Complete mitochondrial genome of *Rivularia auriculata* (Gastropoda, Viviparidae) with phylogenetic consideration

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**ABSTRACT**

Complete mitochondrial genome sequence of *Rivularia auriculata* has a circular genome of 16,552 bp, which is comprised 13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes. The nucleotide composition of the light strand is 43.16% of A, 26.78% of T, 20.18% of C, and 9.88% of G. All genes are encoded on the heavy strand except seven tRNA genes (Met, Tyr, Cys, Trp, Gin, Gly, and Glu) on the light strand. All the protein-coding genes start with ATC initiation codon except ND4 starts with GTG, and two types of inferred termination codons are TAA and TAG. There are 26 intergenic spacers and 4 gene overlaps. It is indicated that *R. auriculata* has closer genetic relationship with *Viviparus chui* (88.64% nucleotide sequence identity between them) than the other snail species.

*Rivularia auriculata* is a kind of rare species of China, which mainly distributes in Xiangjiang River basin of Hunan province, and also scatters in neighboring provinces. The species belongs to the family Viviparidae and the order Architaenioglossa. Due to the destruction of its natural habitats and decreasing of its populations, *R. auriculata* was listed as Extinct Species by China Red Data Book of Endangered Animals. This presents a major obstacle for conservation efforts.

So far there are only a few researches on the population dynamics and morphological structure of *R. auriculata* (Zhou 1996; Pan et al. 2010), and no mitochondrial genomes of genus *Rivularia* in NCBI PubMed. Therefore, we sequenced the complete mitochondrial genome of *R. auriculata* by using the next-generation sequencing (NGS) techniques for its further population genetics and polymorphism studies. *R. auriculata* samples were collected from Poyang Lake in Jiangxi province of China (28°74′ N, 116°41′ E). Specimen (voucher no. zcx20181109-10) was preserved in 95% ethanol and stored at −40 °C refrigerator in the Key laboratory of Eco-circular Agriculture in South China Agricultural University, Guangzhou, China. The procedure referred from Green and Sambrook (2012) was carried out in the total genomic DNA extraction.

We sequenced and characterized the complete mitochondrial genome of *R. auriculata*. The mitochondrial DNA sequence of *R. auriculata* with the annotated genes was deposited in GenBank (accession number: MN264502). Complete mitochondrial genome sequence of *R. auriculata* is a circular one of 16,552 bp containing a total of 37 genes, including 13 protein-coding genes, 2 ribosomal RNA genes (12S-rRNA and 16S-rRNA), and 22 transfer RNA genes (tRNA). All of them are encoded on the heavy strand except seven tRNA genes (Met, Tyr, Cys, Trp, Gin, Gly, and Glu) on the light strand. All the protein-coding genes start with ATC initiation codon except ND4 starts with GTG, and two types of inferred termination codons are TAA and TAG. There are 26 intergenic spacers and 4 gene overlaps. It is indicated that *R. auriculata* has closer genetic relationship with *Viviparus chui* (88.64% nucleotide sequence identity between them) than the other snail species.

**KEYWORDS**

*Rivularia auriculata*; mitochondrial genome; NGS technique

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two tRNA genes vary from 60 to 70 bp in length, and all fold into the typical cloverleaf secondary structure. There are 26 intergenic spacers (total 1567 bp) varying from 1 to 946 bp in length and 4 gene overlaps (total 17 bp), the larger of which is 7 bp between the CYTB and ND5 genes. The tandem repeat sequences are observed in inter genetic space of tRNAThr (TGT).

Phylogenetic analysis covered mitochondrial genomes of R. auriculata and the other 14 species that are from the order Bellamya, Cipangopaludina, Margarya, Rivularia, Viviparus, Pomacea, Marisa, and Obscurella, belong to Architaenioglossa (Figure 1), and Littorina saxatilis was used as an outgroup. Maximum likelihood (ML) method was adopted for phylogenetic analysis (Figure 1). The GTR + I + G model was selected by the Akaike information criterion in jModelTest2.1.7 (https://code.google.com/p/jmodeltest2/). The phylogenetic tree was visualized with MEGA version 6.06 (Tamura et al. 2013). It is indicated that R. auriculata has closer genetic relationship with Viviparus chui (88.64% nucleotide sequence identity between them than the other snail species (Figure 1).

**Disclosure statement**

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

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