *Rita rita* mitogenome sequence (GenBank accession number: KF670723) is 16,475 bp in length. The overall characteristics, including its overall organization and the gene arrangement pattern, are identical to that of the typical vertebrate mitogenome. The complete mitogenome contains 13 protein-coding genes, 2 rRNA, 22 tRNA genes and 1 putative control region (Figure 1). The average base composition of the Rita complete mitogenome is 33.40% for A, 27.41% for C, 14.25% for G and 24.92% for T. All protein-coding genes except (*ND6*) were encoded on heavy strand (H strand). Fourteen tRNA genes were encoded on heavy strand and remainder were encoded on light strand (L strand). The organization of *Rita rita* mitochondrial genome conforms to the consensus of gene order of other fish mitochondrial genome (Figure 1). Eight protein-coding genes use ATG as start codon (*ND1*, *COX2*, *ATPase 8*, *ATPase 6*, *COX3*, *ND3*, *ND4* and *ND5*), two genes use ATA (*cytb* and *ND2*), two genes use GTG (*COX1* and *ND6*) and one gene use TTA (*DN4L*). Five open reading frames end with TAA (*ND1*, *COXI*, *ATPase 8*, *ND4L* and *DN5*); four genes use incomplete stop codon as T** (*ND2*, *ATPase 6*, *ND3* and *cytb*). Two genes (*COX2* and *COX3*) use AGA, one gene (*ND4*) uses AGG, and one gene (*ND6*) uses TAG as stop codon, respectively. The OL (putative light strand origin of replication) is 33 bp in length from 5306 to 5339 bp between *tRNA^Asn* and *tRNA^Cys*. The control region D-loop is located between *tRNA^pro* and *tRNA^phe* with 822 bp in length.

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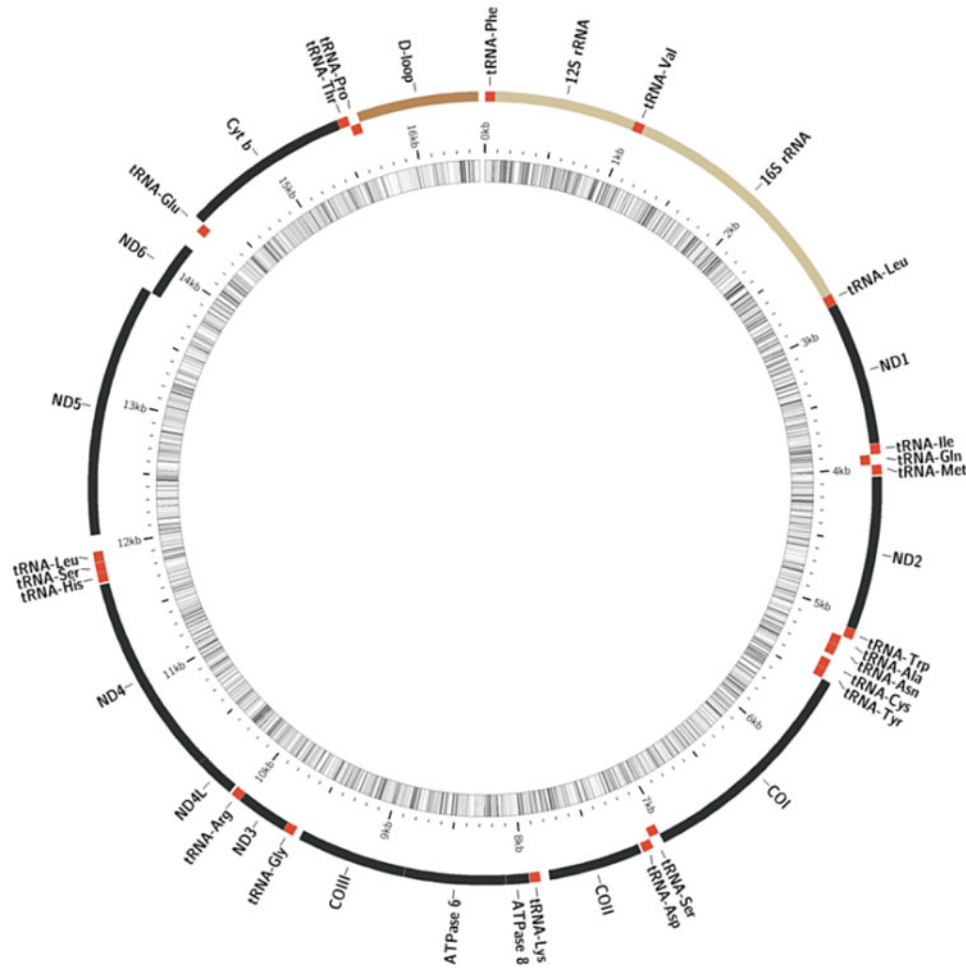
Figure 1. Gene map of the mitochondrial genome of the Catfish *Rita rita*. Black shaded parts represent protein-coding genes. Red and light brown shaded parts represent non-coding regions. Brown part represents control region.

Acknowledgements

Declaration of interest

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