Complete mitochondrial genome sequence for the *Cercopithecus erythrotis camerunensis* (Primate: Cercopithecidae)

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**ABSTRACT**

*Cercopithecus erythrotis camerunensis* a subspecies of *Cercopithecus erythrotis*, endemic primate to West Africa, is listed as a vulnerable species under the IUCN red list, due to a rapid population decline resulting from intense hunting, bushmeat trade and habitat loss. In this study, the complete mitochondrial genome of *C. erythrotis camerunensis* was sequenced and characterized using next-generation sequencing technique. The total length of the complete mitogenome is 16,645 bp, 13 protein-coding genes (PCGs), two ribosomal RNA genes, 22 transfer RNA genes (tRNAs) and a non-coding control region (D-loop region). Its efficient protection from anthropogenic activities has been a major challenge, thus, the complete mitochondrial genome sequence reported here will give molecular information for future evolutionary research and scientific basis for its conservation.

*Cercopithecus erythrotis camerunensis* is a small, colourful monkey with distinctive facial markings, native to Nigeria-Cameroun border, West Africa (Oates et al. 2008; Kingdon et al. 2013). Unfortunately, *C. erythrotis camerunensis* is threatened by deforestation, hunting and bushmeat trade (Fa et al. 2000; Linder 2008; Oates et al. 2008) and has thus led to its population decline. This species has been classified as a Vulnerable species by the International Union for Conservation of Nature (IUCN) on the ‘Red List of Threatened Species’, which makes the protection and conservation of this important species pertinent.

In this study, the complete mitochondrial genome of *C. erythrotis camerunensis* was sequenced. Animal collection permits and ethical approval were obtained from National Park Service, Abuja, Nigeria. This permit and licenses are necessary for collection of samples from the park and transportation of the samples from Nigeria to China. The tissue sample of *C. erythrotis camerunensis* was collected from carcass exhibit seized from poachers in Cross River National Park, Nigeria, West Africa. It was deposited in the Animal Branch of Germplasm Bank of Wild species, Kunming Institute of Zoology, Chinese Academy of Sciences. DNA was extracted using DNeasy Blood & Tissue Kit (Qiagen, Valencia, CA). Library construction and sequencing was done in the Southern China DNA Barcoding Center, with Illumina Miseq platform. Assembling was carried out with SPAdes (http://cab.spbu.ru/software/spades/). Reads were assembled using Linux-OS SPAdes genome assembler v3.12.0 (Bankevich et al. 2012) with k-mer 21, 33, 55. The tRNAs sequences were confirmed using online Search Service tRNAscan-SE (Schattner et al. 2005).

We obtained the complete mtDNA genome of an individual of *C. erythrotis camerunensis* (MH974763). The genome organization consists of 37 genes (13 protein-coding (PCGs), two ribosomal RNA (rRNA), 22 transfer RNA (tRNA) genes, and one control region (D-loop)). Most of the PCGs initiation codons were ATG except for ND3 and ND2 with slight differences in the initiation codon of ATT and ATA respectively. The mitogenome was 16,645 bp in length, with an overall base composition of A: 31.8%, C: 29.7%, G: 12.8% and T: 25.8%. Nucleotide composition was estimated by MEGA 7.0 (Kumar et al. 2016). In addition, nine of the 13 protein-coding genes had complete termination codon TAG, AGG, TAA or GAA, while COIII, ND4, ND3 and CYTB genes terminate with incomplete stop codon (T-). A total of 22 gaps/overlaps were identified among the genes. It has the same gene arrangement and similar codon usage with other Cercopithecidae mitochondrial genome (Li et al. 2009; Lei et al. 2010; Chang et al. 2014; Wang et al. 2014).

To validate the reliability of the sequence, comparison was made with other mitochondrial sequences from *Cercopithecus* species. The phylogenetic position was estimated from complete mtDNA sequences (Figure 1). The newly characterized sequence had 100% bootstrap (Figure 1).
joining tree (NJ) and maximum likelihood (ML) were performed in MEGA 7.0 while maximum parsimony (MP) was estimated using PAUP* (V4.0) (Swofford 2003).

This study will give a useful database for analyzing the phylogenetic relationship of *C. erythrotis camerunensis* and other *Cercopithecus* species. This will provide valuable scientific insights on its conservation and restoration.

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**Disclosure statement**

No potential conflict of interest was reported by the authors.

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![Figure 1. Phylogenetic relationships among *Cercopithecus* based on mtDNA genome of 11 sequences with their species name and accession numbers, Chlorocebus tantalus (EF597502.1) was set as outgroup taxon. *Cercopithecus erythrotis camerunensis* with accession number (JQ256936) was collected from Cameroon (CM) while the new sequence of *Cercopithecus erythrotis camerunensis* (MH974763) was collected from Nigeria (NG). Number above each node indicates the NJ, ML and MP bootstraps support values, respectively.](attachment:image.png)