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metric analysis at population level. The diagnostic SNP markers distinguish with high accuracy between evolutionary lineages, and also between major subspecies, while it is more challenging to differentiate closely related subspecies. This study represents a comprehensive survey of *A. mellifera* genetic diversity in Europe, combining genomic and morphometric data for several hitherto unexamined populations. The identified SNP markers permit a fast and cost-effective subspecies identification, and thus are a valuable tool to be applied for conservation purposes.

038 Applying a SNP-based tool for conservation of wild and managed black bees in Ireland

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Apis mellifera mellifera (black bees) is threatened over much of its natural range. However, in Ireland microsatellite and mitochondrial data have shown that a significant population of this subspecies exists in pure form and spread over a large geographical region on the Island. Black bees have been managed and protected by beekeepers on the island, some of who formed the Native Irish Honeybee Society in 2012. The application of a SNP panel that detects hybridization between M and C lineages clearly supports other data in that the majority of beekeepers included who purported to keep black bees indeed have bees that show very low to no introgression from the C lineage. Furthermore, SNP data has also been applied to the first feral bee colonies located in Ireland subsequent to the introduction of Varroa. Long considered extinct, feral bees sampled to date show high levels of *A. m. mellifera* purity using SNPs. Here we will present this data and also discuss the use of this SNP panel to elucidate patterns in colour variation and honeybee subspecies purity in wild and managed bees towards improving conservation approaches in the face of potential hybridization threat.

039 Genetic models for long-term simulation studies in honeybee breeding

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The EU project SMARTBEES (www.smartbees.eu) will implement breeding programs for various European honeybee races to improve their resilience. For these breeding programs, two conflicting interests have to be met. While striving for gain in the genetic quality of the bees, it is imperative to maintain genetic variability within the population.
In animal breeding, Monte Carlo simulations is a widely used tool to predict the effects of different breeding strategies on the genetic gain, the average inbreeding and the loss of genetic variance in a population. The simulation studies are vital for reliable long-term predictions on the evolution of genetic variability. Thus a suitable model must be chosen in respect of the biological features of honeybees.
There are two main options to model animal genetics in such simulations. In finite locus models (FLM), a trait is genetically controlled by a finite number of gene loci with differing influences. These models yield complex and time intensive simulations. The infinitesimal model (IM) on the other hand assumes infinitely many loci, each of which has the same infinitesimal influence on the trait. This leads to simplifications in the implementation and reduction of the simulation run-times.
We compared the behavior of these genetic models in simulations of honeybee breeding schemes and found major differences in simulations that exceeded the time scale of 20 years. In a simulation setting of a population with 300 colonies per year and intense selection over 100 years, the FLM showed a realistic decrease of genetic variance of 79-92% whereas the variance in the IM only halved (47%).
We therefore conclude that long-term simulation studies in honeybee breeding should rely on FLM as the IM underestimates the dangers of losing genetic variety in the population.
With the FLM, we undertook further investigations, amongst other things on the importance of safe mating control for breeding success.

ORAL PRESENTATIONS