

# Evaluating Regional-scale Genetic Structure of Eastern Honey Bee Populations

Although honey bees (genus *Apis* L.) can be found all over the world, much of their distribution is influenced by human beings because of their importance in agriculture and honey production. *Apis cerana* Fabricius, the principle mainland species of *Apis* s.str. in Asia, remains an amalgamation of populations with considerable variation and regionally specialized morphotypes. A recent, large-scale multivariate analysis of morphometric traits across *A. cerana* populations revealed six of their distinct morphoclusters.

Prof. TAN Ken's team from Xishuangbanna Tropical Botanical Garden (XTBG) and their collaborators evaluated the regional-scale genetic structure of Eastern honey bee populations across the Himalayan region in southwestern China and Nepal using those *mtDNA* markers employed in previous studies. Then they used the data to detect whether or not there existed distinct genetic divisions within the region and to what extent there might be significant retrogression resulting from introductions by apiculturists.

The researchers collected worker bees representing 58 colonies of *A. Cerana* from local apiaries around the Himalayas and southwestern China, including five provinces in China and an area in Nepal. By using the classical phenol-chloroform method, the researchers extracted genomic

DNA from the thorax of individual bees. The *mtDNA* fragment used for this project spanned the COI and COII genes and included both coding and non-coding regions.

A total of 14 haplotypes were detected among the 58 sampled sequences, including 11 newly identified haplotypes and 3 previously reported (Japan1, China2, and China4). The network analysis of haplotypes clustered the samples from Yunnan with those from Nepal, whereas the haplotypes from the southern (Yunnan, Nepal) and northern (Tibet) populations did not form distinct clusters, respectively.

When compared with neighboring areas in southwestern China, a strong divide between southern and northern populations in the Himalayan region (i.e., ranging between Nepal and Tibet) was not recovered.

The result indicated that there was significant gene flow between honey bee populations on the two sides of the Himalayan range.



Eastern honey bee (*Apis cerana*).  
Credit: Charles Lam – Flickr.

Moreover, it is likely that regional beekeepers have moved and traded colonies for centuries across the region, thereby bringing back into genetic contact populations that may have gradually become isolated over larger expanses of geological time.

Their study entitled “Haplotype Diversity and Genetic Similarity among Populations of the Eastern Honey Bee from Himalaya-Southwest China and Nepal (Hymenoptera: Apidae)” has been published in *Apidologie*.

Locations of sampling sites across the Himalayan region.

