Characterization of the complete mitochondrial genome of the Macaroni penguin *Eudyptes chrysolophus* from the Barton Peninsula, King George Island, Antarctica

Jong-U Kim and Jeong-Hoon Kim

Korea Polar Research Institute, Incheon, South Korea

**Abstract**

The Macaroni penguin (*Eudyptes chrysolophus*), a species of crested penguin, is the most abundant penguin species worldwide, distributed from the Antarctic to the Subantarctic regions (Woehler and Poncet 1993). The population of macaroni penguin appears to have declined rapidly over the past three generations (BirdLife International 2020). The taxonomic status of the genus *Eudyptes* and the number of species within it have been repeatedly discussed (Fugone et al. 2018). Complete mitochondrial genomes provide baseline information to understand genomic evolution and facilitate phylogenetic inference (Matsui et al. 2009) and taxonomic clarifications (Sebastian et al. 2018). A mitogenomic study of *E. chrysolophus* have been reported; however, it was incomplete information (Cole et al. 2019). Thus, clarification of complete mitochondrial genome of *E. chrysolophus* is needed to understand their phylogeny and evolution.

Here, we sequenced and analyzed the complete mitogenome of *E. chrysolophus* (GenBank: MW074963). The blood sample (proof number MP1) was obtained at Narebski Point, Antarctica (62°14′14.66″S, 58°46′30.59″W), on 10 January 2010, and stored at the Korea Polar Research Institute (KOPRI), Incheon, South Korea. Total genomic DNA was extracted from the blood sample using a DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany). The complete mitochondrial genome was sequenced and annotated according to our previous study (Kim and Kim 2020). An Illumina paired-end (PE) library was prepared according to the manufacturer’s instructions with 550 bp insert size, and sequencing was performed using an Illumina sequencing platform supplied by a commercial company (Phyzen, Seongnam, South Korea).

The complete mitochondrial genome sequence of *E. chrysolophus* had a circular genome of 17,059 bp in length, containing 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, and two ribosomal RNA (rRNA) genes. The overall base composition is 30.53% (A), 32.86% (C), 13.96% (G), and 22.66% (T), and 46.81% for overall GC contents. The phylogenetic analysis shows a close relationship between *E. chrysolophus* and *E. schlegeli*. Our findings would be useful for further studies on phylogenetics and evolutionary history of the genus *Eudyptes*.

**Keywords**

Crested penguin; *Eudyptes chrysolophus*; Macaroni penguin mitogenome

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**CONTACT**

Jeong-Hoon Kim jhkim94@kopri.re.kr Korea Polar Research Institute, 26 Songdomire-ro, Yeonsu-gu, Incheon 21990, South Korea

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ORCID

Jong-U Kim http://orcid.org/0000-0001-7790-1817
Jeong-Hoon Kim http://orcid.org/0000-0002-2397-2668

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MW074963. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA667576, SRR12778075, and SAMN16378289 respectively.

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Figure 1. Phylogenetic tree of Eudyptes chrysolophus and other Spheniscidae family based on mitochondrial PCGs. The numbers in the nodes indicate bootstrap support values (>50%) from 1000 replicates.