


## The complete mitochondrial genome of Eurasian Sparrowhawk *Accipiter nisus* (Accipitriformes: Accipitridae)

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### ABSTRACT

The mitogenome of the *Accipiter nisus* is a circular module of 18,352 bp, which consists of 39 genes, containing 2 rRNA genes (12S rRNA and 16S rRNA), 13 protein-coding genes, 22 tRNA genes, and two non-coding regions (control region and pseudo control region). The mitogenome of *A. nisus* is composed of 31.3% A, 25.5% T, 30.4% C, 12.8% G, and 76.3% AT. The phylogenetic analysis revealed that *A. nisus* individuals was well grouped in Accipitridae and more closely related to genus *Circus* than other *Accipiter* species

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Mitogenome; *Accipiter nisus*; phylogenetic analysis; Accipitridae

The Eurasian Sparrowhawk (*Accipiter nisus*) is a small-sized raptor species that hunt small and medium-sized passerines in the forest environment (Rytkönen et al. 1998; Lehtikoinen et al. 2010; Hussain et al. 2016). It is distributed in an extremely large range encompassing most of Europe and Asia, and is well adapted to subtropical and temperate areas (Hervías et al. 2017). This species is designated as second-grade endangered species of wild fauna and flora in South Korea (National Institute of Biological Resources 2019).

Muscle tissues of *A. nisus* were collected from the road-killed carcass at Inje-gun, Gangwon-do (38°07'18.4"N, 128°10'10.2"E). A Voucher specimen (KNUWB-04) was deposited in the Wildlife and Fish Conservation Center of the Institute of Forest Science, Kangwon National University. DNeasy Blood & Tissue Kit (Qiagen, Valencia, CA, USA) was used for DNA extraction according to the manufacturer's instruction. A previously published mitogenome (KM360148) of *A. nisus* (Zhang et al. 2016) was used as a reference for PCR primers and Geneious prime (Kearse et al. 2012) was used for gene annotation and aligned with that of the other 13 Accipitridae species using Clustal W implemented in Geneious Prime (Auckland, New Zealand). The phylogenetic tree was constructed by MEGA-X (Kumar et al. 2018) using the Maximum likelihood (ML) based on the mtREV with frequencies (+F) with gamma distributed with invariant sites (G+I) was selected as the best model of evolution (Jones et al. 1992; Kumar et al. 2018). The Eurasian magpie *pica pica* (ND015200) was used as an outgroup.

The complete mitogenome of *A. nisus* (GenBank accession no. MN929010) was 18,352 bp in length and contained two ribosomal RNAs (12S rRNA and 16S rRNA), 13 protein-coding

genes (PCGs), 22 transfer RNAs (tRNAs), and two non-coding regions (control region and the pseudo control region).

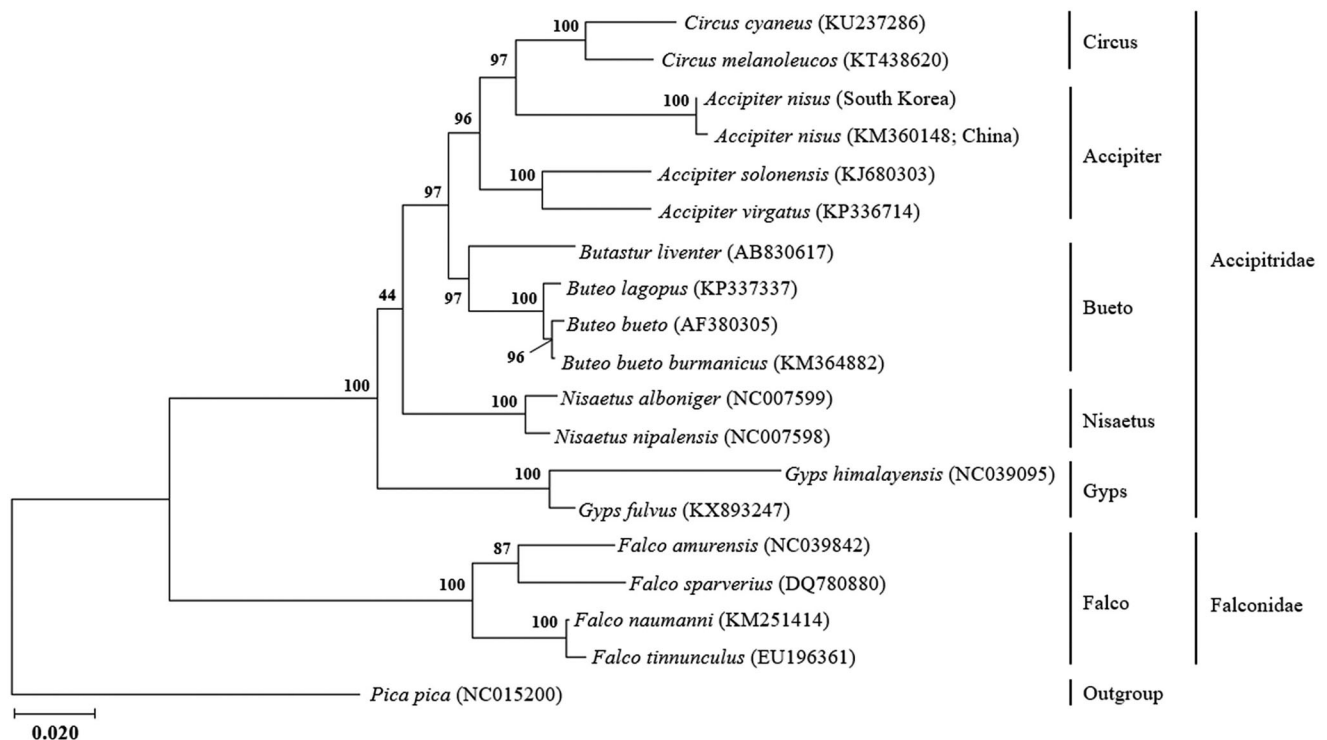
The base composition for the mitogenome sequence is AT-biased, with nucleotide composition of 31.3% A, 25.5% T, 30.4% C, 12.8% G and 76.3% AT. Length of the two rRNA genes (12s rRNA and 16s rRNA) were 971 bp (52.1% A + T) and 1602bp (53.4% A + T), respectively.

The total length of the 13 mitochondrial PCGs of the *A. nisus* is 14,187 bp (57.2% A + T), which encodes 3797 amino acids without stop codons. All protein-coding genes initiate with ATG except COX1 (GTG), ND3 (ATC) and ND5 (ATA). Total 22 tRNA genes, including two leucine-tRNA genes (*tRNA<sup>Leu</sup> (CUN)* and *tRNA<sup>Leu</sup> (UUR)*) and two serine-tRNA genes (*tRNA<sup>Ser</sup> (UCN)* and *tRNA<sup>Ser</sup> (AGY)*), were present in the mitogenome.

Mitochondrial genome of *A. nisus* contains two non-coding regions (D-loop, pseudo control region). D-loop is 2,033 bp in length, located between *tRNA<sup>Thu</sup>* and *tRNA<sup>Pro</sup>*. The Pseudo control region is 760 bp in length, located between *tRNA<sup>Glu</sup>* and *tRNA<sup>Phe</sup>*.

In comparison with the previously published mitogenome of the *A. nisus* (KM360148), which has a total size of 18,647 bp, 99.8% sequence similarity was found in the other regions except for D-loop (96.7%) and pseudo control region (99.7%)

The phylogenetic analysis revealed that *A. nisus* is well placed within the tribe Accipitridae (Figure 1), which forms a sister clade to Chinese *A. nisus* (KM360148). It is analyzed that our sample is more closely related to the genus *Circus* (KT438620, KU237286) than other *Accipiter* species. Earlier datasets have shown genus *Circus* to be sister to the genus



**Figure 1.** The intraspecific phylogeny of *Accipiter nisus* based on mitogenome sequences. The phylogenetic tree was generated using the maximum likelihood based on mtREV with frequencies (+F) with gamma distributed with invariant sites (G+I). The robustness of the tree was tested with 2000 bootstraps. The numbers on the branches indicate bootstrap values.

*Accipiter* (Barrowclough, 2014), but Oatley et al. (2015) suggest that have no strong support in which lineages are the exact sister-group to the *Circus* clade.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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## 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>, reference number MN929010.

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