



Genetic diversity of the honeybee *Apis cerana* in Yunnan, China, based on mitochondrial DNA

L. Yin and T. Ji

College of Animal Science and Technology, Yangzhou University,
Yangzhou, China

Corresponding author: T. Ji
E-mail: jiting12@sohu.com

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ABSTRACT. DNA sequence diversity in the tRNA^{leu}-COII portion of the mitochondrial genome was investigated in samples of *Apis cerana* from Yunnan, China. A fragment of about 480 bp in tRNA^{leu}-COII, including a noncoding area and part of COII, was sequenced. The noncoding area was 97-98 bp; 8 haplotypes were found, among which 5 had been reported previously, while 3 were new. The mean diversity of haplotypes was 0.752 ± 0.030 (0.378-0.698), and nucleotide diversity was 0.01073 ± 0.00087 (0.00412-0.01123). A neighbor-joining tree was constructed based on 73 sequences of noncoding intergenic regions in the mtDNA of *A. cerana* from China and other Asian countries; all haplotypes found in China fell into the mainland Asian group. This result does not support the hypothesis that *A. cerana indica* occurs in southern Yunnan, which was concluded in a recent report based on morphological variation.

Key words: *Apis cerana*; Genetic diversity; Genetic differentiation; mtDNA