

GENOMIC SPOTLIGHT ON A DIVERSITY HOTSPOT OF HONEY BEE–*VARROA* SPP. ASSOCIATIONS

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Abstract

Allopatric speciation is a major driver of biodiversity, particularly in island systems where geographic isolation, environmental heterogeneity, and limited dispersal promote genetic divergence. Islands can thus be used as natural laboratories for studying evolutionary processes, including host–parasite coevolution. The Philippine archipelago represents an ideal region for studying the interactions between honey bees and *Varroa* spp. mites due to the considerable taxonomic diversity of these organisms occurring there. In addition to native Eastern honey bees (*Apis cerana*), Western honey bees (*Apis mellifera*) have been widely introduced for commercial beekeeping. Previous studies indicate that Philippine *A. cerana* and associated *Varroa* spp. populations are genetically distinct from mainland Asian populations, with substantial differentiation also occurring among islands. However, the extent and determinants of this variation remain poorly understood. Here, we use population genomic approaches to characterise genetic variation in *A. cerana*, *A. mellifera*, and their associated *Varroa* spp. mites sampled across multiple islands. Specifically, we investigate how island geography, host ecology, and human-mediated bee movement are associated with patterns of dispersal, gene flow, and adaptation in hosts and parasites. Analyses are ongoing, and results will be presented at the conference. We expect to find (i) ongoing gene flow between allopatric *A. mellifera* populations due to transportation by humans, but not in *A. cerana* populations relying on swarming for dispersal, (ii) host-associated genetic differentiation of *Varroa* spp. mites, with homogenous populations of *V. destructor* of the Korean haplotype primarily linked to introduced *A. mellifera* and more diverse local *Varroa* spp. lineages associated with *A. cerana*, and (iii) candidate genomic regions potentially involved in host-parasite interactions. By integrating genomic data from both hosts and parasites, this study will provide new insights into the drivers of diversification, adaptation, and coevolution of *Apis-Varroa* systems in a biodiversity hotspot.