

Mitochondrial genome of *Stachyris ruficeps* (Aves, Passeriformes, Timaliidae)

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ABSTRACT

Stachyris ruficeps are commonly found in the eastern Himalayas and south China. In our study, we reported the complete mitogenome and obtain basic genetic information of *S. ruficeps* for the first time. The complete mitochondrial genomes of *S. ruficeps* (16 885bp in length) had 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S *rRNA* and 16S *rRNA*) and 2 control regions. All of the 13 PCGs were initiated by ATG. All the genes in *S. ruficeps* were distributed on the H-strand, except for the ND6 gene and eight tRNA genes which were encoded on the L-strand.

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Stachyris ruficeps (Aves, Passeriformes, Timaliidae) was first discovered in India (Blyth 1847), Rufous-Capped Babbler are commonly found in the eastern Himalayas and south China (Liu et al. 2012). *Stachyris ruficeps* is a non-migration oriental bird, it always inhabited broadleaf evergreen forests from 200 to 2500 m (Qu et al. 2015). The length of *S. ruficeps* body was 11cm, the whole body was pale olive, and the back of top head was red brown, throat with thin vertical stripes, chest and central of the abdomen both were yellow-white. The *S. ruficeps* mitochondrial genome could provide the molecular data for the species diversity, genetic diversity and ecological diversity study.

Total mitochondrial genome of *S. ruficeps* was extracted from the muscle tissue by the traditional phenol-chloroform method (Sambrook & Russell 2001). The muscle sample of *S. ruficeps* was collected from Ya'an (N30°01', E103°02') and stored at the Wildlife Conservation Laboratory, Sichuan Agricultural University, Sichuan province, China. Twenty-one primer pairs were designed according to *Garrulax cineraceus* (GeneBank number: NC024553) for amplification and sequencing. The complete mitochondrial genomes of *S. ruficeps* has been submitted to GenBank and the accession number: KU362930 has been obtained.

The complete mitochondrial genome of *S. ruficeps* (16 885bp in length) had 13 protein-coding genes, 22 tRNA

genes, 2 rRNA genes (12S *rRNA* and 16S *rRNA*) and 2 control regions. The nucleotide composition of *S. ruficeps* mitogenome was 30.70% for A, 31.37% for C, 23.43% for T and 14.50% for G (C > A > T > G). The compact arrangement of *S. ruficeps* sequence was similar to the typical avian mitochondrial genome (Huan et al. 2015; Zhou et al. 2015). All of 13 PCGs were initiated by ATG. Nine of 13 PCGs used complete (TAA) or incomplete (TA- or T--) stop codons. *ND1* and *ND5* regarded AGA as the stop codon, *COX1* ended with AGG, and *ND6* used TAG as stop codon. Twelve PCGs, 2 rRNAs, and 14 tRNAs were encoded on the H-strand, whereas the *ND6* and 8 tRNAs (*tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser}*, *tRNA^{Glu}*, *tRNA^{Pro}*, *tRNA^{Gln}*) were encoded on the L-strand. The two control regions of the *S. ruficeps* mitochondrial genome were *D-loop1* (1092 bp) and *D-loop2* (231 bp). *12SrRNA* (974bp) and *16SrRNA* (1601bp) were located between *tRNA^{Phe}* and *tRNA^{Leu}* (UUR) and were separated by *tRNA^{Val}*.

In order to analyse the phylogenetic relationships of *S. ruficeps*, we constructed a phylogenetic tree using MrBayes (Huelsenbeck 2001). In Figure 1, the phylogenetic tree showed that *Macronous* and *Stachyris* were clustered in a clade and *Stachyris rufifrons* was the nearest sister to *S. ruficeps*. This result was consistent with Cibois et al. (2002) and Moyle et al. (2012).

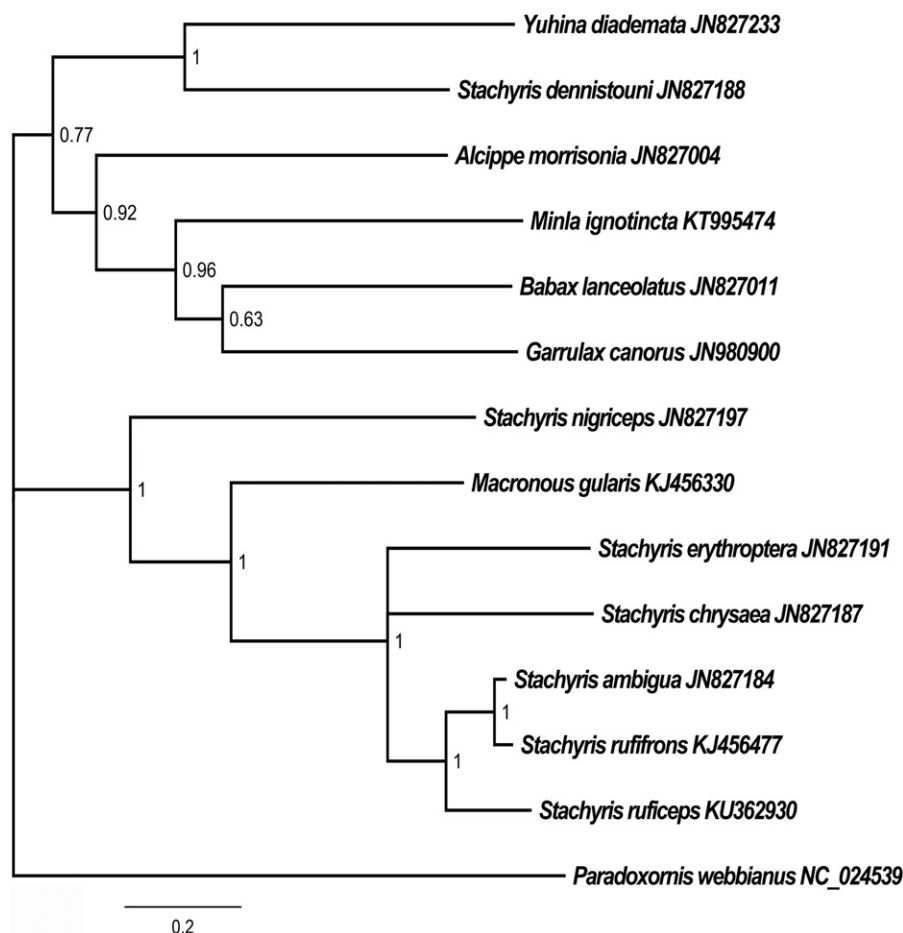


Figure 1. Bayesian tree based on *cytb* sequence of 13 Timaliidae and one *Paradoxornis* birds. The Bayesian tree was reconstructed with general-time-reversible (GTR) model, and the Markov chains for 1 000 000 generations. Numbers on branches represent bootstrap supports (1000 replicates). *Paradoxornis webbianus* were used as outgroup.

Disclosure statement

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