



# Gene organization and characterization of the complete mitogenome of *Hypsugo alaschanicus* (Chiroptera: Vespertilionidae)

J.Y. Kim and Y.C. Park

Division of Forest Sciences, College of Forest & Environmental Sciences,  
Kangwon National University, Chuncheon, Republic of Korea

Corresponding author: Y.C. Park  
E-mail: parky@kangwon.ac.kr

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**ABSTRACT.** We sequenced and characterized the complete mitogenome of *Hypsugo alaschanicus* (Vespertilionidae) to provide more data for comparative mitogenomics of the genus *Hypsugo*. The mitogenome of *H. alaschanicus* is a circular molecule of 17,300 bp, consisting of a control region and a typically conserved set of 37 vertebrate genes containing 13 protein-coding genes (PCGs), 22 tRNA genes, and two rRNA genes (*12S rRNA* and *16S rRNA*). The mitogenome of *H. alaschanicus* is AT-biased, with a nucleotide composition of 34.1 A, 30.9 T, 22.4 C, and 12.6% G. In the 13 mitochondrial PCGs of *H. alaschanicus*, the start codon ATG is used in all PCGs, except *Nd2* and *Nd3* (which use ATT), and *Nd5* (which uses ATA). Eight PCGs (*Nd1*, *Cox1*, *Cox2*, *Atp8*, *Atp6*, *Nd4L*, *Nd5*, and *Nd6*) use TAA as the stop codon, while the stop codon AGA occurs only in *Cytb*. Incomplete stop codons (T-) are used in the other four PCGs (*Cox3*, *Nd2*, *Nd3*, and *Nd4*). These findings contribute to our understanding of the nucleotide composition and molecular evolution of the mitogenomes of the genus *Hypsugo*, and provide more data for comparative mitogenomics and higher phylogeny in the family Vespertilionidae.

**Key words:** Mitogenome; Gene organization; *Hypsugo alaschanicus*; Vespertilionidae