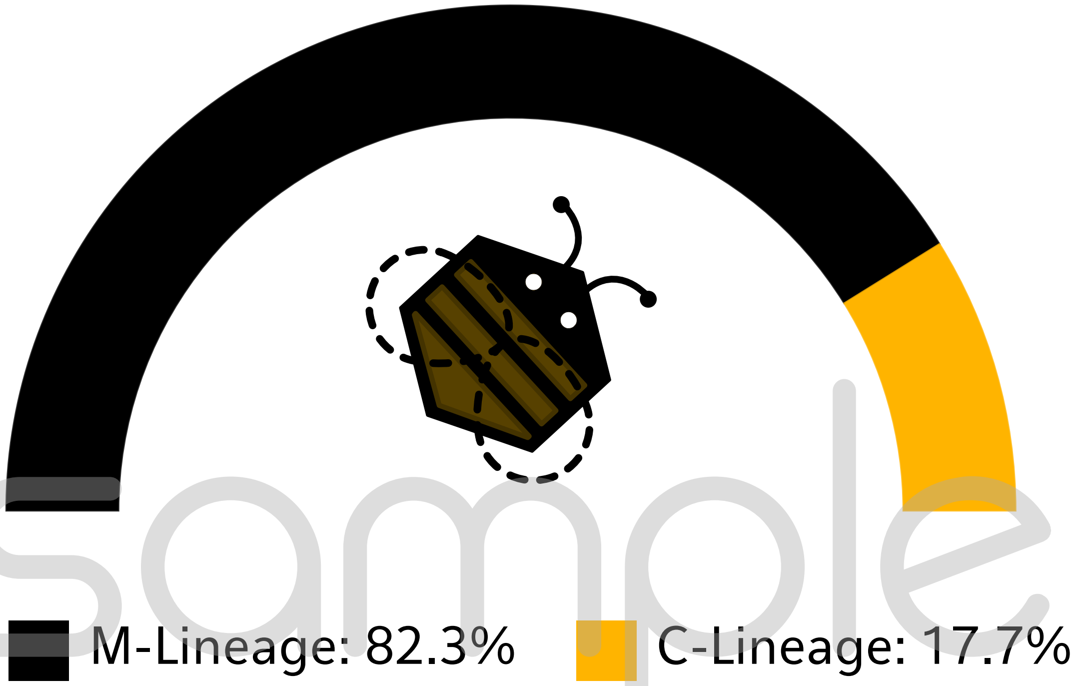
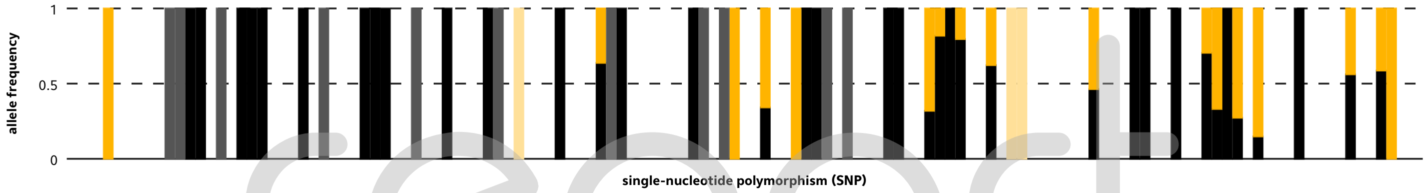
m/c lineage report

Sample ID	Date	Location
0	2021-05-14	56.3,-1.8





m/c lineage admixture assay

This assay analyses a number of variations in the bee's DNA, known as SNPs (single-nucleotide polymorphisms). These SNPs have been shown to differentiate the two main honey bee lineages present in Northern Europe: **M** - *mellifera*, and **C** - *carnica/ligustica*.

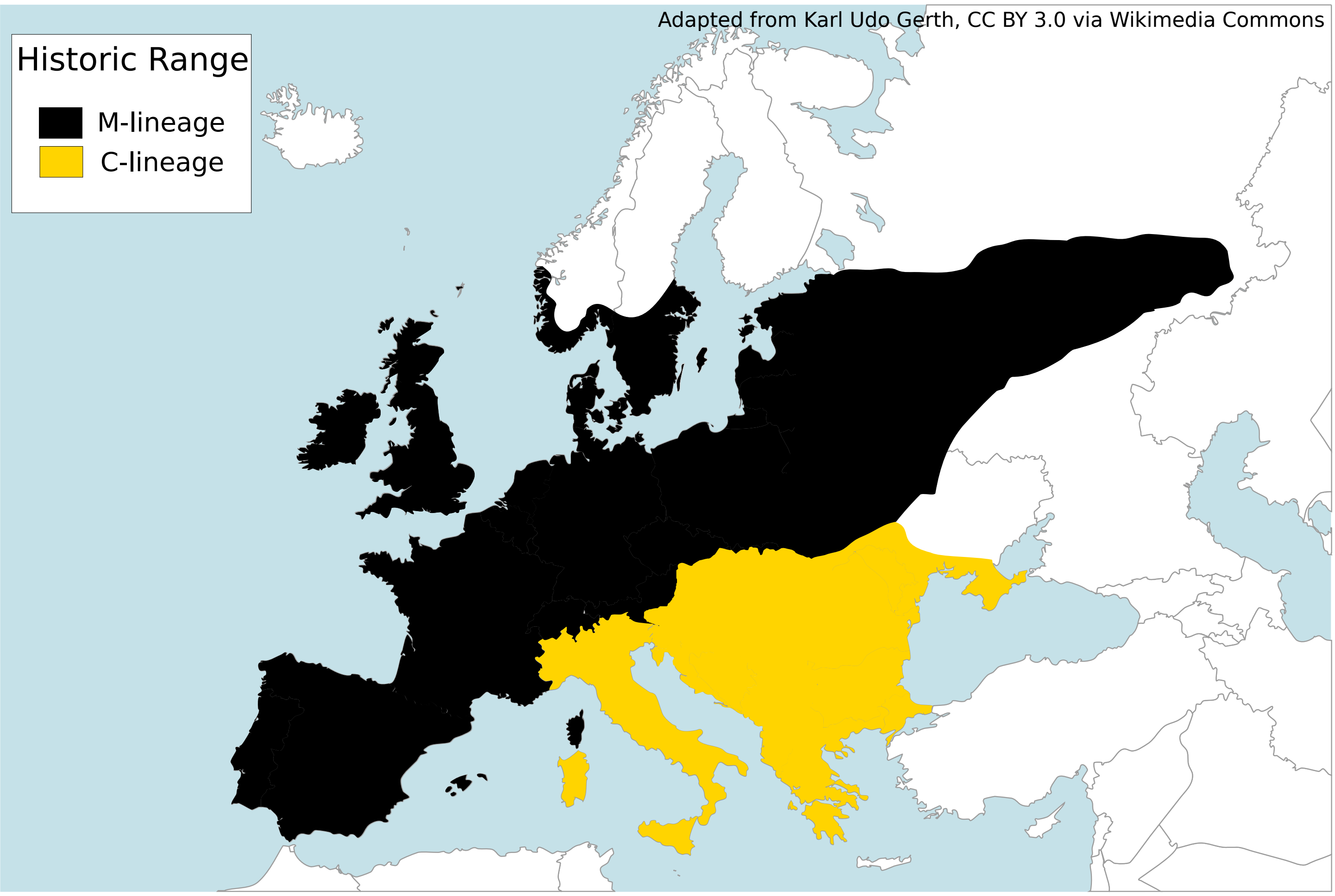
The collective result of the allele frequencies measured across the assay is provided as a "global ancestry estimate", indicated in the top figure. For reference, the stacked bar chart shows the M (black)/C (yellow) lineage allele frequencies at each SNP that passed a certainty threshold. SNPs with allele frequencies that do not pass this threshold are low-confidence, coloured grey and light yellow, and do not contribute to the global ancestry estimate. The y axis ranges from 0 (100% C lineage) to 1 (100% M lineage), providing an indication of admixture levels at discrete regions within the genome. Where a bar is empty that SNP either failed to call for the sample in question, or was excluded from the assay.

honey bee lineages

The Western Honey Bee - *Apis mellifera* - is native to Africa, Europe and western Asia. It can be subdivided into 5 main evolutionary lineages:

- **A** - subspecies from central and southern Africa.
- **C** - subspecies from east and south of the Alps.
- **M** - subspecies from northern and western Europe.
- **O** - subspecies from western Asia.
- **Y** - subspecies from Ethiopia.

Throughout much of Europe the M and C lineages predominate. Rare occurrences of the other lineages can be found where they have been introduced by beekeepers.



Adapted from Karl Udo Gerth, CC BY 3.0 via Wikimedia Commons

Map showing the estimated natural ranges of the M and C lineages prior to human intervention.
Adapted from *A revision of subspecies structure of western honey bee Apis mellifera.* Ilyasov et al. 2020.

Over the last century, high levels of colony movement by beekeepers seeking to develop strains with desired characterstics has resulted in high levels of genetic admixture. Consequently many colonies are now composed of, or exposed to, bees of admixed ancestry. In some areas of the UK and elsewhere reduced levels of admixture can be observed, either through isolation due to landscape topography, reduced beekeeping activity in the area, or through a conscious effort of beekeepers in the area to conserve a particular lineage - such as the dark honey bee on Colonsay (Scotland) and Ouessant (France). The extent of admixture throughout the UK is poorly documented, and through this assay your bees are contributing towards improving our understanding in this area.