



# Complete mitochondrial genome sequence of *Marmota himalayana* (Rodentia: Sciuridae) and phylogenetic analysis within Rodentia

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**ABSTRACT.** This is the first report of a complete mitochondrial genome sequence from Himalayan marmot (*Marmota himalayana*, class Marmota). We determined the *M. himalayana* mitochondrial (mt) genome sequence by using long-PCR methods and a primer-walking sequencing strategy with genus-specific primers. The complete mt genome of *M. himalayana* was 16,443 bp in length and comprised 13 protein-coding genes, 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and a typical control region (CR). Gene order and orientation were identical to those in mt genomes of most vertebrates. The heavy strand showed an overall A+T content of 63.49%. AT and GC skews for the mt genome of the *M. himalayana* were 0.012 and -0.300, respectively, indicating a nucleotide bias against T and G. The control region was 997 bp in size and displayed some unusual features, including absence of repeated motifs and two conserved sequence blocks (CSB2 and

CSB3), which is consistent with observations from two other rodent species, *Sciurus vulgaris* and *Myoxus glis*. Phylogenetic analysis of complete mt DNA sequences without the control region including 30 taxa of Rodentia was performed with Maximum-Likelihood (ML) and Bayesian Inference (BI) methods and provided strong support for Sciurognathi polyphyly and Hystricognathi monophyly. This analysis also provided evidence that *M. himalayana* mt DNA was closely related to that from *Sciurus vulgaris* (Sciuridae) and was similar to mt DNA from *Myoxus glis*.

**Key words:** *Marmota himalayana*; Mitochondrial genome; Rodentia; Phylogenetic analysis