The complete mitochondrial genome of the *Garra tibetana* (Cypriniformes: Cyprinidae)

Chi Zhang\(^a\), Wanliang Wang\(^a\), Jianshe Zhou\(^a\), Meiqun Chen\(^a\) and Xuekai Han\(^b\)

\(^a\)Tibet Academy of Agricultural and Animal Husbandry Sciences, Institute of Fisheries Science, Lhasa, P. R. China; \(^b\)Asian Regional Artemia Reference Center, Tianjin University of Science and Technology, Tianjin, China

**ABSTRACT**

The *Garra tibetana*, an important economic fish belonging to the genus *Garra*, family Cyprinidae, is mainly distributed in Tibet with rare biological resources. Here, we sequenced and characterized the complete mitochondrial genome of *G. tibetana* for the first time, and the results showed that the total length of *G. tibetana* mitogenome was 16,861 bp, consisting of 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes, and 2 control regions. Unlike the typical mitochondrial genome organization in vertebrate, the D-loop region was separated into two part by a tRNA\(^{Pro}\) gene. To further explore the phylogenetic relationship of the *G. tibetana*, we constructed the phylogenetic tree and verified that the *G. tibetana* was a new species of the genus *Garra* and had a closer relationship with *Garra kempi*. This study not only provided valuable evidence on phylogenetic relationship of the *G. tibetana* at the molecular level, but also provided an essential resource for further population genetics research and germplasm conservation on this species.

The genus *Garra* Hamilton 1822 is a group of freshwater fishes, which are of great economic value and widely distributed in southern Asia and northeast Africa. At present, 20 different species of *Garra* have been recognized from the Brahmaputra River basin, of which there are four species in China, namely, *Garra tibetana*, *G. dengba*, *G. motuoensis*, *G. yajiangensis* (Deng et al. 2018; Gong, Freyhof et al. 2018; Gong, Deng et al. 2018). These species mainly inhabited in the rocky or turbulent rivers, and its food includes phyto-detritus in open water habitats, as well as periphyton in substrate-surface habitats (Nebeshwar et al. 2009). Since *G. tibetana* and *Garra kempi* Hora 1921 have many similarities in morphological characterization, *G. tibetana* was misidentified as *G. kempi* for a long period. In recent years, the mitogenome is widely used in the study of population genetics and molecular phylogenetics due to its high substitution rate, non-recombination and nature of maternal inheritance (Galtier et al. 2009). However, so far, there were only six reports about the complete mitochondrial genome of *Garra* and their corresponding molecular evolutions are still limited. Therefore, the complete mitogenome of *G. tibetana* is reported here, which could provide important genomic information for the studies of the evolution relationship and population genetics of genus *Garra*.

Twenty-six fish specimens were collected from lower reach of Brahmaputra River (95°16′56″N, 29°17′52.8″E) in Tibet, China. All voucher specimens were deposited at the Museum of Aquatic Organisms at the Institute of Fisheries Science, Tibet Academy of Agricultural and Animal Husbandry Sciences, Tibet, China. In this study we used the specimen with accession number: 20190006JK. The neighbor-joining (NJ) tree of the *G. tibetana* was constructed using Mega7.0 (Kumar et al. 2016).

The mitogenome of *G. tibetana* was completely sequenced, and our findings revealed that the circular genome was 16,861 bp (GenBank MG999836.1). The whole mitochondrial genome consisted of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S and 16S rRNA), and 2 control regions (D-loop and O\(_{2}\)). Base frequency of the whole mtDNA region was A = 32.3%, T = 26.1%, C = 26.2%, and G = 15.4%, with a relatively lower level of G and a slight A + T bias of 58.4%. The 13 mRNAs contained three start codons, two termination codons, and six overlap regions. The 22 tRNA scattered among the whole mitochondrion, and they were in the range from 68 (tRNA\(^{Pro}\)) to 76 (tRNA\(^{Lys}\) and tRNA\(^{Glu}\)) in length (table1). The D-loop was 1199 bp in length and separated into two parts by a tRNA\(^{Pro}\) gene, which is very similar to *G. kempi* mitochondrial genome (Li et al. 2016).

To further explore the phylogenetic and taxonomic status of *G. tibetana*, a neighbor-joining tree was constructed with 13 species from four genus. Phylogenetic analyses verified that the *G. tibetana* is a member of the genus *Garra* and has a much closer relationship with *G. kempi* compared to other species of *Garra* (*Garra spliota*, *Garra qiaojensis*, *Garra rufa*, *Garra orientalis*, and *Garra flavatra*) (Figure 1).

**CONTACT** Wanliang Wang, 271616863@qq.com, Tibet Academy of Agricultural and Animal Husbandry Sciences, Institute of Fisheries Science, Lhasa, 850000, P. R. China

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Our findings provided valuable evidence on phylogenetic relationship of the *G. tibetana* at the molecular level. Moreover, the complete mitogenome of *G. tibetana* could provide an effective tool for population genetics and evolutionary biology study, as well as the germplasm resources conservation related to this species.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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