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Europe is home to 10 subspecies of *Apis mellifera*, classified into four main lineages sensu Ruttner: M (western and northern European), C (southeastern European), A (African), and O (Middle Eastern). However, large-scale movements of honey bee genetic material—driven by transhumance and, more importantly, queen trading—has intensified gene flow, particularly from the C-lineage subspecies *A. m. carnica* and *A. m. ligustica*, threatening the genetic integrity of several subspecies and blurring the genetic boundaries between subspecies.

Here, we analyzed over 1,200 recently collected samples from apiaries in 33 countries using a multi-marker approach: maternally inherited mitochondrial DNA (tRNA^{Leu}-cox2 intergenic region), nuclear genome-wide single nucleotide polymorphisms (SNPs), and wing shape (DeepWings©) to provide the most updated and extensive account of honey bee genetic variation in Europe. Our results reveal a strong dominance of C-lineage ancestry across Europe, with noteworthy introgression signals in island subspecies and *A. m. mellifera* populations outside conservation apiaries. Notably, all three markers consistently captured these broad introgression patterns.

This unprecedented survey highlights a worrying trend of genetic homogenization in European honey bee populations. Moreover, the widespread prevalence of C-lineage genetic introgression underscores the need for conservation efforts to preserve the diversity shaped by evolution, which is crucial for adaptation to growing environmental challenges.

An unparalleled survey of honey bee genetic diversity in Europe: *insights from wing shape, nuclear whole genome, and mitochondrial DNA data*

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Mountain Regions



APIMONDIA 2025
Copenhagen
Denmark



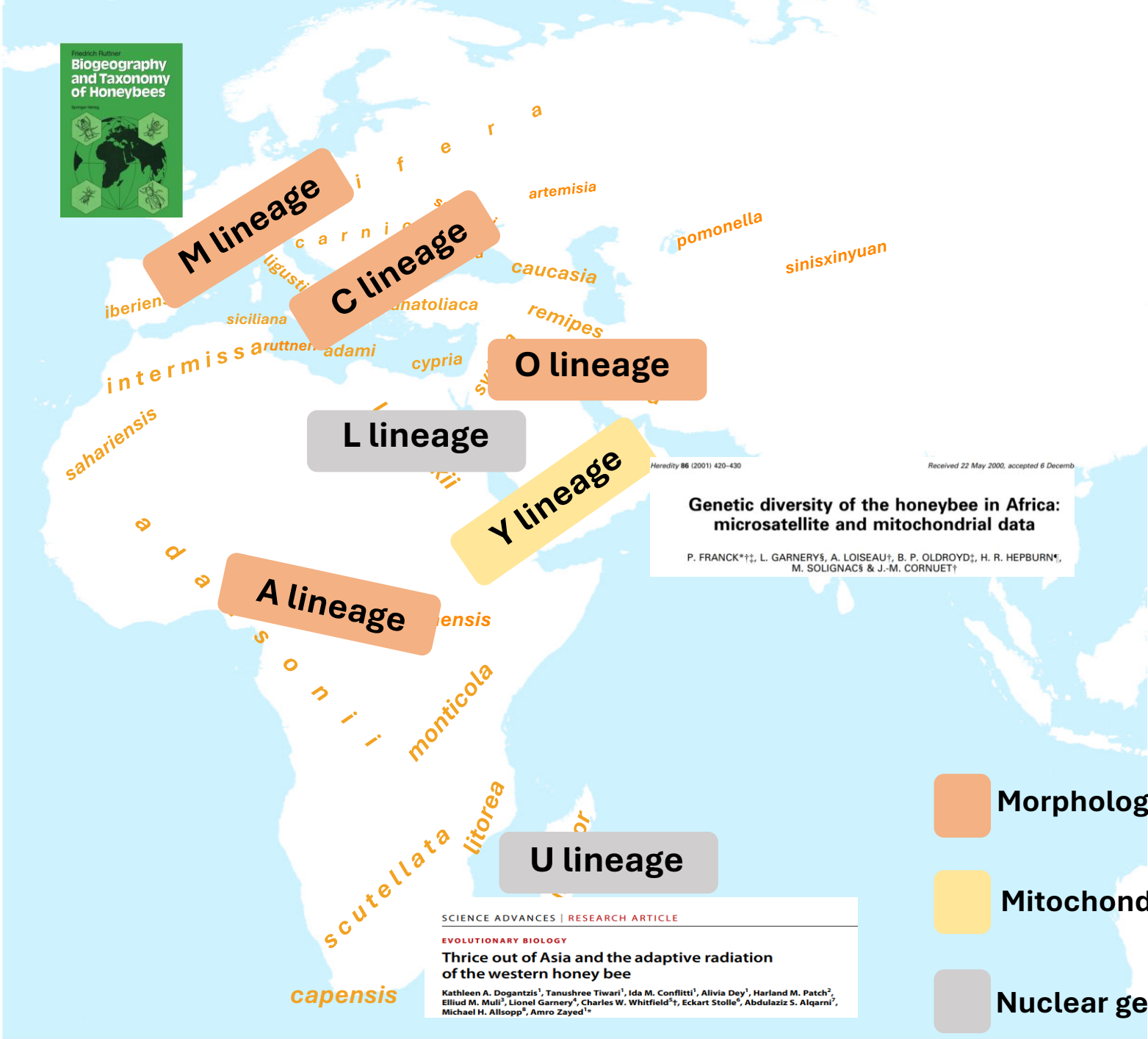
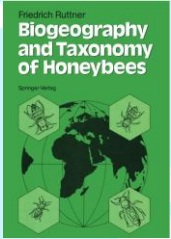
Apis mellifera subspecies

31

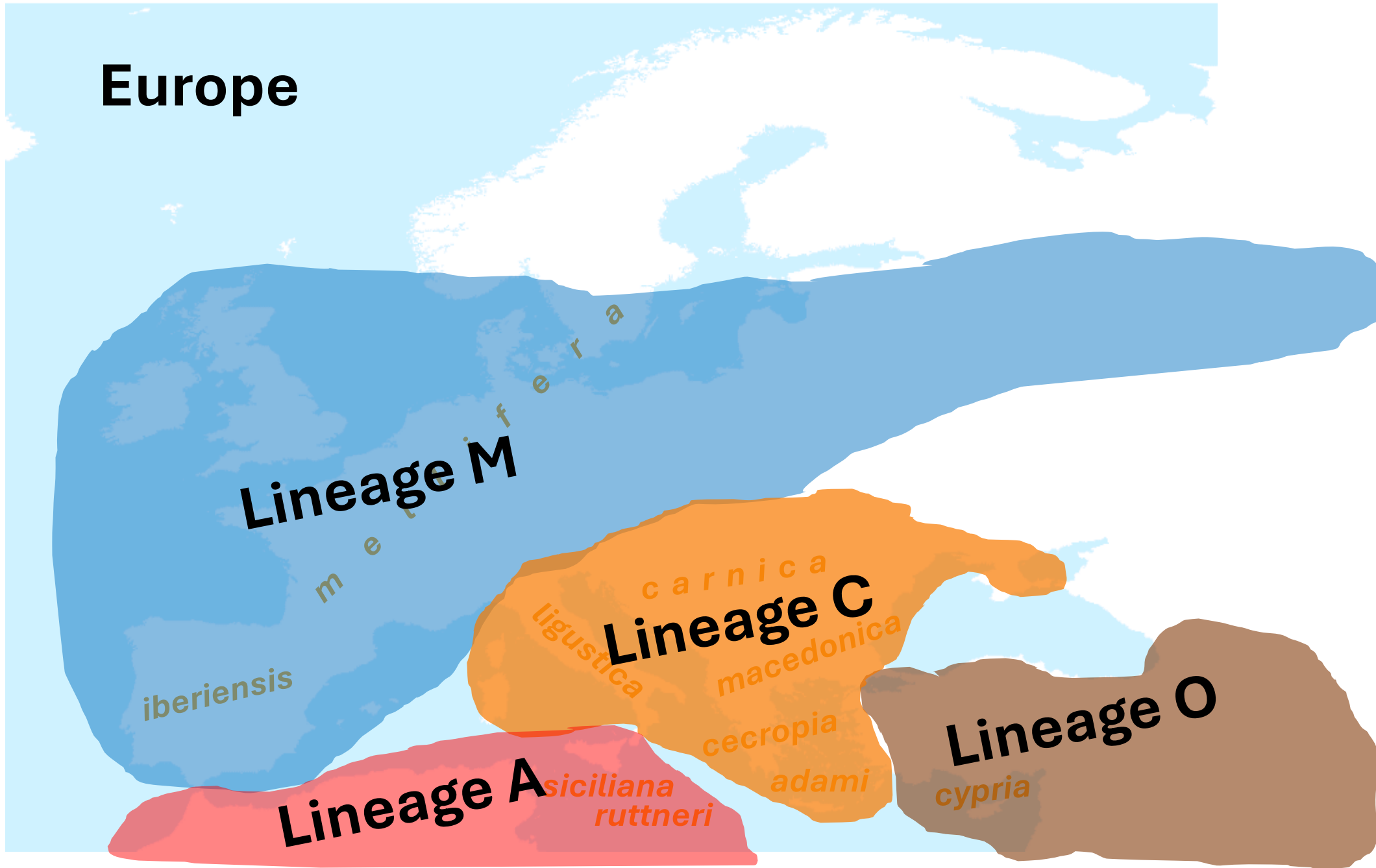
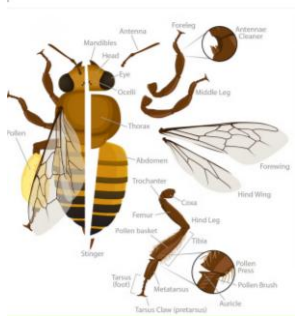


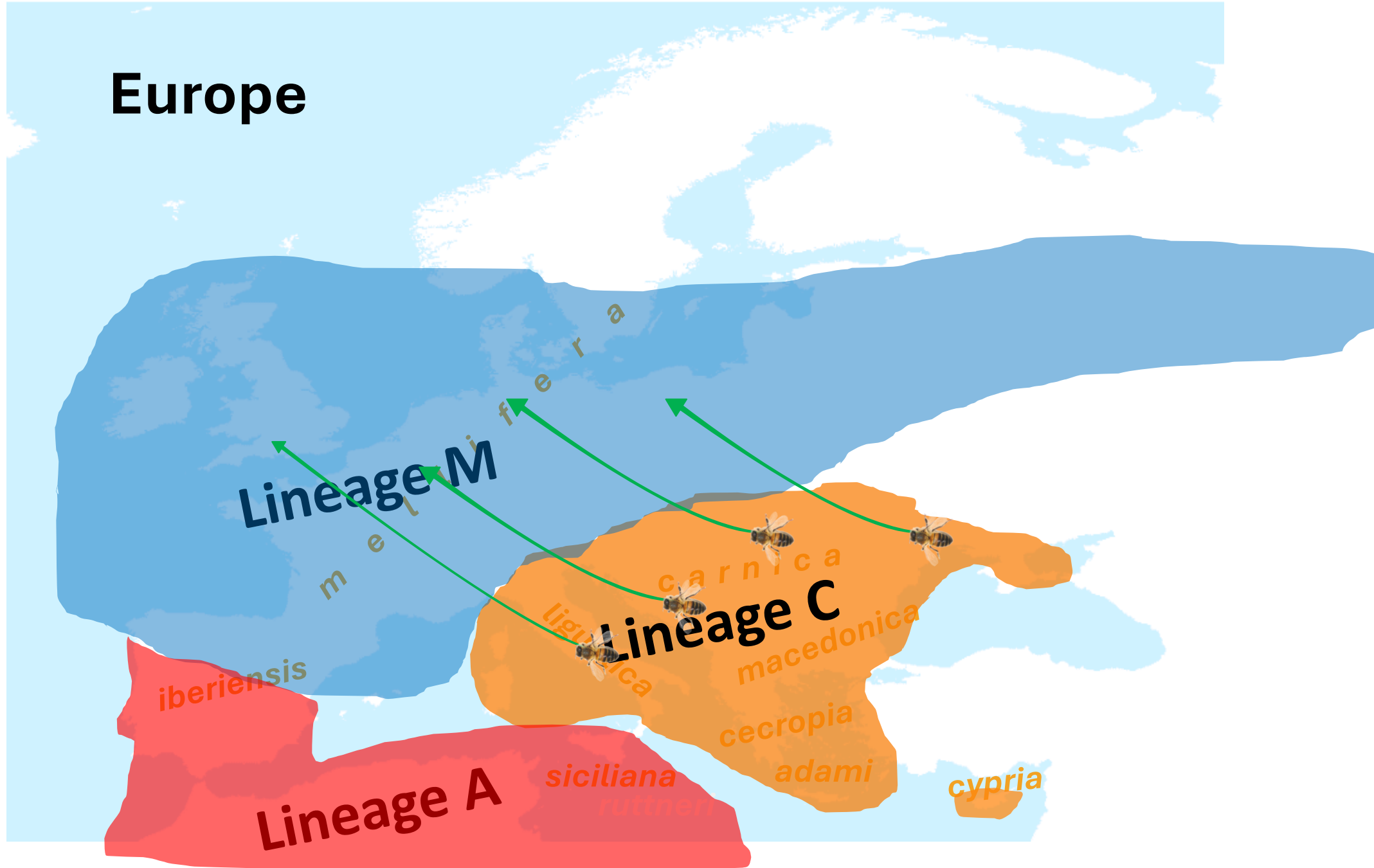
Evolutionary lineages

4-7



Morphological lineages

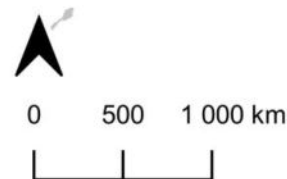




Questions

- ✓ What are the extant lineage patterns in Europe?
- ✓ Do the extant patterns fit the four-lineage scenario originally proposed by Ruttner (1988)?
- ✓ Do the extant patterns fit the expectations in M-lineage (*A. m. mellifera*) conservation apiaries?





Sampling

✓ Sampling 2022-2023

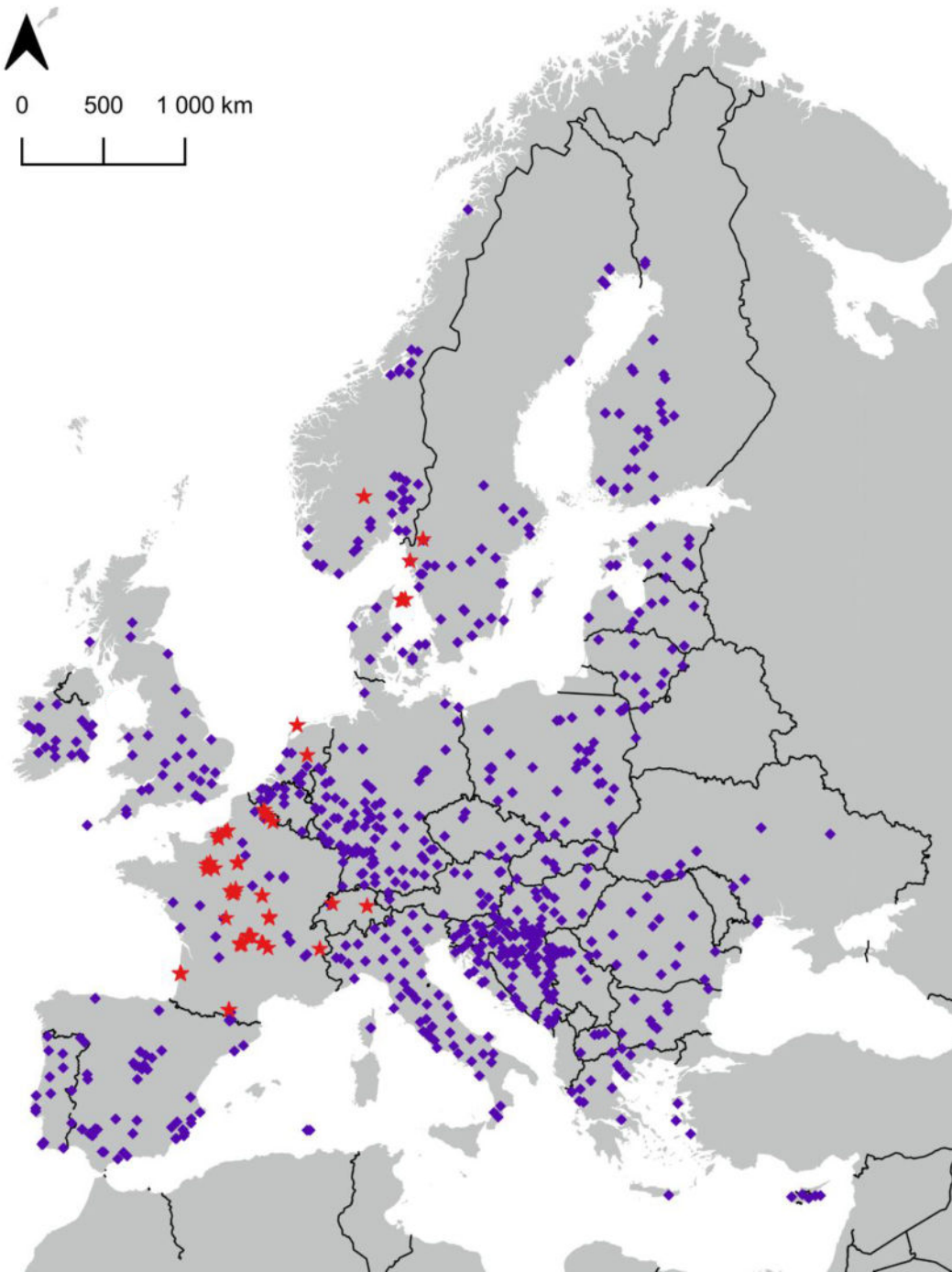
✓ 1311 samples

✓ 1-2 colonies/apiary

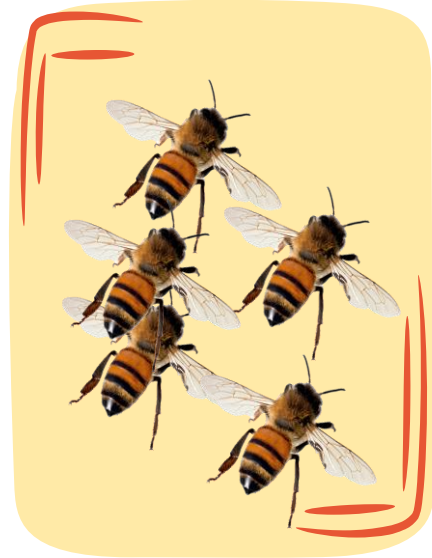
✓ 33 countries

◆ Local bees

★ *A. m. mellifera*
conservation apiaries



Wing geometric morphometrics workflow



5 workers/colony



Right forewing



Stereomicroscope
photo



DeepWings©
5 subspecies classifier

N = 6245

(1249 col.x 5 wings)

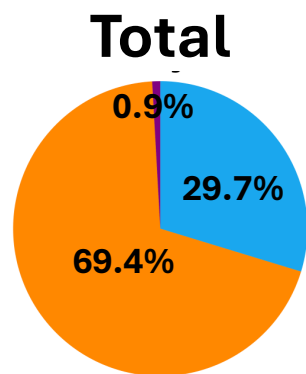




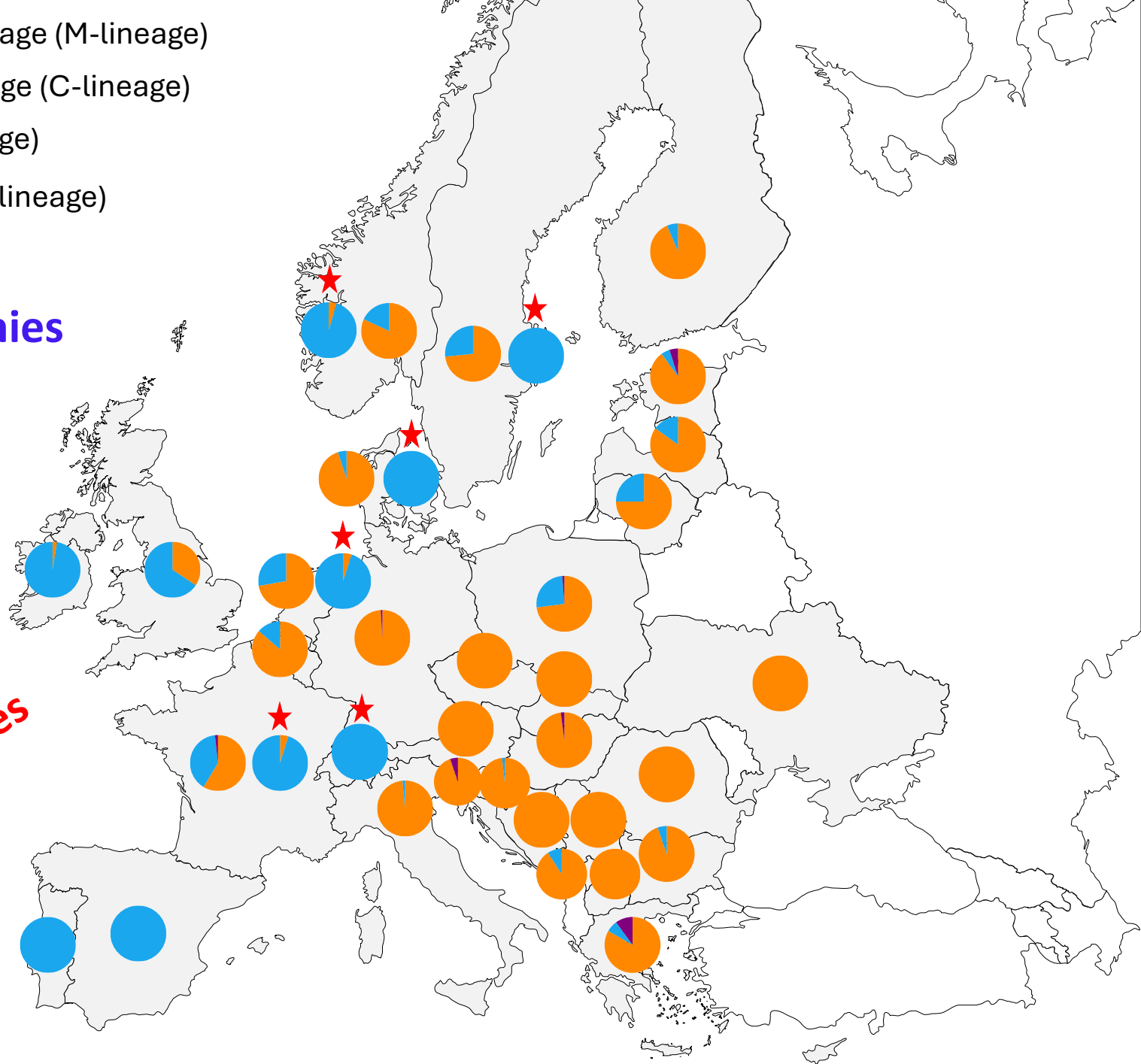
Wing shape
variation

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

Local colonies

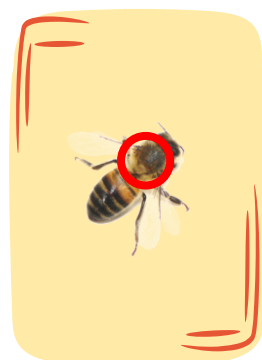
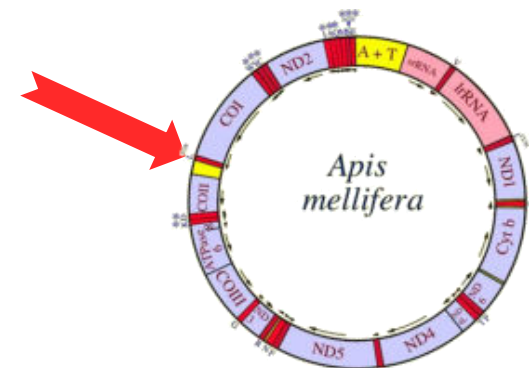


★ Conservation apiaries



Better-B at APIMONDIA 2025

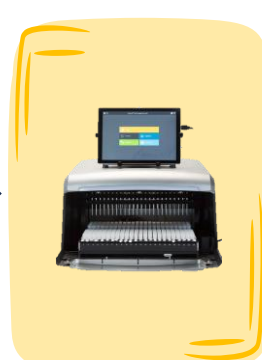
COI-COI intergenic region workflow



1 Thorax



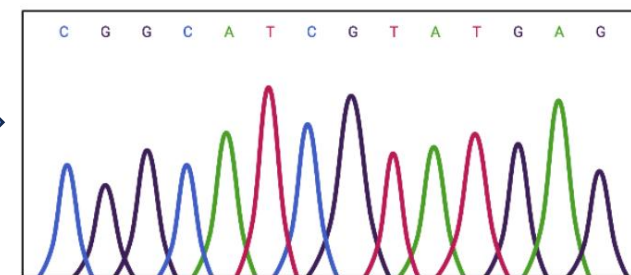
Mechanical
lysis



Automatic
DNA extraction



PCR
amplification

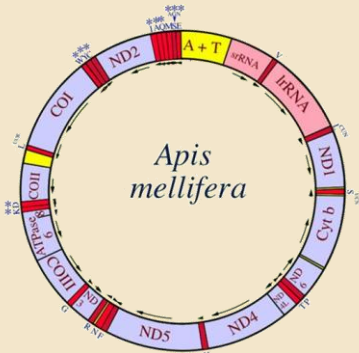


Sanger sequencing
BlastN
MEGA alignment

N=1311



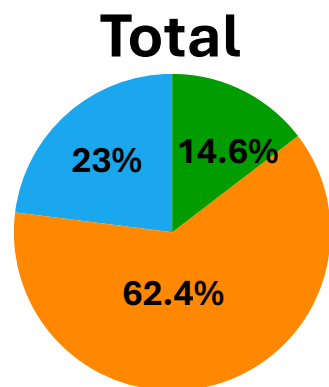
Better-B at APIMONDIA 2025



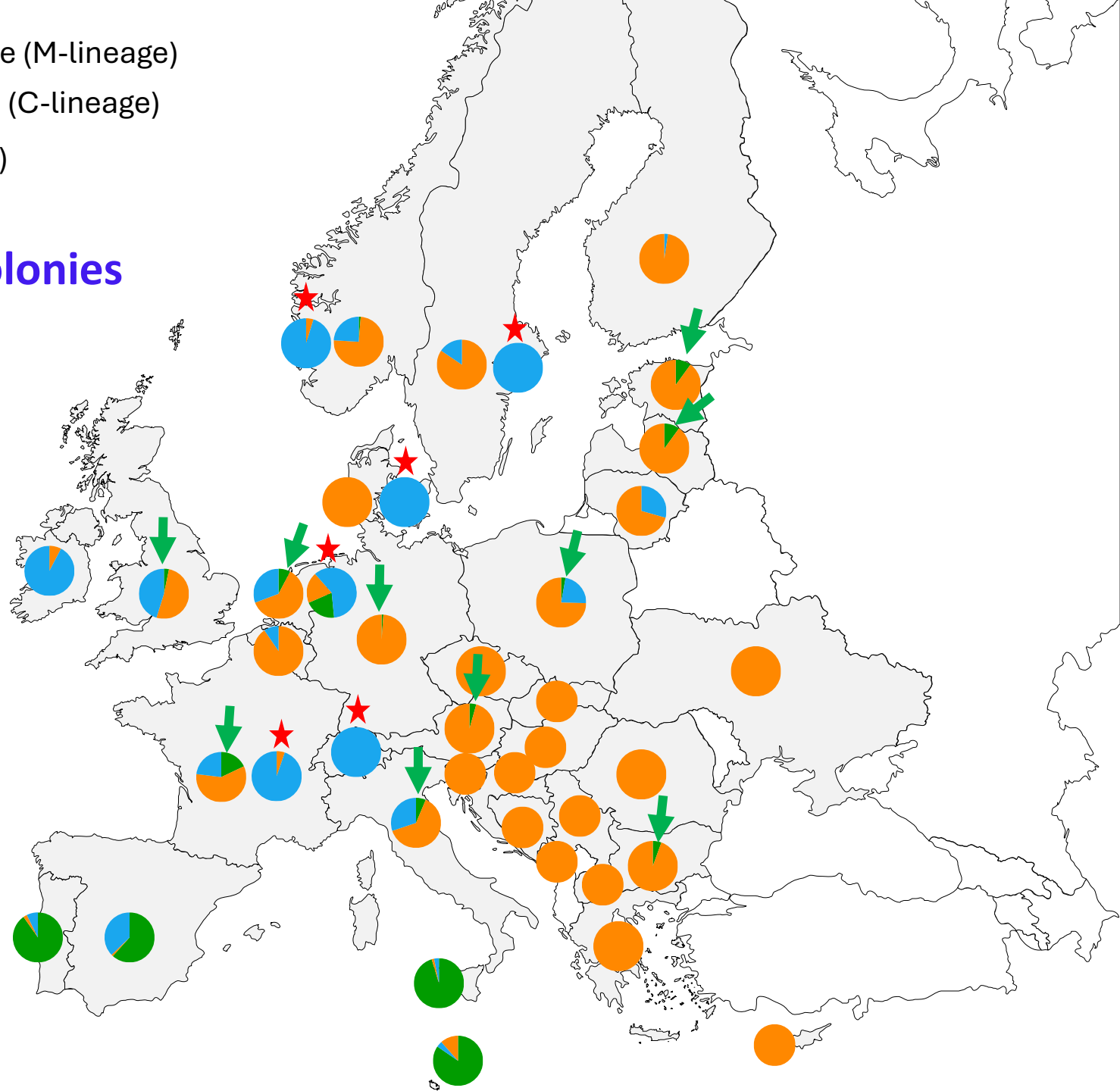
Mitochondrial
COI-COII
variation

- Western European lineage (M-lineage)
- Eastern European lineage (C-lineage)
- African lineage (A-lineage)

Local colonies



★ Conservation apiaries



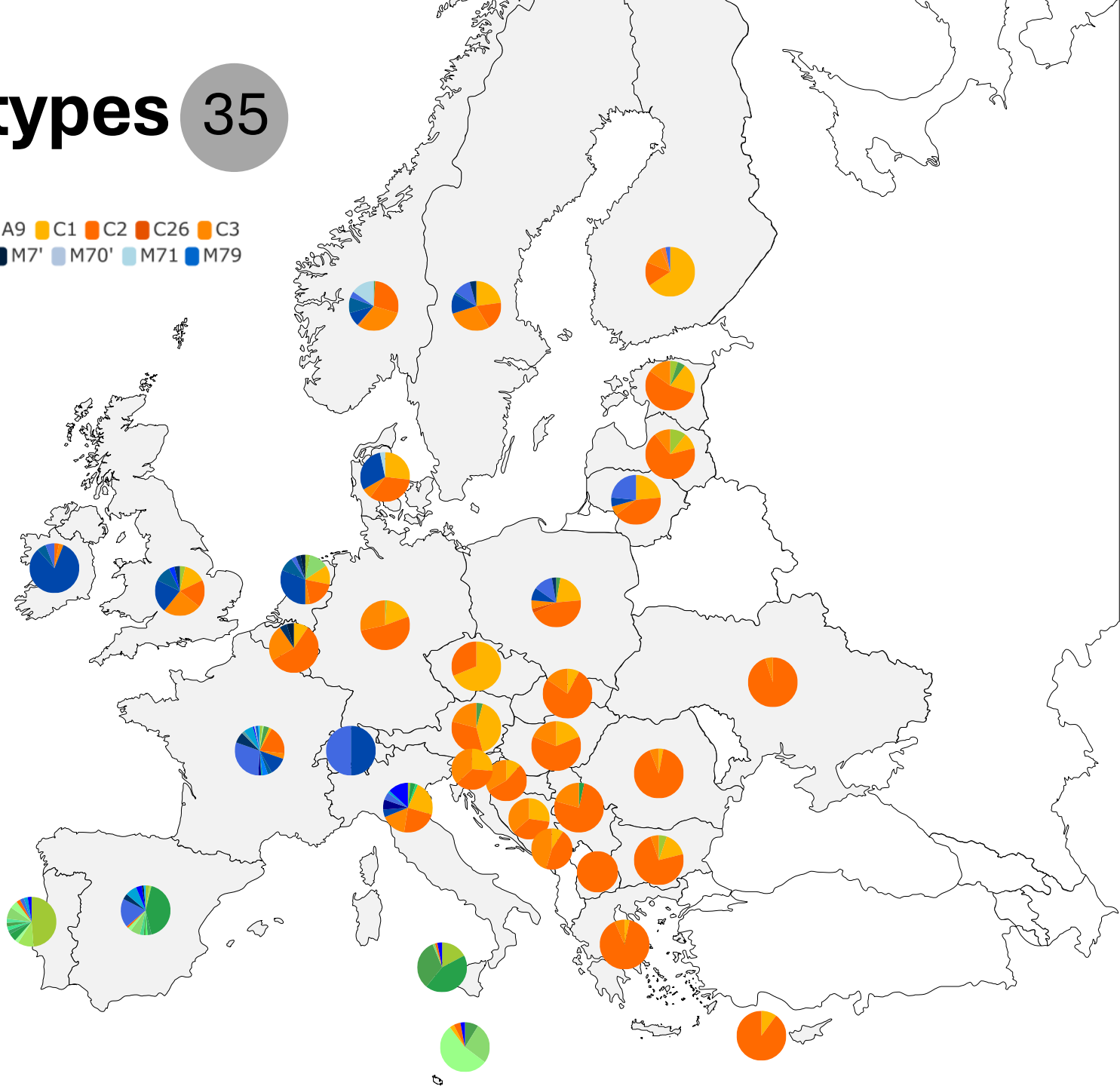
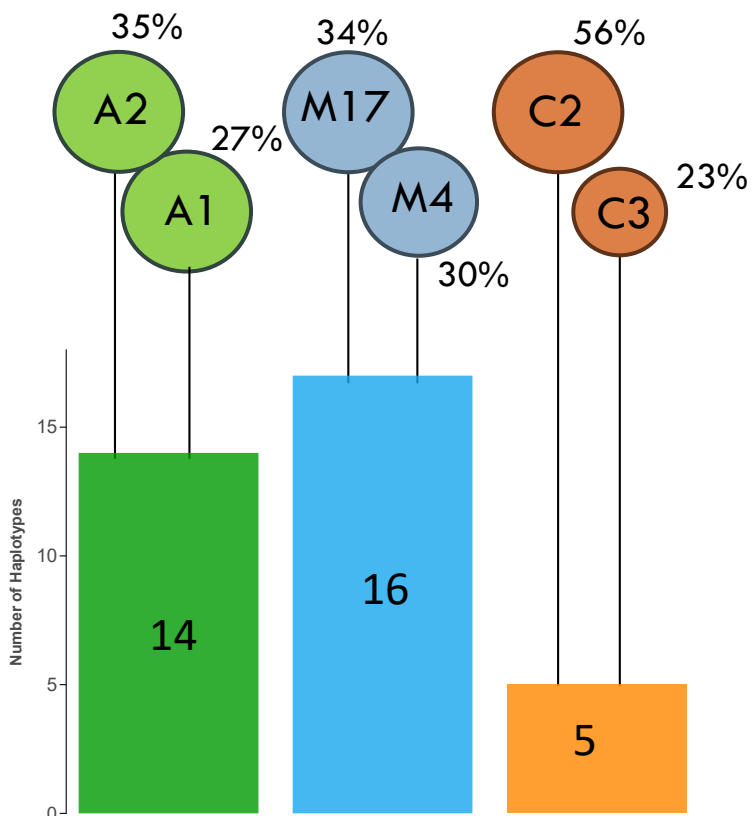
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Mito chondrial haplotypes 35

A1 A11 A14 A16 A2 A26 A3 A3' A39 A4 A48 A56 A8 A9 C1 C2 C26 C3 C4 M17 M17' M19 M19' M20 M3 M4 M4' M68' M69 M7 M7' M70' M71 M79 M8

Most frequent haplotypes

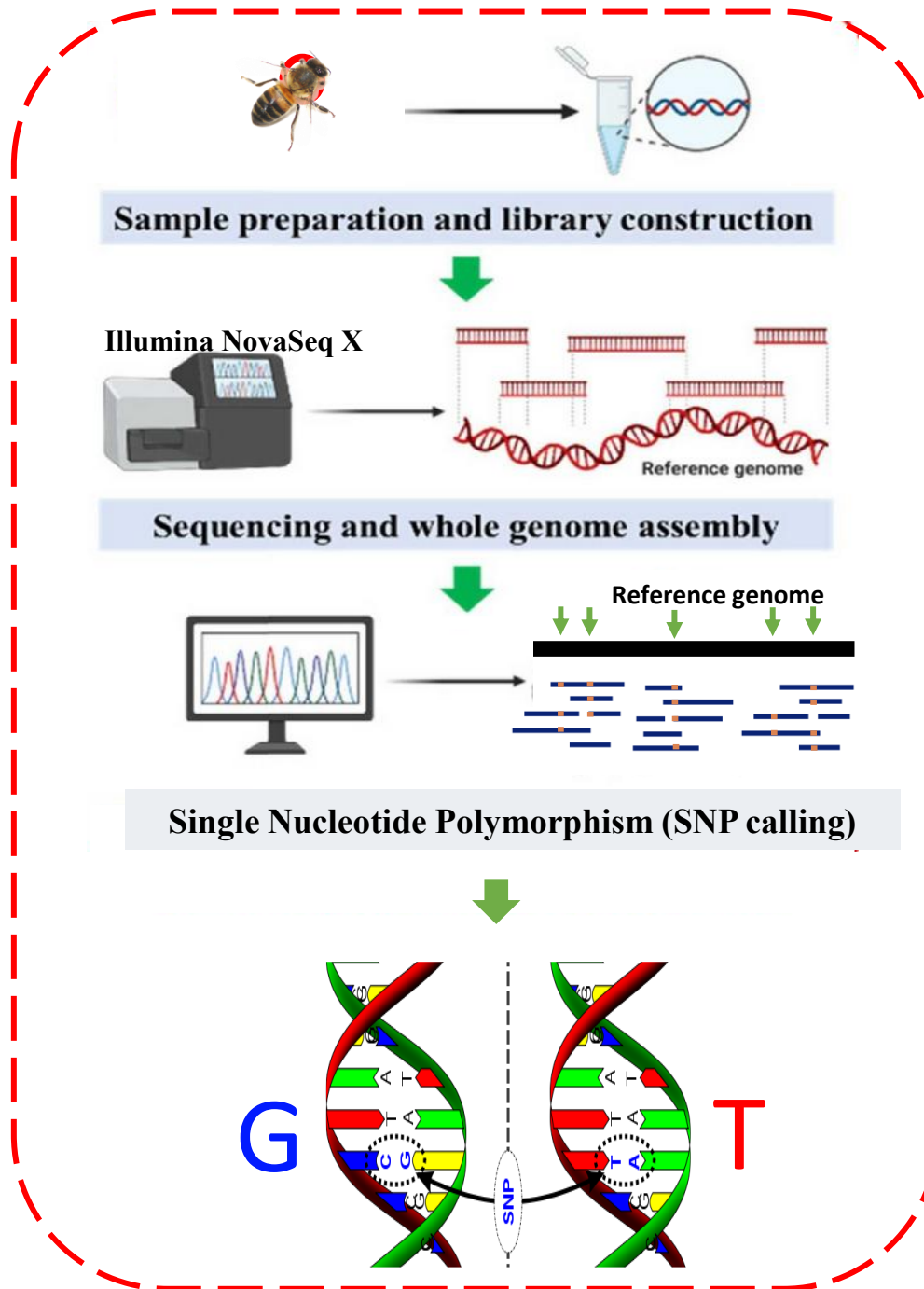


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Whole
nuclear
genomes

Whole genome sequencing workflow



8 million
high-quality
SNPs

N=1091



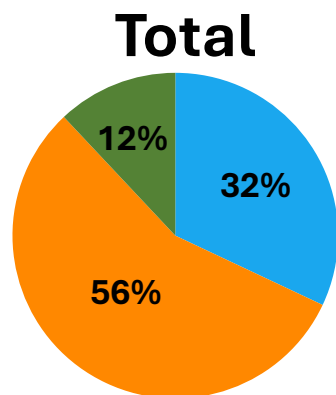
Better-B at APIMONDIA 2025



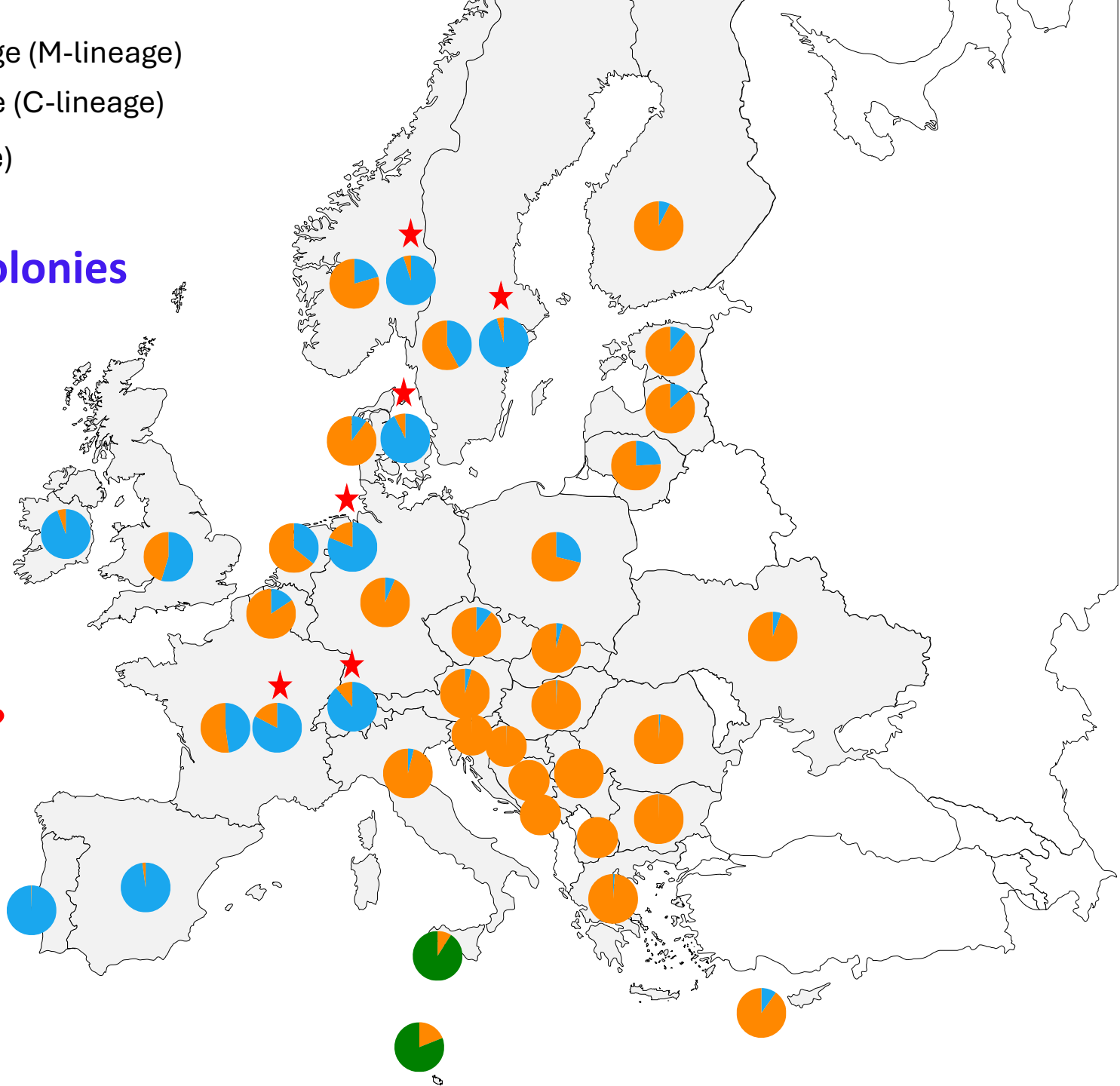
Whole genome variation

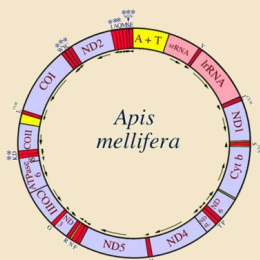
- Western European lineage (M-lineage)
- Eastern European lineage (C-lineage)
- African lineage (A-lineage)

Local colonies

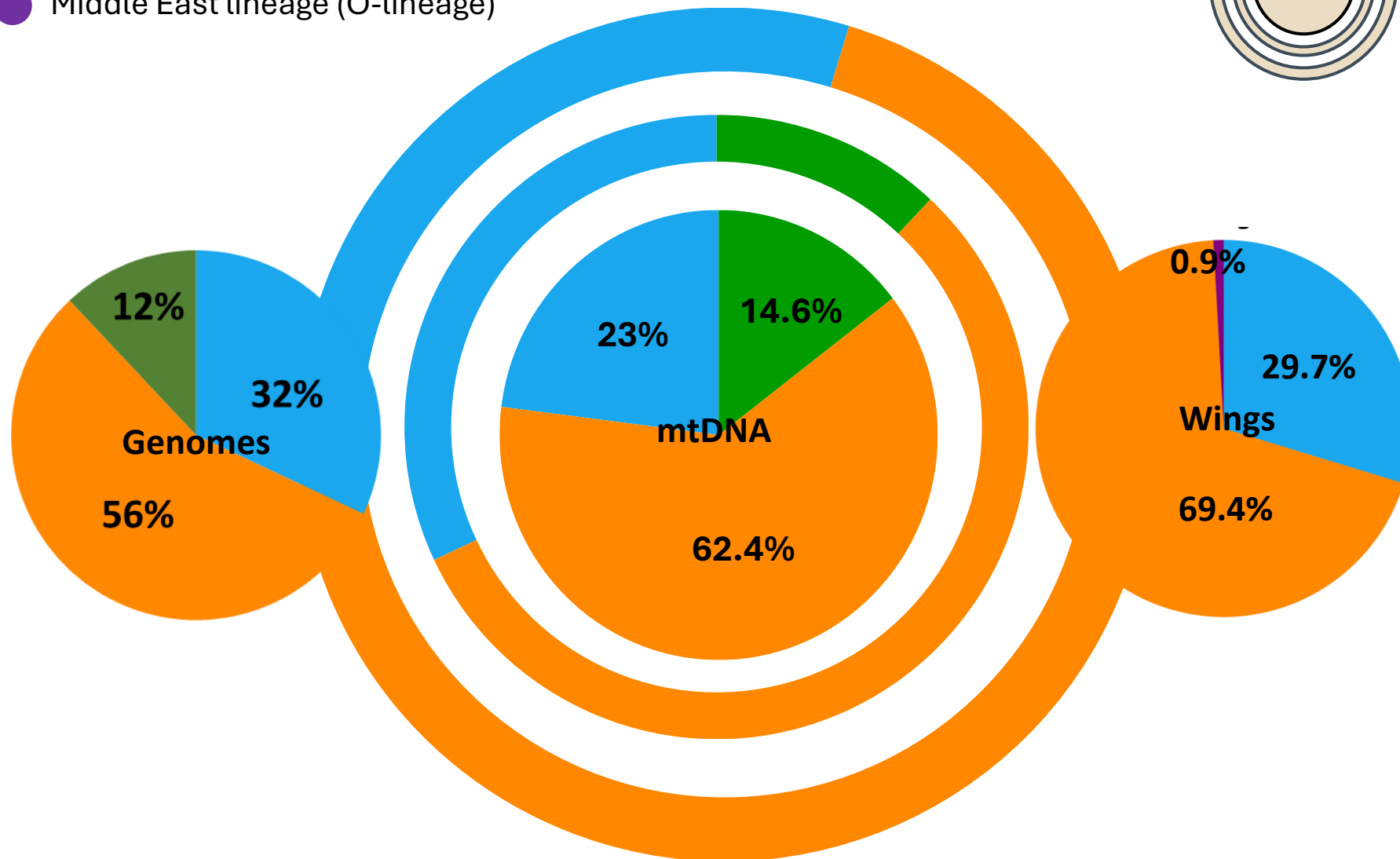
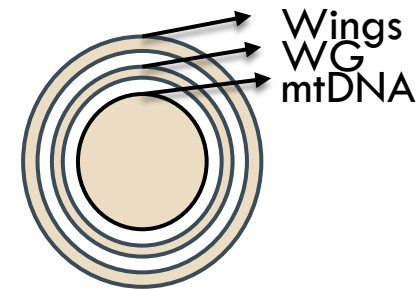


★ Conservation apiaries





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



Highlights

- ✓ C-lineage largely dominates the genetic landscape in Europe;
- ✓ African mitochondrial DNA variants were found in many countries, suggesting that beekeepers are introducing queens from outside the traditional C-lineage range;
- ✓ *A. m. mellifera* conservation apiaries were dominated by M-lineage ancestry, as determined by the 3 datasets, suggesting that beekeepers are successfully protecting the dark bee;
- ✓ Mitochondrial, whole genome, and wing shape data are largely concordant at the lineage level and European scale.

Thank you!



> 300 Beekeepers



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Better-B-project

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Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union, European Research Executive Agency (REA), SERI or UKRI. Neither the European Union nor the granting authorities can be held responsible for them.



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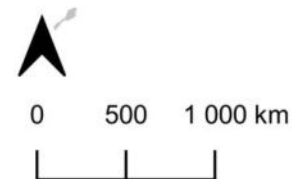


Schweizerische Eidgenossenschaft
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Confederazione Svizzera
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Swiss Confederation

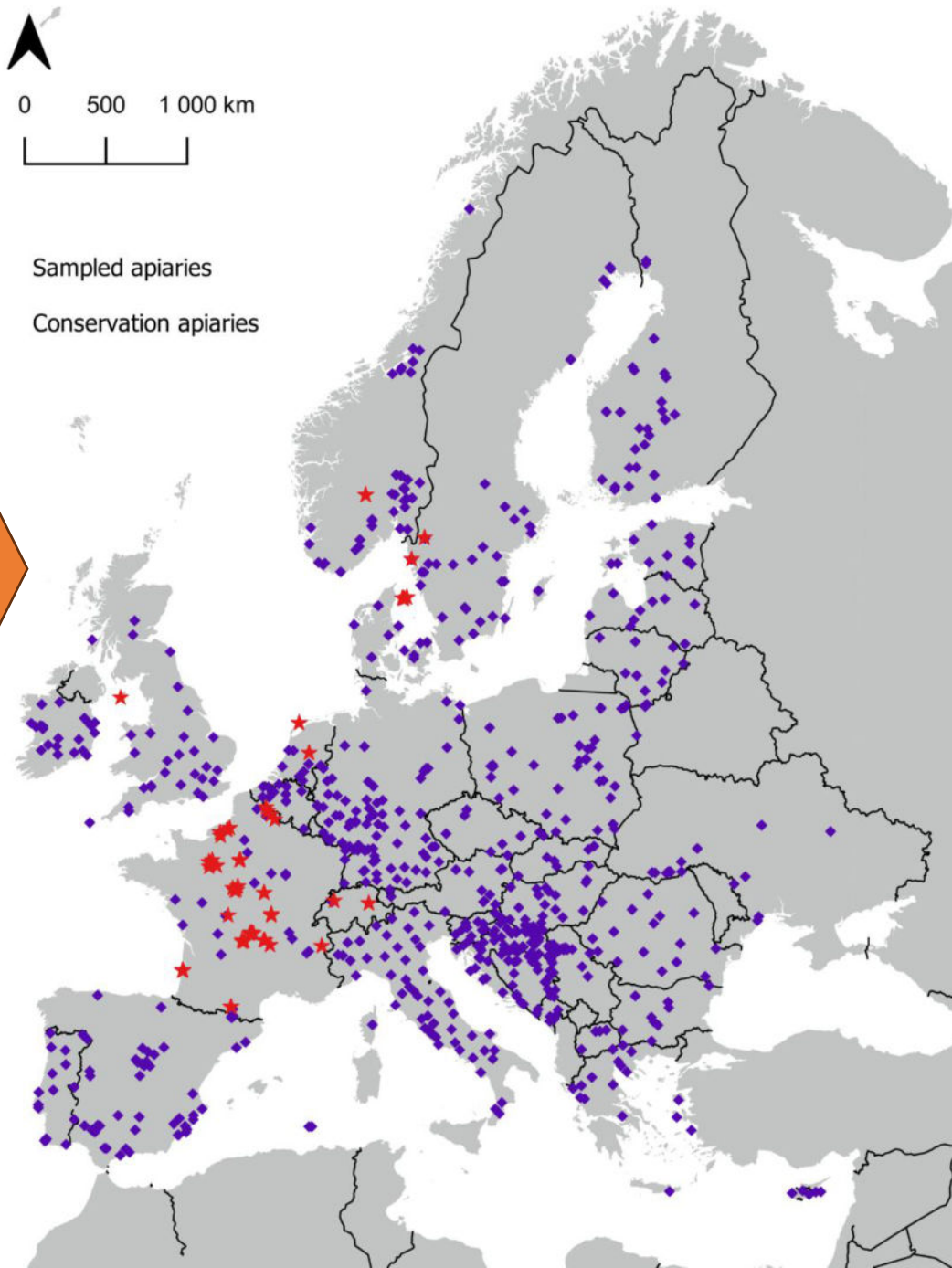
Sampling

COUNTRY	Sample size
AUSTRIA	24
BELGIUM	21
BOSNIA AND HERZEGOVINA	23
BULGARIA	19
CROATIA	56
CYPRUS	10
CZECH REPUBLIC	16
DENMARK	30
ESTONIA	20
FINLAND	42
FRANCE	125
GERMANY	92
GREECE	30
HUNGARY	50
IRELAND	39
ITALY	63
LATVIA	20
LITHUANIA	17
MONTENEGRO	11
NETHERLANDS	33
NORTH MACEDONIA	9
NORWAY	105
POLAND	81
PORTUGAL	41
ROMANIA	34
SERBIA	31
SLOVAKIA	13
SLOVENIA	19
SPAIN	88
SWEDEN	75
SWITZERLAND	17
UKRAINE	25
UNITED KINGDOM	32
TOTAL	1311



◆ Sampled apiaries
★ Conservation apiaries

1311

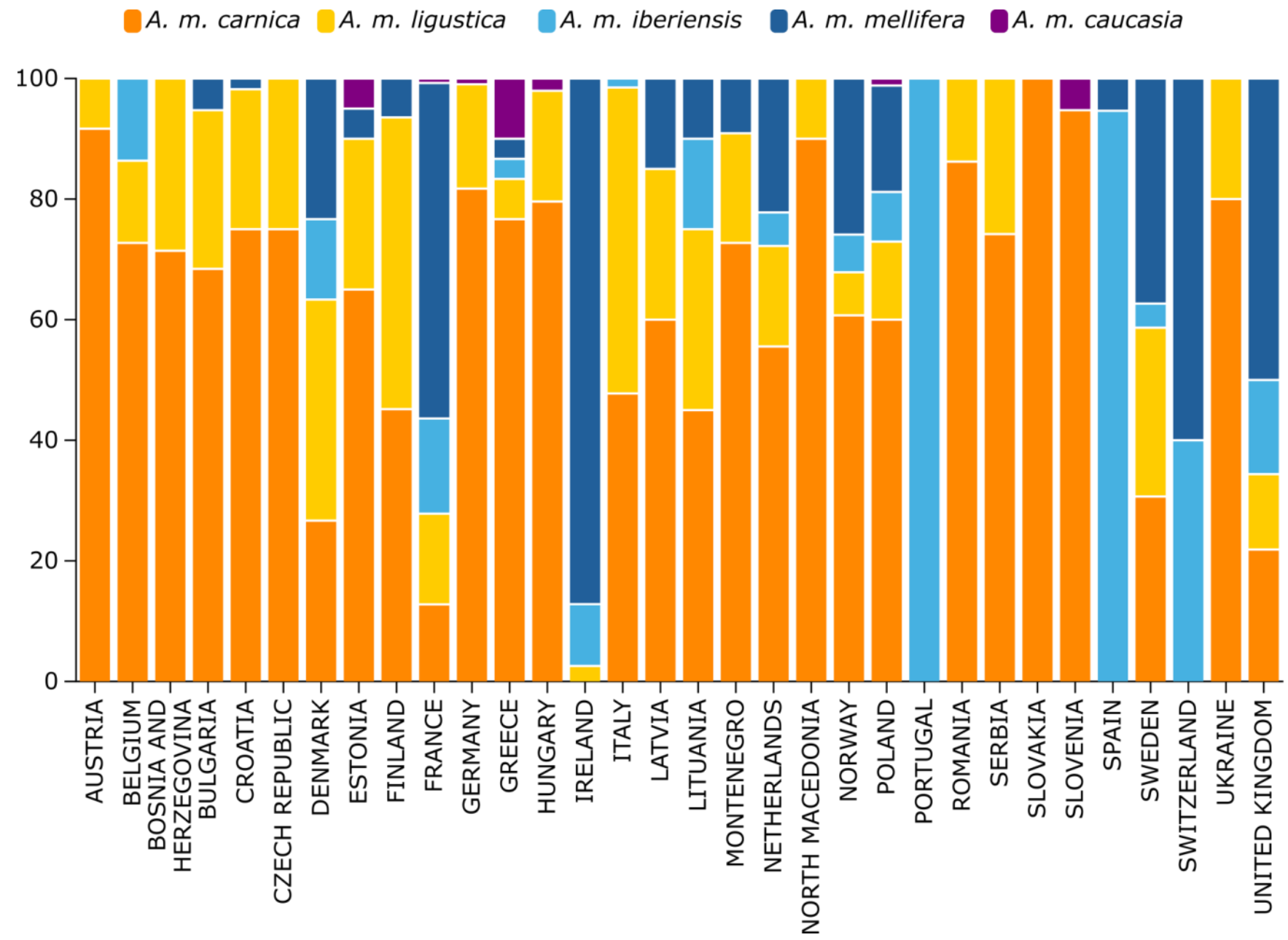


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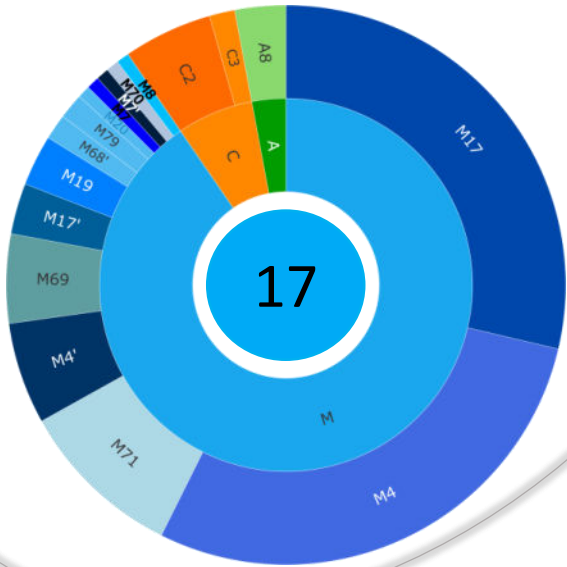


Subspecies classification

DeepWings

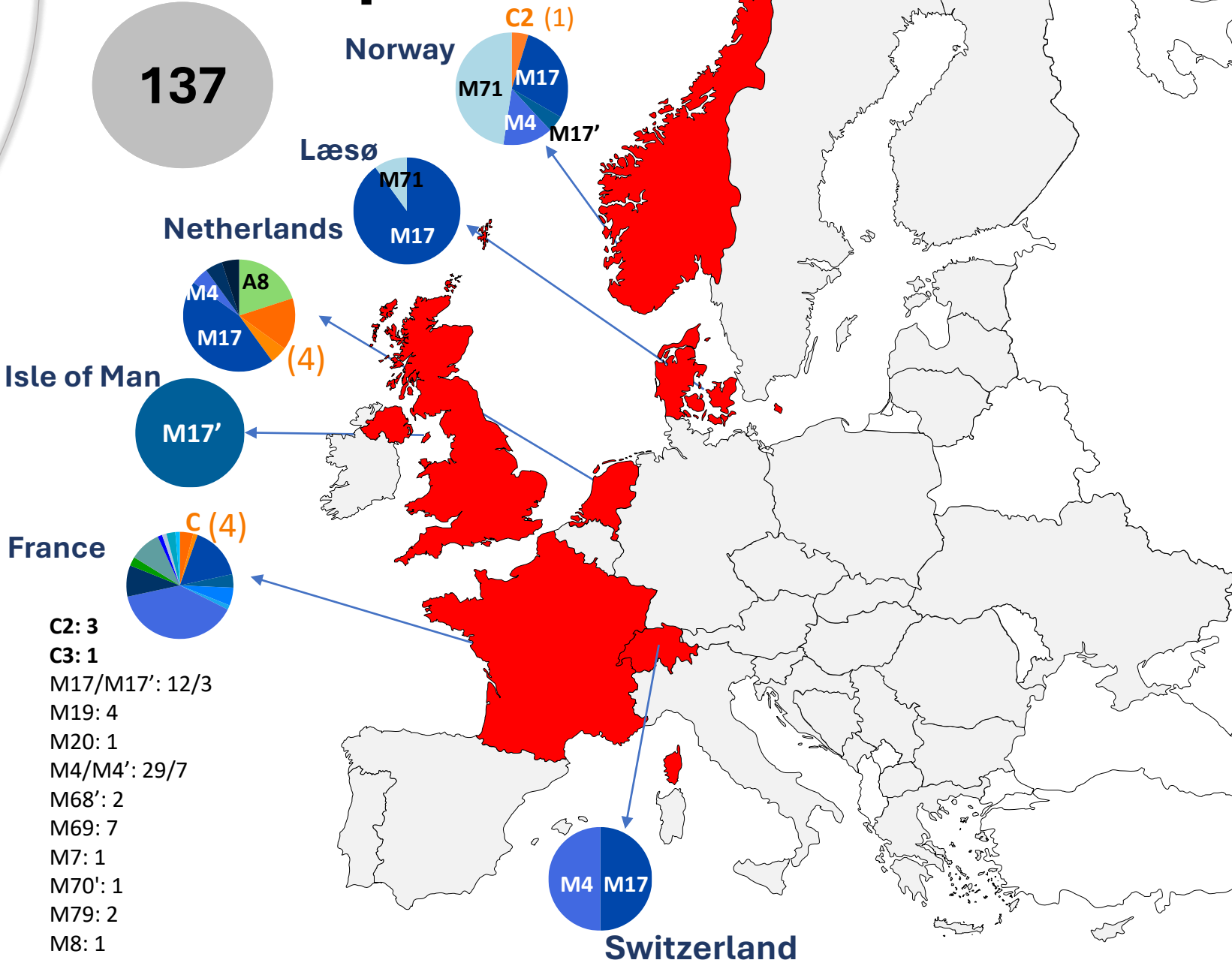


A. m. mellifera conservation apiaries



Country	Sample size
Denmark (Læsø)	10
Netherlands (Terschelling)	14
Netherlands (Nunspeet)	4
France	76
Switzerland	10
UK (Isle of Man)	1
Norway	22

137





Individual-level ancestry

1091

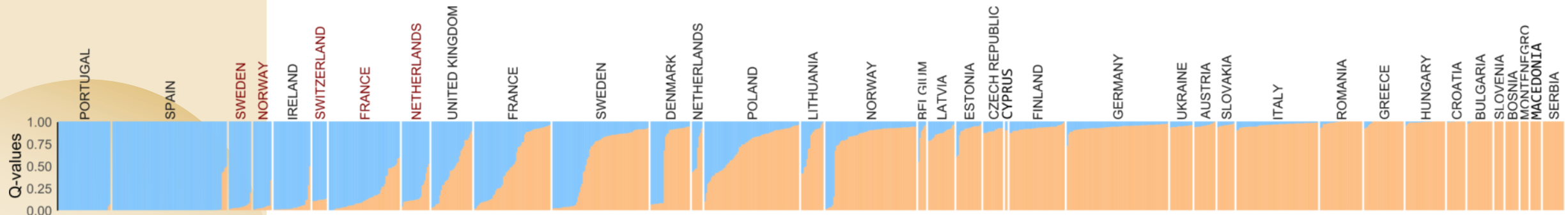
Whole
nuclear
genomes



M-lineage ancestry

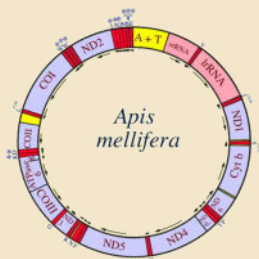


C-lineage ancestry



Admixture plot





Mitochondrial

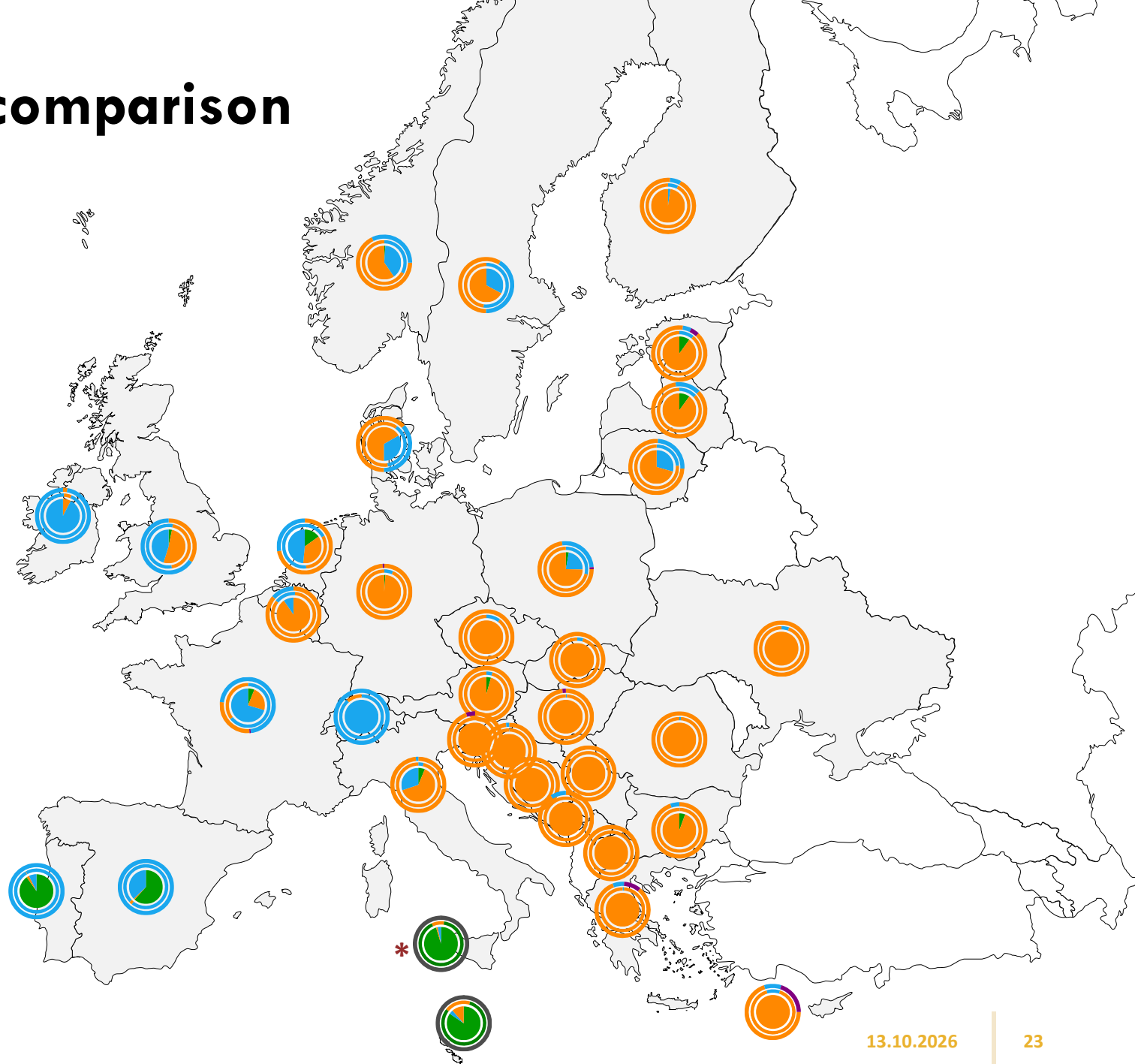
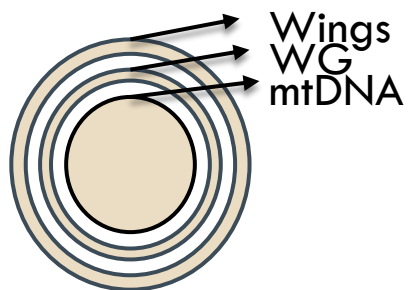


Whole
genomes



Wings

Data sets comparison



■ M ■ C ■ A ■ O
■ No data



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13.10.2026

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