

KU896808. The mitochondrial genome encoded 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs and a non-coding control region, as those found in other *Gymnocypris* species (Qi et al. 2013; Qiao et al. 2014; Zhang et al. 2016). The nucleotide composition of the genome of *G. potanini firmispinatus* is A 28.4%, T 27.2%, G 18.4%, and C 26.0%, with a low A+T content of 56.6%. Except for the *nad6* and eight tRNA genes (tRNA-Gln, tRNA-Aln, tRNA-Asn, tRNA-Lys, tRNA-Tyr, tRNA-SerUCN, tRNA-Glu, and tRNA-Pro) encoded on the light-strand, all others genes were encoded on the heavy-strand. This is a typical gene arrangement conforming to the other *Gymnocypris* species and vertebrate consensus (Qi et al. 2013; Qiao et al. 2014).

All genes use ATG as a start codon, except *cox1* use GTG, which was also discovered in other *Gymnocypris* species (Qi et al. 2013; Qiao et al. 2014). Most open reading frames ended with two types of complete stop codons TAA and TAG, whereas few genes (including *cox2*, *nd4* and *cob*) had an incomplete stop codon: T—. These results showed that the PCGs are stable among the *Gymnocypris* species.

Based on combined nucleotide sequence data of 12 heavy-strand protein-coding genes of *G. potanini firmispinatus*, and together with the sequences of other *Gymnocypris* fishes, phylogenetic trees were constructed using the ME methods (Figure. 1). All *Gymnocypris* species had close relationship, *G. przewalskii*, *G. przewalskii ganzihonensis*, and *G. eckloni* were monophyletic in the trees, which were consistent based on the mitochondrial DNA cytochrome b gene or mitogenoma sequences. In agreement with the findings of previous molecular analyses (Qi et al. 2013;

Zhang et al. 2015), *G. dobula* and *G. namensis* also had a close genetic relationship, however, which had a closer distance with *G. eckloni chilianensis* as the subspecies of *G. eckloni* (Zhang et al. 2015). Thus, the mitochondrial genome data and phylogenetic analysis of the *G. potanini firmispinatus* can enrich the evolution research of *Gymnocypris*.

Disclosure statement

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

References

- Qi D, Chao Y, Zhao L, Shen Z, Wang G. 2013. Complete mitochondrial genomes of two relatively closed species from *Gymnocypris* (Cypriniformes: Cyprinidae): genome characterization and phylogenetic considerations. *Mitochondrial DNA*. 24:260–262.
- Qiao H, Cheng Q, Chen Y. 2014. Characterization of the complete mitochondrial genome of *Gymnocypris namensis* (Cypriniformes: Cyprinidae). *Mitochondrial DNA*. 25:17–18.
- Yue P, Shan X, Lin R. 2000. *Fauna Sinica: Osteichthyes Cypriniformes III*. Beijing (China): Science Press.
- Zhang J, Chen Z, Zhou C, Kong X. 2016. Molecular phylogeny of the subfamily Schizothoracinae (Teleostei: Cypriniformes: Cyprinidae) inferred from complete mitochondrial genomes. *Biochem Syst and Ecol*. 64:6–13.
- Zhang JP, Liu Z, Zhang B, Yin XY, Wang L, Shi HN, Kang YJ. 2015. Genetic diversity and taxonomic status of *Gymnocypris chilianensis* based on the mitochondrial DNA cytochrome b gene. *Genet Mol Res*. 14:9253–9260.