NUS National University of Singapore
Department of Biological Sciences
Faculty of Science

BIOLOGY COLLOQUIUM

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Museum samples reveal population genomic changes associated with a rapid evolutionary response by wild honey bees (*Apis mellifera*) to a novel parasite

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Understanding genetic changes caused by novel parasites can reveal mechanisms of adaptation and genetic robustness. Here we examine the population genomic changes in wild colonies of honey bees (Apis mellifera) following exposure to the ectoparasitic mite (Varroa destructor), the main causative agent of high levels of colony mortality in Europe and North America. Using a novel PCR-free library preparation method, we sequenced whole genomes from museum specimens collected from a population of wild, mite-free colonies in 1977, and directly compared their allele frequencies to those of specimens collected from the same population in 2010, more than decade after the arrival of the mites. Although the density of colonies in this population is the same today as in the past, suggesting a tolerance to the parasite, the comparison reveals evidence of a drastic mitochondrial bottleneck, resulting in the loss of virtually all haplotypic diversity. In contrast, nuclear genetic diversity is unchanged. At least 232 genes, spread throughout the genome, show signs of selection, but there is no evidence of 'hard' selective sweeps, and corresponding islands of reduced genetic diversity, suggesting a complex polygenic response. These data show the robustness of honey bee populations that are genetically diverse and can evolve rapid tolerance to introduced diseases, while also maintaining much of the standing genetic variation.

About the Speaker

I have broad interests in evolutionary biology, focusing mainly on leveraging the power of next-generation tools for answering long-standing basic questions. As a result, I like to explore new techniques, be they laboratory, computational, or involving new sequencing technologies. Although I started my career in the laboratory and in the field, presently I am more of a bioinformatician. Over the past couple of years, I became increasingly interested in applying short-read sequencing to degraded DNA, such as that found in museum, archaeological or other poorly preserved specimens. Having developed a range of tools for high-throughput processing of degraded insects, are harnessing these tools for projects ranging from ecosystem phylogenetics and phylogeography, to studying evolutionary processes using museum samples. Additionally, I maintain an interest in social insect systems, which I worked on during my graduate studies, and also nurture a more recently acquired research program using snake venoms to understand adaptation.

Artwork by Ann Nee, DBS, NUS