



Short Communication

Complete mitochondrial genome and codon usage of the Nepalese whiskered bat *Myotis muricola* (Vespertilionidae)

K.B. Yoon and Y.C. Park

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

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

Genet. Mol. Res. 14 (4): 14637-14645 (2015)

Received July 10, 2015

Accepted September 30, 2015

Published November 18, 2015

DOI <http://dx.doi.org/10.4238/2015.November.18.27>

ABSTRACT. We sequenced and characterized the complete mitogenome of the Nepalese whiskered bat *Myotis muricola* (Vespertilionidae) to provide more data for comparative mitogenomics and codon usage in the genus *Myotis* (Vespertilionidae). The mitogenome of *M. muricola* is a circular molecule of 17,224 bp, consisting of a control region and a conserved set of 37 genes containing 13 protein-coding genes (PCGs), 22 tRNA genes, and two rRNA genes (*12S rRNA* and *16S rRNA*). The mitogenome of *M. muricola* is AT-biased, with a nucleotide composition of 33.6% A, 29.7% T, 23.3% C, and 13.4% G. The total length of the 13 mitochondrial PCGs, excluding stop codons, is 11,376 bp, or 3792 amino acids. The relative synonymous codon usage (RSCU) of codons ending in A/T was generally higher than that for codons ending in G/C. The most frequently used codons are CTA(Leu) and CGA(Arg), with RSCU values greater than 2.0. The most rarely used codons, all terminating in G, are TCG(Ser), CCG(Pro), GCG(Ala), AAG(Lys), TGG(Try), CGG(Arg), and ACG(Thr), with RSCU values below 0.2. TCG(Ser) occurs only five times, and has the lowest

RSCU value (0.091). These results are valuable for a better understanding of the molecular evolution of mitogenomes in the genus *Myotis*.

Key words: Mitochondrial genome; Codon usage; Nepalese whiskered bat; *Myotis muricola*; Vespertilionidae