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Poster P24 Session 2, Room 2

The Azores archipelago harbours heterogeneous honey bee populations shaped by recent human-mediated processes

Henriques, D; Lopes, AR; Pinto, MA

Centro de Investigação de Montanha, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal

The Azores offers a unique stage for studying the impact of human-mediated processes on the genetic composition of honey bee populations. Through beekeeping activities, humans can shape gene pools directly, by selective breeding or by mediating gene flow between geographically isolated lineages, and indirectly, by introducing novel parasites and pathogens. These processes can change dramatically and rapidly in insular populations, due to their geographical isolation and their typically small effective population sizes. Recently, we performed a genetic survey of the Azorean honey bee populations (N=474) using a combination of mtDNA and SNP markers. This survey revealed a very heterogeneous composition across the archipelago, which has been shaped by historical and contemporary human-mediated processes. The most ubiquitous haplotypes (62%) were of African ancestry (sub-lineage AIII), supporting an introduction of the Iberian honey bee *Apis mellifera iberiensis* from the north of mainland Portugal during historical times. However, a tentative breeding program in the 1980s, involving the importation of honey bee queens from a highly divergent eastern European lineage (aka lineage C), associated with the accidental arrival of the dangerous ectoparasitic mite *Varroa destructor* in 2000, led to a dramatic change in the composition of populations from Pico, Faial and Graciosa and, to a lesser extent, from Terceira, São Miguel, Flores, and especially Santa Maria. The SNP and mitochondrial data were not concordant ($r^2=0.082$). In São Miguel, most of the individuals did not show any signal of C-lineage introgression in the nuclear genome although 27% of the colonies harbored a C-lineage mitotype. Contrarily, in Terceira and São Jorge, C-lineage mitotypes were undetected, yet many individuals (84%) showed some level of nuclear introgression ($0.050=Q\text{-values}=0.181$). Graciosa, Pico, and Faial harbour the most introgressed population, as revealed by both markers, and the latter two islands are also colonized by *V. destructor*. Santa Maria harbours the best preserved population, with virtually no C-lineage introgression at both nuclear and mitochondrial compartments, and it is free of *V. destructor*. This is the first genetic study performed in the Azores, offering unique baseline data that can be used for better managing and preserving Azorean populations.