

# The mitochondrial genome organization of the rice frog, *Fejervarya limnocharis* (Amphibia: Anura): a new gene order in the vertebrate mtDNA

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## Abstract

The mitochondrial DNA of the rice frog, *Fejervarya limnocharis* (Amphibia, Anura), was obtained using long-and-accurate polymerase chain reaction (LA-PCR) combining with subcloning method. The complete nucleotide sequence (17,717 bp) of mitochondrial genome was determined subsequently. This mitochondrial genome is characterized by four distinctive features: the translocation of ND5 gene, a cluster of rearranged tRNA genes (tRNA<sup>Thr</sup>, tRNA<sup>Pro</sup>, tRNA<sup>Leu</sup><sup>(CUN)</sup>), a tandem duplication of tRNA<sup>Met</sup> gene, and eight large 89-bp tandem repeats in the control region, as well as three short noncoding regions containing two repeated motifs existing in the gene cluster of ND5/tRNA<sup>Thr</sup>/tRNA<sup>Pro</sup>/tRNA<sup>Leu</sup>/tRNA<sup>Phe</sup>. The tandem duplication of gene regions followed by deletions of supernumerary genes can be invoked to explain the shuffling of tRNA<sup>Met</sup> and a cluster of tRNA and ND5 genes, as observed in this study. Both ND5 gene translocation and tandem duplication of tRNA<sup>Met</sup> were first observed in the vertebrate mitochondrial genomes.

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**Keywords:** *Fejervarya limnocharis*; Rice frog; Complete mtDNA sequence; Unique ND5 gene order

## 1. Introduction

The content of the mitochondrial genome, including 13 protein-coding genes, two rRNA genes, and 22 tRNA genes, as well as a control region, is highly conserved in vertebrates, with only a few exceptions. To date, complete mitochondrial

genomes have been determined in 321 species of vertebrates, but among these, there are only six species of amphibians: the frogs *Xenopus laevis* (Roe et al., 1985) and *Rana nigromaculata* (Sumida et al., 2001), the caecilian *Typhlonectes natans* (Zardoya and Meyer, 2000), and the salamanders *Mertensiella luschani* (Zardoya et al., 2003), *Ranodon sibiricus* (Zhang et al., 2003a), and *Andrias davidianus* (Zhang et al., 2003b). Characteristic descriptions of these vertebrate mitochondrial genomes show that few of them either bear pseudogenes of tRNA or even lost certain individual genes (Macey et al., 1998; Kumazawa et al., 1998).

Although gene order is also highly conserved in most of vertebrate mtDNAs, it is found that 81 out of 321 known mitochondrial genomes possess a rearranged gene order, and many of these rearrangements involve tRNA genes only.

**Abbreviations:** ATP6, ATPase subunit 6; ATP8, ATPase subunit 8; COI-III, cytochrome *c* oxidase subunit I-III; Cyt *b*, cytochrome *b*; D-loop, displacement loop; H-strand, heavy strand; L-strand, light strand; LA-PCR, long-and-accurate polymerase chain reaction; ND1-6, 4L, NADH dehydrogenase subunit 1-6, 4L; PCR, polymerase chain reaction; tRNA, transfer ribonucleic acid.

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