Better-B newsletter

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Genetic diversity is crucial for resilience**. Honeybee colonies with high genetic variation are healthier and more able to deal with stressors. Genetic diversity is also the raw material for evolution, enabling honeybee populations to adapt to local climates and environmental conditions and to evolve resistance to pathogens. To better understand how genetic diversity promotes resilience, the Better-B project has sequenced the entire genomes of over one thousand honeybees. The results have identified genes that are likely important for adaptation to different climates. We have also used genome sequencing to study the genetic changes that occur when honeybee populations survive exposure to the Varroa mite without treatment, highlighting the natural ability of honeybees to maintain genetic diversity. **Ultimately, the goal of this research is to allow beekeepers to select honeybees with genetic backgrounds that are resilient and well-adapted to their local environments.

How are honeybees adapted to their local environments?

Beekeeping in Europe is practiced in diverse climates, ranging from the hot and arid Mediterranean summers to long Scandinavian winters, in conditions that are altering rapidly due to climate change. It is crucial to ensure that honeybees are genetically adapted to their local climatic conditions to promote resilience and colony survival. To uncover the genes that are important for adaptation to climate, the research groups of Matthew Webster (UU) and Alice Pinto (IPB), in collaboration with many other Better-B partners, have sequenced the genomes of more than 1000 honeybees collected from all over Europe.

The evolutionary history of honeybees

If we want to understand how honeybees are adapted to their environment, then we need to know their evolutionary history. Honeybees have been present in Europe for nearly one million years, long before people arrived. Due to massive climatic fluctuations of ice ages and geographical barriers such as mountain ranges, two major evolutionary lineages became isolated from each other and accumulated large genetic differences. These are called the M lineage - to which the Dark bee (*Apis mellifera mellifera*) and the Iberian bee (*A. m. iberiensis*) belong- and the C lineage- to which the Italian bee (*A. m. ligustica*) and the Carnolian bee (*A. m. carnica*) belong. The native range of the M lineage in Europe stretches throughout the west from Scandinavia to the Iberian Peninsula, whereas the C lineage is restricted to the southeast of Europe, the Italian peninsula and the Balkans.

Much more recently, in the last 150 years, the natural distribution of honeybees in Europe has been disrupted by movement of colonies and importation of queens by beekeepers. This has mainly involved importation of C-lineage to countries in the north, which has affected the genetic background of M-lineage honeybees native to those areas. The mixture of honeybee lineages increases genetic diversity, but can also disrupt adaptations between genes and environment, reducing resilience of local populations. By studying honeybee genomes, we aim to uncover the effect of transport of bees on how well they are genetically adapted to their environments. We also aim to identify genes that control traits important for adaptation to climate.

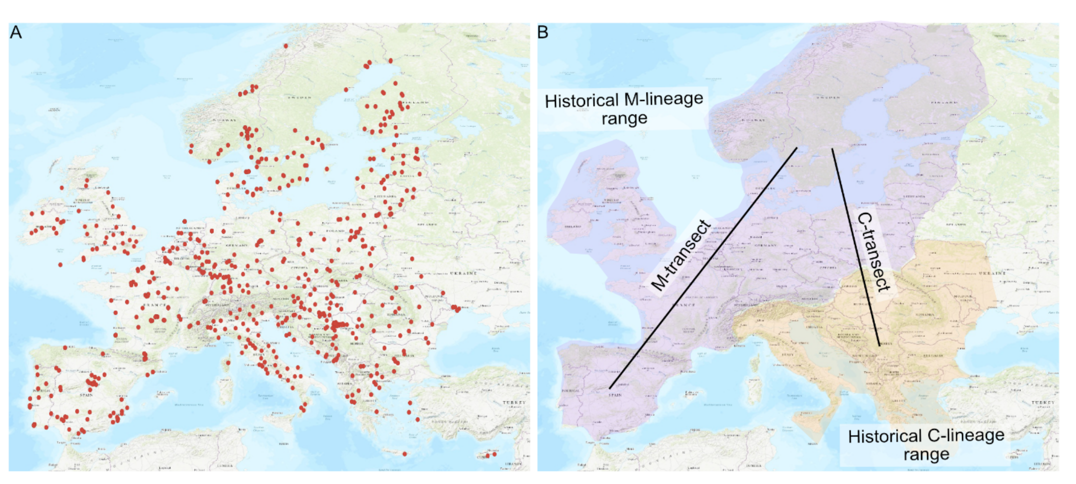

Figure 1: (A) Sampling locations of over 1000 bees from 33 European countries that have had their genomes sequenced by Better-B. (B) The historical range of M and C lineage bees that are native to Europe are shaded. This distribution has been disrupted by transport of bees from the C lineage further north. We have compared the genomes of bees along two north-south transects to find genes that control adaptation to climate.

1000 honeybee genomes

The Better-B project has sequenced genomes of worker bees collected throughout Europe (Fig 1A). These data have revealed that transport of honeybees has had a massive effect on their genetic composition. Countries including Germany, Belgium, Netherlands, and those in Scandinavia now commonly have >90% of their genetic background made up of the imported C lineage. It is possible that this large-scale importation has disrupted adaptation to local environment, resulting in bees that are less resilient.

Taking this mixed genetic background into account, we compared honeybee populations along two north-south transects to identify genes that could explain adaptation to climate (Fig 1B). The M-lineage transect compares honeybees in the Iberian Peninsula with those in northern Europe, which must be collected from specific "conservation" populations unaffected by importation of C-lineage bees. The C-lineage transect compares honeybees from southeastern Europe with those from northern Europe. By making these comparisons, we can identify specific genetic variants that differ in frequency between northern and southern populations and can explain adaptation to different climates.

Genes for climate adaptation

We have used a wide range of statistical methods to identify genes for adaptation to climate. These involve comparing genomes of bees living at different latitudes. We also search for correlations between gene frequencies and climatic measurements such as temperature and rainfall. Using these methods, we have identified several genes with different variants in northern and southern countries. One particularly interesting gene belongs to the "myosin heavy chain" family, which produces proteins that are important components of muscle. Honeybees use their large flight muscles to regulate temperature in the hive, either by generating heat in cold weather or increasing airflow to the hive to cool it down. We hypothesise that different variants of this gene are beneficial depending on whether a colony is in a hot or cold climate. By promoting the use of bees with genetic variants in this gene that match the climate, we can increase resilience and survival of honeybee colonies.

How do honeybees evolve resistance to *Varroa*?

The *Varroa* mite is the main cause of honeybee colony losses in Europe, and most colonies cannot survive without chemical treatment. Nevertheless, over the last two decades, several honeybee populations have evolved natural resistance to this parasite and can survive without intervention by beekeepers. The Better-B project has investigated four existing *Varroa*-surviving populations and established new populations that are not treated for *Varroa* in nine different locations across Europe. By sequencing the genomes of these populations, we can analyse the changes in genetic variation that occur as populations acquire resistance to *Varroa*.

Genetics of Varroa-surviving colonies

The locations of Varroa-surviving populations are shown in Figure 2. We identified four existing populations in Cluj-Napoca (Romania), Gjerdrum (Norway), De Hoge Veluwe (the Netherlands) and Kalmthout (Belgium). All these populations have survived *Varroa* for many years. The Norwegian population was initiated as early as 1999 and the Dutch population in 2007, whereas both the Belgian and Romanian populations have been treatment-free since 2019. Better-B partners also started nine new populations at the beginning of the project in 2023 in regions with different climates all over Europe. Each location began with an average of ~56 colonies that were managed according to the "Darwinian black box" approach. This protocol ensures that the populations evolve under natural selection by *Varroa* and includes yearly colony splitting for swarm prevention. Out of these populations, two did not survive the first year without *Varroa* treatment, demonstrating its devastating effect on honeybee colonies.

We studied the evolution of all the *Varroa*-surviving populations using whole genome sequencing. We were interested in a few main questions: 1) Do population bottlenecks due to natural selection cause decreased genetic variation? 2) Does low genetic variation increase the risk of population extinction due to *Varroa*? 3) What genetic variants are under selection because they increase resistance to *Varroa*?

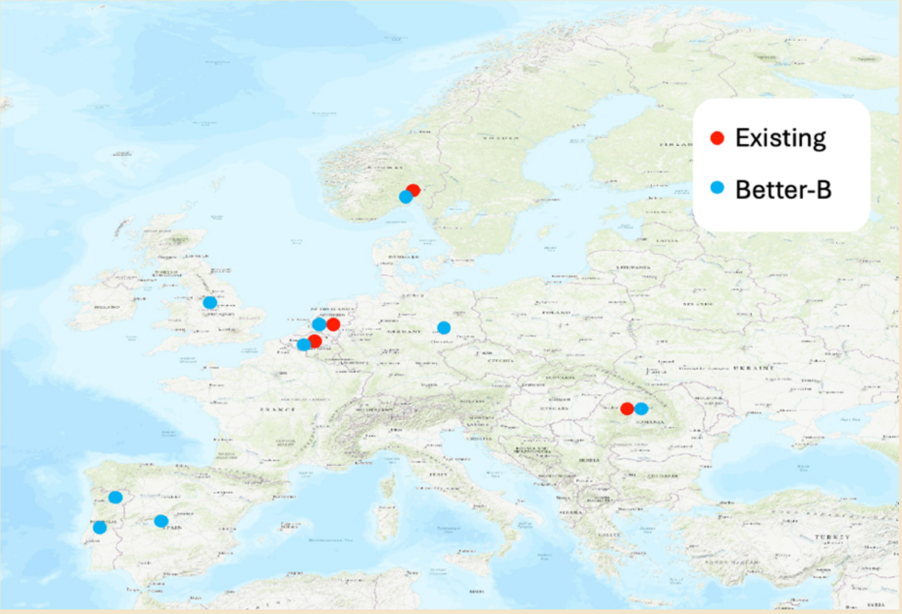

Figure 2: Locations of Varroa-surviving honeybee populations studied as part of Better-B

High levels of genetic diversity in European honeybees

We compared levels of genetic diversity in the four existing *Varroa*-surviving populations with honeybee colonies in nearby regions that were treated for *Varroa*. Surprisingly, there were no consistent differences. This is surprising because the untreated populations experienced substantial reductions in size due to colony mortality, which might be expected to lead to reduced genetic diversity. The results therefore emphasise the natural ability of honeybees to maintain genetic variation through processes such as queens mating with multiple drones.

When we compared genetic diversity among all populations, we found that it correlated most strongly with their historical origins: colonies with a hybrid ancestry were more genetically diverse. However, we did not identify any effect of genetic diversity on the survival of the "Darwinian black box" populations, suggesting that genetic diversity in all these populations is sufficiently high, and that mortality due to *Varroa* is due to other factors.

Comparisons of the four established *Varroa*-surviving populations with surrounding populations that are treated for *Varroa* did not reveal any specific genes responsible for *Varroa* resistance. This is probably because a large number of genes are important for resistance to *Varroa*, and that the genetic variants under selection differ between populations and environments. The "Darwinian black box" experiments performed as part of Better-B will generate several additional *Varroa*-surviving populations, which will be a crucial resource for understanding the genetics of *Varroa* resistance.

What's next?

In the next phase of the project, we will model the future effects of climate change on how bees are adapted to their environment. This will help us to predict the effects of climate change on resilience of honeybee colonies and determine if certain regions of Europe are particularly at risk of colony loss due to changing climate. By identifying specific genetic variants that are matched to a certain climate, we also hope to advise beekeepers on the best adapted honeybee strains for their local conditions.

Darwinian selection experiments are ongoing in nine locations as part of Better-B. These populations are evolving resistance to *Varroa*. By analysing the genetic changes in populations that survive or fail, and by comparing them between populations, we hope to uncover genetic factors that promote colony resilience.

Do you want to know more?

Please join us for our next upcoming public event, which will take place on 25 November 2026 in Bragança, Portugal, and online. We will be holding the event in both English and Portuguese (and a little bit of Spanish).

We will further explore the genetics of the honey bee and local adaptation, learn how the landscape affects resistance to pesticides, and gain an understanding of thermoregulation within the hive. We warmly invite you to discuss with us the Better-B concept for sustainable beekeeping by a two-track management approach separating production and reproduction. In the afternoon, there will be a practical session where we will learn how best to help the bee colony regulate the temperature inside the hive.

Learn more
www.better-b.eu

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Better-B Project

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