

## **Complete mitochondrial genome sequence of the Indian pipistrelle *Pipistrellus coromandra* (Vespertilioninae)**

### **ABSTRACT**

We characterized the complete mitogenome of *Pipistrellus coromandra* (Indian pipistrelle) for comparative analysis of mitogenomes and for resolving the phylogenetic relationship of four tribes in the subfamily Vespertilioninae. The mitogenome size of *P. coromandra* was 17,153 bp, with a control region and a typical set of 37 mitochondrial genes. The nucleotide composition of the *P. coromandra* mitogenome showed an AT bias with a nucleotide composition of 33.5% A, 30.7% T, 13.3% G, and 22.5% C. The mitochondrial protein-coding genes in *P. coromandra* use the standard start codon (ATN), two stop codons (TAA and AGA), and two incomplete stop codons (TA- and T--). The intertribal relationship of four tribes was highly resolved from the phylogenetic analysis of mitogenome sequences.

**Keyword:** Mitogenome; Pipistrellini; *Pipistrellus coromandra*; Vespertilioninae