Analysis of complete mitochondrial genome sequence of bar-tailed Treecreeper 

**ABSTRACT**

Bar-tailed Treecreeper *Certhia himalayana* Vigors, 1832) inhabits coniferous or mixed broadleaf-conifer forest at an altitude of 1000–3500 meters, occasionally occurs in the shrub to c.500 m (BirdLife International 2016). *C. himalayana* occurs in Central Asia and southwest of China (Yunnan, Sichuan and Shanxi provinces) (Harrap and Quinn 1996). This species has an extremely large range, and hence does not approach the thresholds for Vulnerable under the range size criterion (BirdLife International 2016). Molecular studies supported *C. himalayana* closely related with Sittidae and Troglodytidae by highly probability based on mitochondrial genes, nuclear genes, both nuclear and mitochondrial genes, or mitochondrial and morphological data (Jonsson and Fjeldsæ 2006). Barker et al. (2002) and Fregin et al. (2012) also proved it used nucleotide sequence or mitochondrial and nuclear genes. The complete mitochondrial genome of *C. himalayana* has not been determined and characterized until now. Therefore, the aim of this study was to first assemble and characterize the complete mitochondrial genome of *C. himalayana*.

The specimen (Duan-025) was collected from Zixi Mountain (25.02N, 101.41E), which was located central Yunnan Province in China, and stored at the Herbarium of Southwest Forestry University. The total mitochondrial DNA was extracted from the muscle tissue using the Ezup Column Animal Genomic DNA Kit (Sangon, Shanghai, China). The complete mitochondrial genome was annotated using MITOS Web server (http://mitos2.bioinf.uni-leipzig.de/index.py) (Bernt et al. 2013) and OGDRAW 1.3.1 (Greiner et al. 2019). The complete mitochondrial genome of *C. himalayana* was submitted to the NCBI database under the accession number MN624167. A maximum likelihood (ML) tree was implemented in RAxML v7.7.1 (Stamatakis 2014) under the GTR-Gamma model, and node support was calculated with 1000 bootstrap replications (Wei et al. 2016). Sequences of *Lorius chlorocercus* and *Psittacula alexandrae* obtained from GenBank (MN_515396 and MK_986660) were used as outgroups to root trees following Jonsson and Fjeldsæ (2006).

The complete mitochondrial genome of *C. himalayana* was found to be a circular double-stranded 16,814 bp in length. A total of 38 mitochondrial genes were identified, including 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes, and 1 non-coding control region (D-loop). All the 13 protein coding genes contained the same start codon TTA/ATA, except that nad6 and nad4 gene started with ATG, nad5 gene started with TCT, cox1 gene started with CCT. Furthermore, eleven of the PCGs used complete ATT/ATG or incomplete AT(A) stop codon, and other two types were AGG[nad6], ATC[5t8].

Among these genes, nad6 and 8 tRNAs (trnE, trnP, trnS, trnY, trnC, trnN, trnA and trnQ) were located on the light strand (L-strand), while all of the remaining genes were located on the heavy strand (H-strand). The overall base composition of *C. himalayana* mitogenome was 25.1% for A, 29.2% for T, 14.5% for C, 31.2% for G, with a GC content of 45.7%. A phylogenetic tree strongly supported that *C. himalayana* closely related with Family Troglodytidae by highly probability.

**KEYWORDS**

Mitogenome; gene arrangement; phylogeny; Bar-tailed Treecreeper

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**CONTACT**

Yubao Duan: boyciana@163.com

Faculty of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, China

These authors contributed equally to this work.

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which is higher than G + C content of 45.7%, similar to other Psittaciformes (Barker 2014; Song et al. 2018).

The reconstructed phylogenetic tree showed that *C. himalayana* grouped with Family Troglodytidae (*Campylorhynchus brunnicepilus*, *C. zonatus* and *Henicorhina leucosticta*) with strong support (100% bootstrap support value) by the analyses of protein-coding genes (Figure 1). *C. himalayana* closely related with Family Troglodytidae, which is congruent with previous studies (Jonsson and Fjeldsa 2006). The complete mitochondrial genome of *C. himalayana* reported here will be useful for future population genetic studies of this species and will provide essential genome resources for the ecologically important species.

**Disclosure statement**

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**ORCID**

Yubao Duan http://orcid.org/0000-0002-6458-9585

**Data availability statement**

The data that support the findings of this study are openly available in NCBI at https://www.ncbi.nlm.nih.gov/, reference number [MN624167], or available from the corresponding author.

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