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MITOGENOME REPORT

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The complete mitochondrial genome of *Tauraco livingstonii* (Musophagidae: Tauraco)

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ABSTRACT

Livingstone's turaco, *Tauraco livingstonii*, belongs to the family Musophagidae. In this study, we obtained the complete mitochondrial genome sequence of Livingstone's turaco by high-throughput sequencing technology and constructed a phylogenetic tree. It was found that the mitochondria of this species are 19,015 bp in length and contain a total of 37 genes, comprising 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. The base composition of the mitochondrial genome is 31.61% A, 24.22% T, 30.64% C, and 13.52% G, with a GC content of 44%. Notably, an intriguing phenomenon of mitochondrial genome rearrangements was observed, characterized by the duplication of the tRNA Glu-L-CR gene order. In addition, the results of the phylogenetic tree analysis shed light on the taxonomic position of Livingstone's turaco and supported the taxonomy of Otidimorphae. The study provides a basis for future phylogenetic and taxonomic investigations of Musophagiformes.

Introduction

Livingstone's turaco (*Tauraco livingstonii*, g. r. gray, 1864) belongs to the family Musophagidae and is typically found in humid regions throughout Burundi, Malawi, Mozambique, Tanzania, and Zimbabwe. Specifically, this species is known to inhabit mountainous and coastal forests below 2500 m above sea level (Forshaw 2002). Livingstone's turaco is a medium-sized scansores, measuring approximately 45 cm from beak to tail and weighing between 262 and 380 g. One of the distinctive features that identifies this species is the tipped crest measuring approximately 6.5–7.5 cm on the top of the head. The white tipped crest is also anteriorly pointed when erect. In this study, we have sequenced the complete mitochondrial genome of Livingstone's turaco and analyzed its phylogenetic relationships. The findings of this research may contribute to species identification and genetic evolution studies (Figure 1).

Materials and methods

Muscle tissue samples of Livingstone's turaco were collected from Chongqing zoo (Latitude** 106.50174 and Longitude** 29.50547) and the specimen was deposited at the College of Wildlife and Protected Areas of Northeast Forestry University (https://wildlife.nefu.edu.cn/, Xuedong Liu: liuxuedong89@

126.com) under the voucher number H2201. High-throughput sequencing technology was utilized to sequence the mitochondrial genome of Livingstone's turaco. The sequencing data were submitted to the National Center for Biotechnology Information (NCBI; http://www.ncbi.nlm.nih.gov, accession number: OR094904).

The whole genomic DNA was extracted from the sample, and a DNA library was constructed using TruSeq Nano DNA HT Sample Prep Kit. The library was then sequenced on an Illumina HiSeq/NovaSeq platform with a 2×150 paired-end sequencing strategy, and the depth of coverage is shown in Supplementary Figure S1. FASTQ was used for data quality control (Chen et al. 2018), and the sequence was assembled into contigs using metaSPAdes software (Nurk et al. 2017). mitoMaker was used for annotating mitochondrial genes (Schomaker-Bastos and Prosdocimi 2018) (Figure 2).

Mitochondrial genome sequences of Livingstone's turaco, seven additional species from the family Musophagiformes, Cuculiformes, and Otidiformes found in GenBank, and *Caprimulgus indicus* as outgroup members were used to construct a phylogenetic tree. Sequence alignment was performed using the Muscle method in MEGA11 (Edgar 2004; Tamura et al. 2021), MrModeltest 2 was used to select the optimal model (Darriba et al. 2020). Bayesian phylogenetic inference was performed using the Markov chain Monte Carlo (MCMC) methods in MrBayes3.2.7 (Ronquist et al. 2012),

CONTACT Gaoxiang Kuang ✉ 16468545@qq.com 🏢 Chongqing Zoo, Chongqing, China; Kun Jin ✉ jk2002@caf.ac.cn 🏢 Ecology and Nature Conservation Institute, Chinese Academy of Forestry, Beijing, China; Xuedong Liu ✉ liuxuedong89@126.com 🏢 College of Wildlife and Protected Area, Northeast Forestry University, Harbin, China

the run length was set to 1,000,000, and the diagnostics were calculated every 1000 generations. The phylogenetic tree is visualized in iTOL (Tyagi et al. 2020) (Figure 3).

Results and discussion

The mitochondrial genome is 19,015 bp long and encodes a total of 37 genes, including 13 protein-coding genes, 22 tRNA genes, two rRNA genes (12S rRNA and 16S rRNA), and two control region (CR) (D loop). The overall nucleotide

Figure 1. Species reference image of Livingstone's turaco. The image is referenced from the iNaturalist (Marc Henrion 2023). This figure is attribution noncommercial sharing. https://www.inaturalist.org/photos/250606396?size=original.

composition is 31.61% A, 24.22% T, 30.64% C, and 13.52% G. All protein-coding genes, except for ND3(ATC), start with the codon ATG. Most end with the codon TAA (COX1, COX2, ATP8, ATP6, ND3, ND4L, ND4, ND5, and CYTB), while three genes (ND1, ND2, and ND6) have the stop codon TAG, and COX3 ends with TGA. In addition, we found the mitochondrial genome rearrangements phenomenon (duplicate tRNA Glu-L-CR gene order) in the mitochondria of Livingstone's turaco (Kang et al. 2018). Compared to the classical mitochondrial structure, Livingstone's turaco has four additional duplicate genes (ND6, trnT, trnP, and trnE) and an extra CR, referred to as a pseudo-control region (YCR). The YCR is present in the mitochondrial genomes of numerous bird species (Eberhard and Wright 2016). and studies found that the duplication of CRs in the mitochondrial genome is associated with longer lifespan in birds compared to mammals of similar weight (Skujina et al. 2016).

Initially, the dactyly of Musophagidae and Cuculidae is zygodactyl. This morphological similarity has prompted the inference of a potential evolutionary relationship between these avian taxa. Consequently, both Musophagidae and Cuculidae are classified under Cuculiformes. But studies based on whole genome sequencing have reclassified Musophagidae as Musophagiformes. Musophagiformes is most closely related to Otidiformes, followed by Cuculiformes. Together, they are classified as Otidimorphae (Jarvis et al. 2014). The results of the phylogenetic analysis of this study also support this classification criterion.
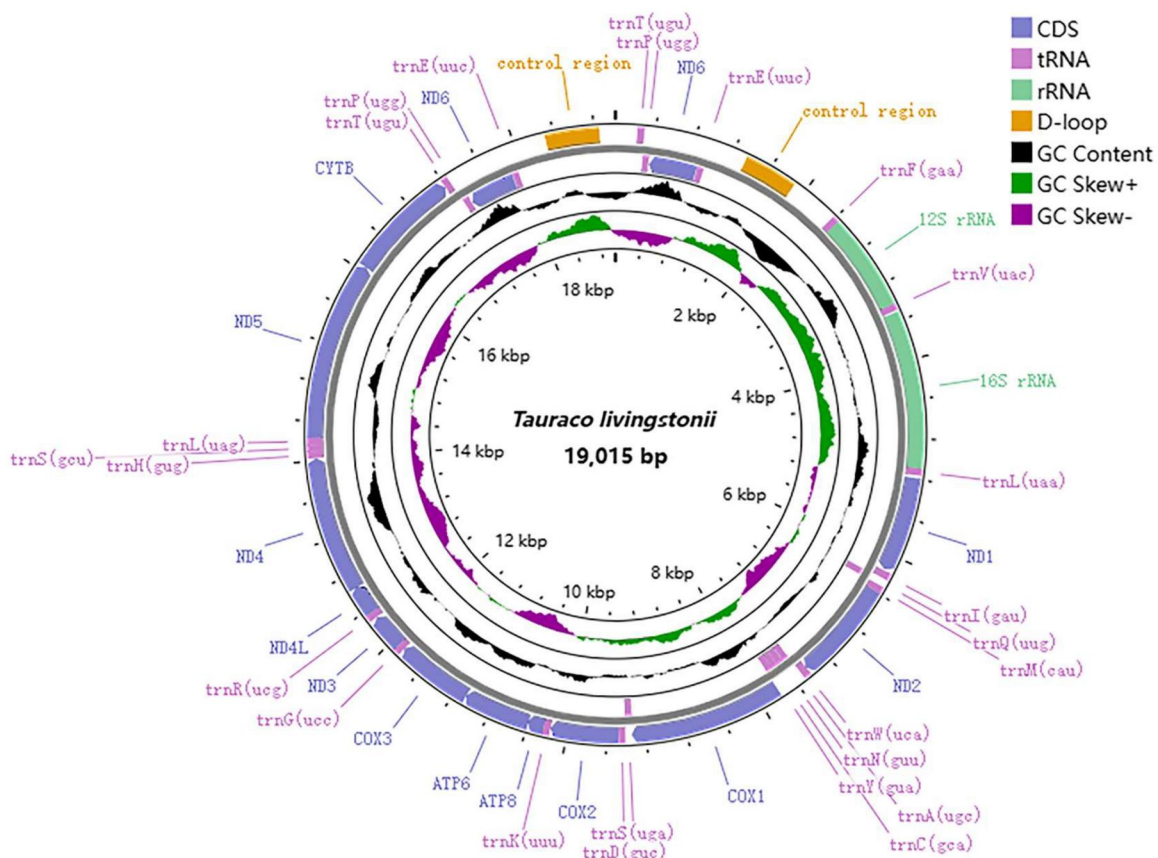

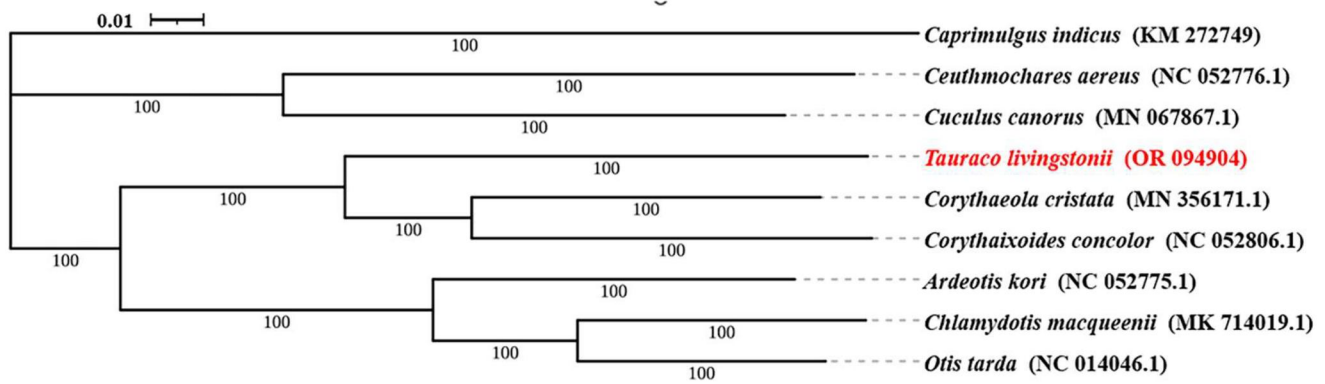**Figure 2.** The circular mitogenome map of Livingstone's turaco.

Figure 3. A phylogenetic tree based on the complete mitochondrial genomes of nine species was constructed by MrBayes 3.2.7, with *Caprimulgus indicus* (KM272749) as the outgroup. The accession number of *Tauraco livingstonii* (OR094904) obtained in this study was represented by red letters. The other mitochondrial genome sequences used in this tree are: *Ceuthmochares aereus* (NC052776.1), *Cuculus canorus* (MN067867.1), *Corythaeola cristata* (MN356171.1), *Corythaixoides concolor* (NC052806.1), *Ardeotis kori* (NC052775.1), *Chlamydotis macqueenii* (MK714019.1), and *Otis tarda* (NC014046.1).

Ethical approval

The muscle samples of Livingstone's turaco were extracted from a Livingstone's turaco which died of illness in the Chongqing zoo. Ethical approval is not required in this case.

Author contributions

Xiaojia Wang was responsible for sample collection; Xuanye Wu conducted experiments, analyzed data, and wrote the paper; Gaoxiang Kuang, Kun Jin, and Xuedong Liu participated in the conception and design of the paper, as well as providing financial support. All authors agree to take responsibility for all aspects of the work.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/nuccore/OR094904 under the accession. BioProject, SRA, and Bio-Sample numbers are PRJNA967797, SRR24511900, and SAMN34722102, respectively.

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