# Phylogeography of *Bryoria fuscescens* (=*B. capillaris*) across the Euro-Mediterranean región: Panmixia or ancestral shared alleles?

## Carlos Galan Boluda

International Association for Lichenology, 9th symposium 1-6 August-2021
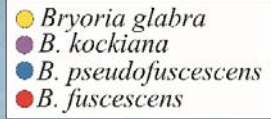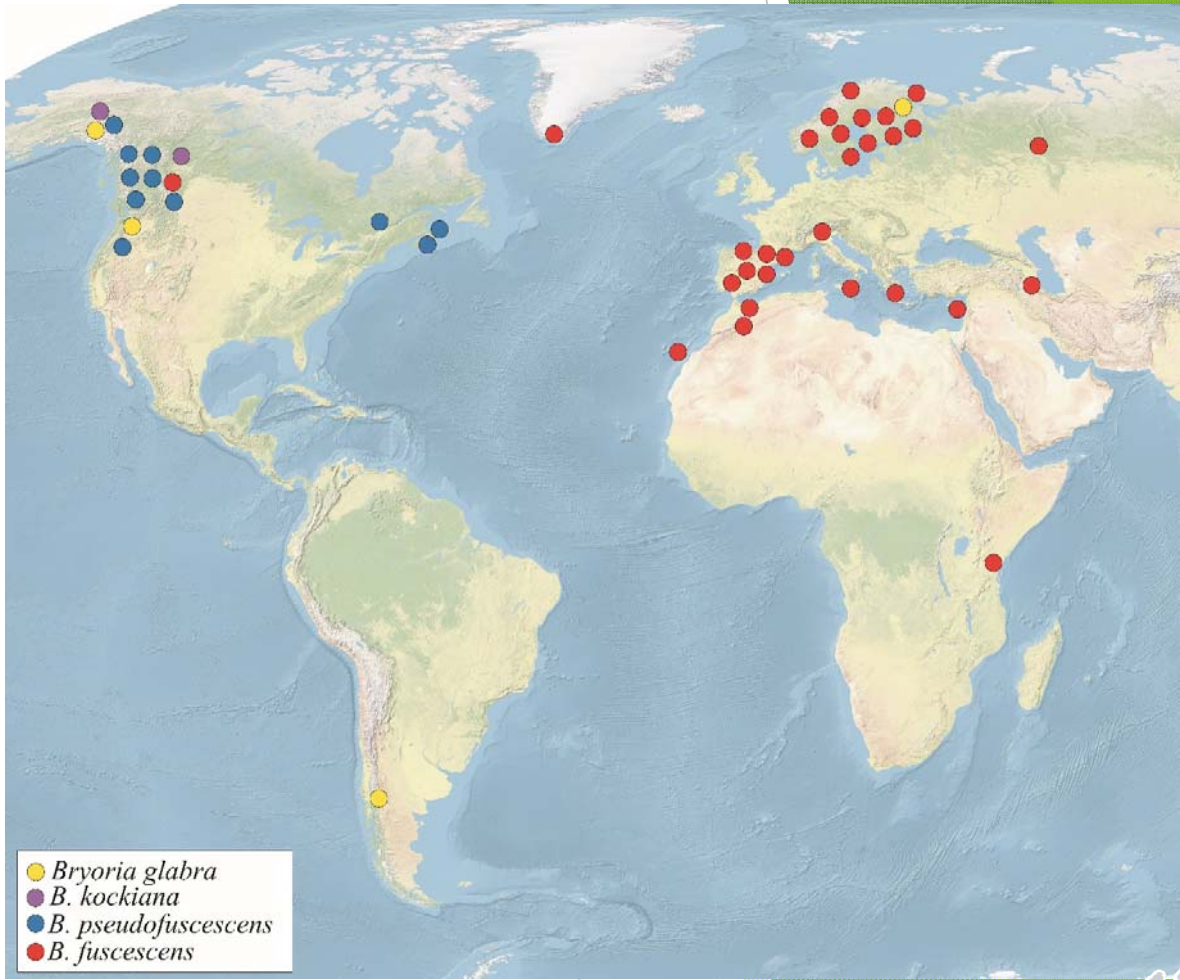
# Introduction
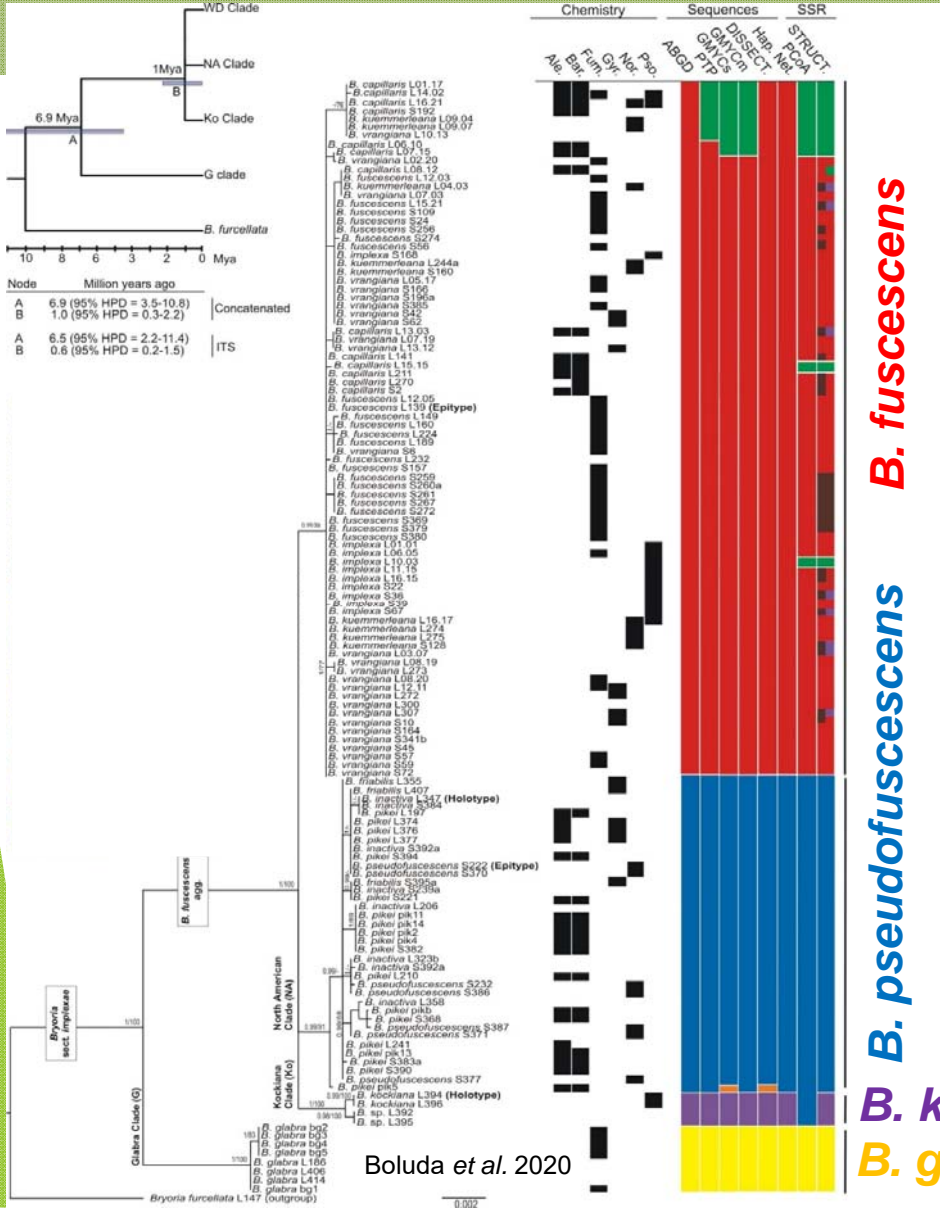


Boluda *et al.* 2020

*B. fuscescens*

*B. pseudofuscescens*

*B. kockiana*

*B. glabra*

Legend:
- Bryoria glabra
- B. kockiana
- B. pseudofuscescens
- B. fuscescens
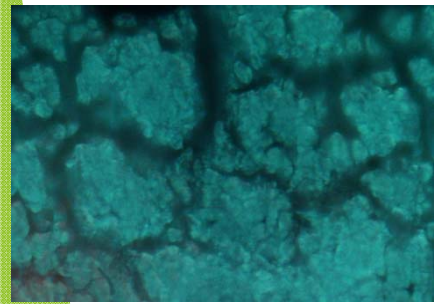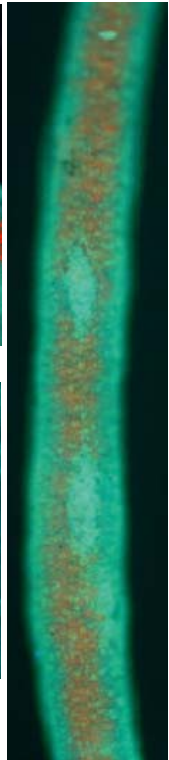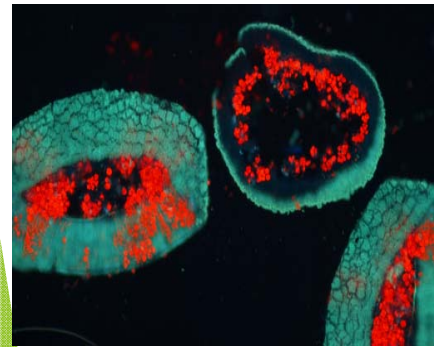
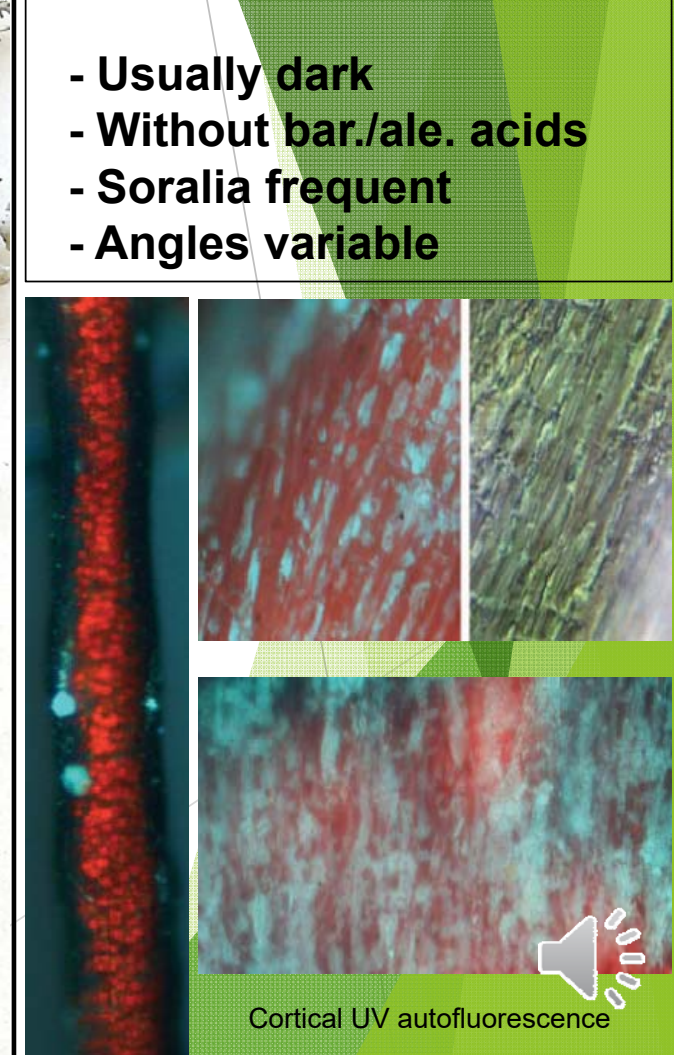# Introduction



**Phenotype-*capillaris***

- Usually pale
- With bar./ale. acids
- Soralia rare
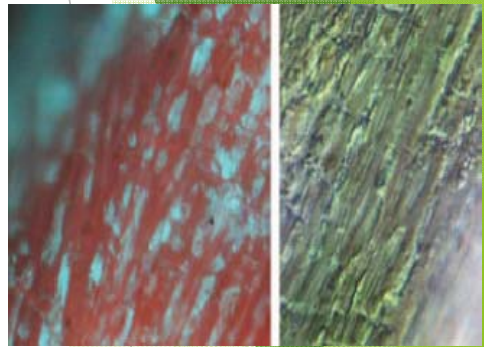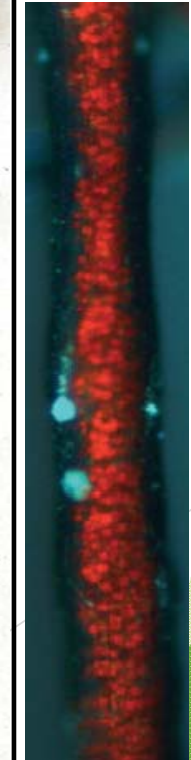- Angles usually acute

*Bryoria fuscescens*

**Phenotype-*fuscescens***

- Usually dark
- Without bar./ale. acids
- Soralia frequent
- Angles variable

Cortical UV autofluorescence
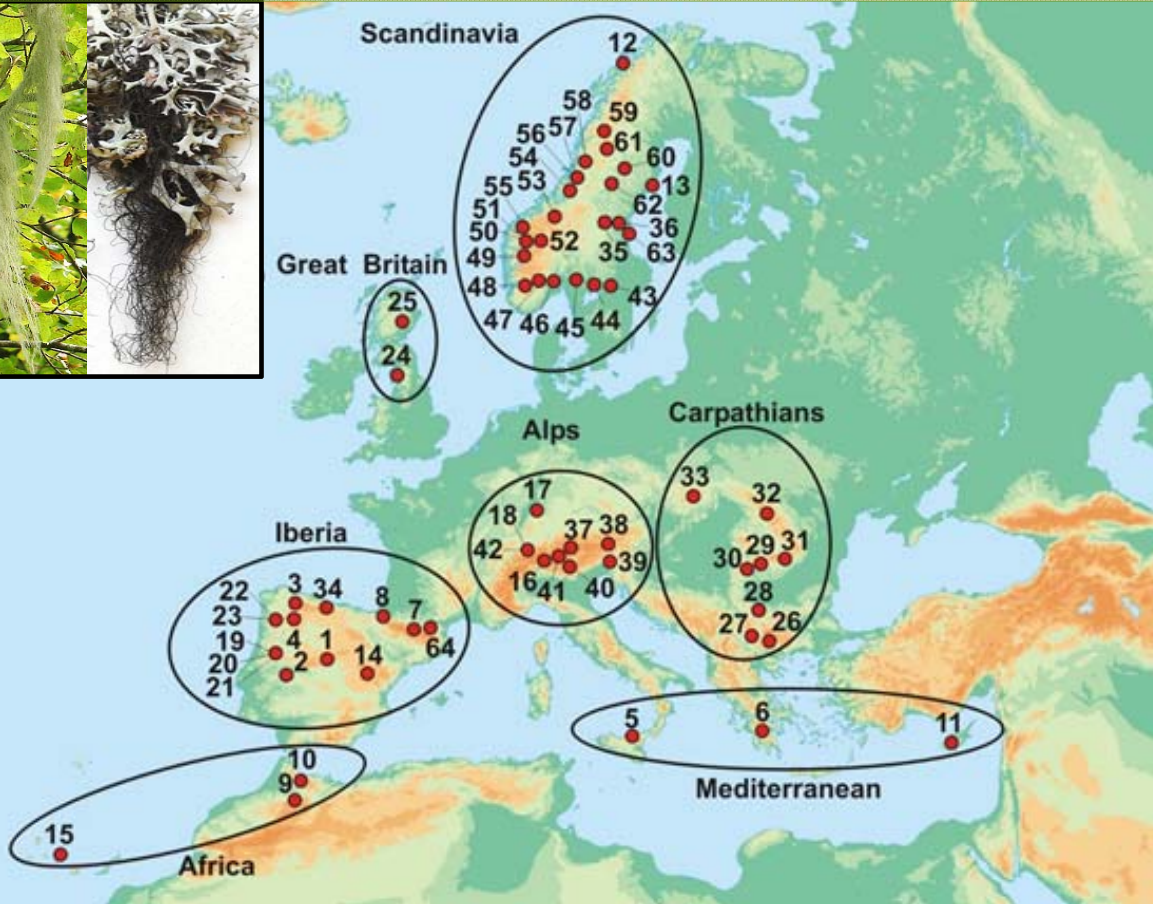
Cortical UV autofluorescence

# Sampling



Table 1. Amplified and analysed SSRs. Left: Number of specimens with successful amplification for each locus, and its respective number of alleles. Right: Selected loci and specimens for the analyses after remove unexpected alleles and specimens with missing data.

| Locus | Amplified SSRs | | SSRs used for the analyses | |
|---|---|---|---|---|
| | Specimens | Alleles | Specimens | Alleles |
| Bi01 | 1384 | 22 | Not used | Not used |
| Bi02 | 1123 | 6 | Not used | Not used |
| Bi03 | 1391 | 5 | 1359 | 5 |
| Bi04 | 1388 | 8 | 1359 | 7 |
| Bi05 | 1359 | 14 | 1359 | 10 |
| Bi06 | 1366 | 22 | 1359 | 21 |
| Bi07 | 1368 | 6 | 1359 | 6 |
| Bi08 | 1385 | 5 | 1359 | 5 |
| Bi09 | 597 | 3 | Not used | Not used |
| Bi10 | 1393 | 5 | 1359 | 3 |
| Bi11 | 1391 | 12 | 1359 | 10 |
| Bi12 | 1399 | 22 | 1359 | 21 |
| Bi13 | 1359 | 18 | 1359 | 18 |
| Bi14 | 1391 | 4 | 1359 | 3 |
| Bi15 | 1071 | 3 | Not used | Not used |
| Bi16 | 1360 | 6 | 1359 | 6 |
| Bi18 | 1359 | 9 | 1359 | 9 |
| Bi19 | 1388 | 8 | 1359 | 6 |

**1.400 specimens, 64 populations, 18 microsatellites**

Data curation

**1.359 specimens
14 microsatellites
No missing data**

**35 specimens used for a phylogenetical reconstruction
(3 standard loci, and 5 new loci)**

# Results: Diversity per areas
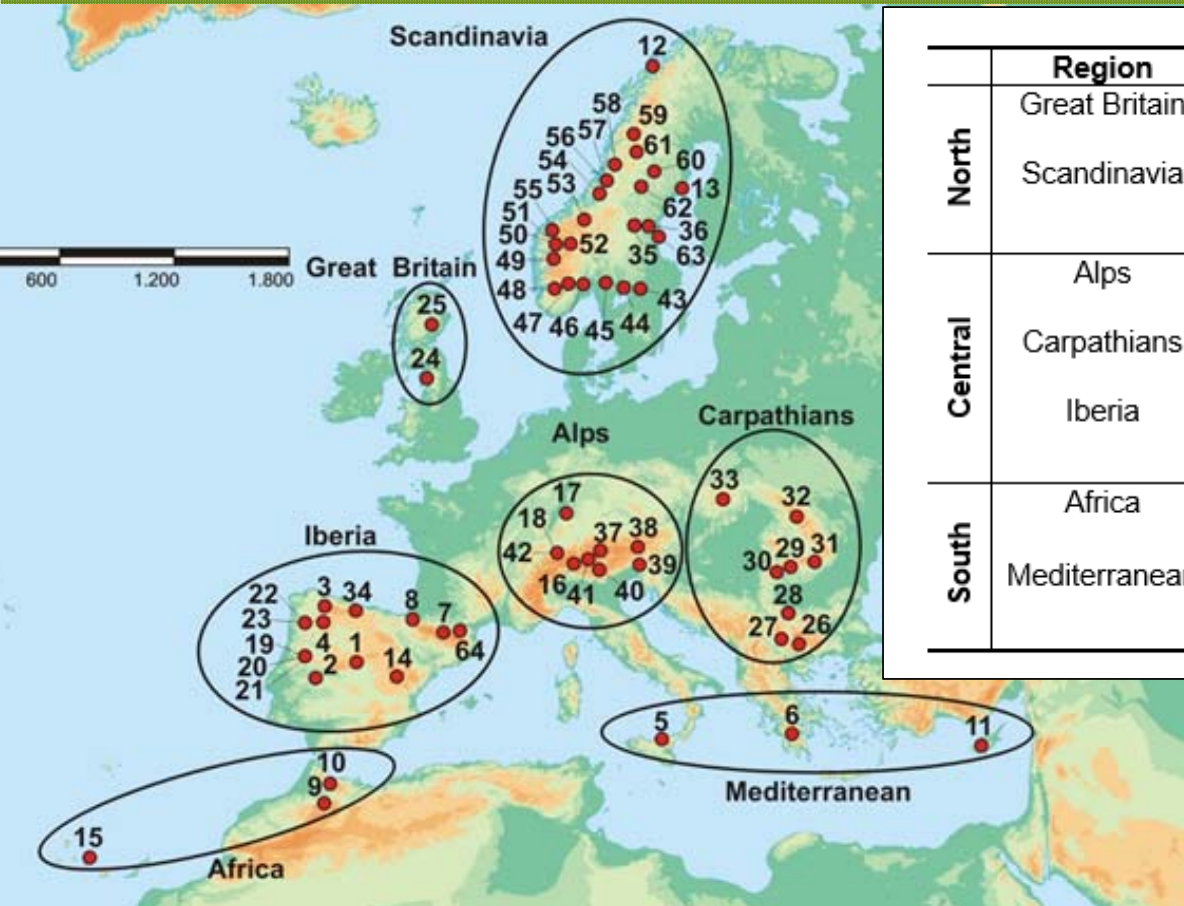


| | Region | specimens | AR | PAR | specimens | AR | PAR |
|---|---|---|---|---|---|---|---|
| North | Great Britain | 32 | 2.642 (0.439) | 0.000 (0.000) | 588 | 7.500 (1.207) | 1.357 (0.452) |
| | Scandinavia | 556 | 7.428 (1.170) | 1.357 (0.452) | | | |
| Central | Alps | 189 | 5.357 (1.014) | 0.357 (0.199) | 641 | 7.071 (1.442) | 0.857 (0.274) |
| | Carpathians | 179 | 5.428 (0.976) | 0.000 (0.000) | | | |
| | Iberia | 273 | 5.571 (0.976) | 0.285 (0.125) | | | |
| South | Africa | 65 | 4.571 (0.947) | 0.428 (0.227) | 130 | 5.571 (1.087) | 0.500 (0.251) |
| | Mediterranean | 65 | 4.214 (0.575) | 0.071 (0.071) | | | |

Scandinavia: ⬆⬆
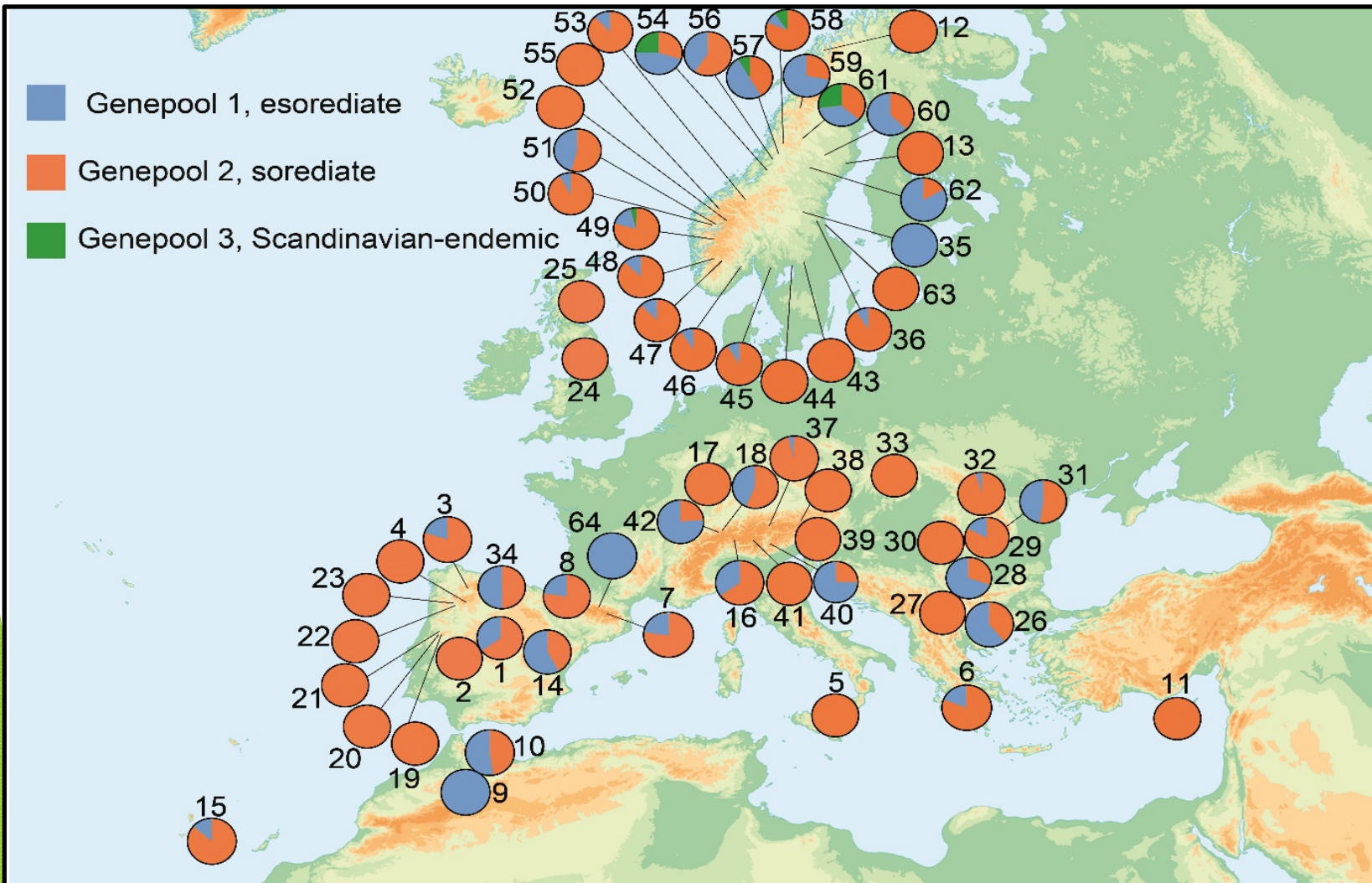Alps: ⬆
Iberia: ⬆
Carpathians: ⬆⬇
Great Britain: ⬇

⬆ High diversity
⬇ Low diversity

# Results: Genepools distribution



**DAPC Genepools**

**Genepool 1**
Soralia: Frequent
Fum.: Variable
Ph. *capillaris*: 13%
Ph. *fuscescens*: 87%

**Genepool 2**
Soralia: Absent
Fum.: No
Ph. *capillaris* : 87%
Ph. *fuscescens* : 13%
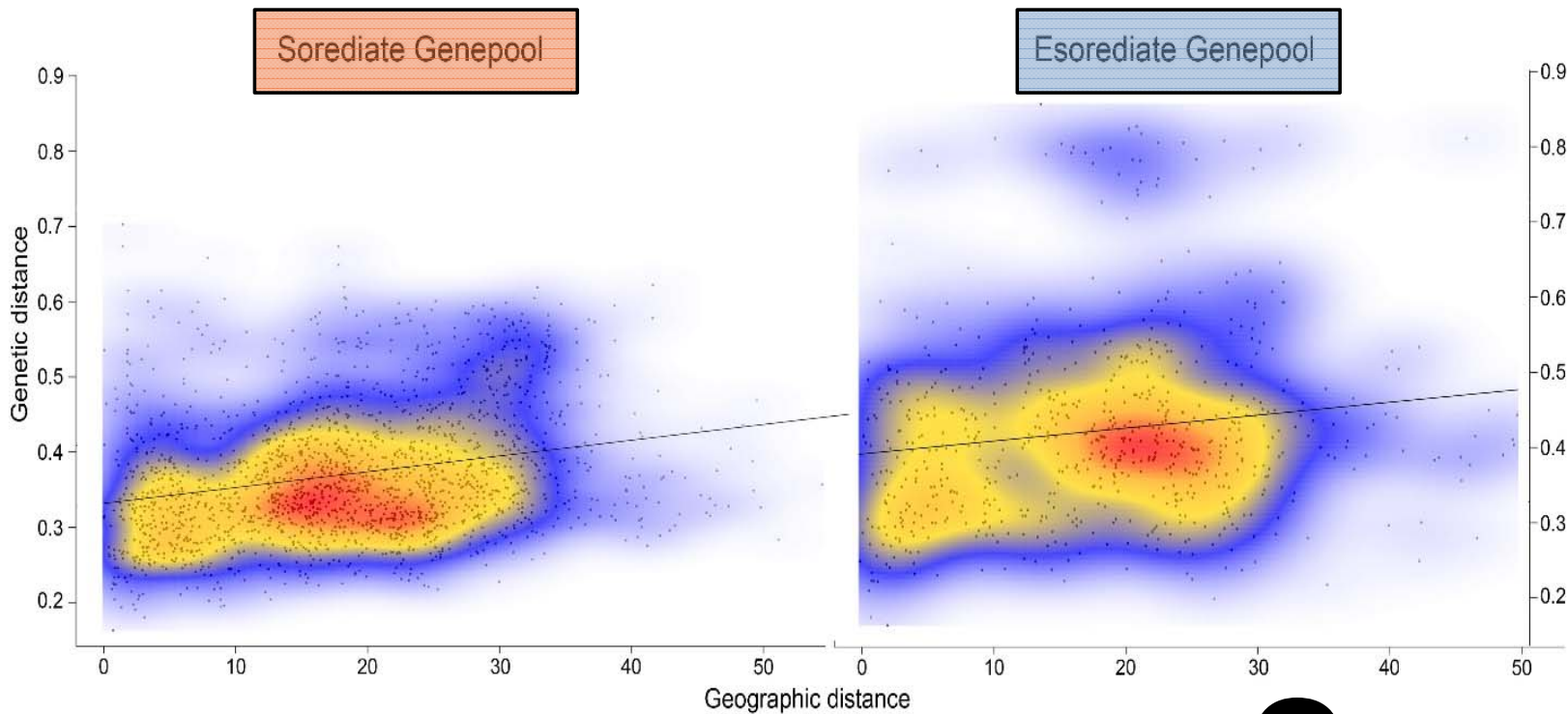
**Genepool 3**
Soralia: Absent
Fum.: No
Ph. *capillaris* : 100%
Ph. *fuscescens* : 0%

Legend:
- Genepool 1, esorediate
- Genepool 2, sorediate
- Genepool 3, Scandinavian-endemic

# Results: Isolation by distance

**Analysis to detect genetic isolation by geographic distance between pairs of populations**



Sorediate Genepool

Esorediate Genepool

Genetic distance

Geographic distance

**Soralia are not favouring dispersion**

?

## DAPC Genepools

### Genepool 1
**Soralia: Frequent**
**Fum.: Variable**
**Ph. *capillaris*: 13%**
**Ph. *fuscescens*: 87%**

### Genepool 2
**Soralia: Absent**
**Fum.: No**
**Ph. *capillaris* : 87%**
**Ph. *fuscescens* : 13%**

### Genepool 3
**Soralia: Absent**
**Fum.: No**
**Ph. *capillaris* : 100%**
**Ph. *fuscescens* : 0%**

# Results: Past potential distribution
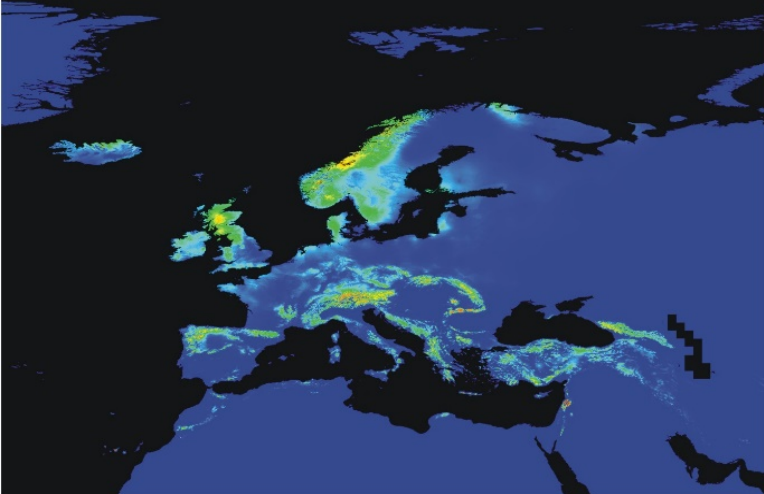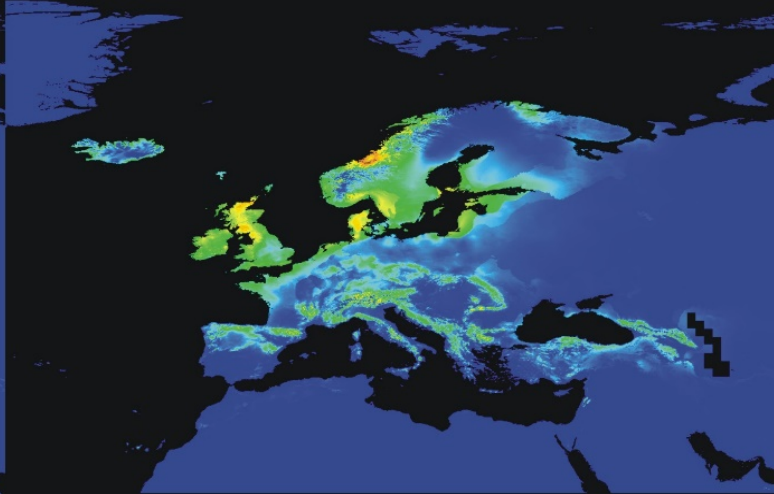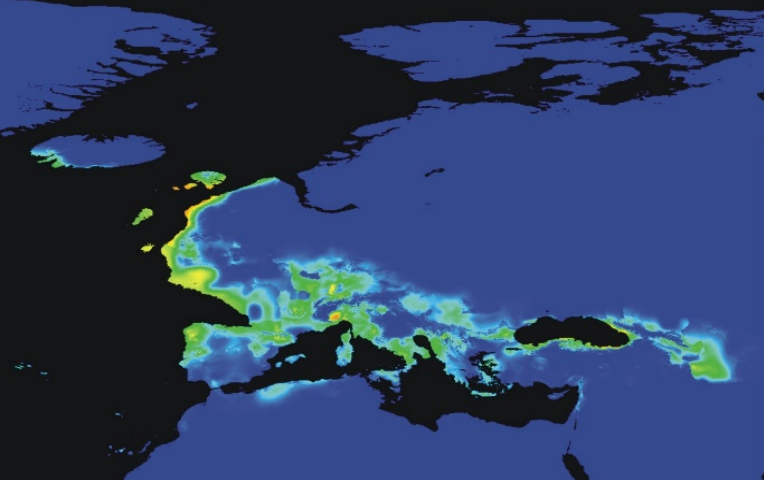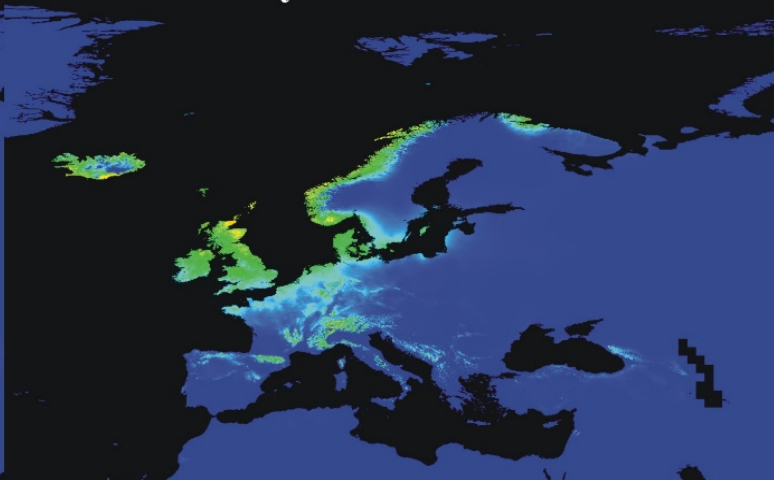


**Glacial refugia candidates:**

**East of British Isles**

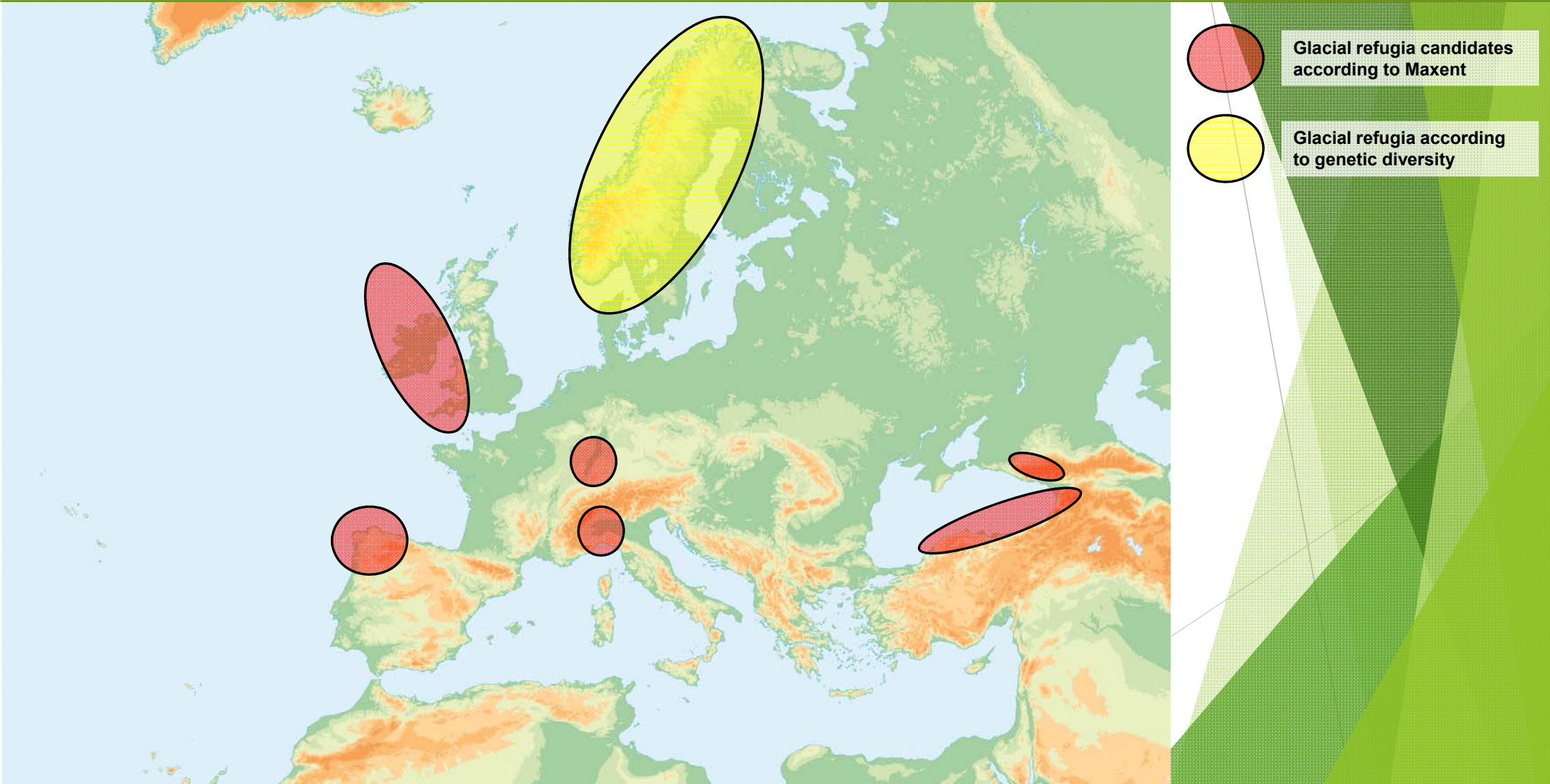**Northwest of Iberian Peninsula**

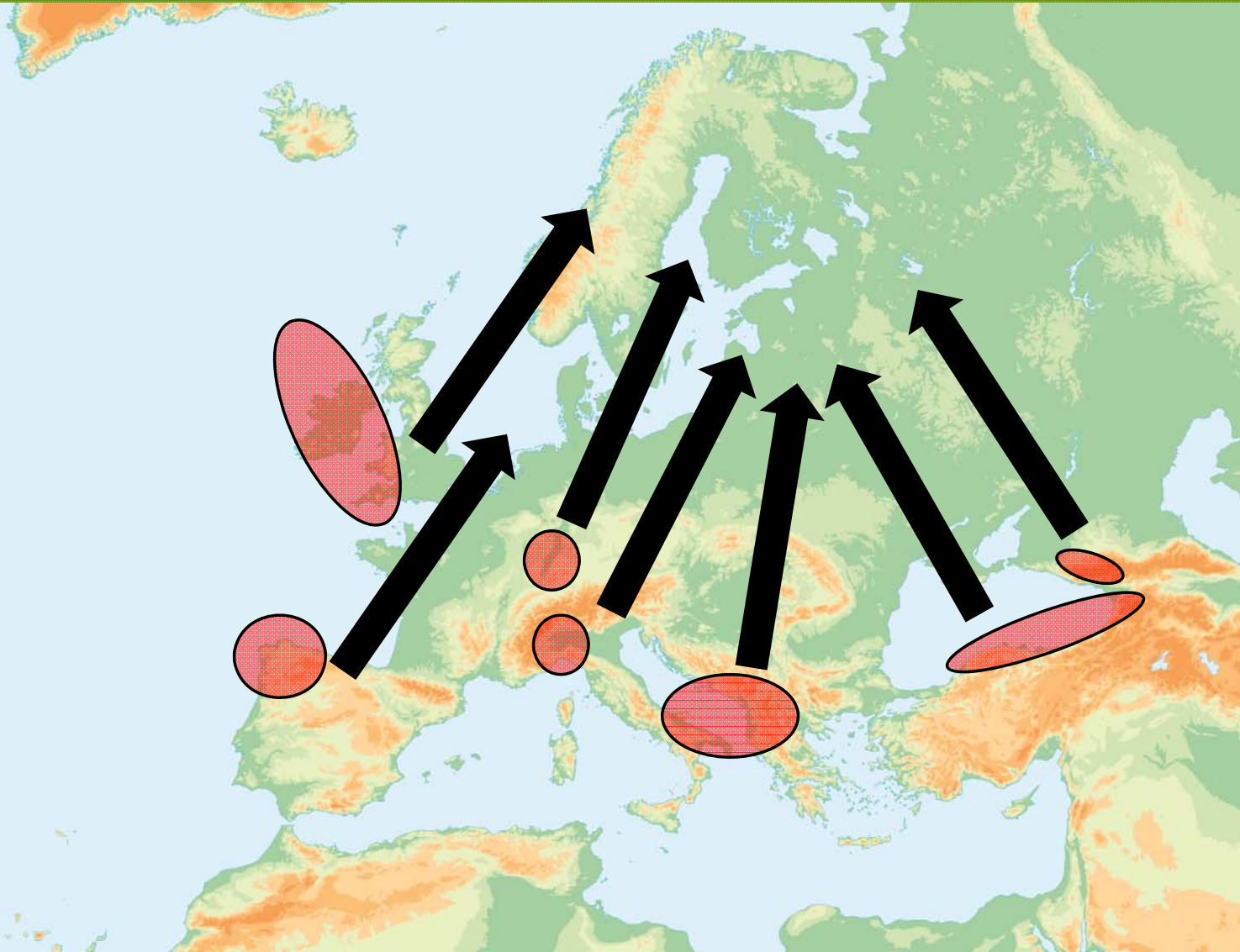**Alps lowlands**

**Black sea**

Potential distribution prediction for *Bryoria fuscescens s. str*. using Maxent and 11 bioclimatic layers
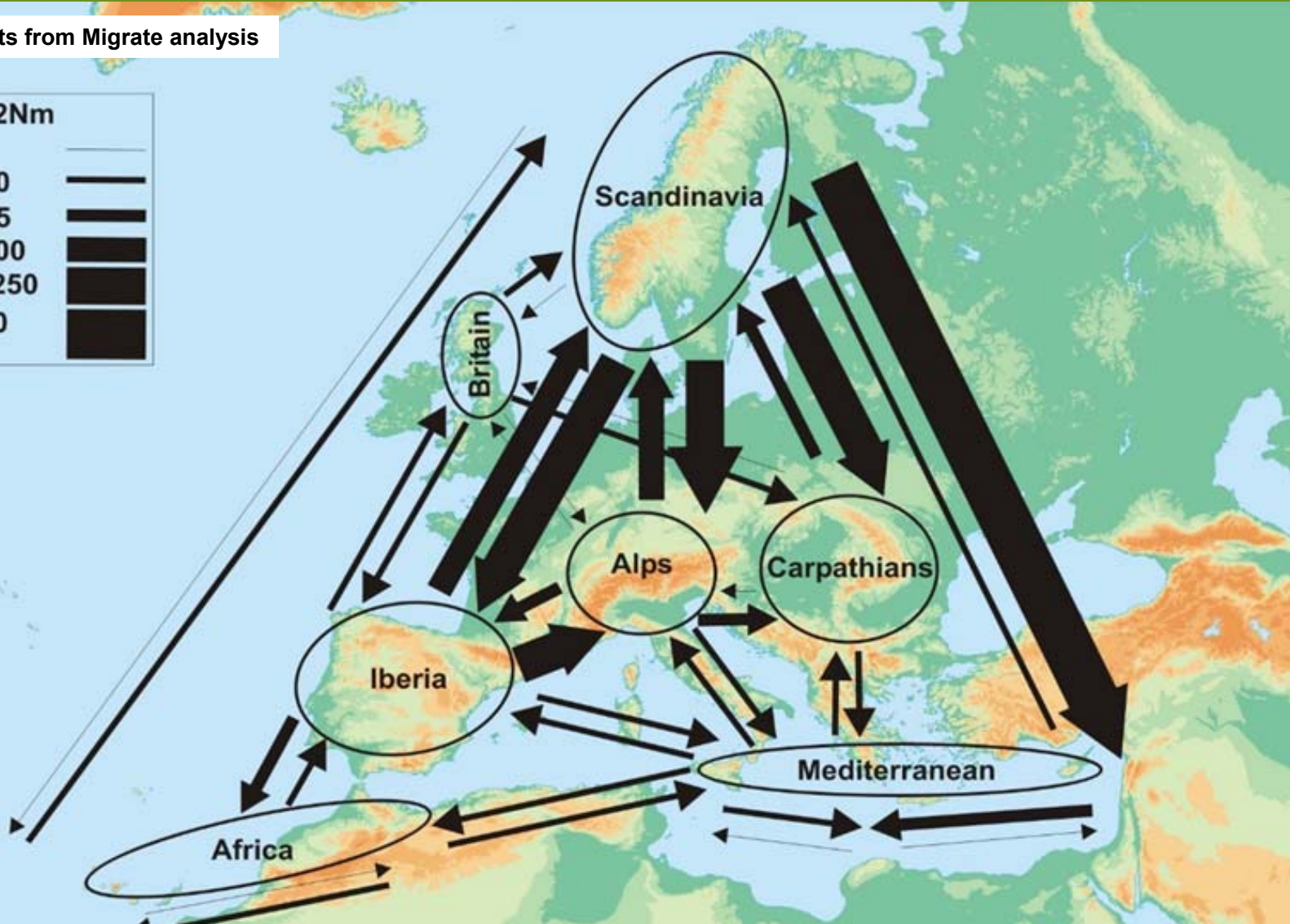
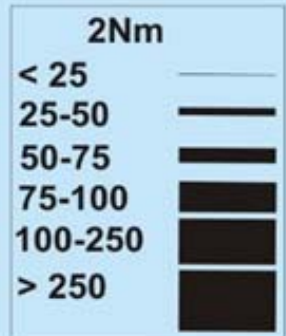# Results: Putative refugia according Maxent
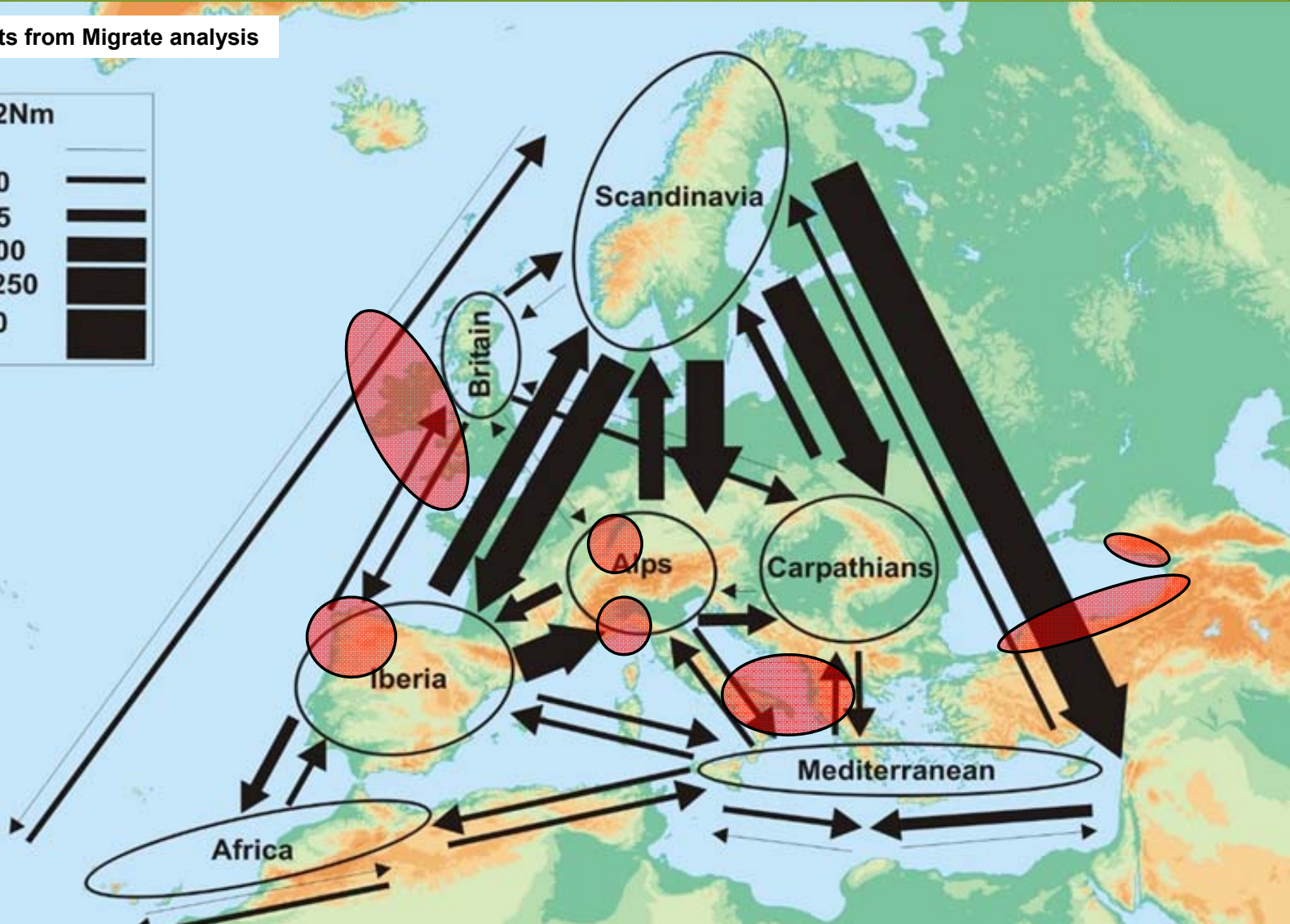
Glacial refugia candidates according to Maxent

Glacial refugia according to genetic diversity

# Results: Expected migration



Glacial refugia candidates according to Maxent

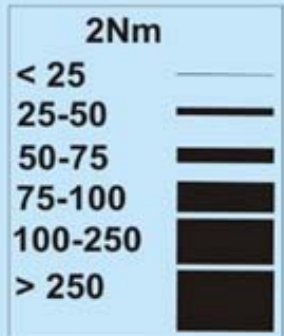# Results: Detected migration

# Results: Mismatch between results



Results from Migrate analysis

2Nm
< 25
25-50
50-75
75-100
100-250
> 250

Scandinavia
Britain
Alps
Carpathians
Iberia
Mediterranean
Africa

Glacial refugia candidates according to Maxent

# Discussion: Example of putative migrations
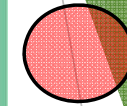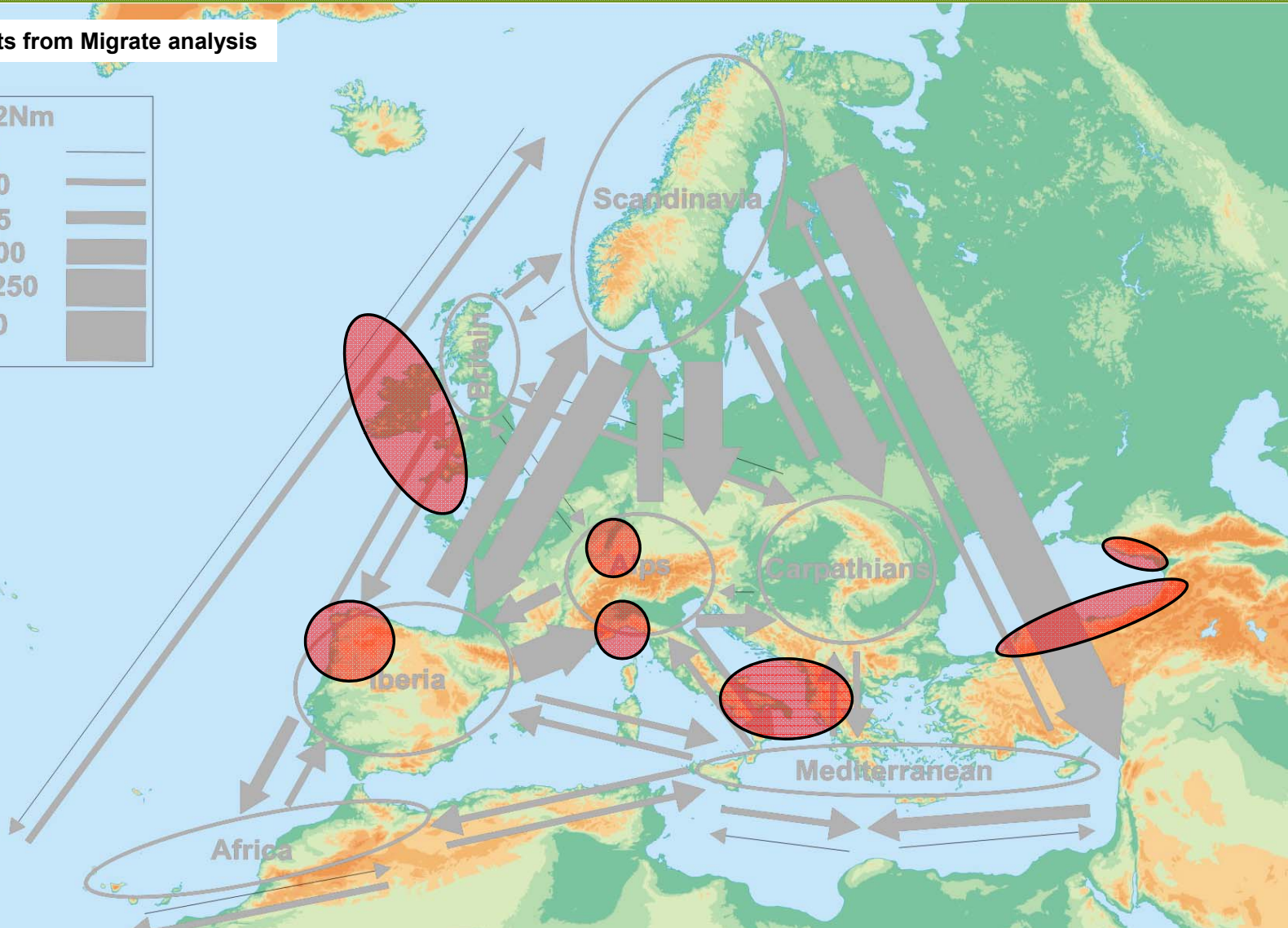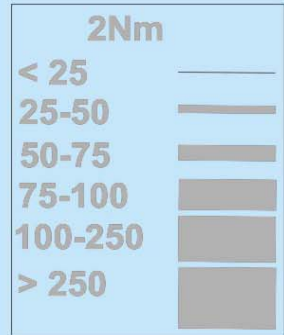


Results from Migrate analysis

2Nm
< 25
25-50
50-75
75-100
100-250
> 250

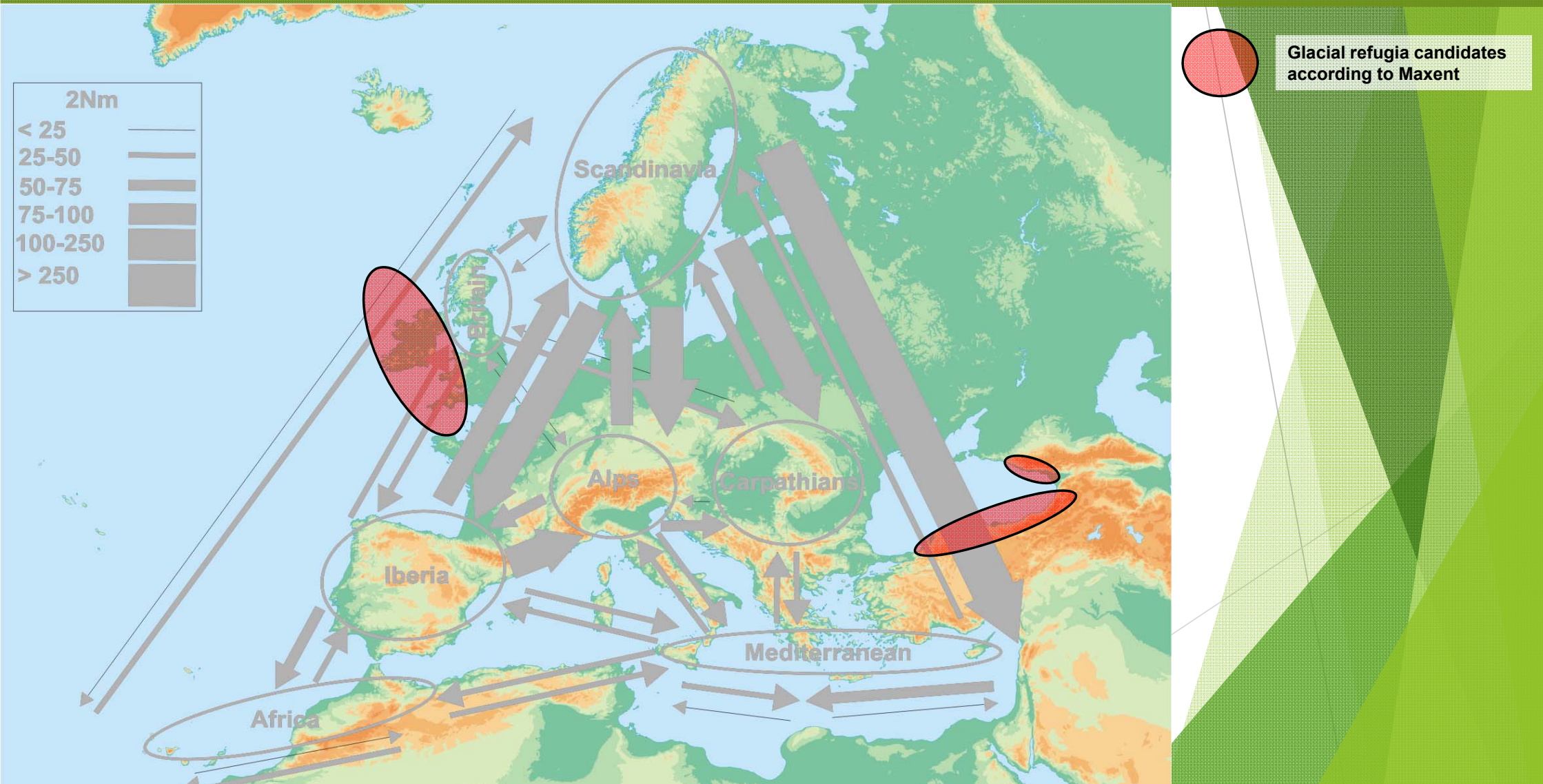Glacial refugia candidates according to Maxent

Scandinavia

Britain

Alps

Carpathians

Iberia

Mediterranean

Africa

# Discussion: Example of putative migrations

# Discussion: Example of putative migrations



Results from Migrate analysis

2Nm
< 25
25-50
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Scandinavia

Alps

Carpathians

Iberia

Mediterranean

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Glacial refugia candidates according to Maxent

Hypothetical migrations

# Discussion: Example of putative migrations



Results from Migrate analysis

2Nm
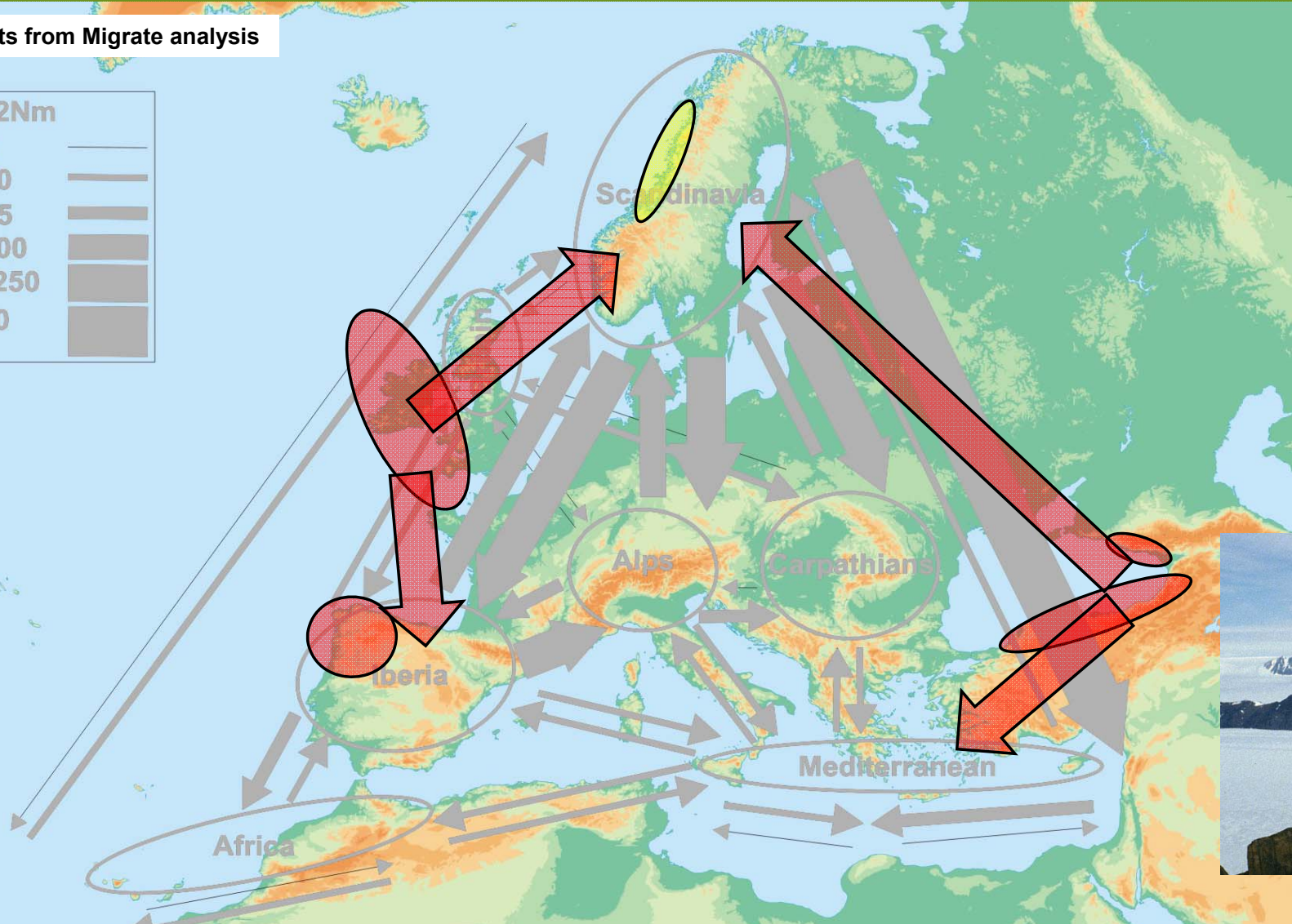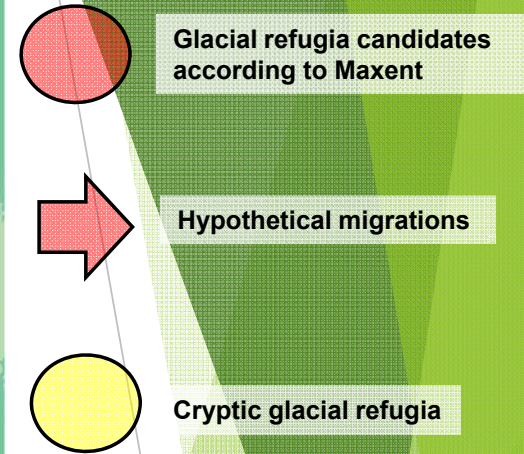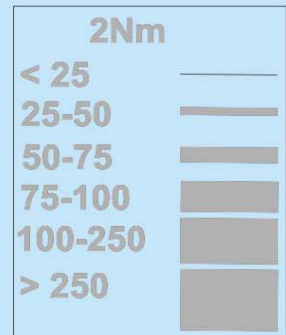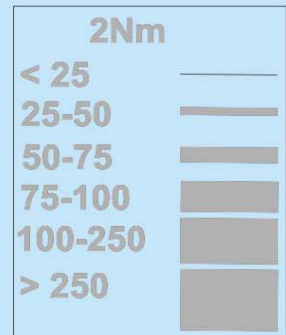< 25
25-50
50-75
75-100
100-250
> 250

Scandinavia

Alps

Carpathians

Iberia

Mediterranean

Africa

Glacial refugia candidates according to Maxent

Hypothetical migrations

Cryptic glacial refugia

Example of nunataks

# Discussion: No isolation by distance
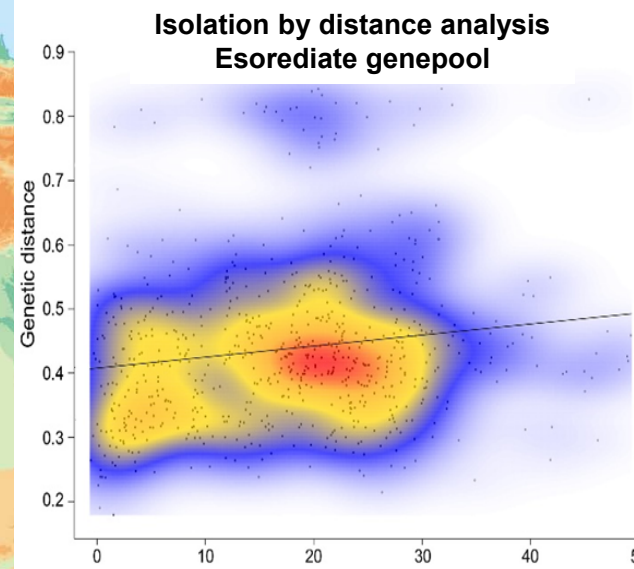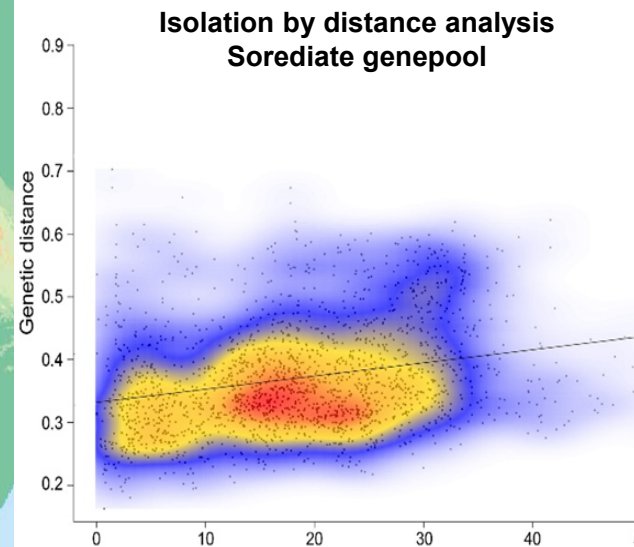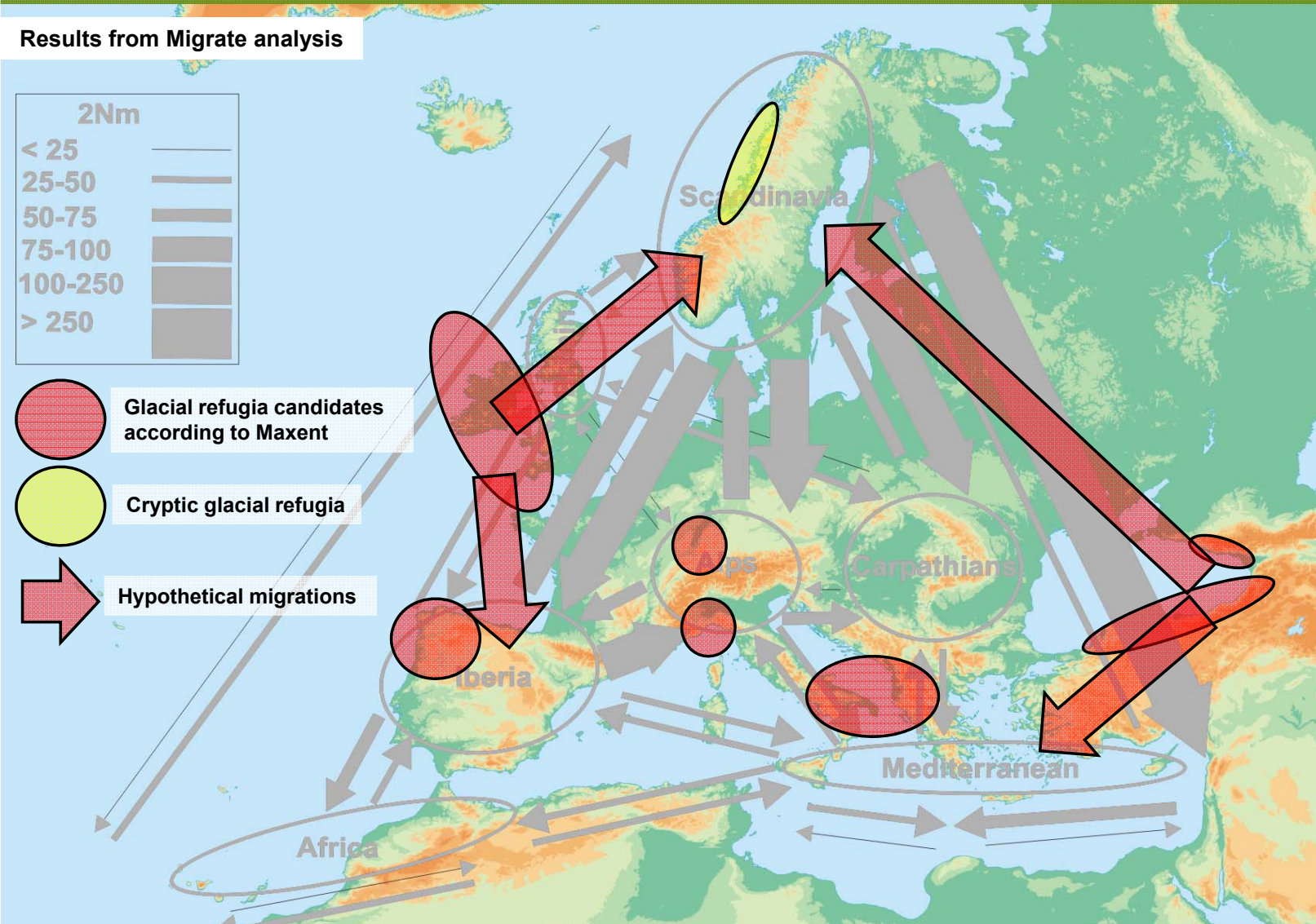
Results from Migrate analysis

2Nm
< 25
25-50
50-75
75-100
100-250
> 250

Glacial refugia candidates according to Maxent

Cryptic glacial refugia

Hypothetical migrations

Scandinavia

Alps

Carpathians

Iberia

Mediterranean

Africa

Isolation by distance analysis
Sorediate genepool

Genetic distance

Isolation by distance analysis
Esorediate genepool

Genetic distance

# Discussion: Ancestral shared alleles

**Results from Migrate analysis**

2Nm

| | |
|---|---|
| < 25 | |
| 25-50 | |
| 50-75 | |
| 75-100 | |
| 100-250 | |
| > 250 | |

Glacial refugia candidates according to Maxent

Cryptic glacial refugia

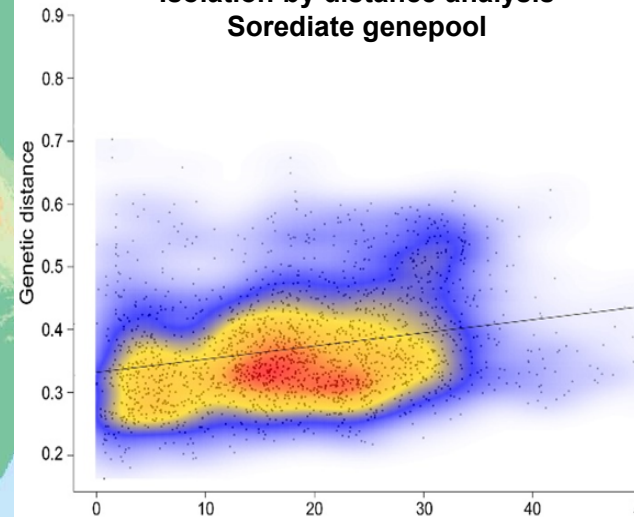Hypothetical migrations

Scandinavia

Africa

**Migration:**
Far pair populations much more differentiated than closer ones.
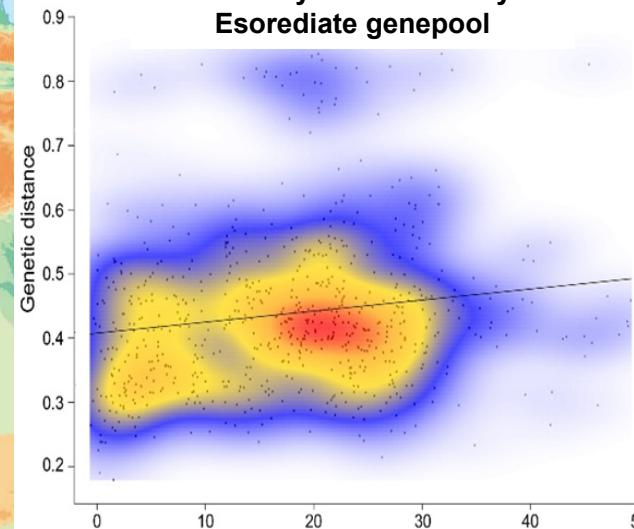
**Ancestral shared alleles:**
Far pair populations not much more differentiated than closer ones.
(usually linked to incomplete lineage sorting)

Isolation by distance analysis
Sorediate genepool

Isolation by distance analysis
Esorediate genepool

# Discussion: Ancestral shared alleles



nuITS, IGS, GAPDH

Intergenic sequence close to the microsatellite 13

Intergenic sequence close to the microsatellite 15

Intergenic sequence close to the microsatellite 16

Intergenic sequence close to the microsatellite 18

Intergenic sequence close to the microsatellite 19

Evidence of incomplete lineage sorting

# Discussion: Ancestral shared alleles

**Results from Migrate analysis**

2Nm
< 25
25-50
50-75
75-100
100-250
> 250

**Nunataks across Europe**

Scandinavia

Glacial refugia candidates according to Maxent

Cryptic glacial refugia

Hypothetical migrations

Africa

**Migration:**
Far pair populations much more differentiated than closer ones.

**Ancestral shared alleles:**
Far pair populations not much more differentiated than closer ones.
(usually linked to incomplete lineage sorting)
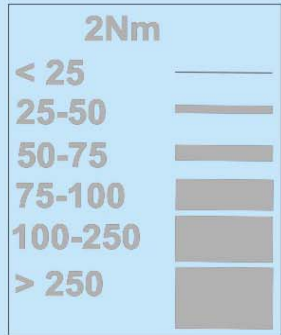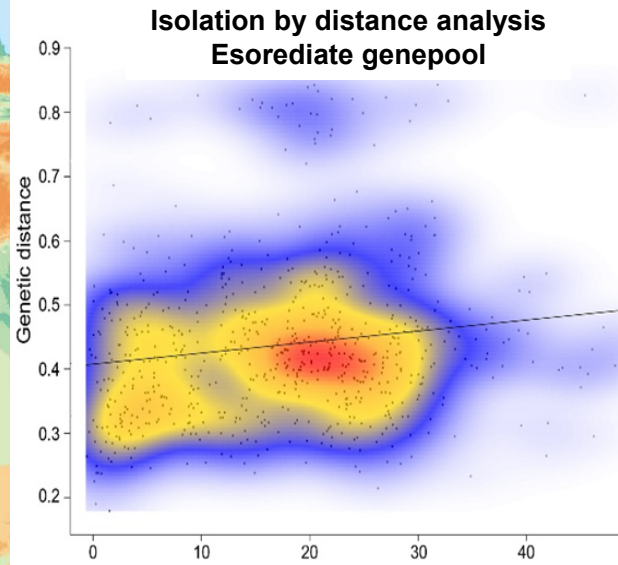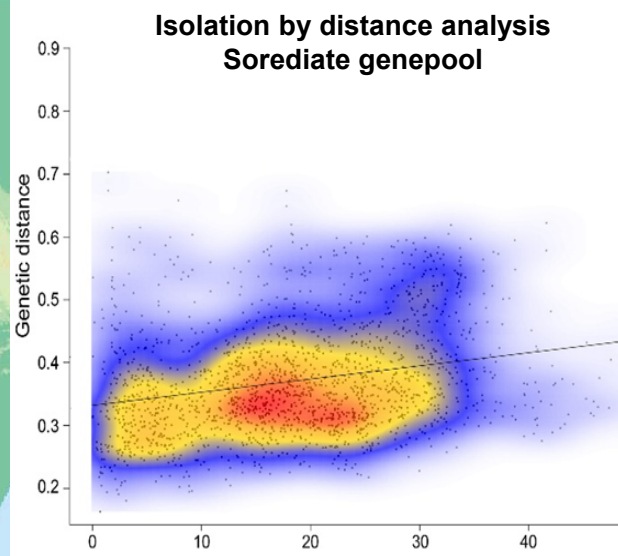
Isolation by distance analysis
Sorediate genepool

Isolation by distance analysis
Esorediate genepool

Genetic distance

# Thanks for your attention

# For any question please contact carlos.g.boluda@gmail.com

**Carlos G. Boluda**     **Víctor J. Rico**     **Yamama Naciri**     **David L. Hawksworth**

**Christoph Scheidegger**