



MICROSATELLITE DIVERSITY OF DALMATIAN SAGE POPULATIONS FROM THE BALKAN AND APENNINE PENINSULAS

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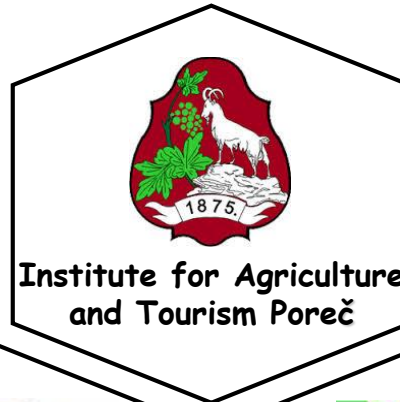
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CMAPSEEC 2018, Split

CoE CroP-BioDiv

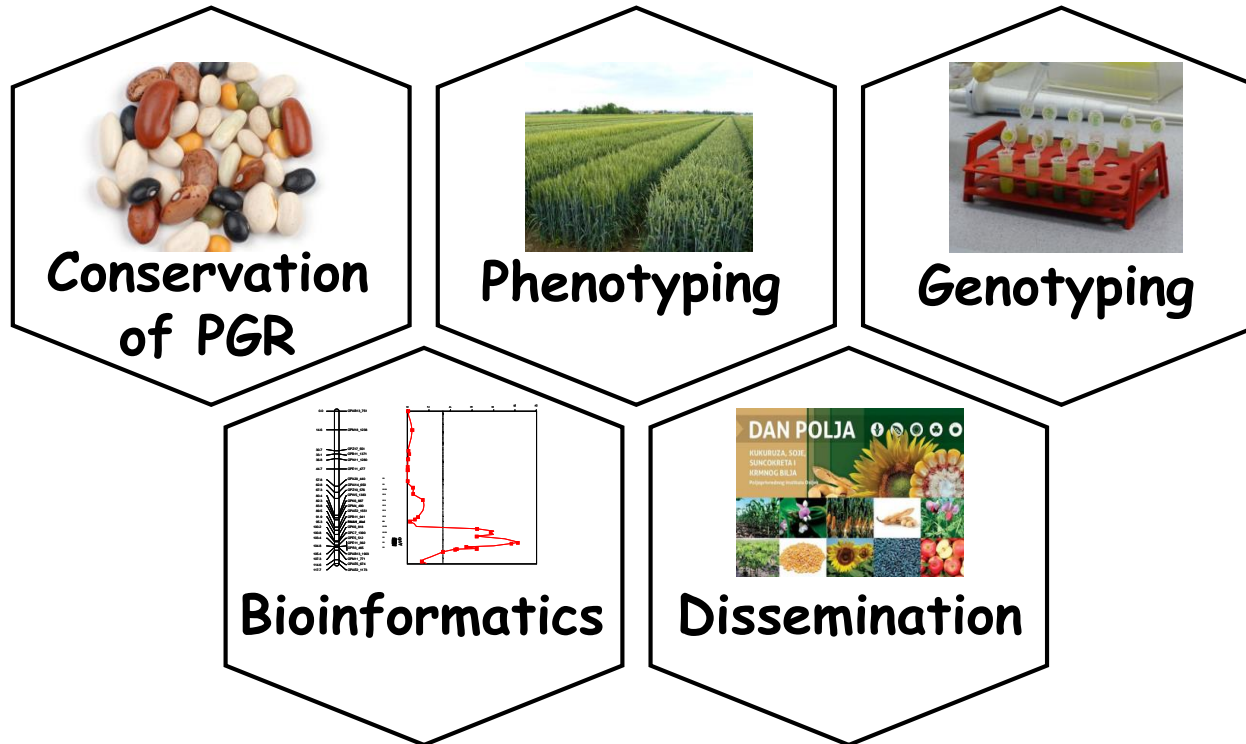
+ 5 Member Institutions

Host
Institution



CoE CroP-BioDiv

OBJECTIVES



Conservation of Plant Genetic Resources >> increase the benefits

Phenotyping >> high-throughput phenotyping (HTP) platforms

Genotyping >> next-generation sequencing (NGS) techniques

Bioinformatics >> genome-wide association studies (GWAS)

Dissemination >> workshops, summer schools

MODEL PLANT SPECIES

Major Crops



Maize



Wheat



Soybean

Traditional Crops



Grapevine



Olives

Promising Crops



**Brassicas
Alliums**



Common bean



**Dalmatian pyrethrum
Dalmatian sage**



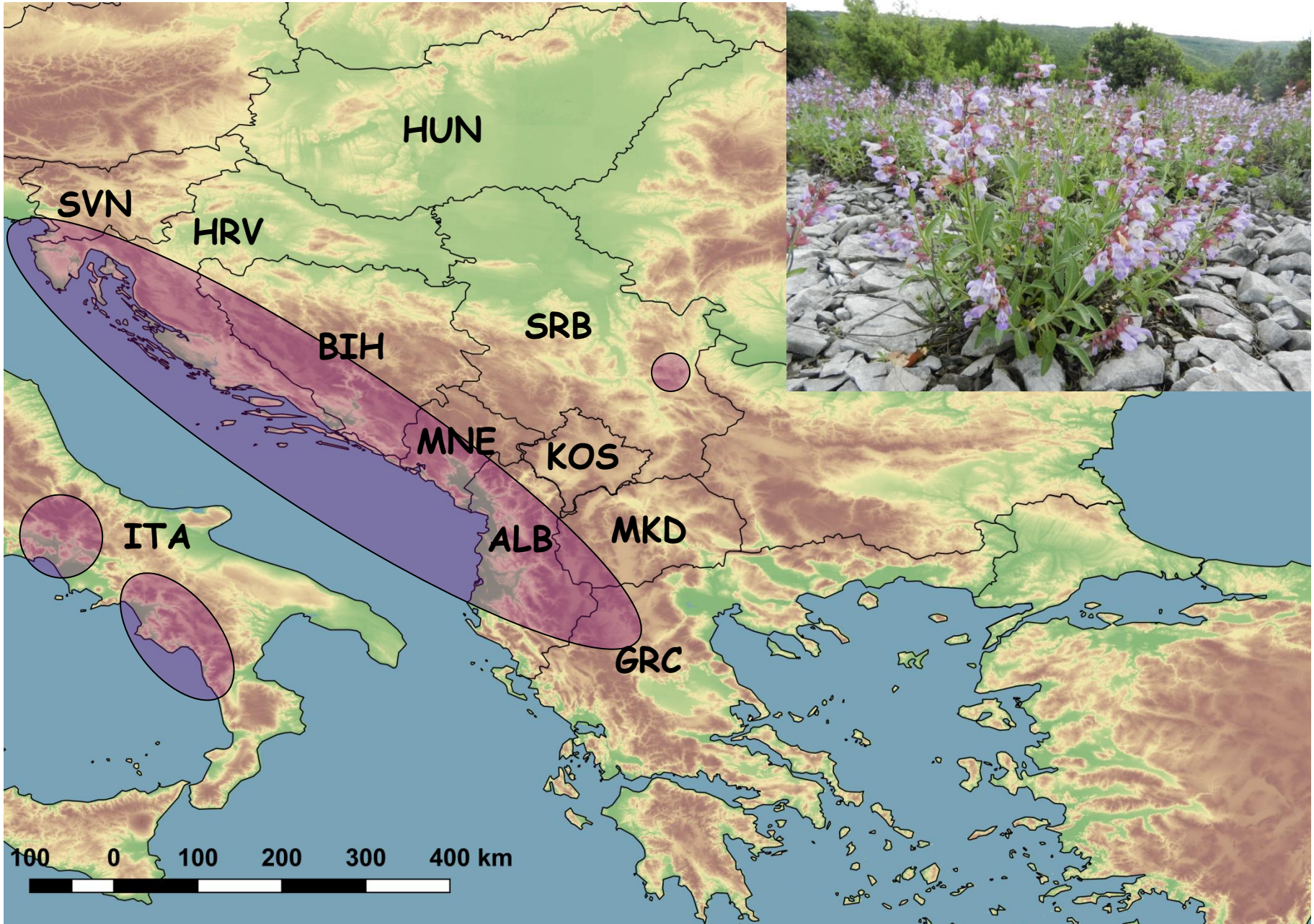
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CMAPSEEC 2018, Split

PLAN

- (1) Natural distribution
- (2) Genetic diversity
- (3) Genetic structure
- (4) Ecological niche modelling

NATURAL DISTRIBUTION OF DALMATIAN SAGE



SAMPLES / ANALYSES

- **samples:**

 - 62 populations / 1,350 plants

 - Italy (13), Slovenia (2), Croatia (23),

 - Bosnia and Herzegovina (2), Montenegro (7), Serbia (2),

 - Albania (5), Macedonia (1), Greece (7)

- **molecular analysis:**

 - 8 microsatellite markers

 - 191 alleles

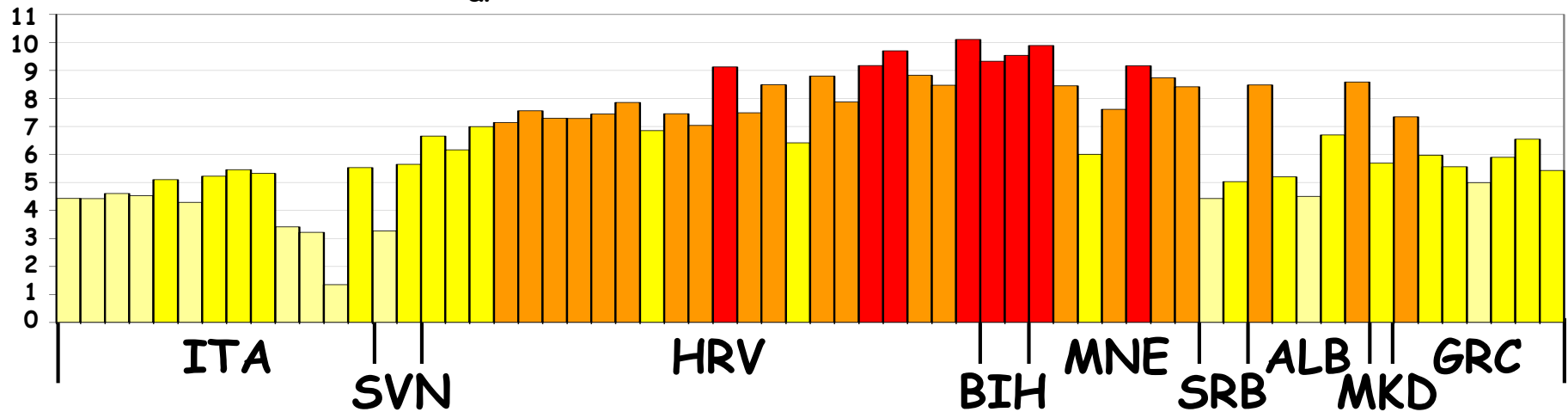
PLAN

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GENETIC DIVERSITY

Parameter	Mean	Range
Allelic richness (N_{ar})	6.669	1.35-10.11
Observed heterozygosity (H_O)	0.665	0.081-0.832
Expected heterozygosity (H_E)	0.683	0.087-0.846

Allelic richness (N_{ar})



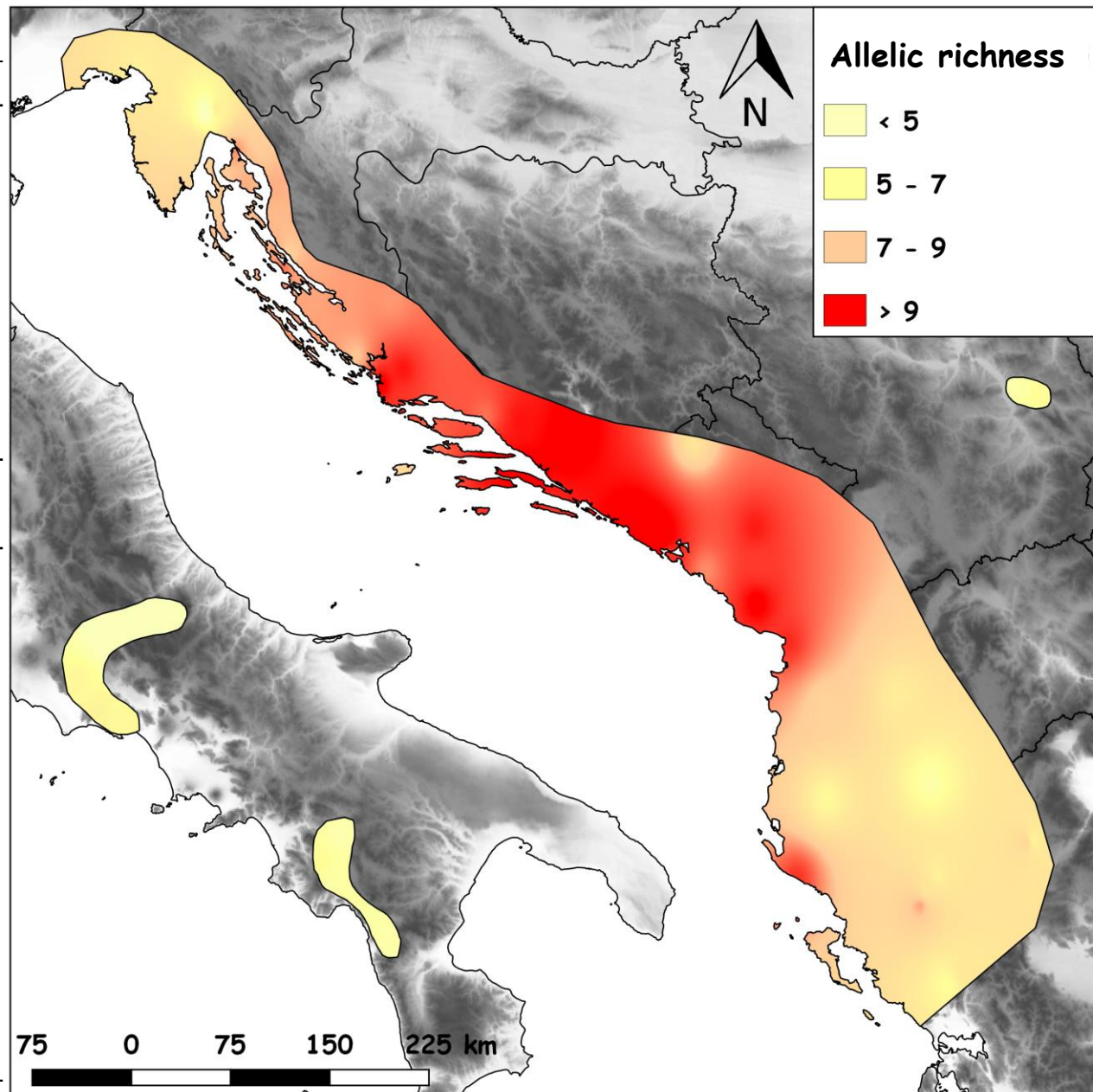
ALLELIC RICHNESS

■ $N_{ar} > 9$

Br.	Population	Country
P38	Konavle	HRV
P41	Vrbanj	MNE
P35	Pelješac	HRV
P40	Mostar	BIH
P39	Međugorje	BIH
P34	Hvar	HRV
P45	Rumija	MNE
P28	Šparadići	HRV

■ $N_{ar} < 5$

P59	Arta	GRC
P03	Maratea	ITA
P04	Cilento	ITA
P52	Prespa	ALB
P01	Pollino 2	ITA
P48	Miljkovac	SRB
P02	Pollino 1	ITA
P06	Savoia	ITA
P10	d'Antino	ITA
P14	Novokračine	SVN
P11	M. Salviano	ITA
P12	Maiella	ITA



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GENETIC STRUCTURE

- Bayesian model-based clustering method for inferring population structure

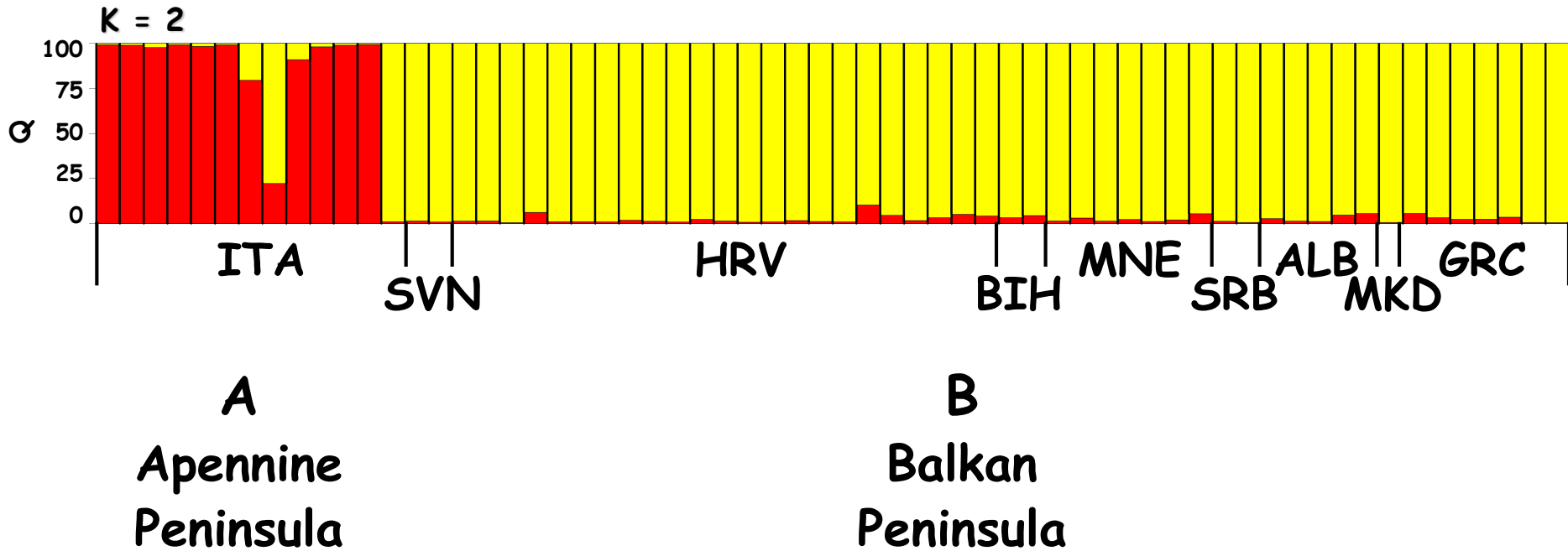
Assumption:

- there are K populations of origin each of which is characterized by a set of allele frequencies at each locus

Goal:

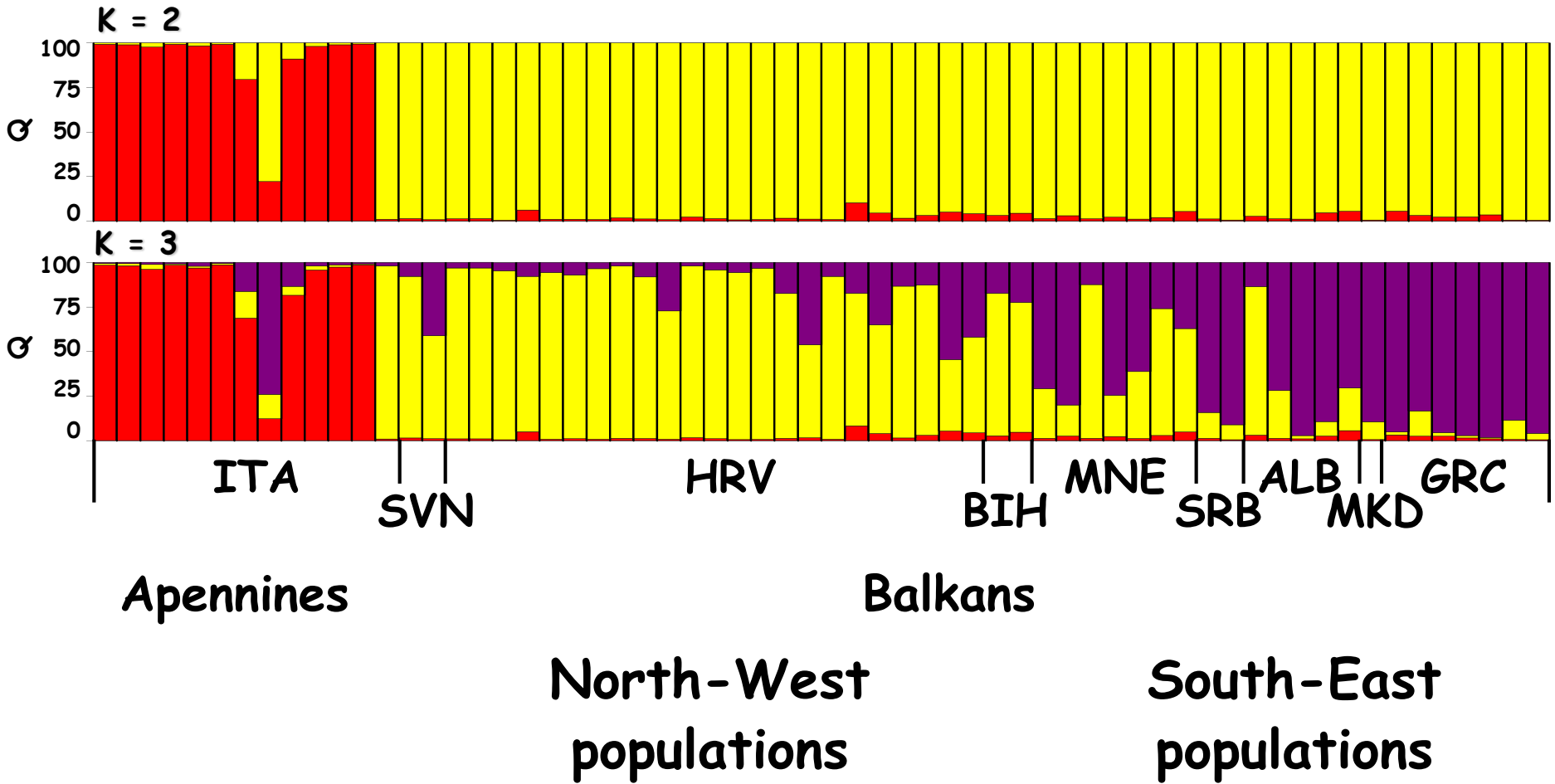
- assign individuals to populations of origin in such a way that within each population the departures from:
 - (1) Hardy-Weinberg equilibrium (HWE) and
 - (2) linkage equilibrium (LE)are minimized

$$K = 2$$



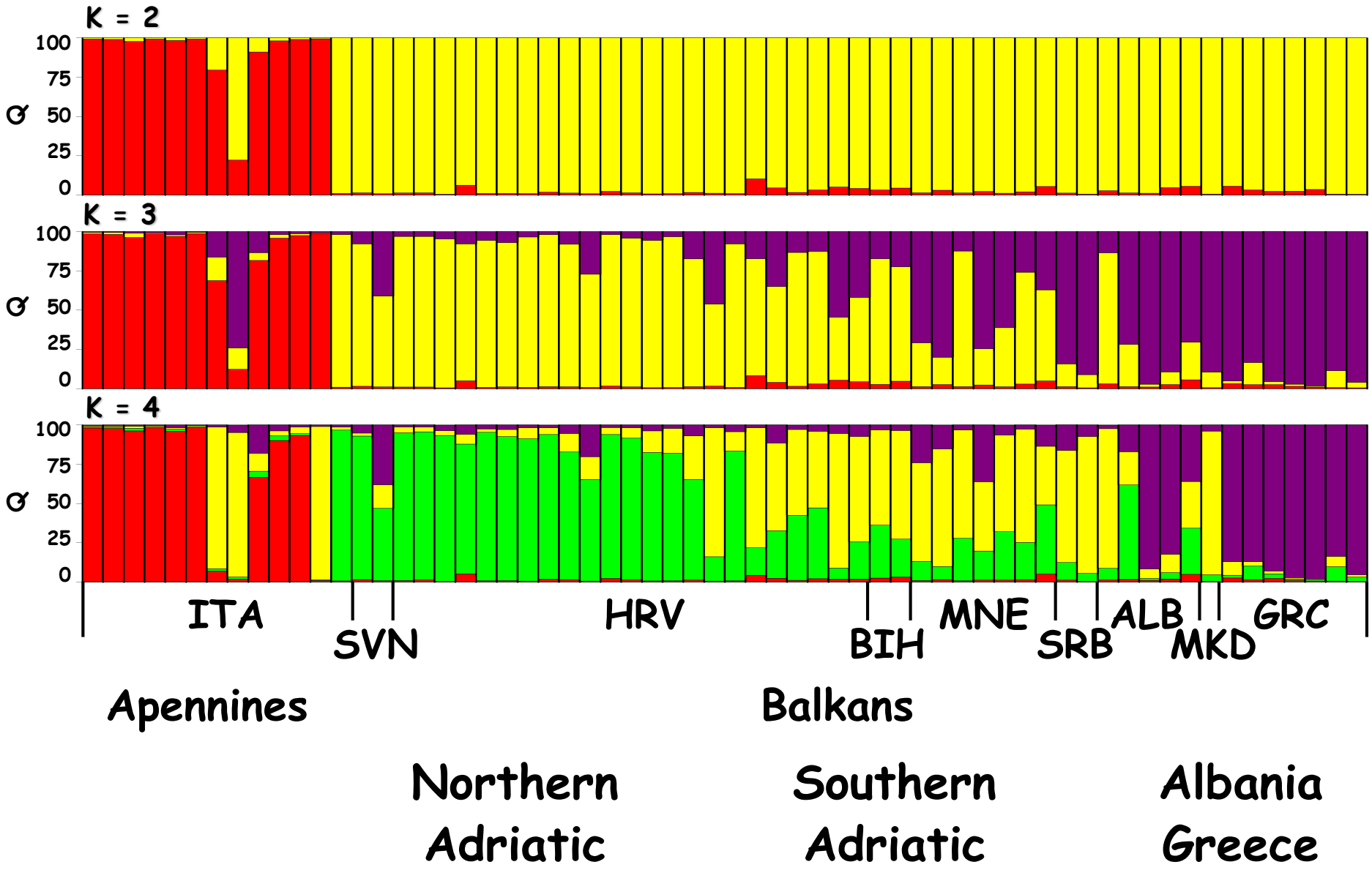
- proportions of membership (Q) of each individual plant in each of the two clusters (populations of origin):
 - each individual plant is represented by a single vertical line divided into colors representing different clusters
 - the length of the colored segment shows the individual's estimated proportion of membership in that cluster

K = 3



- the cluster B (Balkan) is at K = 3 split into two clusters according to geographical locations:
North-West: Slovenia-Croatia-BiH
South-East: Montenegro-Albania-Macedonia-Greece

K = 4

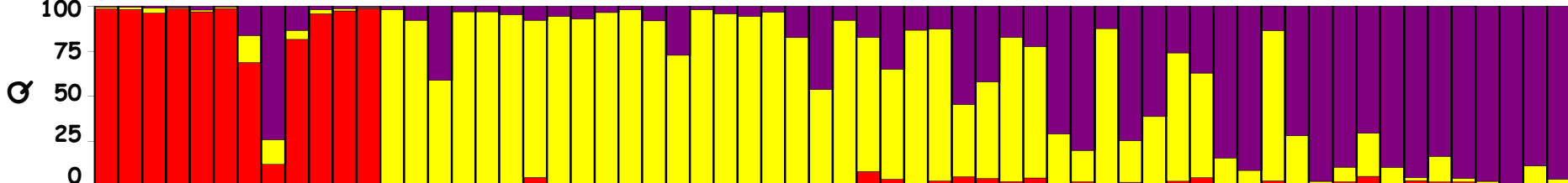


K = 5

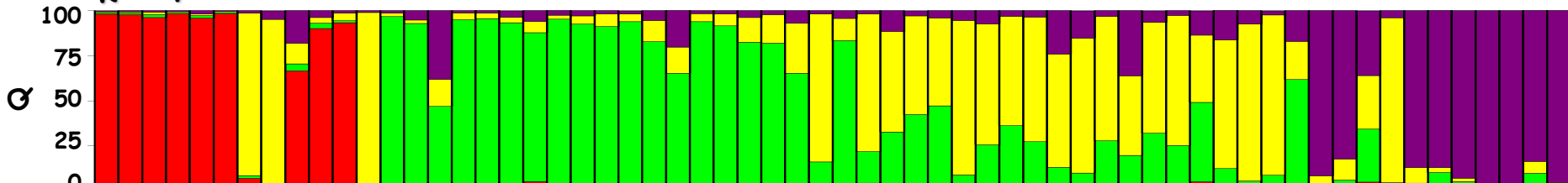
K = 2



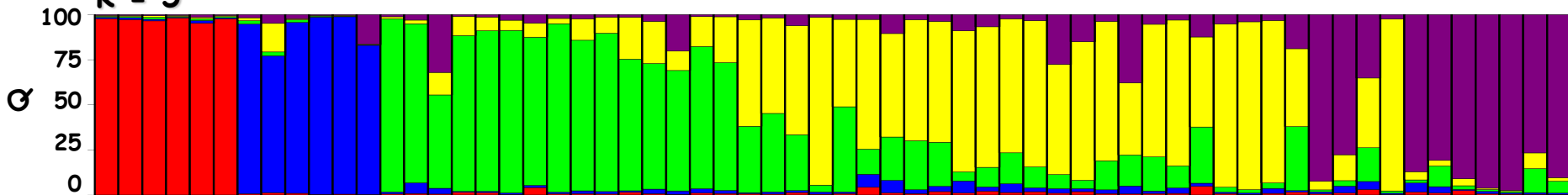
K = 3



K = 4



K = 5



A B

C

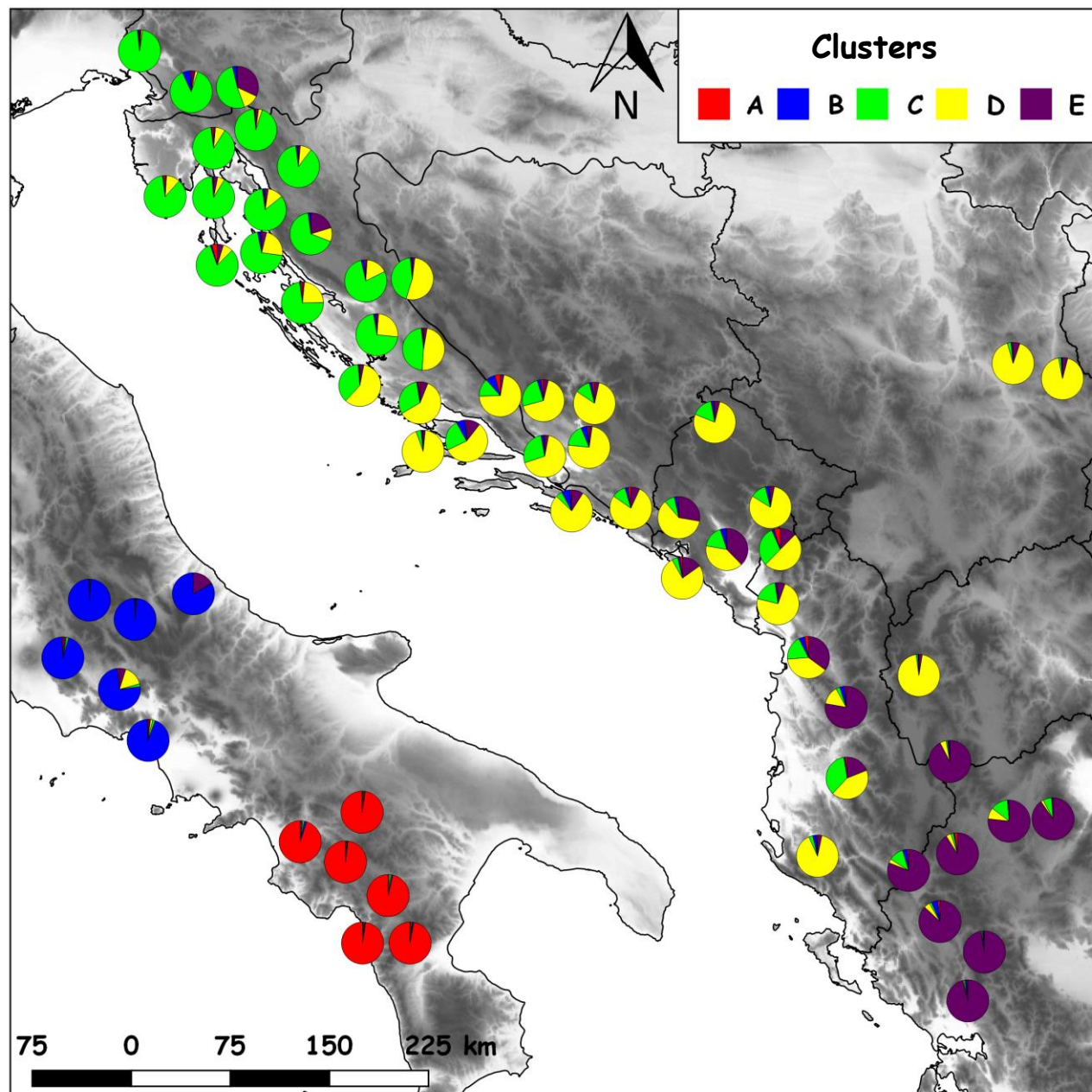
D

E

GENETIC CLUSTERS

Cluster

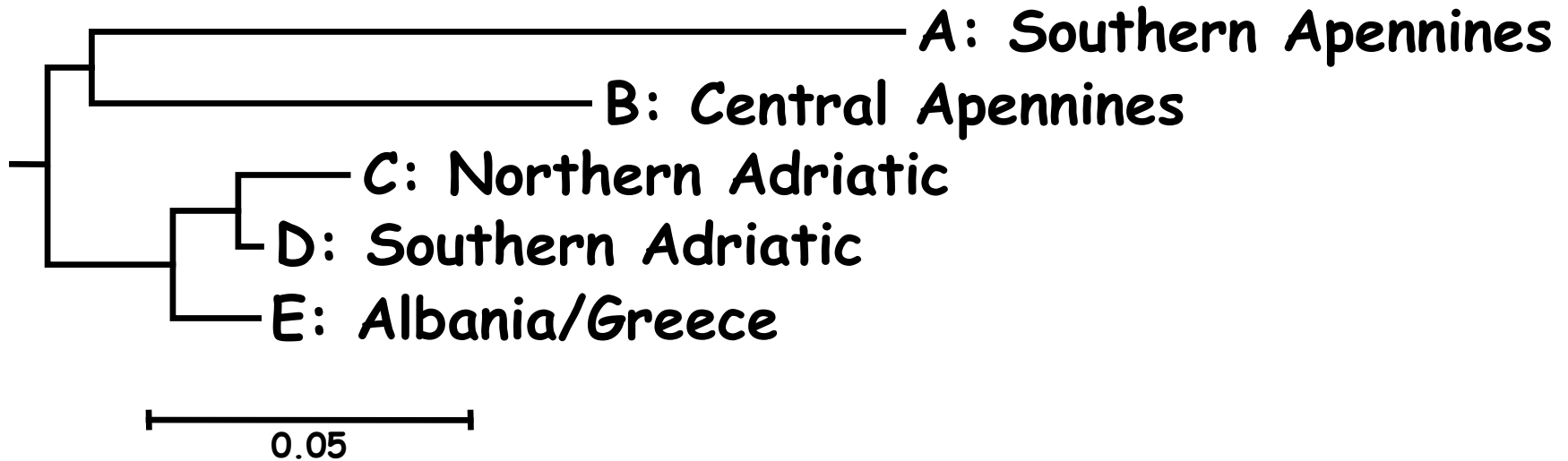
- A** Southern Apennines
- B** Central Apennines
- C** Northern Adriatic
- D** Southern Adriatic
- E** Albania Greece



TREE

Distance measure: net nucleotide distance

Tree algorithm: Neighbor-Joining



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ECOLOGICAL NICHE MODELLING

- species distribution modelling (SDMs)

- estimate the relationship between species records at sites and the environmental characteristics of those sites
- predict the suitability of sites for occupation or persistence of the species

- input data:

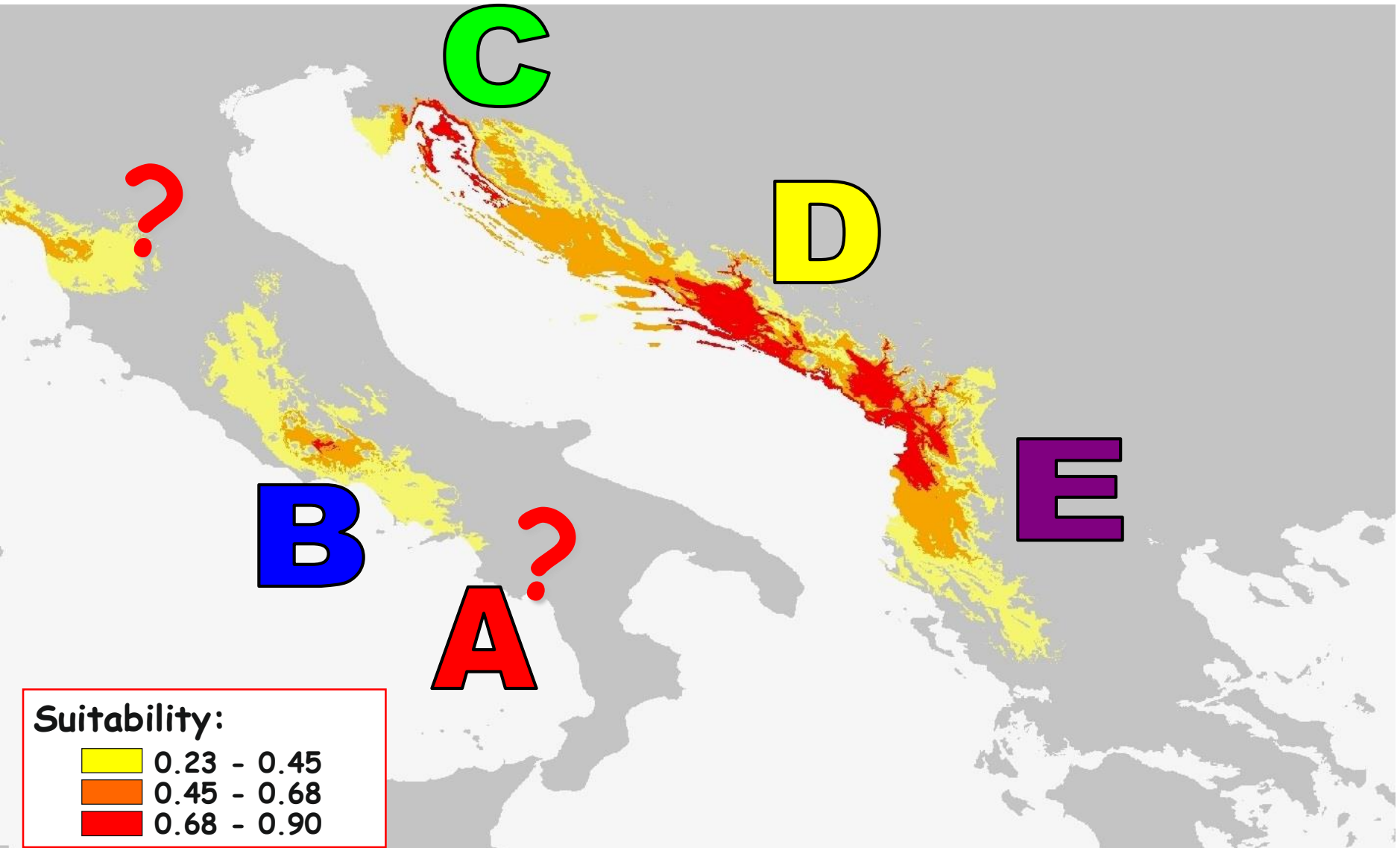
(1) geographic distribution

68 data on occurrence (evenly distributed)

(2) environmental characteristics of the sites

19 bioclimatic variables (WorldClim database)

ENM: PRESENT DAY CONDITIONS



SUITABILITY: EDAPHIC FACTORS

(1) Balkans

■ Leptosols

Shallow soils
over limestone

(2) Apennines

■ Cambisol

Moderately
developed
brown soil



Collaborators:

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