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Whole-genome re-sequencing of museum specimens reveals resilience to disease in a feral population of European honey bees

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Gould Seminar Room (Rm 235) Gould Building (Bldg. 116), Linnaeus Way, ANU



For several decades colonies of honeybees (*Apis mellifera*) managed by beekeepers have suffered high mortality due to parasites and pathogens, most notably the ectoparasitic mite *Varroa destructor* and its associated viruses. In contrast, feral colonies are thriving in many places. Little is known about the historical abundance of feral colonies in the United States, but one well-studied population near Ithaca, NY now has the same population density as it did in 1978, despite the arrival of *Varroa* and other diseases in the intervening years (Seeley, 2007). To investigate what selective events occurred in this population during this time, we conducted whole-genome re-sequencings of worker bees collected from feral colonies, using a novel low-error PCR-free library preparation technique. An analysis of 516,702 SNPs reveals evidence for numerous 'soft' selective sweeps in the genomes of these feral honey bees, but no reduction of the effective population size. These results suggest that feral honeybee colonies may be resilient to disease and capable of rapid selective responses when faced with novel parasites and pathogens.

Presented by

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