Pollenize Project

Devon Honeybee Lineage
01/12/2023

Background

The honey bee subspecies *Apis mellifera mellifera* is native to the United Kingdom and North-Western Europe. Since the mid-19th century, other subspecies of honey bee have been imported into the UK, particularly those from Italy (*A. m. ligustica*) and the Carniola region of Eastern Europe (*A. m. carnica*). These bees have mated with the native bee, resulting in genetic introgression. As a result, it has been suggested that all honey bees in the UK may now be hybridised. However work is ongoing to investigate the level at which introgression has occurred, and whether or not native genetics are still present at significant levels.

Honey Bee Sampling

A call-out was made to beekeepers in Devon who would be willing to sample their colonies to identify the level of hybridisation present across the county. A single adult honey bee was selected from each colony and sent to Beebytes for admixture analysis[1], along with extra information about the colony (geographical location, history etc).


[1] Henriques, D., Browne, K.A., Barnett, M.W. et al. High sample throughput genotyping for estimating C-lineage introgression in the dark honeybee: an accurate and cost-effective SNP-based tool. Sci Rep 8, 8552 (2018).

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Results

Summary

Analysis was successfully performed on 165 samples collected from a wide variety of locations across Devon. DNA was extracted individually from each bee, and analysed to estimate the proportions of M-lineage (*mellifera*) and C-lineage (*ligustica, carnica*) genetic ancestry. The results were analysed in three ways: simple statistical analysis; admixture analysis; and geographical analysis.

Statistical and Admixture Analysis

The samples presented a gradient of genetic admixture, ranging from near-pure M lineage (**94.5% M**) to near-pure C lineage (**92.5% C**). The average (mean) M lineage ancestry observed was **58%** (median **60.7%**, mode **61.4%**, standard deviation **15.5%**). While samples with high C-lineage ancestry may be explained by recent imports, the presence of relatively pure M-lineage bees, as well as a general bias towards M-lineage overall provides evidence that native honey bee genetics continue to persist in England. This is contrary to claims that the native bee was wiped out by the Isle of Wight disease in the early 1900s.[2]
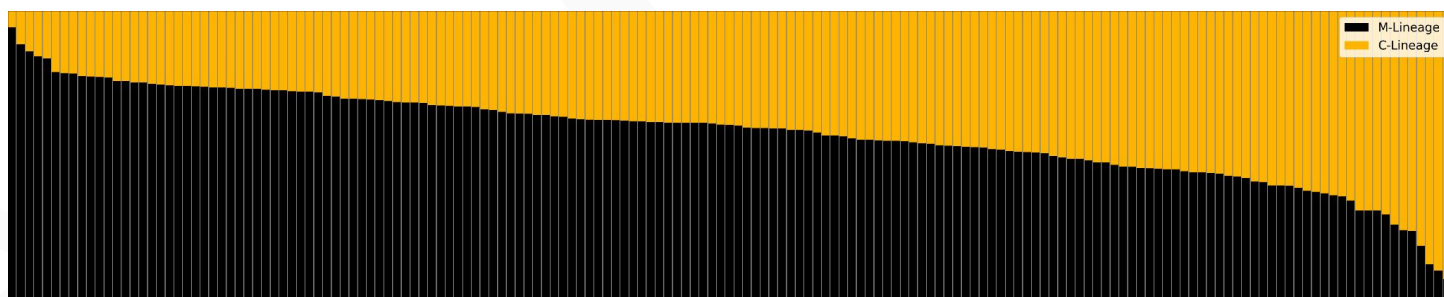
*Admixture Analysis: Each bar represents a single sample, ordered by introgression.*

2   Adam, Brother (1954). Bee Breeding. Bee World, 35(1), 4–13.

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Geographical Analysis

The geographical location of each colony was provided by the beekeeper submitting the sample in the form of either a postcode, what3words reference, or latitude/longitude coordinates. Samples were mapped accordingly, both as individual data points, and also averaged over larger areas .

The individual sample map indicates that admixture proportions appear to be unrelated to geographical location. In some areas, such as around South Molton we observe high M and C scoring samples in neighbouring colonies, where we might otherwise expect more hybridisation from cross-mating.

In other areas however we see neighbouring colonies with similar scores, such as around Torquay. More work is needed to identify whether this is due to colony movement and selection by beekeepers, or a result of matings..
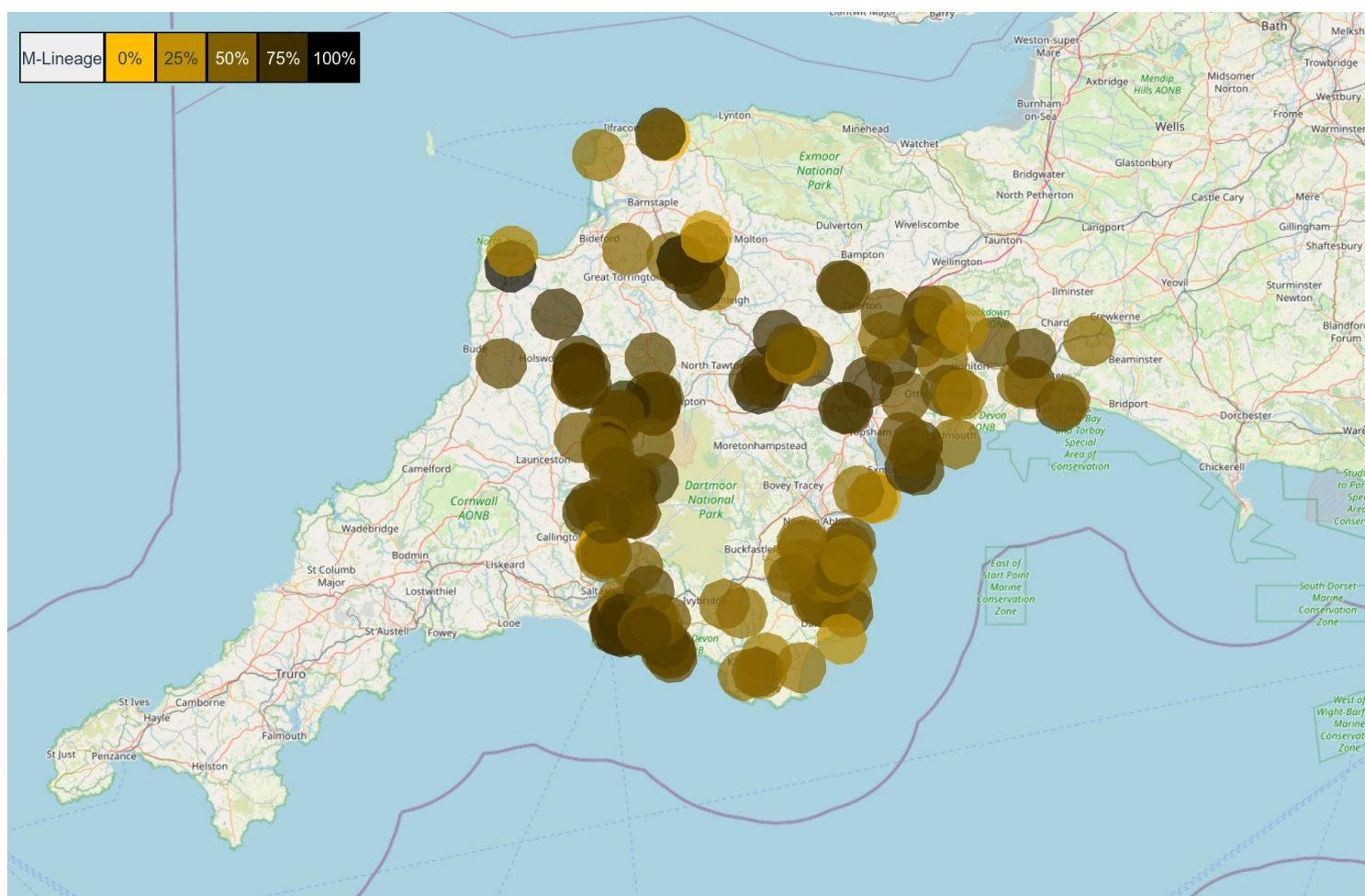

Individual samples, expanded to 5km circles to indicate likely area of forage/mating.

(point centres have been displaced for apiary anonymity)

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Results

By averaging the results geographically we see that admixture levels across Devon fall into a smaller range, with a uniformity that reflects the results of the admixture analysis. While there is variation across the county, there do not appear to be any obvious geographical or topographical effects on hybridisation.

As with the individual samples, we do see some areas with more bias, such as in the north-west and around Plymouth. Again, further work looking at the beekeeping practices in these areas may help identify the cause.
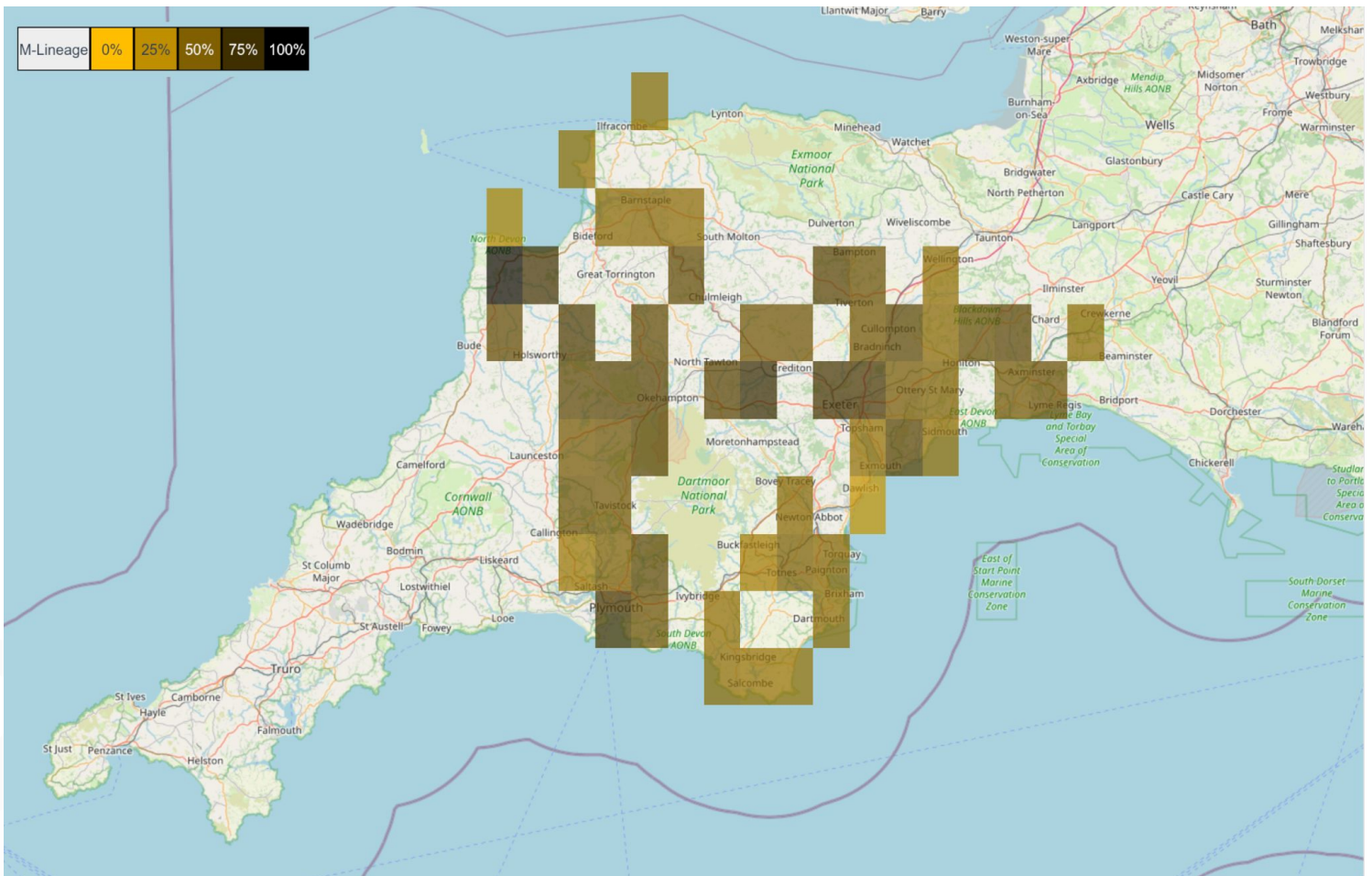
Samples averaged to lat/long 10km x 6km grid squares

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Results

Beekeeper Responses

As part of the sampling process, beekeepers were asked to provide information on the history of their colonies as free-form text. These results were analysed to see if there was a correlation between words potentially associated with M-lineage (*mellifera mellifera, black, dark, native*), C-lineage (*carni, ital, ligustica, yellow*), *Buckfast* and Hybrid (*hybrid, mixed*) samples.

The graph below shows the admixture results accompanied by a second series coloured for samples where a matching word was found in the sample information.

Claims for M-lineage occur across the whole sample range, but with some grouping towards samples with correspondingly high scores. Only 2 samples were explicitly claimed as C-lineage (*Carniolan*), while a number of others were claimed as Buckfast.

The C-lineage claims can be seen to not correspond to samples with high C-lineage purity. It is not clear if these bees were obtained already hybridised from breeders, or if there has been hybridisation since the bees were introduced into Devon.

The Buckfast claims span a wide range of actual results. While there is no formal definition of genetic make-up for the Buckfast strain, M-lineage ancestry commonly accounts around 10% to 20% of the genome.[3] However most of the samples claimed as Buckfast in this study fall outside this range.

While claims of M-lineage ancestry occur across the whole range, it is interesting to note that C-lineage, Hybrid and Buckfast claims all occur in samples with relatively high levels of introgression.
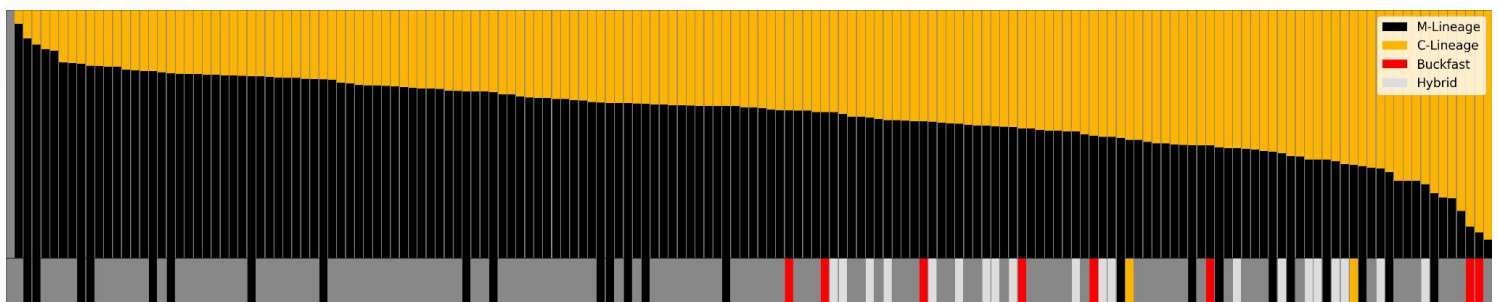
Admixture 'claim' for each sample, shown below actual results

3. Parejo, M, Wragg, D, Gauthier, L, Vignal, A, Neumann, P, Neuditschko, M. Using Whole-Genome Sequence Information to Foster Conservation Efforts for the European Dark Honey Bee, Apis mellifera mellifera. Frontiers in Ecology and Evolution. 4 (2016)

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