Complete mitochondrial genome of a hen harrier *Circus cyaneus* (Accipitriformes: Accipitridae) from South Korea

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**ABSTRACT**

A hen harrier *Circus cyaneus* (Accipitriformes: Accipitridae), a migrant raptor having a wide breeding range from Europe to Northeast Asia, migrates to more southerly areas (Southern Europe, China, Korea and Japan) in winter. In this study, the complete mitochondrial genome of *C. cyaneus* was completely sequenced and characterized. It was 20,173 bp in length being composed of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes and two control regions. It has a base composition of A (32.2%), G (12.6%), C (30.5%) and T (24.7%). The phylogenetic tree reconstructed based on the maximum likelihood (ML) method confirms that *C. cyaneus* places within the clade of the family Accipitridae in the monophyletic avian order Accipitriformes.

The mitochondrial genome of *C. cyaneus* is 20,173 bp long (GenBank accession no. KU237286), which exhibits the same gene order with that of the order Accipitriformes. It contains total 37 genes including 13 PCGs (COX1-3, ND1-6, ND4L, CYTB, ATP6 and ATP8), 2 rRNAs (16S rRNA and 12S rRNA), 22 tRNAs and 2 control regions (CR and 3'CR), of which 28 genes places on the heavy strand (H-strand) and the remaining 9 genes are located on the light strand (L-strand). The overall genome components and gene orders are identical to those of *C. cyaneus* published with the specimens of Inner Mongolia (Gao et al. 2018). The overall A + T content of *C. cyaneus* mitogenome is 56.9%: 53.7% for PCGs, 56.7% for tRNAs, 53.2% for rRNAs and 67.0% for CRs. In the PCGs (11,400bp long), 12 are encoded in the H-strand, and the only one (CYTB) is located in the L-strand. All PCGs use the conventional start codons ATN except for COX1 using GTG which was also employed as the initiation-codon in other avian species (Slack et al. 2003). CR (3,571bp long) locates between *trnT* and *trnP*, which is divided into three domains of Domain I, Central Conserved Domain II, and Domain III. Domain II exhibits only five conserved boxes of F, E, D, C and B-box, generally existing in Aves, is not found.

The maximum likelihood (ML) tree was reconstructed with 13 PCGs among 27 accipitriform species (Figure 1). The best fitting model mtVer + I+G4 was selected for the ML analysis. The ML tree confirms that *C. cyaneus* places within the clade of the family Accipitridae in the monophyletic avian order

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Accipitriformes. Within the family Accipitridae, there are found four different clades of Clade 1, 2, 3 and 4. In Clade 2, *C. cyaneus* from South Korea is grouped with *C. cyaneus* from Inner Mongolia within the monoclade of the genus *Circus*. *Accipiter* is a sister genus of *Circus*. The relationships of the four families of Accipitriformes are consistent with those of Burleigh et al. (2015) and Jiang et al. (2015).

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study are openly available in NCBI at [https://www.ncbi.nlm.nih.gov/nuccore/KU237286.1](https://www.ncbi.nlm.nih.gov/nuccore/KU237286.1). The information of the supplementary table was deposited in Figshae DB ([https://doi.org/10.6084/m9.figshare.13139693.v1](https://doi.org/10.6084/m9.figshare.13139693.v1)).

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