

OP-075 [Bee Biology]

Whole genome sequencing reveals resilience of European honeybees to climate change

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Climate change is a threat to the health of honeybee (*Apis mellifera*) populations in Europe. Honeybees can thrive across a large range of climates, and evolution by natural selection has resulted in local populations with traits suited to local environments. Genetic adaptation of bees to their local climate is an important factor that determines how they will react to warming temperatures. However, movement of bees by humans could potentially disrupt associations between these traits and local environments. Furthermore, management and breeding practices can affect their genetic variation and their potential to adapt to a changing climate.

We have analyzed the genomes of 1096 honeybees sampled from all over Europe to understand how they are adapted to their local environments and to predict how future climate change will affect their resilience. The genomes reflect extensive translocation of C-lineage bees (mainly *A. m. ligustica* and *A. m. carnica* subspecies) from southeastern Europe, which have hybridized with and replaced M-lineage bees (*A. m. mellifera* subspecies) in the north and west. Our analysis uncovers the genetic basis of adaptations to different climates in Europe, and identifies genes that control these adaptations.

We combined our results on how bees are adapted to their local environment with predictions of local climate in the future throughout Europe. This allows us to predict which populations are most susceptible to climate change. We can also address two important questions: 1) in which parts of Europe are honeybees most sensitive to climate change? 2) what effect have human management and hybridization between subspecies had on honeybees' resilience to climate change? Our findings have implications for beekeeping practices in future.

Whole genome sequencing reveals resilience of European honeybees to climate change

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APIMONDIA 2025
Copenhagen
Denmark

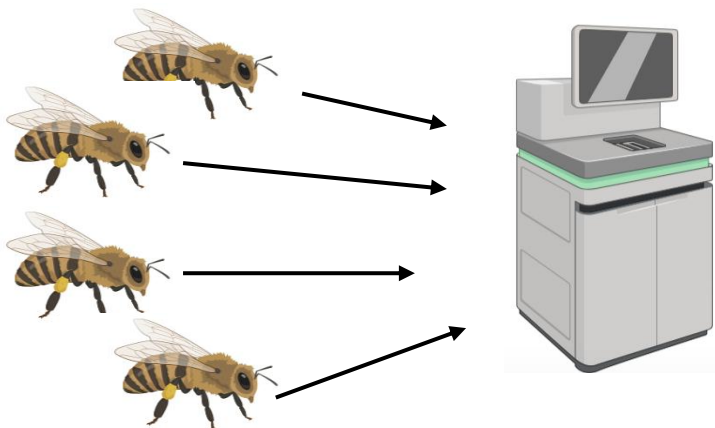




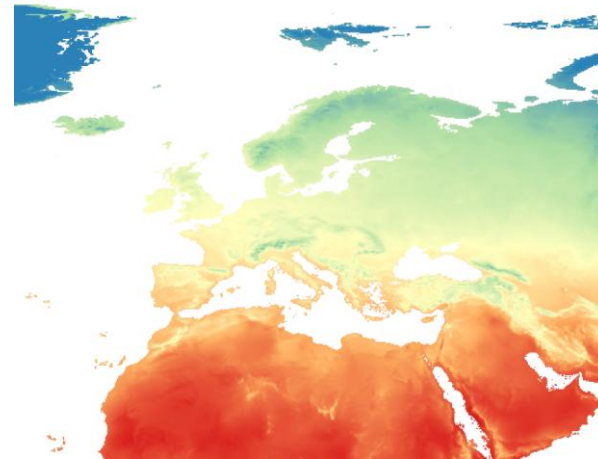
Aim: Improve the resilience of beekeeping to abiotic stresses

How are honeybees genetically adapted to their local climates?

How will climate change disrupt these adaptations?



whole genome sequencing

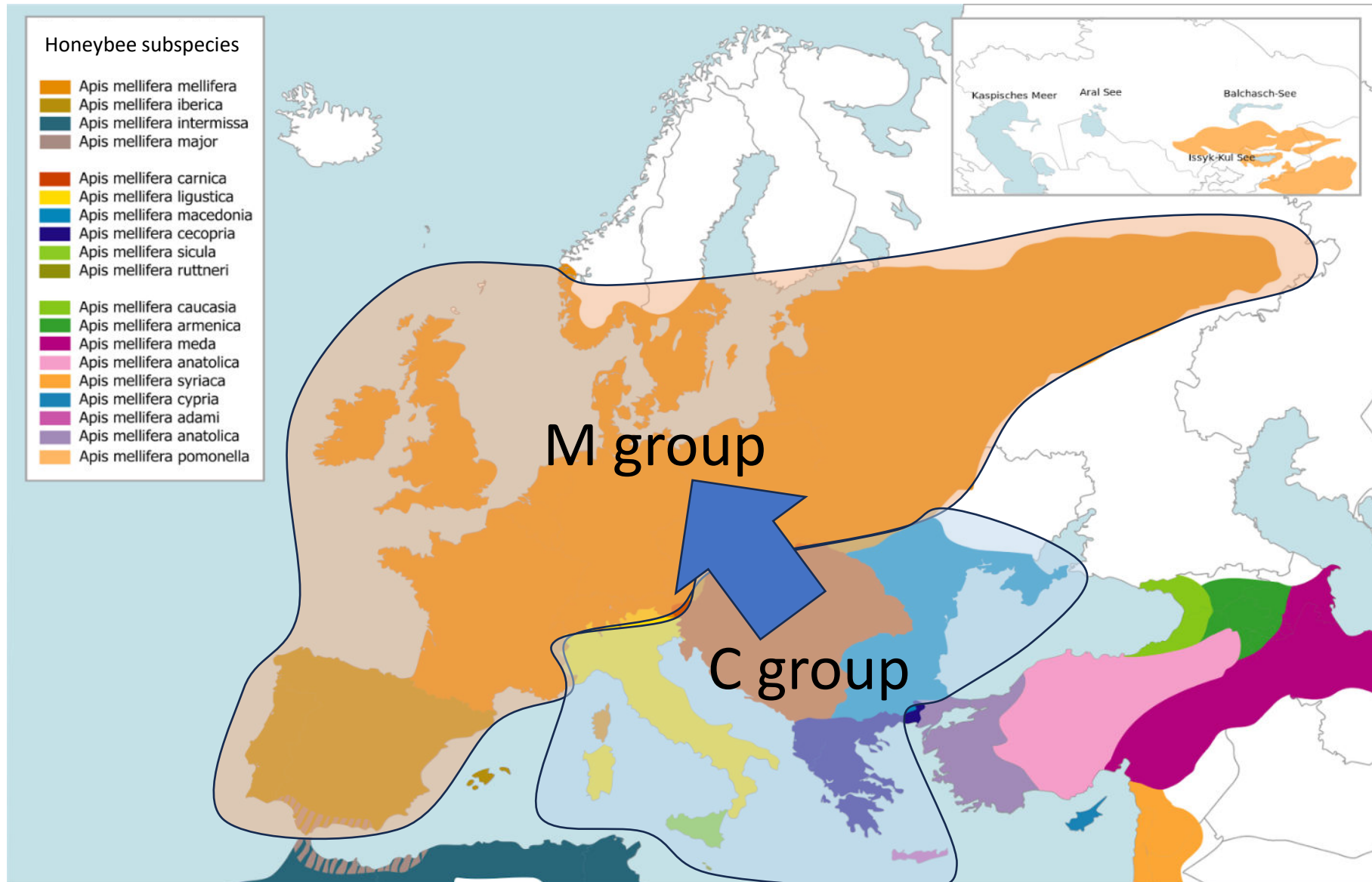


gene-environment associations

Honeybee subspecies in Europe

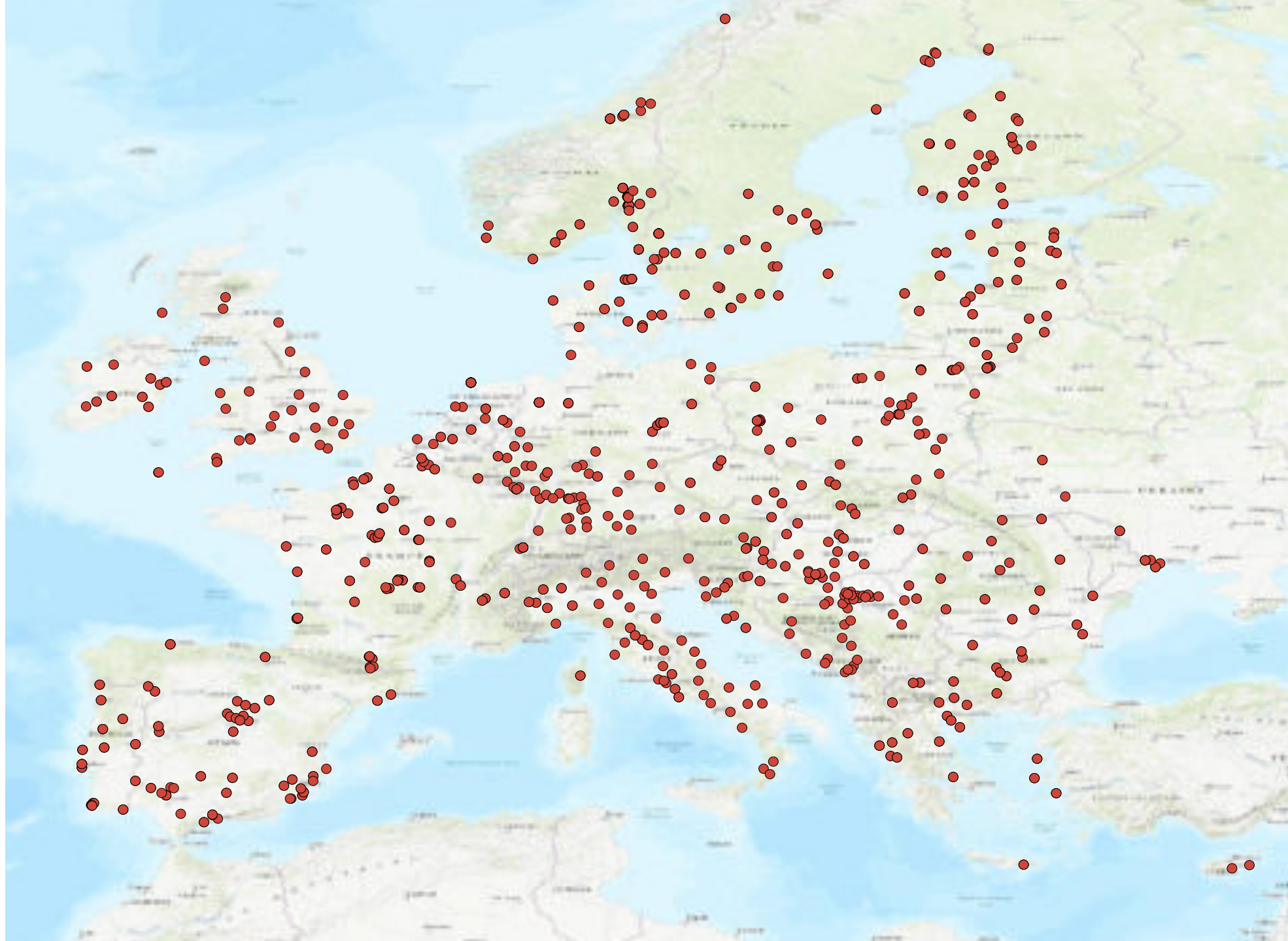


Two divergent lineages



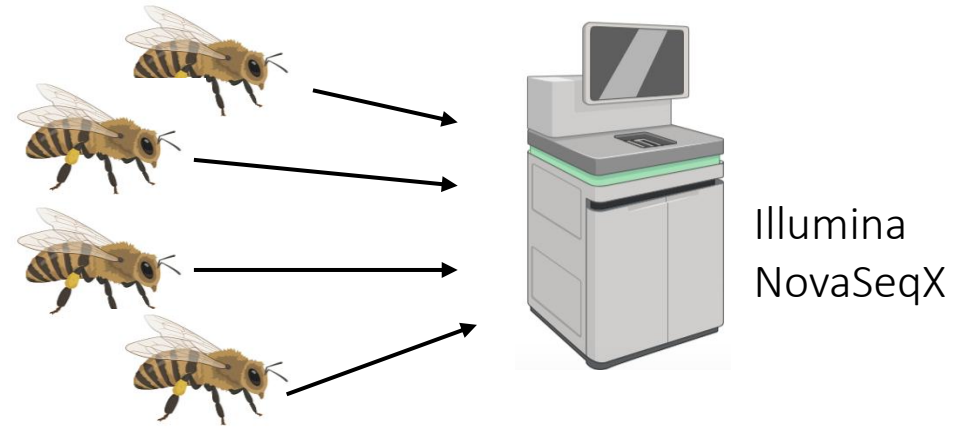
Whole genome sequencing
of 1094 samples

Sampling from
1) random apiaries
2) conservation projects

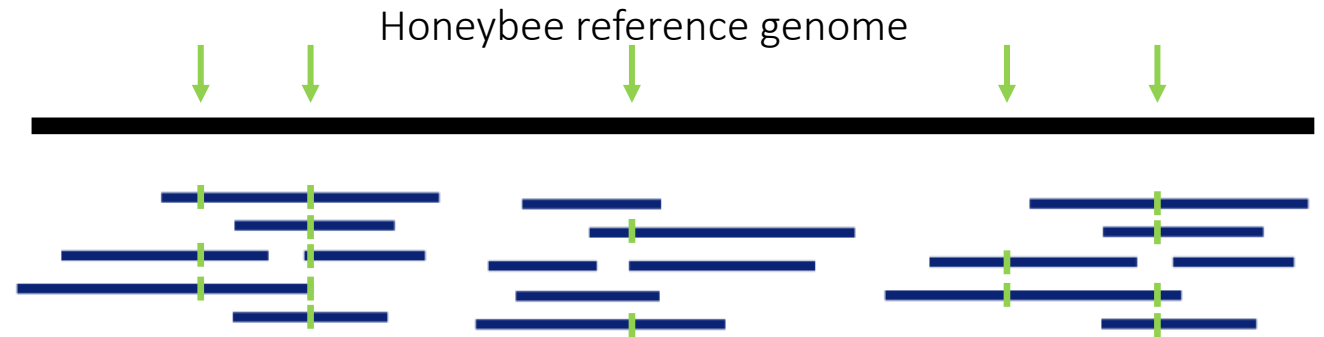


Whole-genome sequencing

1) Sequence bee genomes



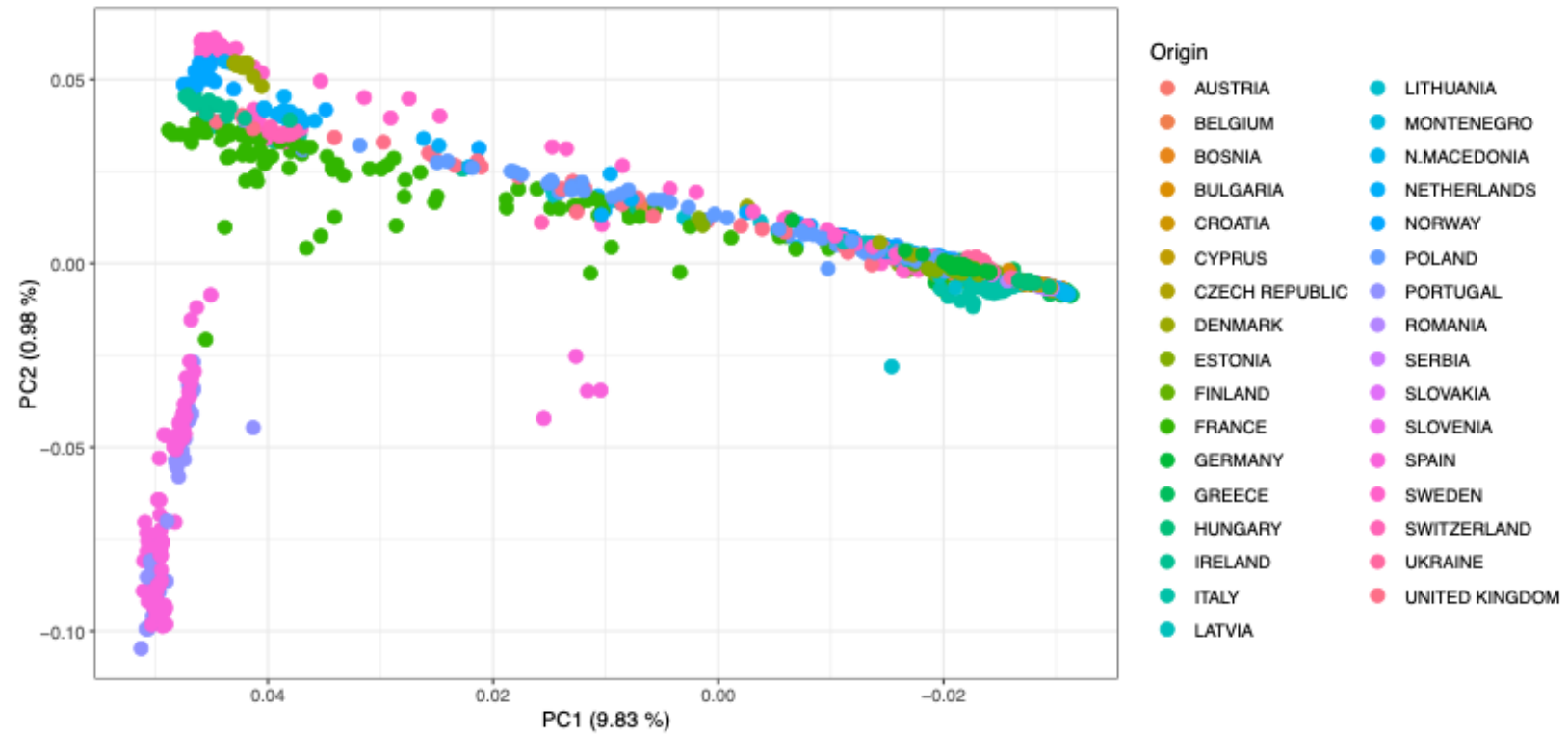
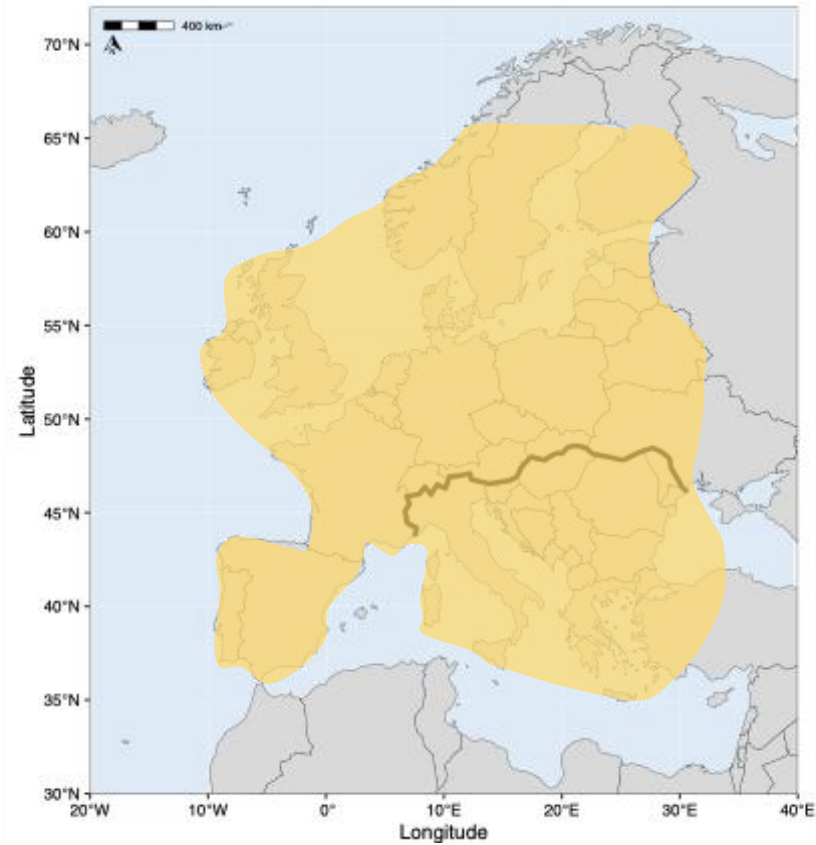
2) Map sequences to reference genome,
identify genetic variants



16 million single-nucleotide polymorphisms

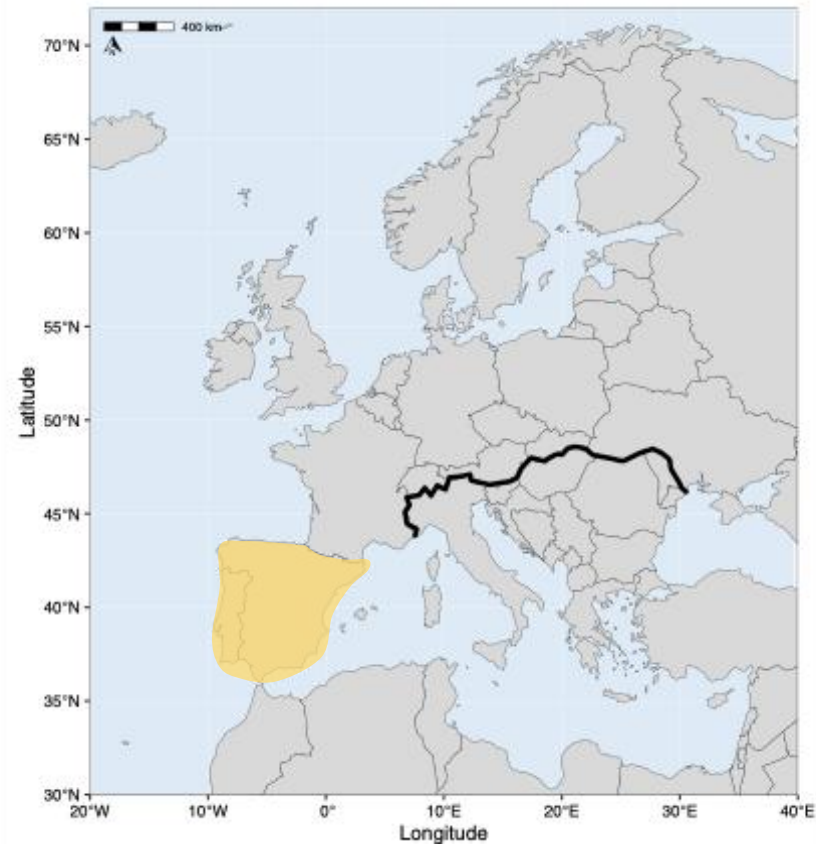
Genetic structure

M ← ————— → C

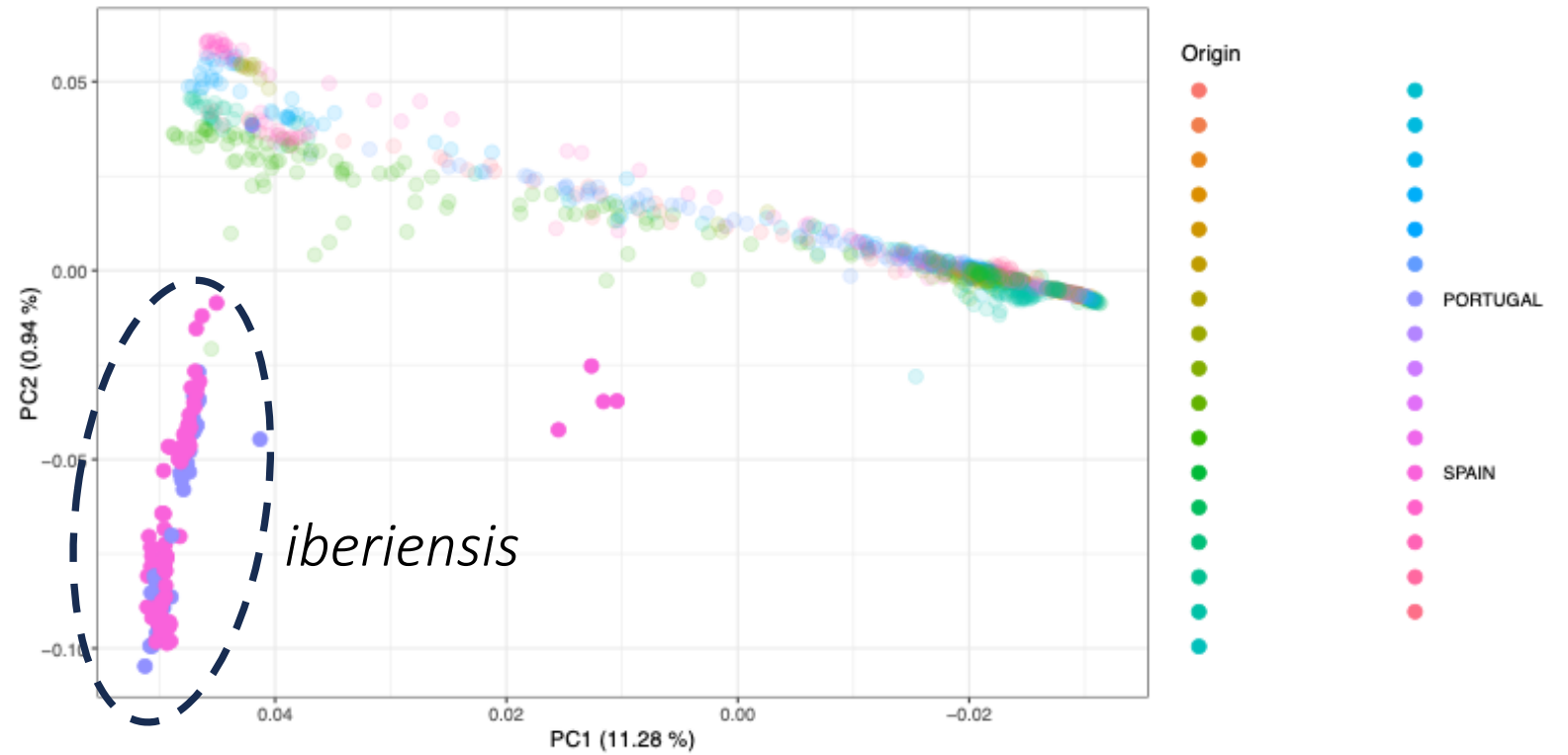


Genetic structure

SW Europe

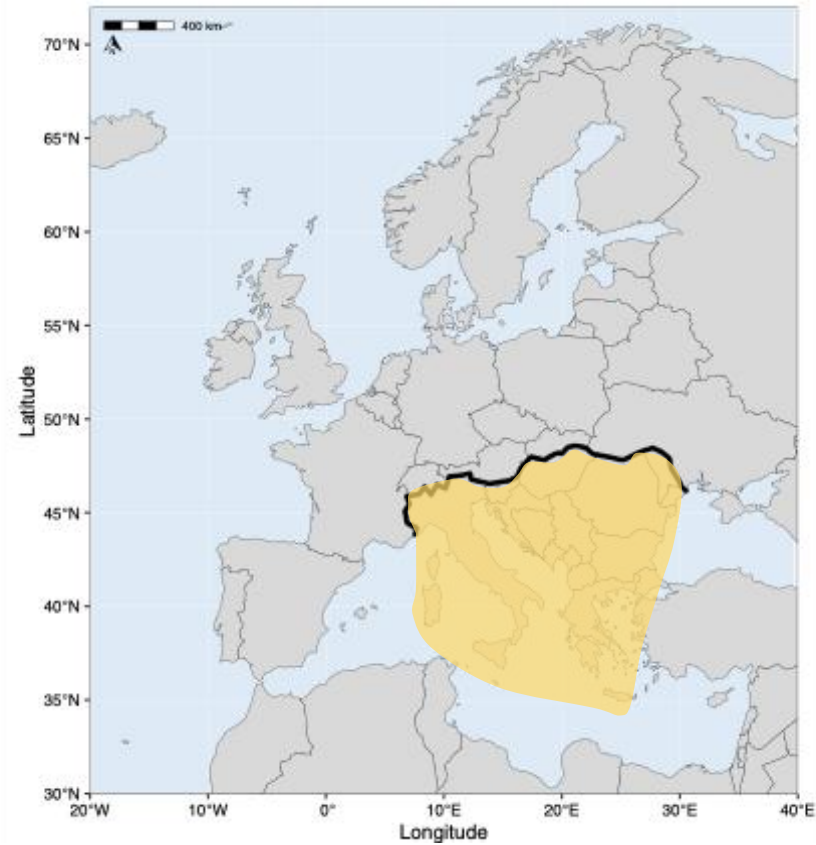


M ← ————— → C

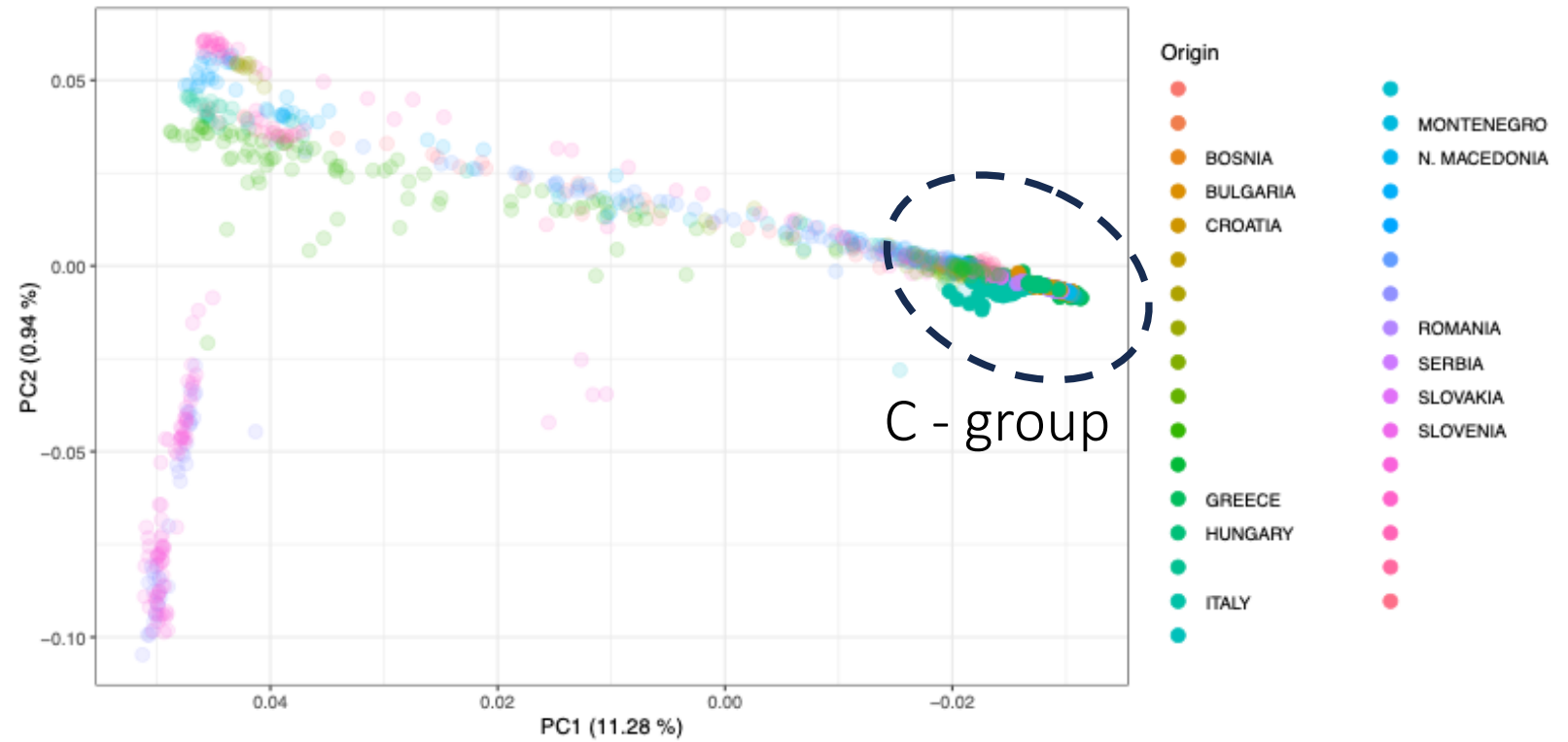


Genetic structure

SE Europe

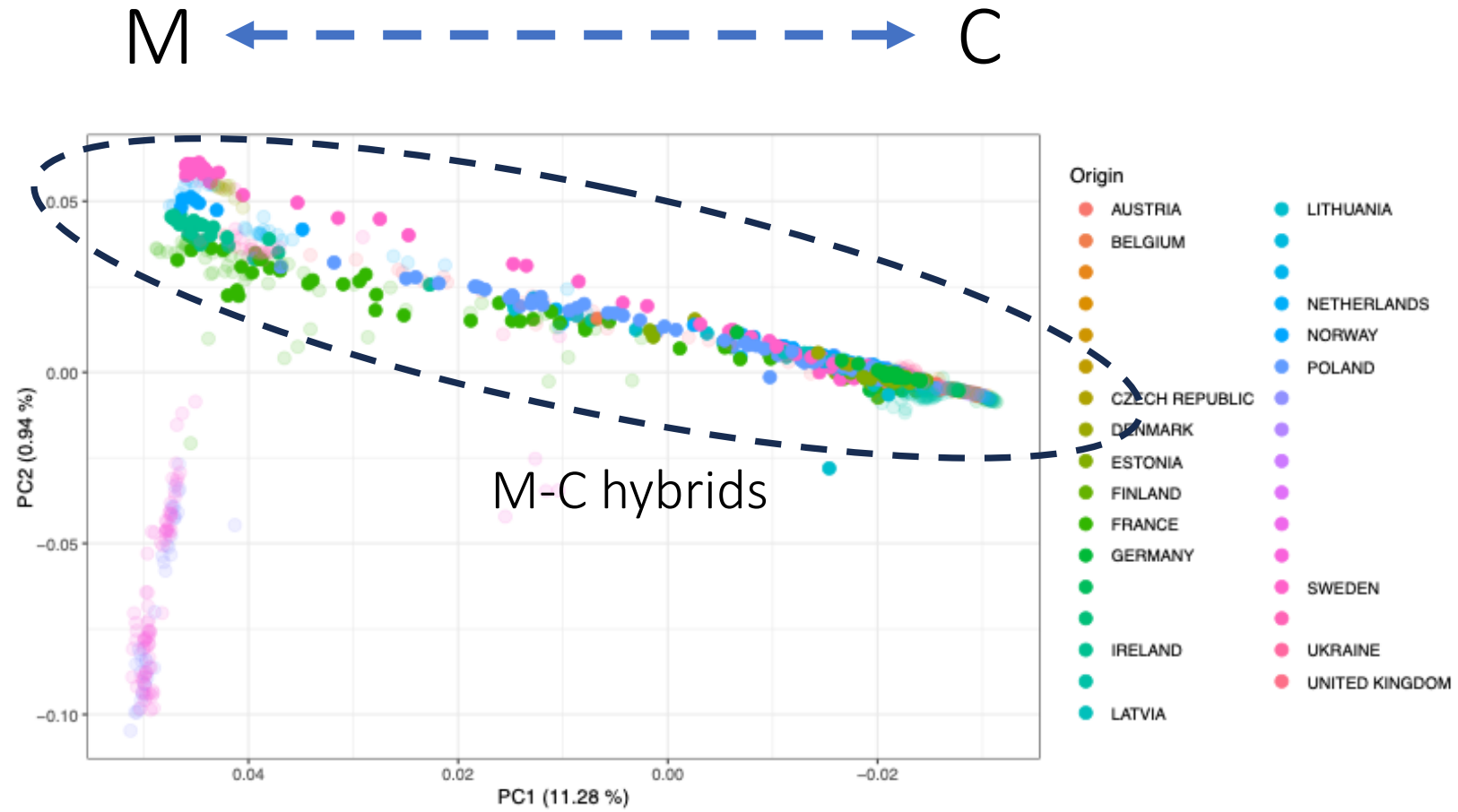
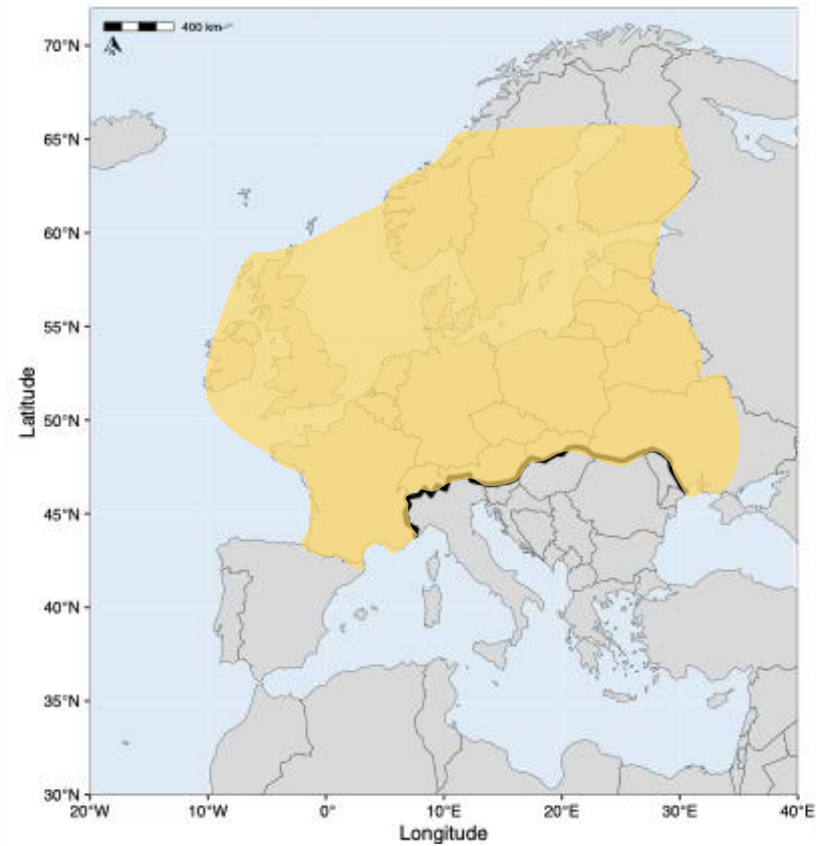


M ← ————— → C



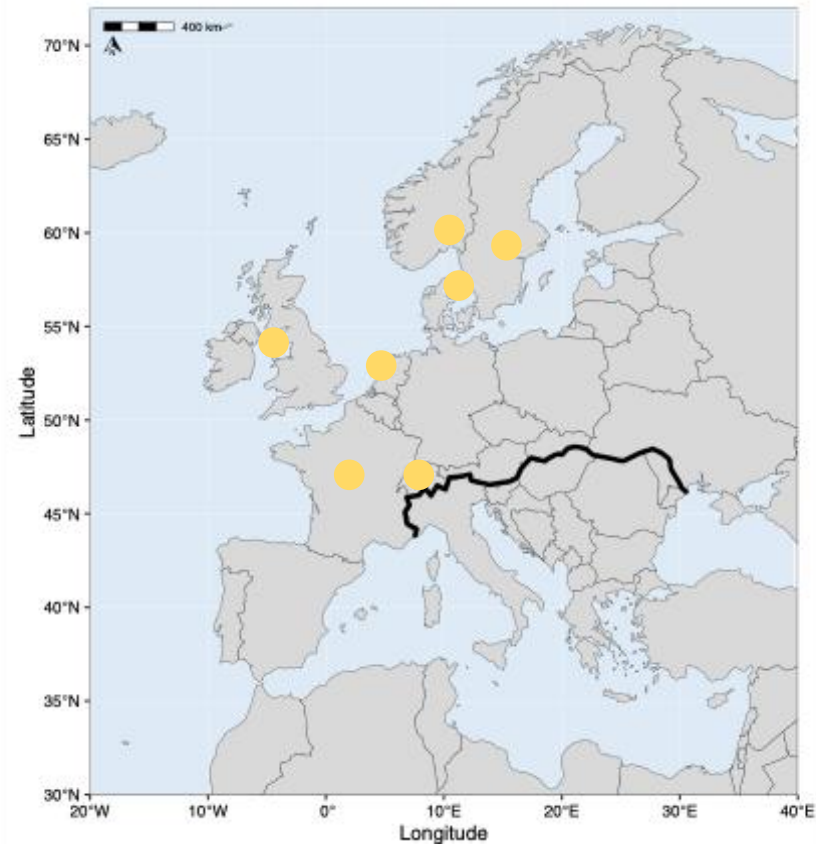
Genetic structure

N Europe

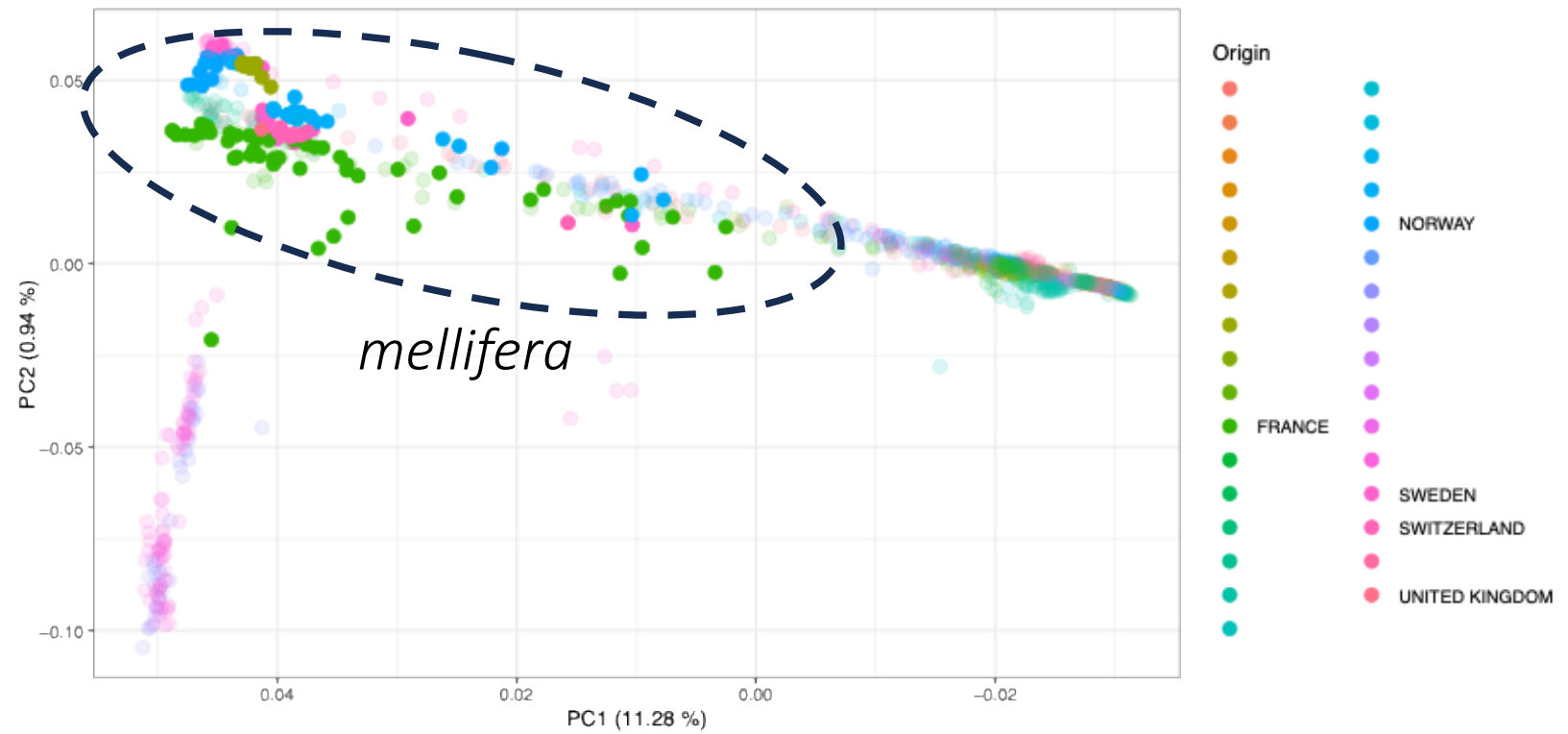


Genetic structure

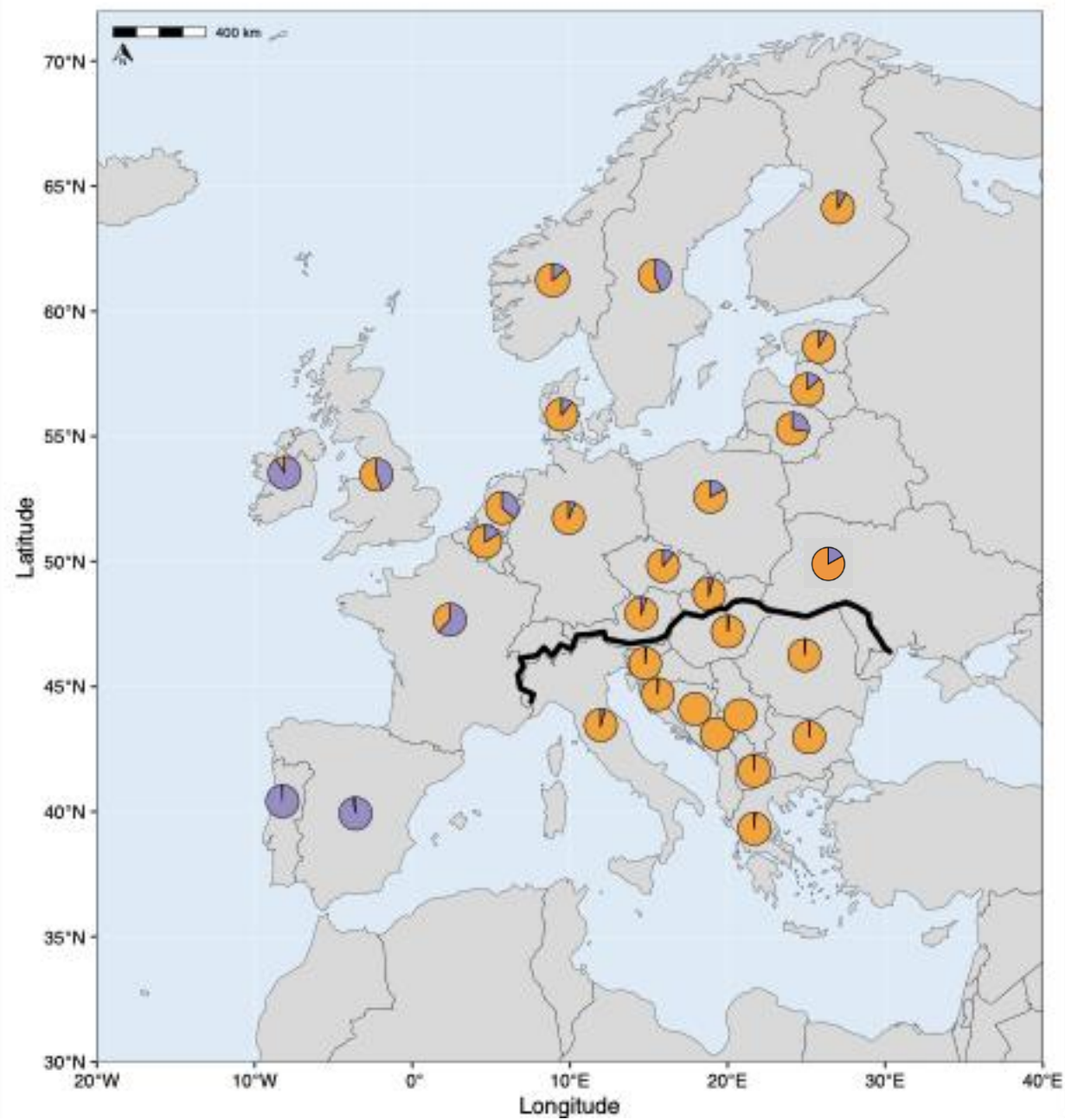
M conservation projects



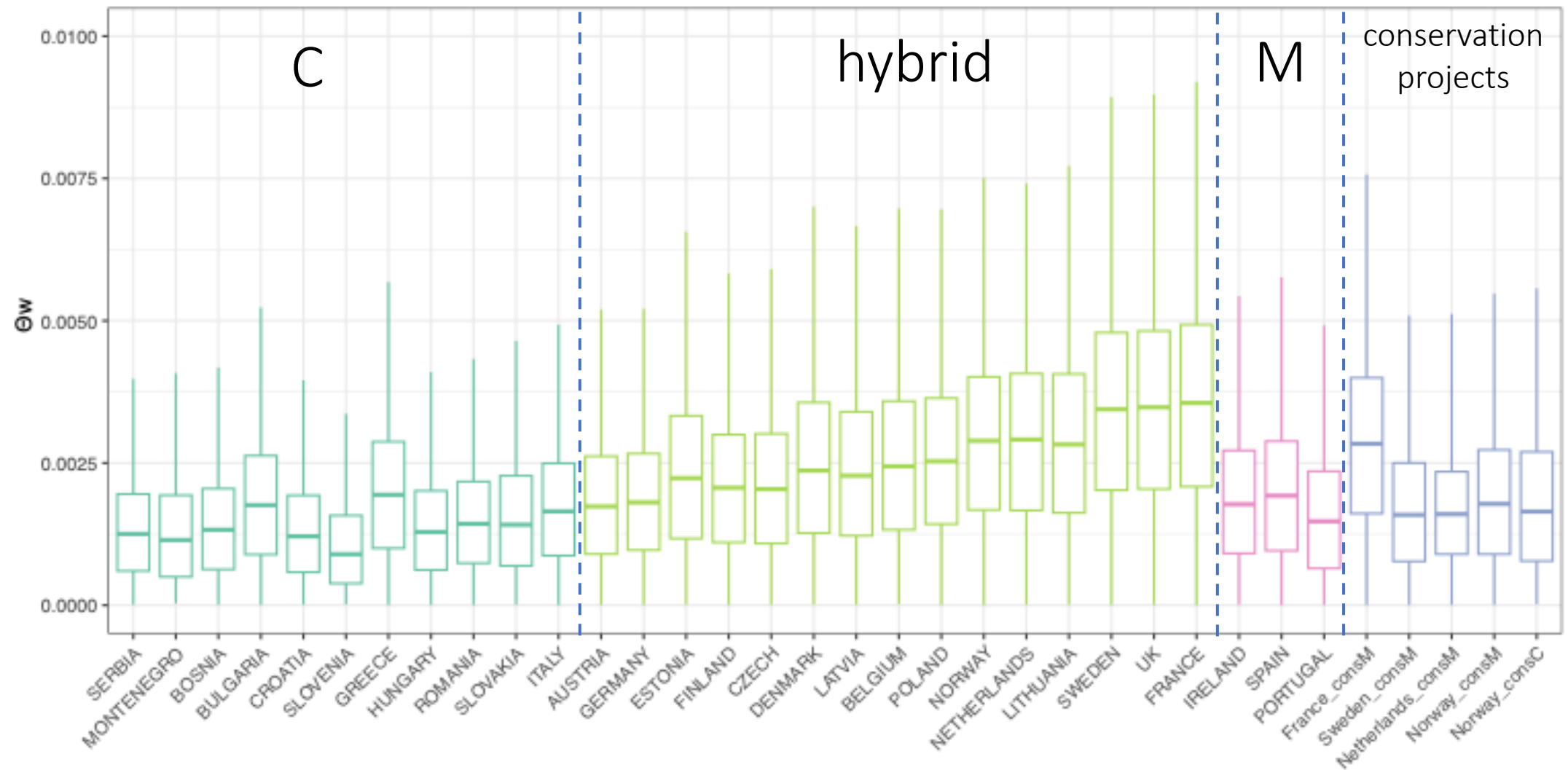
M ← ————— → C



■ C-ancestry ■ M-ancestry



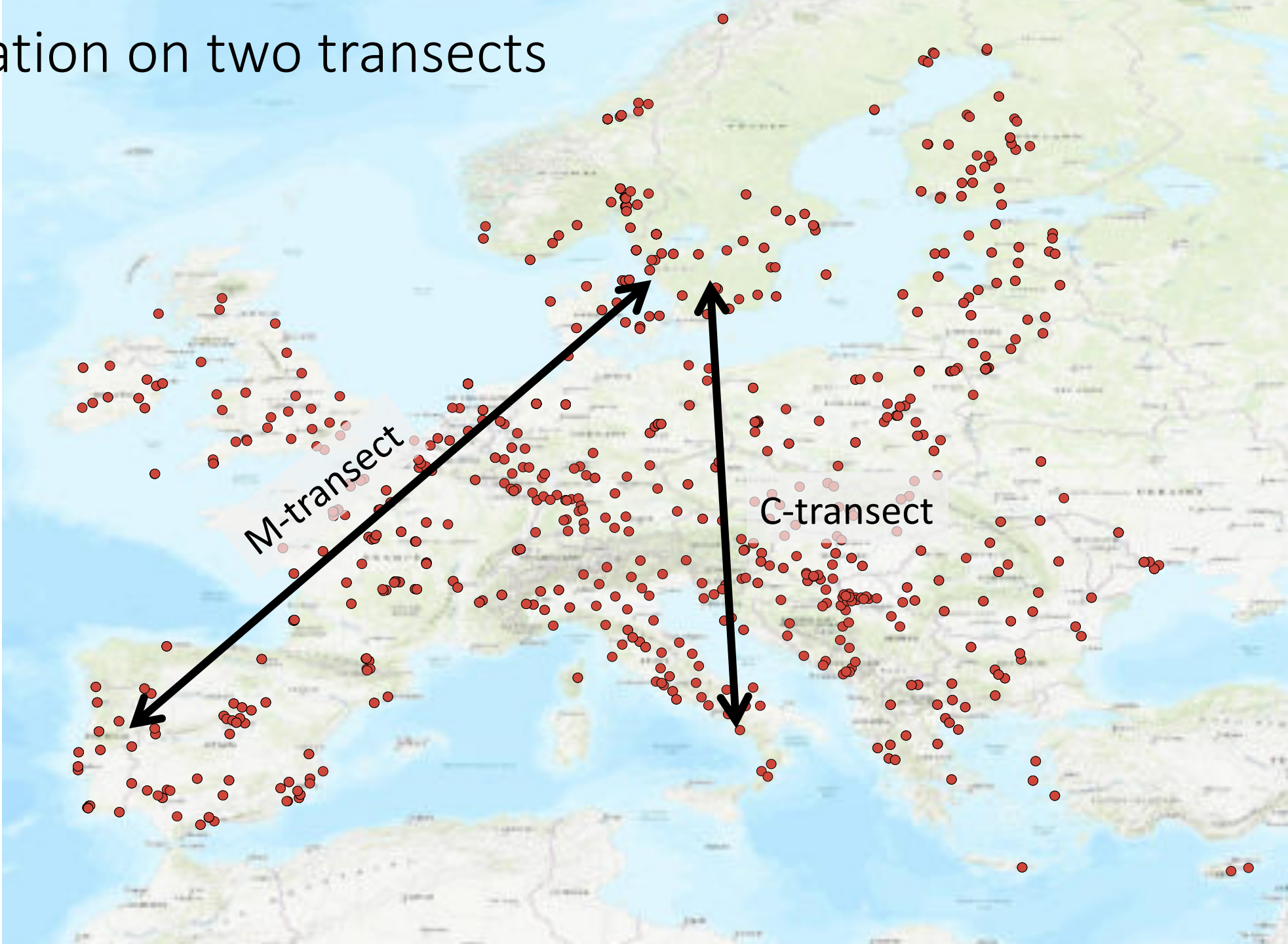
Genetic variation



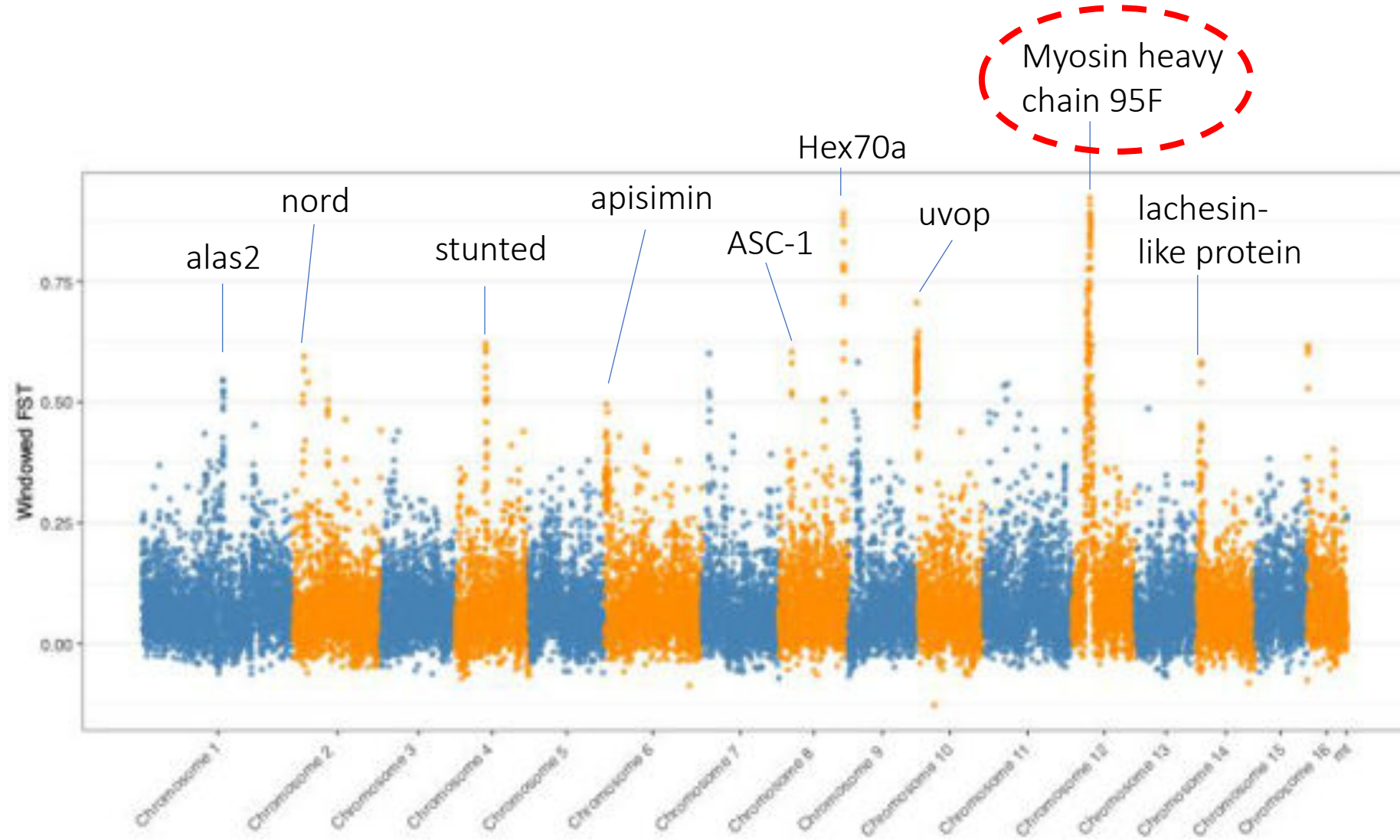
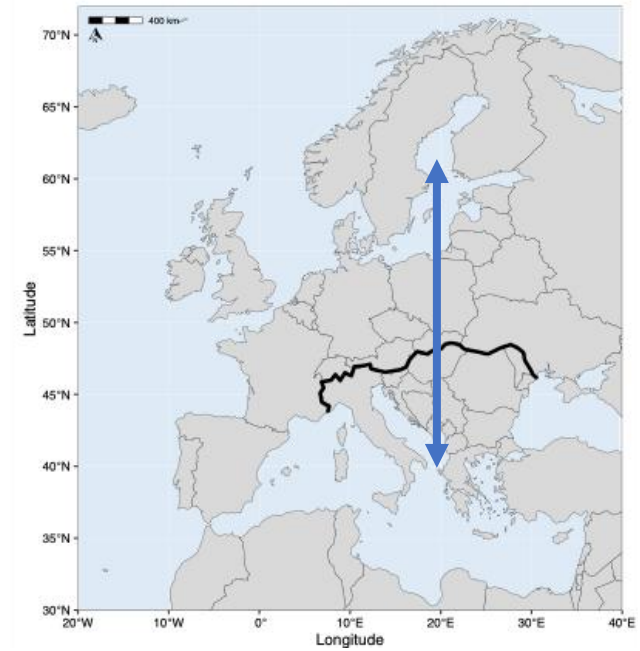
Climate adaptation on two transects

M-lineage transect
ancient adaptation to local
conditions

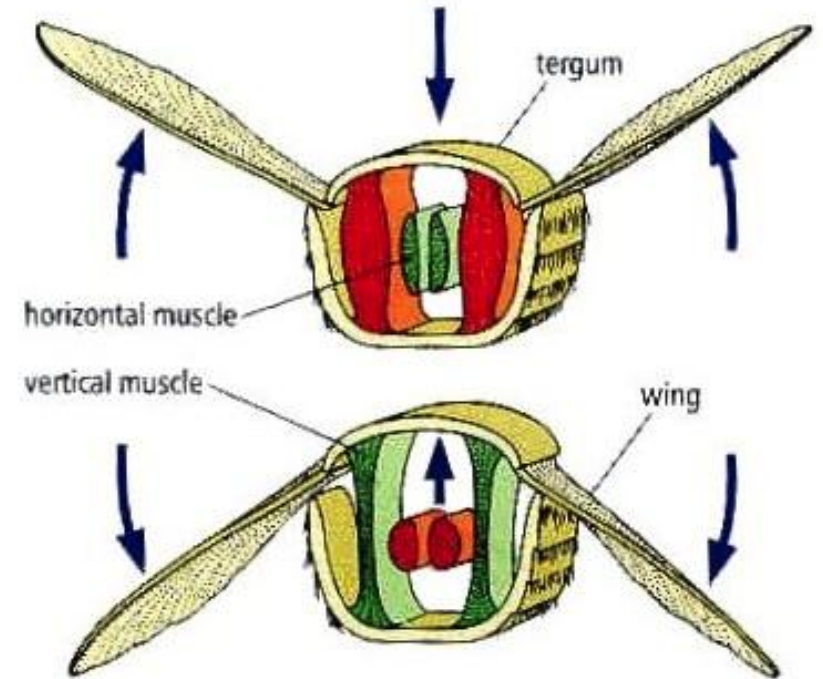
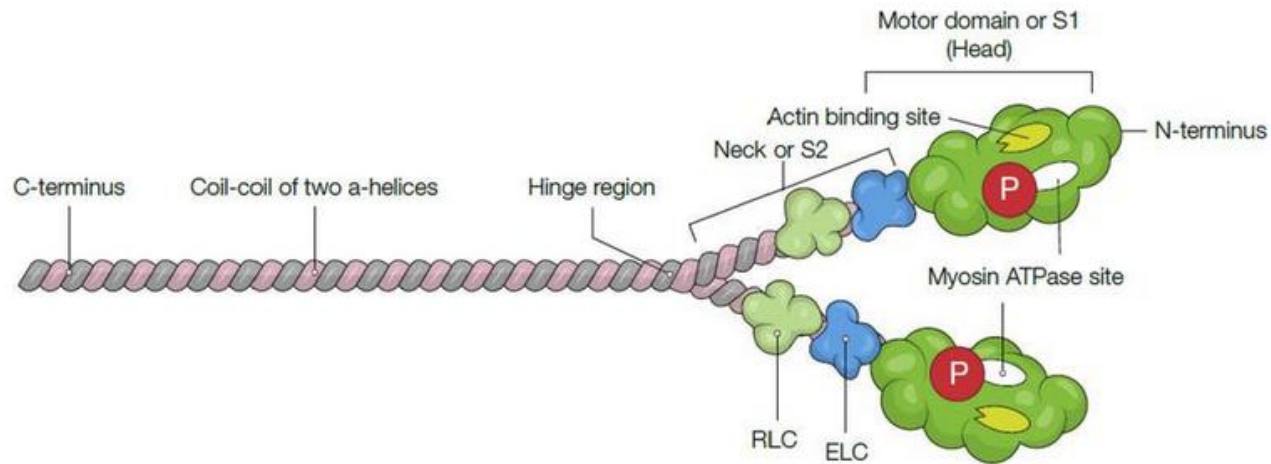
C-lineage transect
recent adaptation after
introduction to north



C transect (Eastern Europe)

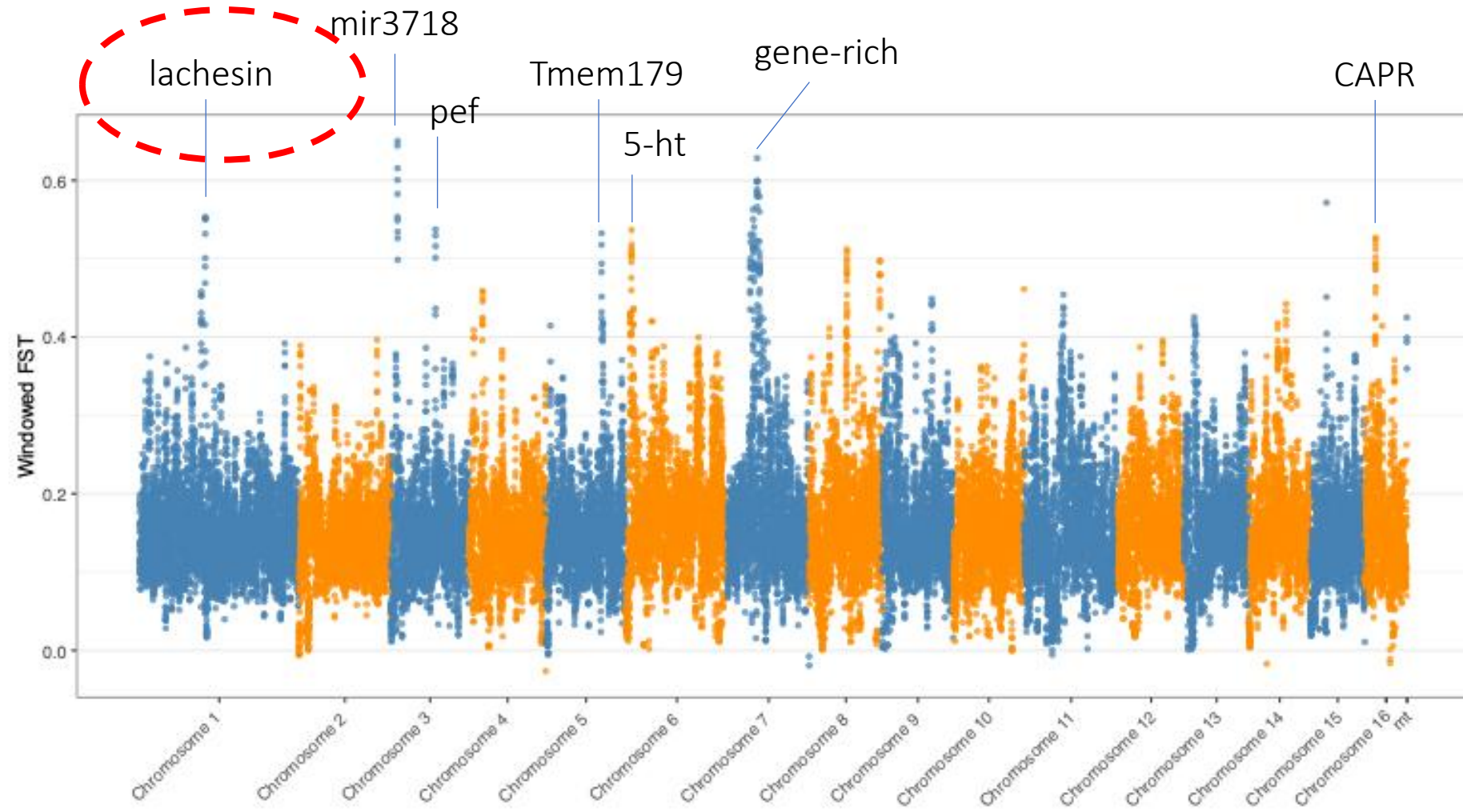
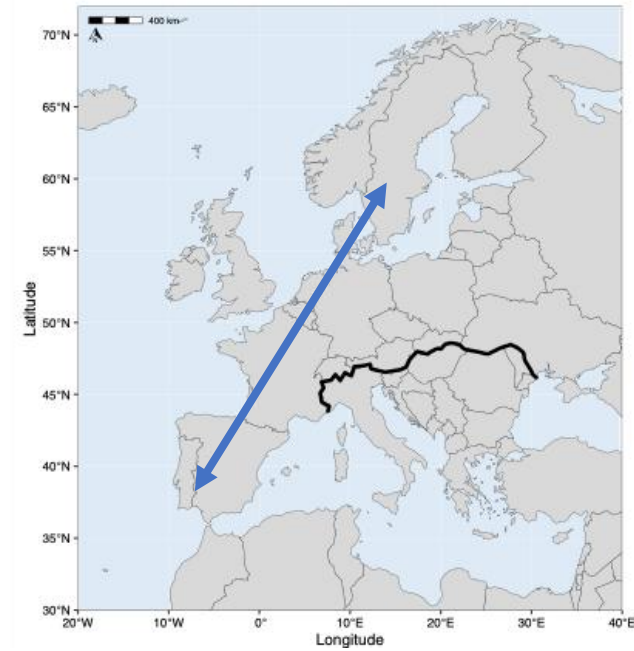


Myosin heavy chain 95F

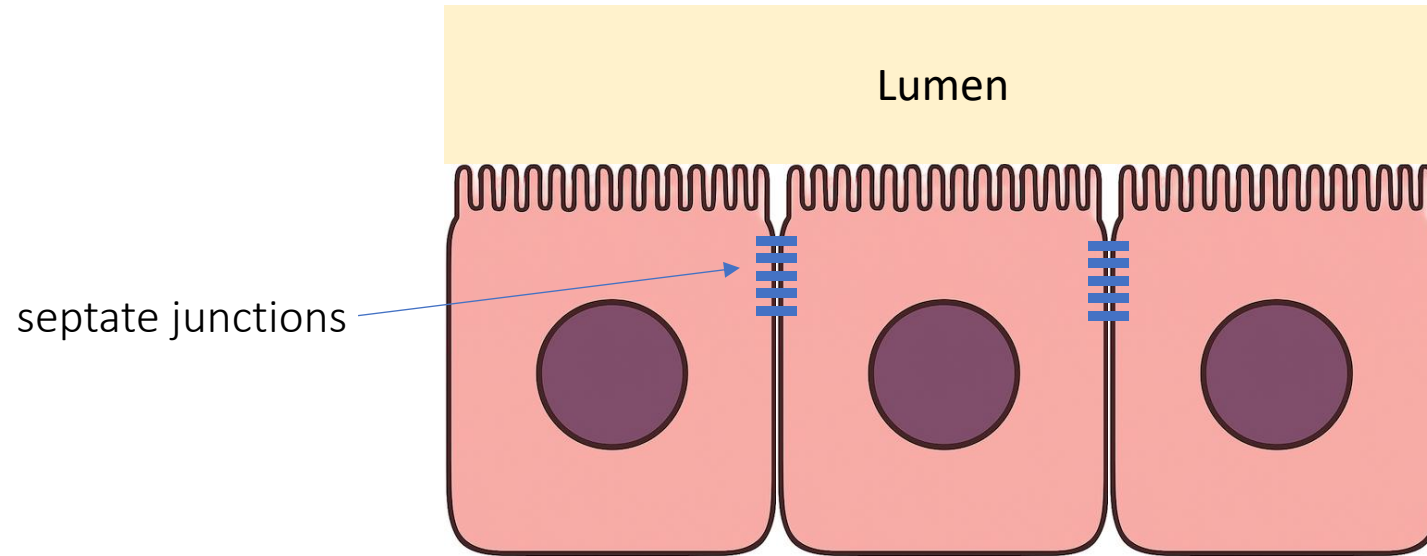


Myosin heavy chain is a key motor protein important in muscle contraction

M transect (Western Europe)



Lachesin



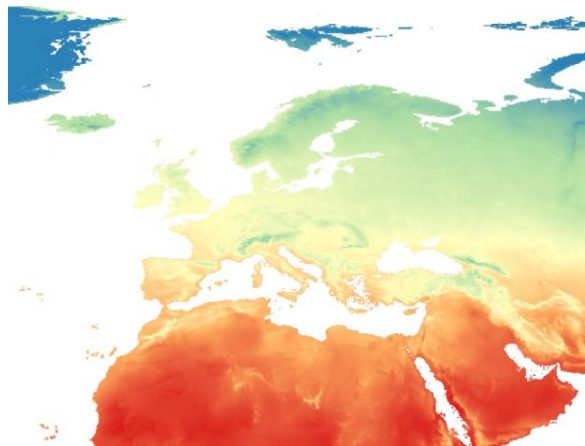
Lachesin is a component of junctions between cells of epithelia
Could be important for resistance to desiccation

Gene-environment associations

Redundancy Analysis (RDA)

Temperature

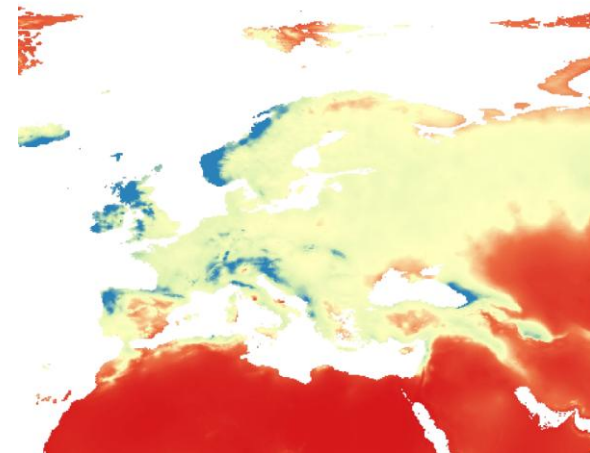
AMT	Annual Mean Temperature
MDR	Mean Diurnal Range
Isotherm	Isothermality
StD	Temperature Seasonality
MaxW	Max Temperature of Warmest Month
MinCool	Min Temperature of Coldest Month
TAnnRange	Temperature Annual Range
MeanTwet	Mean Temperature of Wettest Quarter
MeanTdry	Mean Temperature of Driest Quarter
MeanTwarm	Mean Temperature of Warmest Quarter
MeanTcool	Mean Temperature of Coldest Quarter



AMT

Precipitation

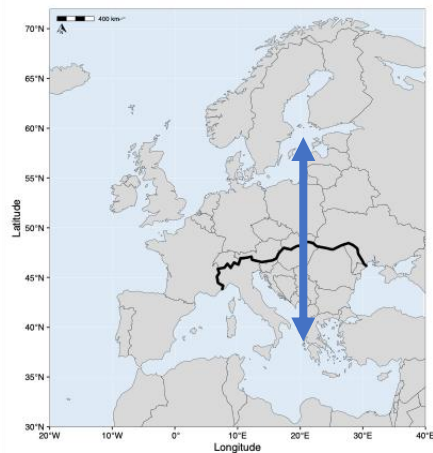
AnnPress	Annual Precipitation
PressWet	Precipitation of Wettest Month
PressDry	Precipitation of Driest Month
PressVar	Precipitation Seasonality (Coefficient of Variation)
PressWetQ	Precipitation of Wettest Quarter
PressDryQ	Precipitation of Driest Quarter
PressWarmQ	Precipitation of Warmest Quarter
PressColdQ	Precipitation of Coldest Quarter



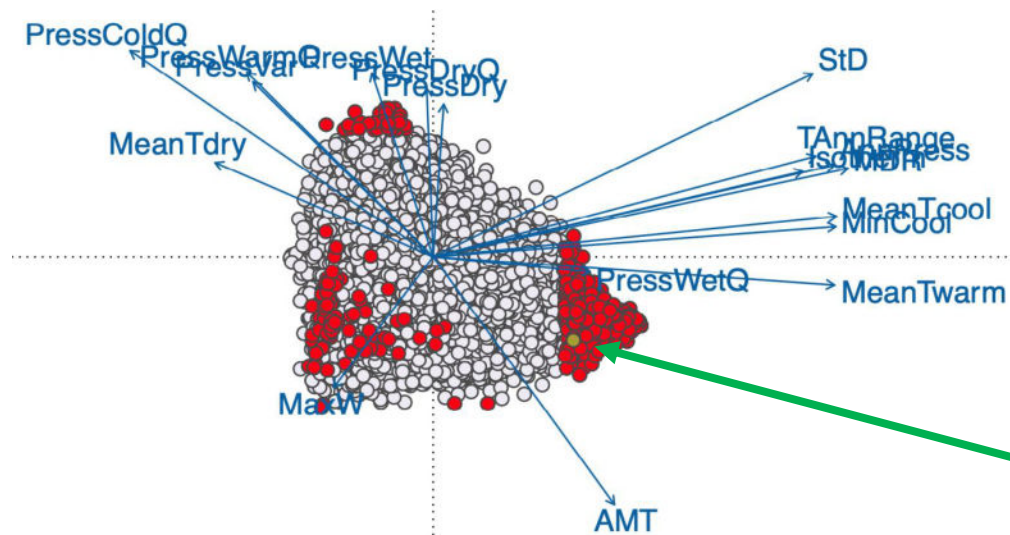
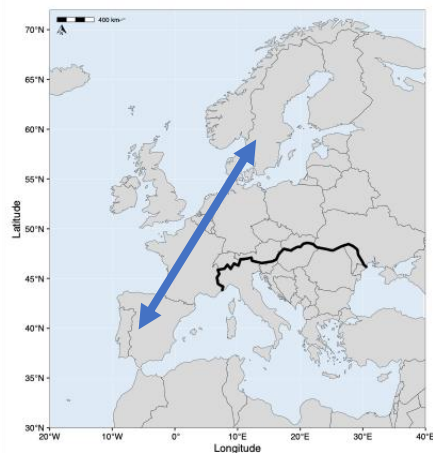
AnnPress

RDA analysis

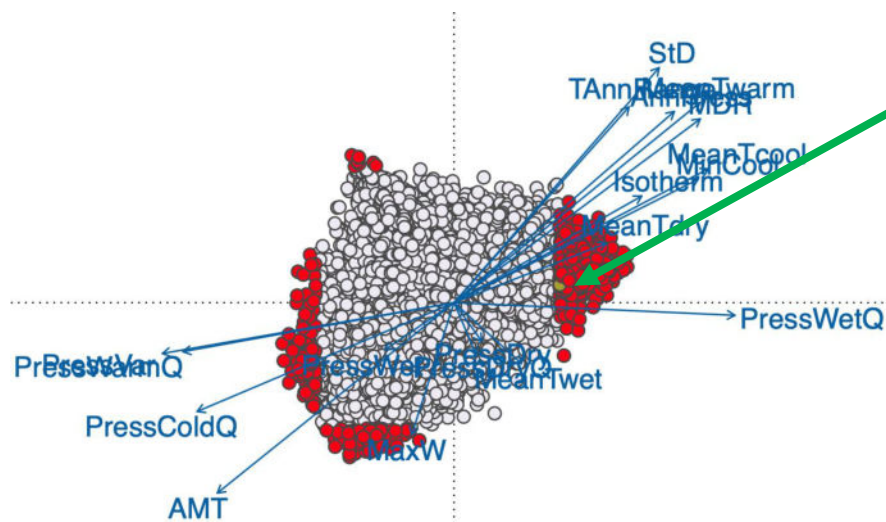
C



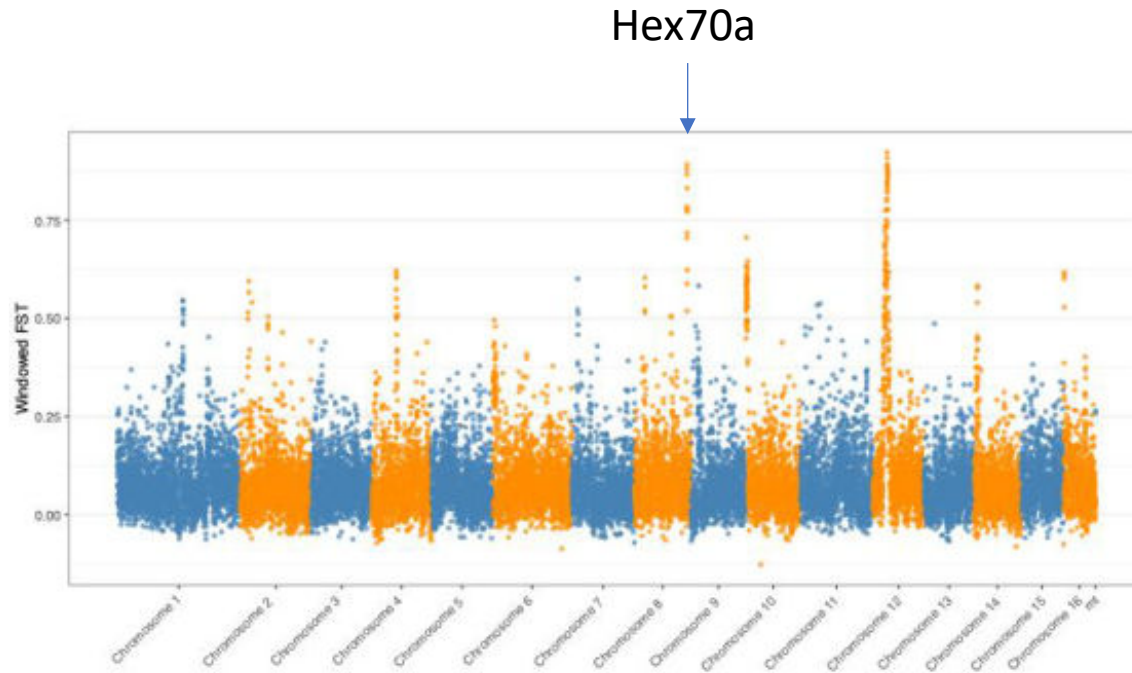
M



Hex70a



Hex70a



Hexamerin protein
identified in all analyses

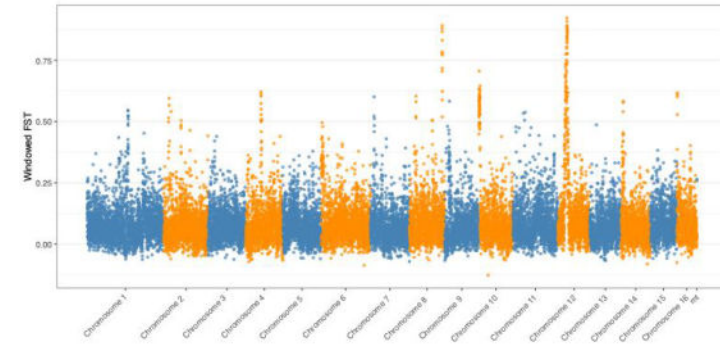
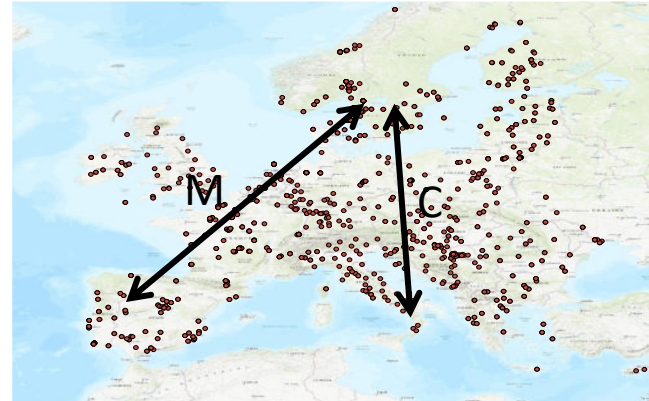
Storage protein for amino acids during metamorphosis
Regulated by Juvenile Hormone
Role in oogenesis and spermatogenesis



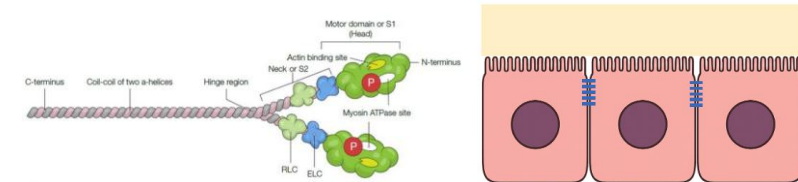
Conclusions

Identification of genes involved in adaptation

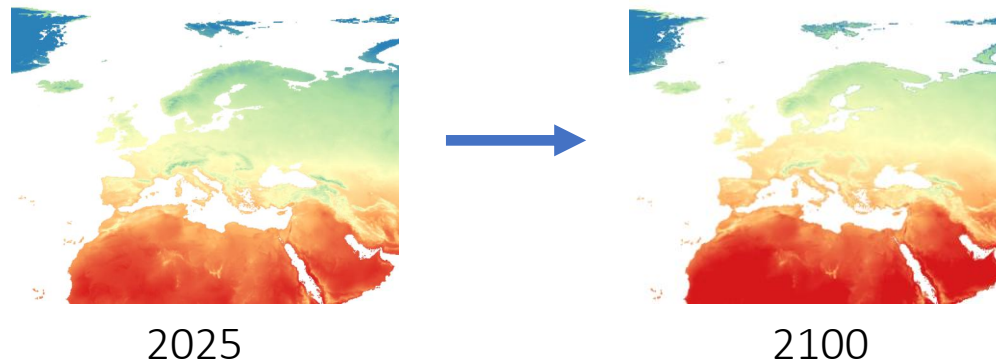
- ancestral (western M-group) transect
- introduced (eastern C-group) transects



Candidate genes suggest molecular and cellular mechanisms for how bees are adapted to climate



Prediction of effects of climate change



Better-B

FOR RESILIENT BEEKEEPING



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National Genomics Infrastructure
Sweden

Thanks to hundreds of beekeepers throughout Europe!





Thank you for your attention!



www.better-b.eu



Better-B-project

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