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Phylogenetic relationships of Russian far-east *Apis cerana* with other North Asian populations

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Abstract

Apis cerana Fabricius, 1793 is the eastern honeybee species distributed throughout Asia from the tropical climate in the southern part to the temperate climate in the northern part. We sequenced and annotated the complete mitochondrial DNA (mtDNA) of *A. cerana* from Vladivostok, Primorsky Krai of the Russian Far East and uploaded it to the database GenBank (AP018450). MtDNA sequence has 15,919 bp length, AT-content 84% and GC-content 16% and contains 22 tRNA genes, 13 protein-coding genes, two ribosomal RNA genes, one AT-rich region and four non-coding intergenic regions (NC1-4). All protein-coding genes start with ATT and ATG codons, except for ATC, the start codon of the ATP8 gene, which and stop with the common stop codons TAA and TAG. A comparative analysis of complete mtDNA of *A. cerana* from China, Indonesia, Korea, Malaysia, Russia, Taiwan, Thailand, Vietnam, and Japan found that the Russian Far East *Apis cerana* differed from others on the subspecies level. Based on the comparative analysis of complete mtDNA (~16,000 bp), nuclear DNA (nDNA) gene Vitellogenin (VG) (~4,100 bp) and morphological measurements (six parameters), we assumed that the Russian Far-East *A. cerana* can be a distinct northern Asia population and can be described as a separate unique subspecies of *Apis cerana ussuriensis* subsp. nov. *Apis cerana koreana* subsp. nov. is also validated and described as a new subspecies.

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