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Morphometric and mitochondrial COI-based genomic variability probation in Asian honeybees, *Apis cerana* F. (Hymenoptera: Apidae)

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Honeybees support biodiversity and agricultural productivity by pollinating native plants and important crops. The present investigation examined the morphometric and mitochondrial cytochrome oxidase subunit I (*COI*) gene-based molecular variability of *Apis cerana* F. across twenty locations in Himachal Pradesh, India, varying in agro-climatic conditions. Morphometric analysis revealed significant variations in body length (11.088–12.999 mm), head length (2.785–3.120 mm), thorax length (3.198–3.972 mm), abdomen length (4.350–6.266 mm), antennal length (4.098–4.488 mm), proboscis length (5.262–5.820 mm), forewing (8.608–8.950 mm) x (2.760–3.145 mm), hindwing (6.068–6.426 mm) x (1.665–1.795 mm), and hamuli number (17.550–19.600). Such variations may suggest the impact of environmental factors and other natural influences. The mitochondrial *COI* gene analysis revealed genetic similarity between the Himachal Pradesh population and its neighbouring Chinese *A. cerana*. Phylogenetic analysis delineated two distinct clades, reflecting population structure influenced by environmental and genetic factors. This combined approach allows for cross-species comparisons, shedding light on the evolutionary relationships between *A. cerana* and other native bees.

Keywords: *mtCOI*, Genetic variability, North Western Himalaya