

## Complete mitochondrial genome of two endemic species to China: *Discocheilus wui* and *Discocheilus wuluoheensis* (Cypriniformes, cyprinidae)

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### ABSTRACT

The genus *Discocheilus* is endemic to China and only distributed in the Pearl River. The complete mitochondrial genome of *Discocheilus wui* and *Discocheilus wuluoheensis* were successfully sequenced in this study. The complete mitochondrial genomes of these two species are 16,589 bp and 16,587 bp in length, respectively. They both consist of 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes and a control region. The gene compositions and genome organizations of the two species are similar to other fish. The complete mitochondrial genome sequence of these two species will contribute to reveal the genetic backgrounds for their conservation.

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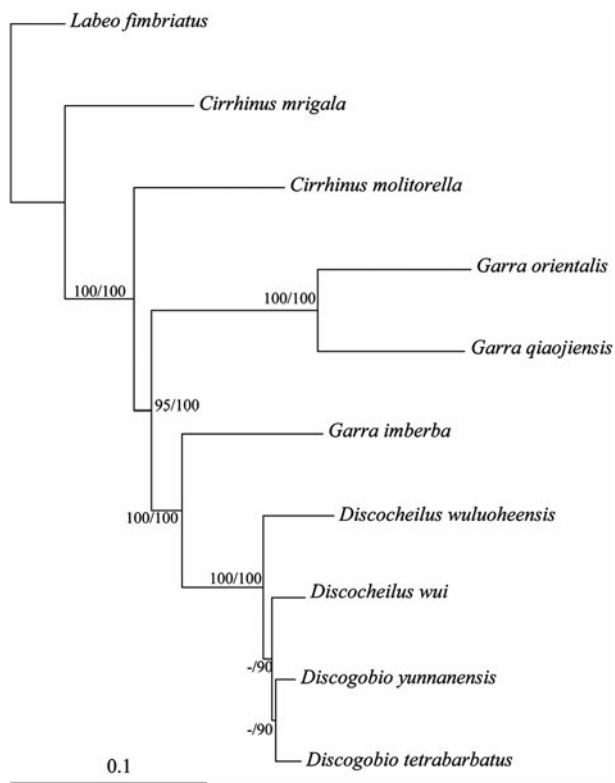
### KEYWORDS

*Discocheilus wui*;  
*Discocheilus wuluoheensis*;  
complete mitochondrial  
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The genus *Discocheilus* is a member of subfamily Labeoninae in the family Cyprinidae and is endemic to the Pearl River in China (Li et al. 1996; Zhang et al. 2000). Up to now, only a few studies involved the phylogenetic positions of *Discocheilus wui* and *Discocheilus wuluoheensis* have been reported (Zheng et al. 2010; 2016). The complete mitochondrial genomes of the two species were presented in this study. The specimens sequenced in this study are deposited in the Kunming Institute of Zoology, Chinese Academy of Sciences. The sequences were deposited in GenBank with the accession numbers KX840358 and KX840359, respectively. *Discocheilus wui* (voucher no. KIZ20080045) was collected from Leye, Guangxi (24°40'03.6"N, 106°25'13.5"E); and *Discocheilus wuluoheensis* (voucher no. KIZ20080429) was collected from Luoping, Yunnan (24°45'49.1"N, 104°29'46.0"E).

Total DNA was extracted from the fin using the standard phenol-chloroform method, and pair-end sequencing were generated from Illumina Hiseq 2500. The DNA sequences were annotated using MitoAnnotator (Iwasaki et al. 2013), and nucleotide composition were calculated by MEGA7 (Kumar et al. 2016). The gene compositions and genome organizations of the two species are similar to other fish (Miya et al. 2003). The complete mitochondrial genome of *D. wui* and *D. wuluoheensis* are 16,589 and 16,587 bp in length, respectively. They both include 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes, and a control region (D-loop).

The overall base composition of the heavy strand are: A 32.2%, T 26.6%, C 26.0%, G 15.3% for *D. wui*, and A 32.1%, T 26.6%, C 25.9%, G 15.4% for *D. wuluoheensis*. Both AT contents are higher than GC contents, which are consistent with other fishes (Miya et al. 2003). All genes of these two species are encoded on the H-strand, with the exception of one protein-coding gene (ND6) and eight tRNA genes. Two overlaps were identified between protein-coding genes (ATP8–ATP6, and ND4L–ND4) on the same strand. Although ND5 and ND6 also overlapped, they were encoded on the opposite strands. All protein-coding genes start with an ATG codon except for COI with a GTG start codon. Six genes end with complete stop codon (TAA) while seven genes have incomplete stop codon (TA or T), which were presumably completed as TAA by post-transcriptional polyadenylation (Nardi et al. 2001). All tRNA genes of two species ranged from 66 bp to 76 bp and 67 bp to 76 bp in length respectively. The 12S and 16S rRNA genes were 952 bp and 1684 bp in length for *D. wui*, while 952 bp and 1685 bp for *D. wuluoheensis* respectively. The control regions are 934 bp and 931 bp in length, respectively. The phylogenetic tree showed that *D. wui* and *D. wuluoheensis* are most closely related to the genus *Discogobio* (Figure 1), and the results are consistent with that of several mitochondrial genes (Zheng et al. 2010). The data of mitochondrial genome combined with the nuclear genes will be better to understand the genetic relationships of these endemic



**Figure 1.** Molecular phylogeny of *Discocheilus* and the related species in Labeoninae based on complete mitochondrial genome. The phylogenetic tree is constructed with maximum likelihood and Bayesian method. The nodal numbers are ML bootstrap and BPP values, respectively. Only values above 50% are given. The accession number for tree construction is listed as follows: *Labeo fimbriatus* (KP025676), *Cirrhinus mrigala* (JQ838173), *Cirrhinus molitorella* (KF160921), *Garra imberba* (KM255666), *Discogobio yunnanensis* (KJ997760), *Discogobio tetrabarbatus* (KJ669372), *Garra orientalis* (JX290078), and *Garra qiaojiensis* (KF727438).

fish. The complete mitochondrial genome sequence of these two species will contribute to reveal the genetic backgrounds for their conservation.

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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