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P133 High sample throughput genotyping for estimating C-lineage introgression in the dark honeybee: an accurate and cost-effective SNP-based tool

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The natural distribution of the honeybee (*Apis mellifera* L.) has been changed by humans in recent decades to such an extent that the formerly widest-spread European subspecies, *Apis mellifera mellifera*, is threatened by extinction through introgression from highly divergent commercial strains in large tracts of its range. Conservation efforts for *A. m. mellifera* are underway in multiple European countries requiring reliable and cost-efficient molecular tools to identify purebred colonies. Here, we developed four ancestry-informative SNP assays for high sample throughput genotyping using the iPLEX Mass Array system. Our customized assays were tested on DNA from individual and pooled, haploid and diploid honeybee samples extracted from different tissues using a diverse range of protocols. The assays had a high genotyping success rate and yielded accurate genotypes. Performance assessed against whole-genome data showed that individual assays behaved well, although the most accurate introgression estimates were obtained for the four assays combined (117 SNPs). The best compromise between accuracy and genotyping costs was achieved when combining two assays (62 SNPs). We provide a ready-to-use cost-effective tool for accurate molecular identification and estimation of introgression levels to more effectively monitor and manage *A. m. mellifera* conservatories.

P134 A collection status of the world biogeography and population genomics of *Varroa destructor* project

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Globalization has provided opportunities for species to cross geographical barriers and establish outside their native range. The Western honey bee previously geographically isolated from all other *Apis* species was introduced in Asia for more than a century. One unfortunate consequence of this new sympatry was the successful host switch of *Varroa destructor* from the Asian honeybee to the Western honeybee. While the Asian honeybee, original host, co-evolved with *Varroa* mites and developed defense strategies, the Western honeybee was naïve toward this parasite leading to important colony damages. Following beekeeping and honey bee movements, *V. destructor* spread nearly worldwide and is considered as the major destructive force behind colony global collapse. Despite several efforts to track accurately *Varroa* invasion since its host switches, the ancestral origins and pathways of introductions remain unclear. In order to better understand the world biogeography of this successful biological invader, we started to build a *Varroa* mites world collection since 2017. Whole genome sequencing of *V. destructor* collected from different continents, countries, and honey bee subspecies will be used i) to reconstruct the demographic history of the parasite, and ii) study the genetic diversity and connectivity of invasive populations. The current collection contains female mites collected from 560 colonies of *Apis mellifera* from 22 countries resulting from a huge collaborative effort from the honey bee research and beekeeping community. Efforts on improving collection size and coverage are ongoing. A subset of samples has been selected for preliminary sequencing to assess the genetic diversity level within and among apiaries. The results from world population genomics will be valuable to identify the demographic key factors behind the global success of Varroa invasion.