

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the *Onychostruthus taczanowskii* (Aves, Passeridae) and its phylogenetic analysisYonggui Ma^{1,2}, Xiaoyang Wang¹, Yuan Huang¹, and Fumin Lei³¹Co-Innovation Center for Qinba Regions' Sustainable Development, College of Life Sciences, Shaanxi Normal University, Xi'an, China, ²Ministry of Education Key Laboratory of Qinghai-Tibet Plateau Resources and Environment, Qinghai Normal University, Xining, China, and ³Key Laboratory of the Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China

Abstract

The complete mitochondrial genome sequence of *Onychostruthus taczanowskii* consisted 16 917 bp, the genome harbored the same gene order with that of other birds, contained 13 protein-coding genes, 22 tRNAs, 2 rRNAs and 1 non-coding control region. The all tRNAs formed typical cloverleaf secondary structures, except *tRNA^{Ser} (AGN)* and *tRNA^{Phe}*. The control region was located between *tRNA^{Glu}* and *tRNA^{Phe}* with 1310 bp in length, which consist of three domains: highly variable domain I, central conserved domain II and conserved sequence domain III. According to the phylogenetic analysis, *Onychostruthus taczanowskii* had a closer relationship with *Pyrgilauda ruficollis*, and *Passer montanus* were sister to them.

Keywords

Mitochondrial genome, *Onychostruthus taczanowskii*, phylogeny

History

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The White-rumped Snowfinch (*Onychostruthus taczanowskii*) belongs to Passeridae, *Onychostruthus*. It is a typical songbird in alpine grassland and alpine meadow, and endemic to the Tibetan plateau. The upper part of this species is pale brown, and it has white forehead, supercilium and a black eye print. It shows adaptability to higher altitude environment, but its taxonomic status is controversial. Historically, the taxonomic status of *Onychostruthus taczanowskii* changed several time. It was placed under *Onychospiza*, then revised as *Onychostruthus*. However, Zheng (2002) placed it in *Montifringilla*. Qu et al. (2006) used mitochondrial gene *cytb* and nuclear myoglobin gene to do the phylogenetic analysis. It showed that *Onychostruthus taczanowskii* belonged to *Onychostruthus*, which was widely accepted (Gill et al., 2013).

In this study, the sample was collected from Xizang, China. The complete mitochondrial genome sequence of *O. taczanowskii* (GenBank accession number: KJ148631) was amplified and sequenced by long PCR and conserved primers walking approaches. The results showed that the full-length mitochondrial genome of *O. taczanowskii* is 16 917 bp with 54.5% A + T content, and consists of 37 genes which had the same gene order with other birds of Passeriformes. ATG was used as a start codon of most the genes, only except ND3 which used GTG as start codon. TAA or TAG is the termination codon for most genes,

except ND1 and COI using AGG, ND5 using AGA, COIII and ND4 had an incomplete termination codon T. The secondary structure of 22 tRNAs were predicted and found typical structures like that in most of tRNAs, except *tRNA^{Ser} (AGY)* with the absence of DHU arm, and *tRNA^{Phe}* with an extra nucleotide which inserted in the T ψ C arm. The predicted secondary structures of 12S rRNA and 16S rRNA exhibit 47 helices in three domains and 60 helices in six domains, respectively. The control region was located between *tRNA^{Glu}* and *tRNA^{Phe}* with 1310 bp in length, which consist of three domains: highly variable domain I, central conserved domain II and conserved sequence domain III.

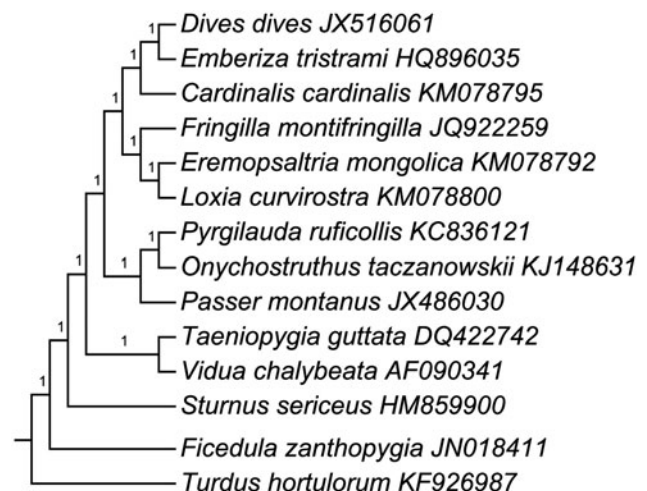


Figure 1. The Bayesian Inference tree of *O. taczanowskii* together with another 13 passerine species. The number of branches is the posterior probability values.

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Phylogenetic tree was estimated by Bayesian inference (BI) using MrBayes 3.2 (Ronquist & Huelsenbeck, 2003) and analyzed under the GTR+ Γ +I model. *Sturnus sericeus*, *Turdus hortulorum* and *Ficedula zanthopygia* as outgroups. The results of phylogenetic study strongly supported the previous taxonomic status of *O. taczanowskii* (Figure 1). Based on phylogenetic analysis of 13 mitochondrial protein-coding gene data of some passerines, the result revealed that *O. taczanowskii* has the closest relationship with *Pyrgilauda ruficollis*, and Passeridae (including both species and *Passer montanus*) forms a sister group with six species from Fringillidae.

Declaration of interest

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

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