

Maternal origin of honeybee (*Apis mellifera*) colonies from across Europe



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Better-B

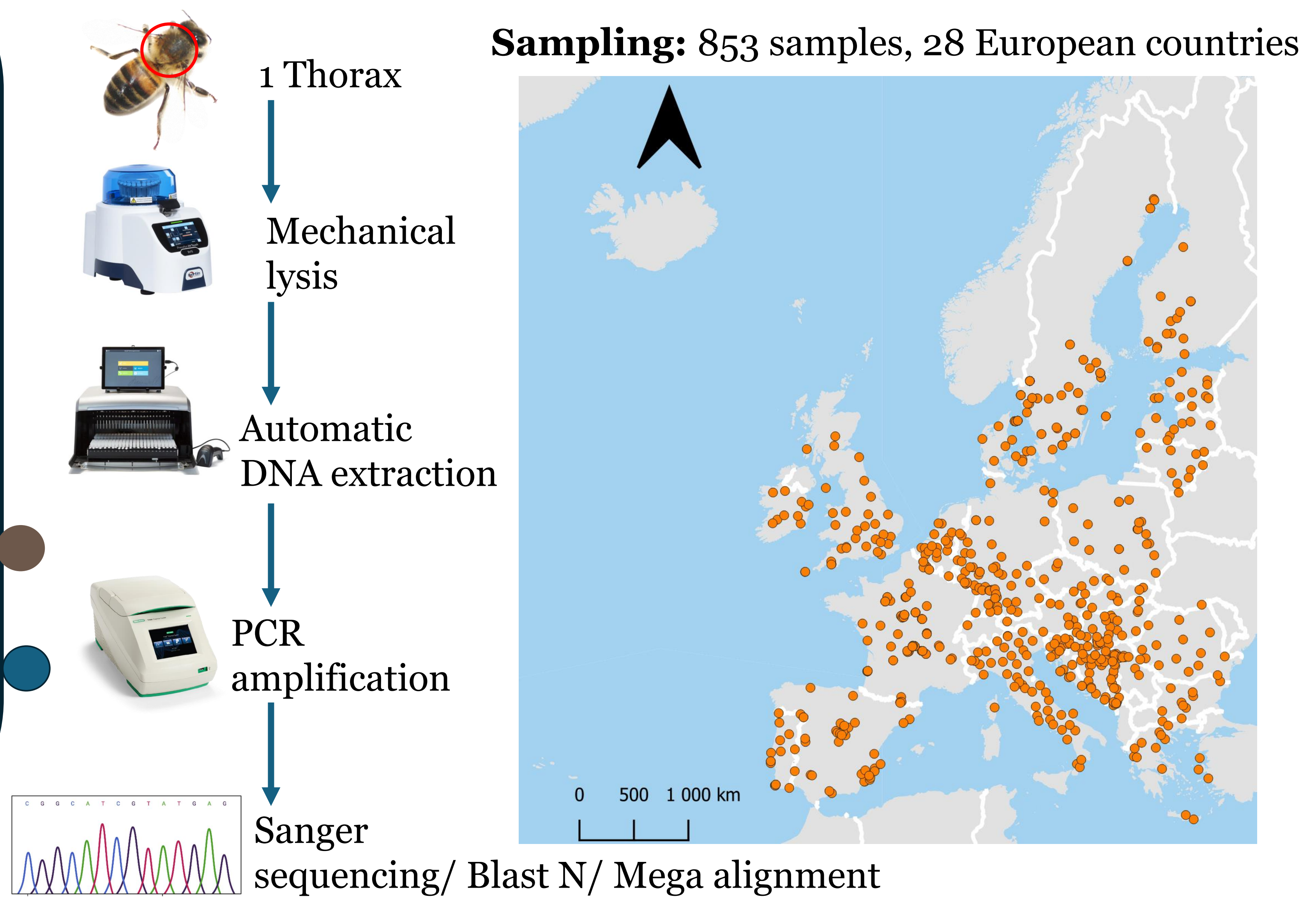
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Introduction

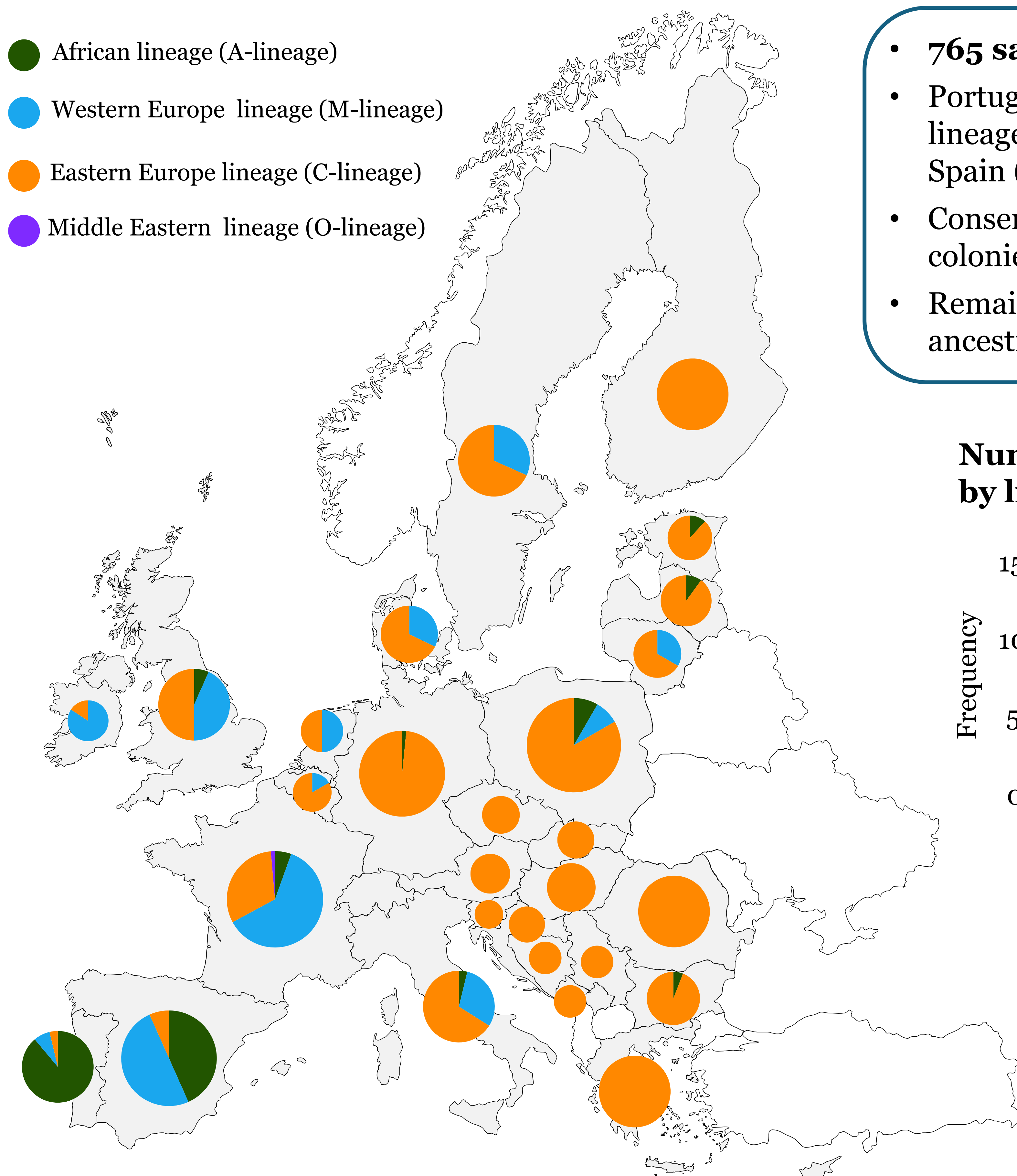
Worldwide commercial beekeeping threatens the native origin of the honeybee (*Apis mellifera*), with beekeepers favouring subspecies of Eastern European C-lineage ancestry due to their docile behaviour and high honey production traits. In many parts of Western and Northern Europe, queens of Western European M-lineage ancestry have been massively replaced by queens of C-lineage ancestry, and this has led to the development of conservation programs aiming at recovering native lines. The maternally-inherited mitochondrial DNA (mtDNA), particularly the intergenic region tRNA^{leu}-cox2, has been the marker of choice for assessing honeybee variation at large geographical scales.

GOAL: assess the mtDNA variation across 28 European countries

Materials & Methods

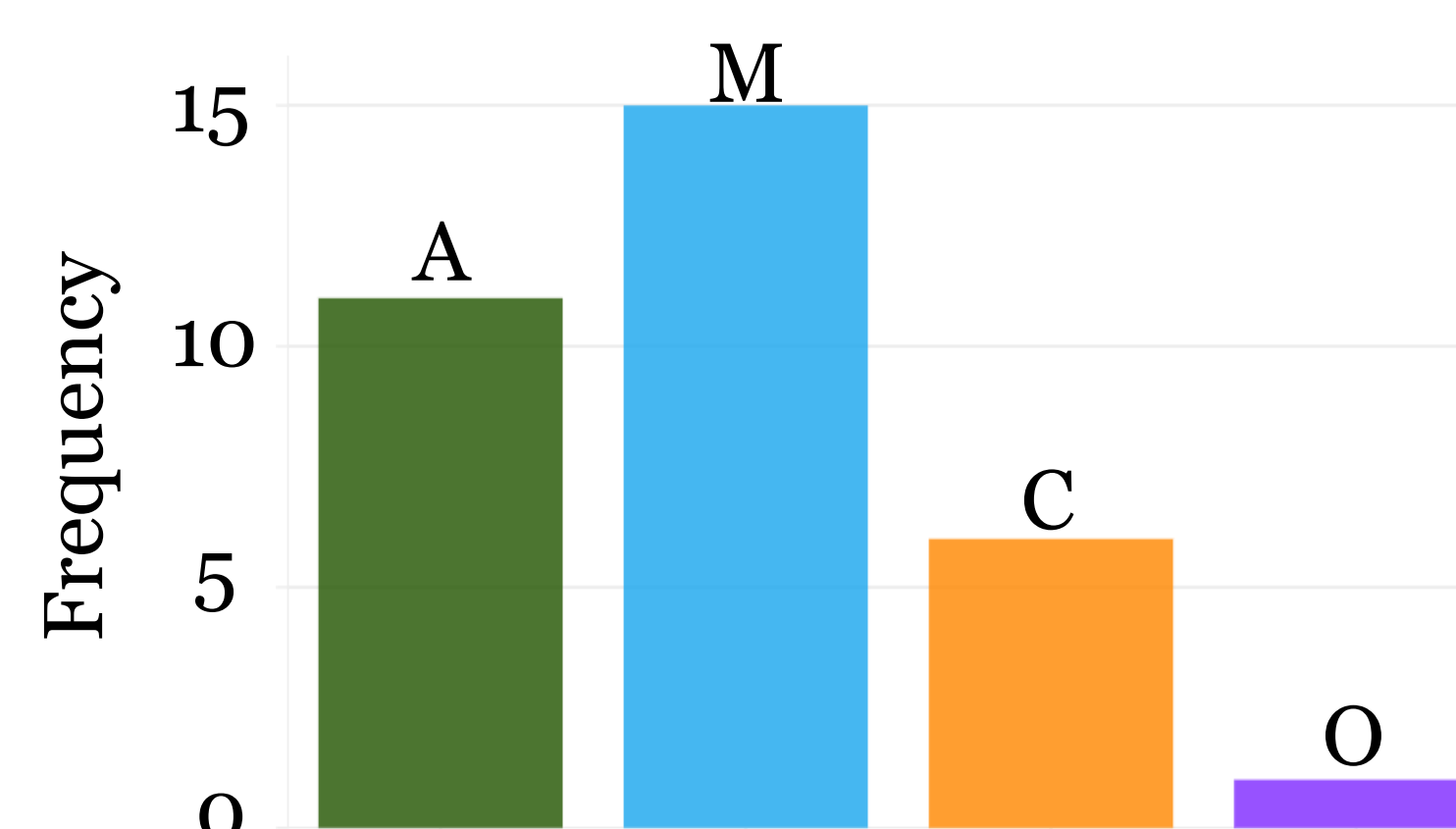


- African lineage (A-lineage)
- Western Europe lineage (M-lineage)
- Eastern Europe lineage (C-lineage)
- Middle Eastern lineage (O-lineage)



- 765 samples** demonstrated good sequencing quality (missing data = 10%)
- Portugal and Spain with a higher number of colonies exhibiting A and M lineage. However, C-lineage colonies were also detected in Portugal (1) and Spain (2).
- Conservation centres in France and Denmark (Læsø) exhibiting M-lineage colonies.
- Remaining countries are dominated by colonies of C-lineage maternal ancestry.

Number of haplotypes by lineage



Haplotypes:

Most frequent **A**:

- A1** (mainly found in Portugal)

Most frequent **M**:

- M4** (France, Denmark, Spain, Ireland, Italy)

Most frequent **C**:

- C2** (Germany, Greece, Italy, and most of eastern countries)
- Only the **Czech Republic** showed exclusive **C1** colonies.

This unprecedented mtDNA analysis across Europe **underscores the worrying dominance of C-lineage genetic variation**, highlighting the **urgent need for strategic conservation efforts to preserve the native genetic diversity of *Apis mellifera***.

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