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PP-453 [Bee Biology]

Genetic diversity in honey bees:
a glimpse into long-term evolutionary history and recent human impacts

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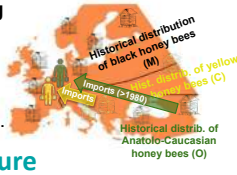
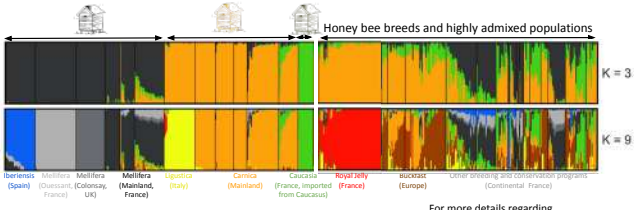
Background & Main Results

For *Apis mellifera*, as with any species, **preserving high genetic diversity is key to maintaining adaptability** and ensuring long-term persistence. However, the dynamics of its genetic diversity and the impacts of modern beekeeping remain debated.



During the last decade, we collected **and whole genome sequenced 1000+ haploid males from several subspecies** (including M, C and O lineages) and breeds (including Buckfast and Royal Jelly-producing ones) in Europe.

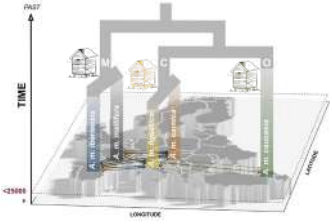
1 Population structure



We revealed clear genetic structure, with distinct lineages corresponding to regions of origin, as well as specific backgrounds for the Buckfast and Royal Jelly breeds *A. m. mellifera* populations conserved on small islands exhibited no introgression.

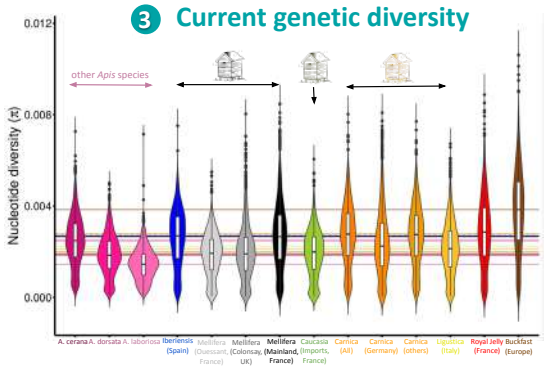
For more details regarding the genetic structure:

2 Long-term evolutionary history



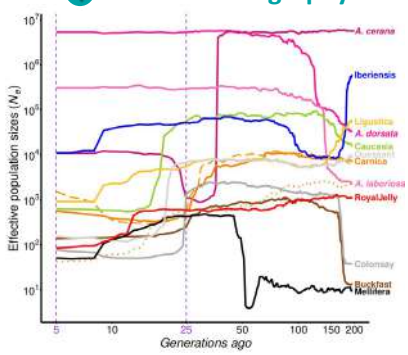
Using demographic modeling based on Approximate Bayesian Computation, we inferred long divergence (up to 1 million generations) and relatively recent (postglacial) secondary contacts pre-dating modern beekeeping.

3 Current genetic diversity



We observed variable levels of diversity among the different clusters. Black honey bee populations from island conservatories exhibited the lowest genetic diversity.

4 Recent demography

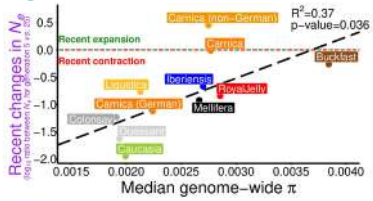


We inferred recent changes in population sizes (*Ne*) and detected bottlenecks in most populations over the last 25 gen.

Conclusions

We uncovered secondary contacts between lineages pre-dating modern beekeeping. However, recent practices have induced bottlenecks, reducing their genetic diversity, especially in black honey bees from conservatories, raising concerns about the long-term sustainability.

5 Recent human impacts



We observed that the widespread bottlenecks over the past 25 generations, consistent with the impact of modern beekeeping practices, explains their present-day diversity.

Prospects

We aim to explore how reduced genetic diversity translates into deleterious mutation load. Although an increased load is expected under the nearly neutral theory of molecular evolution, haplodiploidy may counterbalance its accumulation.

More in our recent paper:

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For Apis mellifera, as for any species, preserving a sufficiently high genetic diversity is essential for adaptability and, consequently, long-term persistence. This explains (i) why genetic diversity is considered as one of the three fundamental units of biodiversity and (ii) why goal A of the UN CBD 15 (2022 Kunming-Montreal conference) emphasizes the importance of maintaining genetic diversity in both wild and domesticated species to safeguard species' adaptive potential. In practice, tracing genetic diversity over time is complex, but demographic modeling using large genomic datasets can provide insights into both natural processes and human-driven impacts. We have recently conducted a large-scale genomic analysis to trace honey bee evolution and assess diversity across three main lineages (M, C and O). Using whole-genome resequencing from 9 genetic groups, we investigated the history of divergence, gene flow, and recent changes in effective population sizes. Our demographic inferences based on Approximate Bayesian Computations suggest that A. mellifera diversity was partly shaped by past climate events, with spells of isolation during glacial periods, and secondary contacts with gene flow between lineages following postglacial expansions. These processes predate beekeeping, supporting historical gene flow between the M and C lineages. Demographic modeling based on linkage disequilibrium revealed moderate to strong bottlenecks over the past 25 generations. Coupled with whole-genome diversity analyses, our results suggest that modern beekeeping practices (e.g. queen rearing) have substantially reduced the diversity of honey bees. In particular, we highlight genetic bottlenecks in black honey bee (A. m. mellifera) populations from two island conservatories. Our study provides key insights about the determinants of present-day genetic diversity in honeybees. Given the pivotal role of A. mellifera for wild plant and crop pollination, the observed loss of diversity raises concerns about the long-term sustainability of the current trajectory. We stress the need for increased public funding for conservatories to safeguard genetic resources.