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NEW ZEALAND

Genetic Structure of the New Zealand Honey Bee

Unexpected African lineage markers and their implications for selective breeding

Between 2022 and 2023, honey bee samples were collected from four distinct regions of New Zealand. DNA analysis and SNP genotyping were conducted to determine genetic origins and assess hybridisation levels. The study focused on identifying markers distinguishing Eastern European (C lineage), Western European (M lineage), African (A lineage), and Middle Eastern (O lineage) genetic origins.

New Zealand's honey bee populations present a unique case study in genetic isolation and controlled breeding. This research investigated the genetic structure of *Apis mellifera* populations in New Zealand, focusing on unexpected African genetic markers and their implications for breeding programs. The study utilized high-resolution SNP genotyping to characterize genetic admixture patterns and evaluate their potential significance for apicultural practices.

METHODS

- Comprehensive genetic analysis revealed varying levels of lineage admixture across sampled populations (see figure. 1):
 - Eastern European (C) lineage was dominant, comprising 78-94% of genetic composition
 - Western European (M) lineage was consistently present in all samples, ranging from 4.2% to 22.1%
 - African (A) lineage markers were either absent or present at low levels (0.7-6%)
 - Middle Eastern (O) lineage showed minimal contribution
- The presence of African genetic markers, despite no historical records of direct African honey bee introductions, suggests complex patterns of genetic inheritance through indirect pathways.
- The consistent presence of M-lineage markers in all samples indicates the persistent influence of historical *A. m. mellifera* imports.

Three primary hypotheses explain the presence of African genetic markers:

- Indirect introduction through Australian imports, where honey bees contain ~4-5% African genetic admixture
- Possible undocumented historical imports of reproductive material
- Natural selection favoring specific African genetic traits beneficial in local conditions

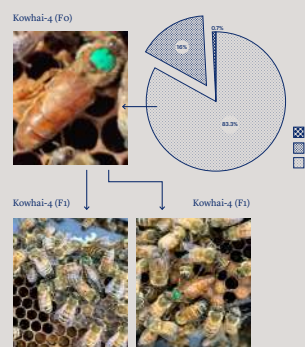
Regional variations in genetic composition were observed. This genetic heterogeneity across regions likely reflects the complex interplay between human-mediated breeding choices and the historical development of beekeeping in different parts of New Zealand, rather than representing a single causative factor. While previous understanding of New Zealand honey bee populations was based on managed European lineages, our findings reveal more complex patterns of genetic admixture. The detection of African genetic markers, even at low levels, highlights the importance of using advanced genetic monitoring tools in breeding programs. This unexpected genetic complexity emphasizes the need for more precise molecular diagnostic approaches in selection programs, as even moderate levels of genetic introgression can affect breeding outcomes and population management strategies. (see figure. 2)

CONCLUSION

Our research demonstrates the complexity of honey bee genetic structure in isolated populations and highlights the importance of comprehensive genetic monitoring in breeding programs. Future breeding strategies should focus on maintaining beneficial genetic diversity while ensuring population stability and preventing uncontrolled hybridisation.

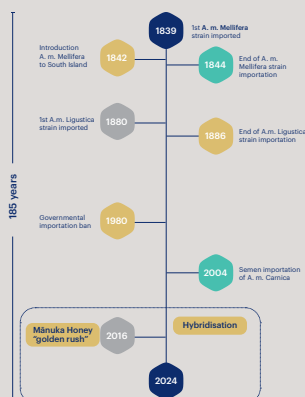
The findings contribute to our understanding of honey bee evolution in isolated environments and provide valuable insights for apicultural practices worldwide. This research emphasizes the need for continued genetic monitoring and evidence-based breeding strategies in maintaining sustainable honey bee populations NZ.

Figure 1. Proportion of ancestry from Eastern European (C), Western European (M), and African (A) lineages.



Genomic ancestry of queen Kowhai-4 (F), inferred from SNP-based admixture analysis. Results indicate predominance of C lineage (Carniolan, 83.3%), with minor M (16.6%) and A (0.7%) lineage components. Analysis performed externally; reference panel not disclosed.

Figure 2. History Timeline (185 years)



Genetic structure of new zealand honey bees: unexpected african lineage markers and their implications for selective breeding

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Between 2022 and 2023, honey bee samples were collected from four distinct regions of New Zealand.

1. Comprehensive genetic analysis revealed varying levels of lineage admixture across sampled populations:
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 - African (A) lineage markers were either absent or present at low levels (0.7-6%)
 - Middle Eastern (O) lineage was not detected
2. The presence of African genetic markers, despite no historical records of direct African honey bee introductions, suggests complex patterns of genetic inheritance through indirect pathways.
3. The consistent presence of M-lineage markers in all samples indicates the persistent influence of historical *A. m. mellifera* imports.

Regional variations in genetic composition were observed. This genetic heterogeneity across regions likely reflects the complex interplay between human-mediated breeding choices and the historical development of beekeeping in different parts of New Zealand, rather than representing a single causative factor. While previous understanding of New Zealand honey bee populations was based on managed European lineages, our findings reveal more complex patterns of genetic admixture. This unexpected genetic complexity emphasizes the need for more precise molecular diagnostic approaches in selection programs, as even moderate levels of genetic introgression can affect breeding outcomes and population management strategies. Our research demonstrates the complexity of honey bee genetic structure in isolated populations and highlights the importance of comprehensive genetic monitoring in breeding programs. The findings contribute to our understanding of honey bee evolution in isolated environments and provide valuable insights for apicultural practices worldwide. This research emphasizes the need for continued genetic monitoring and evidence-based breeding strategies in maintaining sustainable honey bee populations NZ.