

Recolonisation post-glaciaire de l'ouest de l'Europe par la vipère péliade (*Vipera berus*)

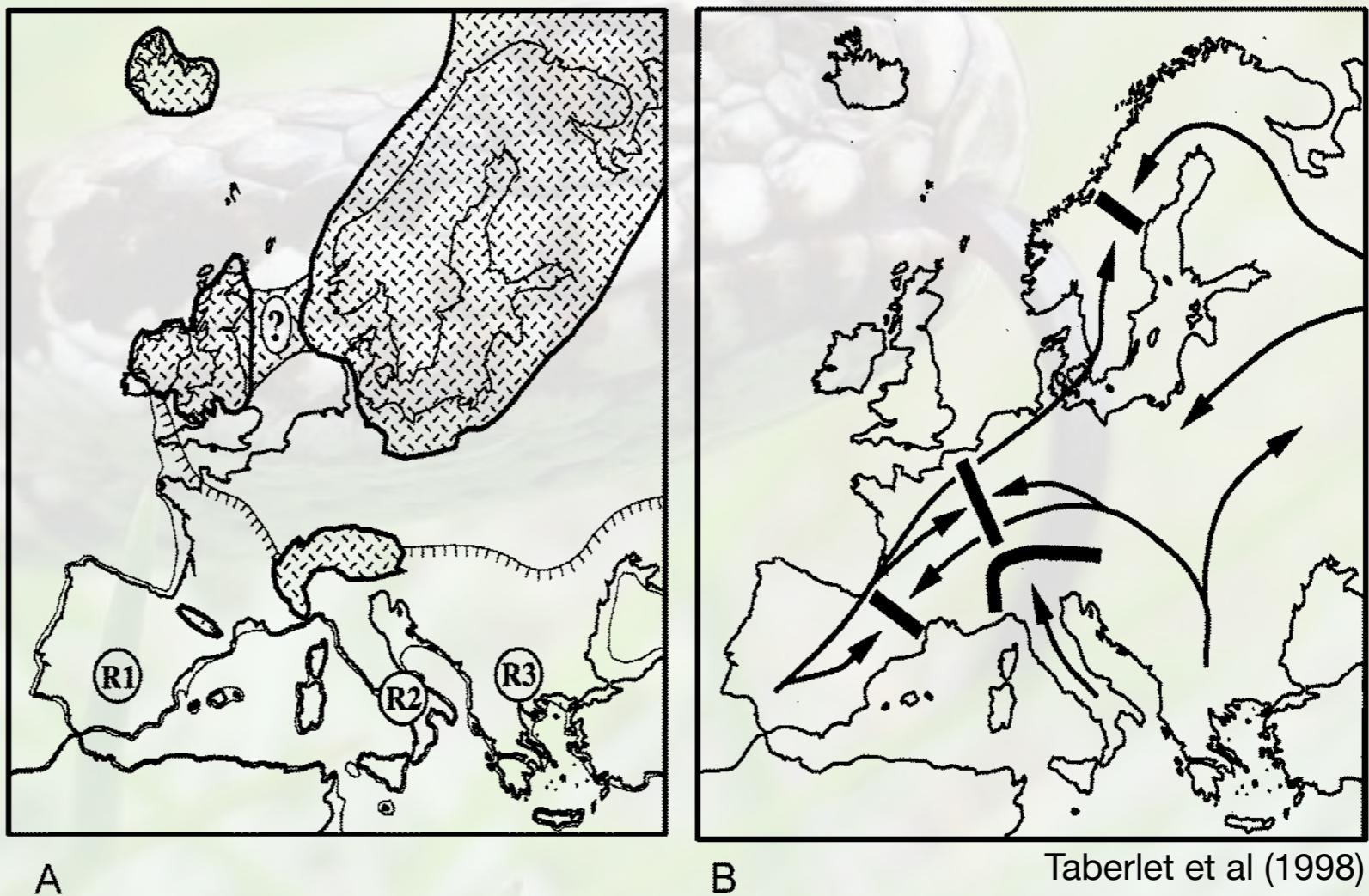
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Phylogeography in Europe

- genetic structure mainly influenced by the glaciations
- general pattern of genetic structure (animals and plants)
- P Taberlet /
GM Hewitt



Central-marginal hypothesis

- during colonisation events, genetic diversity is progressively lost
(Carson 1959)
 - peripheral populations have lower genetic diversity
 - genetic diversity \propto [distance to the centre of the range/refugia]



Central-marginal hypothesis

- hypothesis supported by numerous studies, but still debated
- alternative hypothesis:
 - Fisher (1930): selection of highly variable populations at the peripheral
 - Kark et al (2008): non-linear association, with higher diversity at sub-peripheral zones



The adder (*Vipera berus*)

- small venomous snakes: 60-70 cm



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2^{ème} rencontres herpétologiques du Grand Est

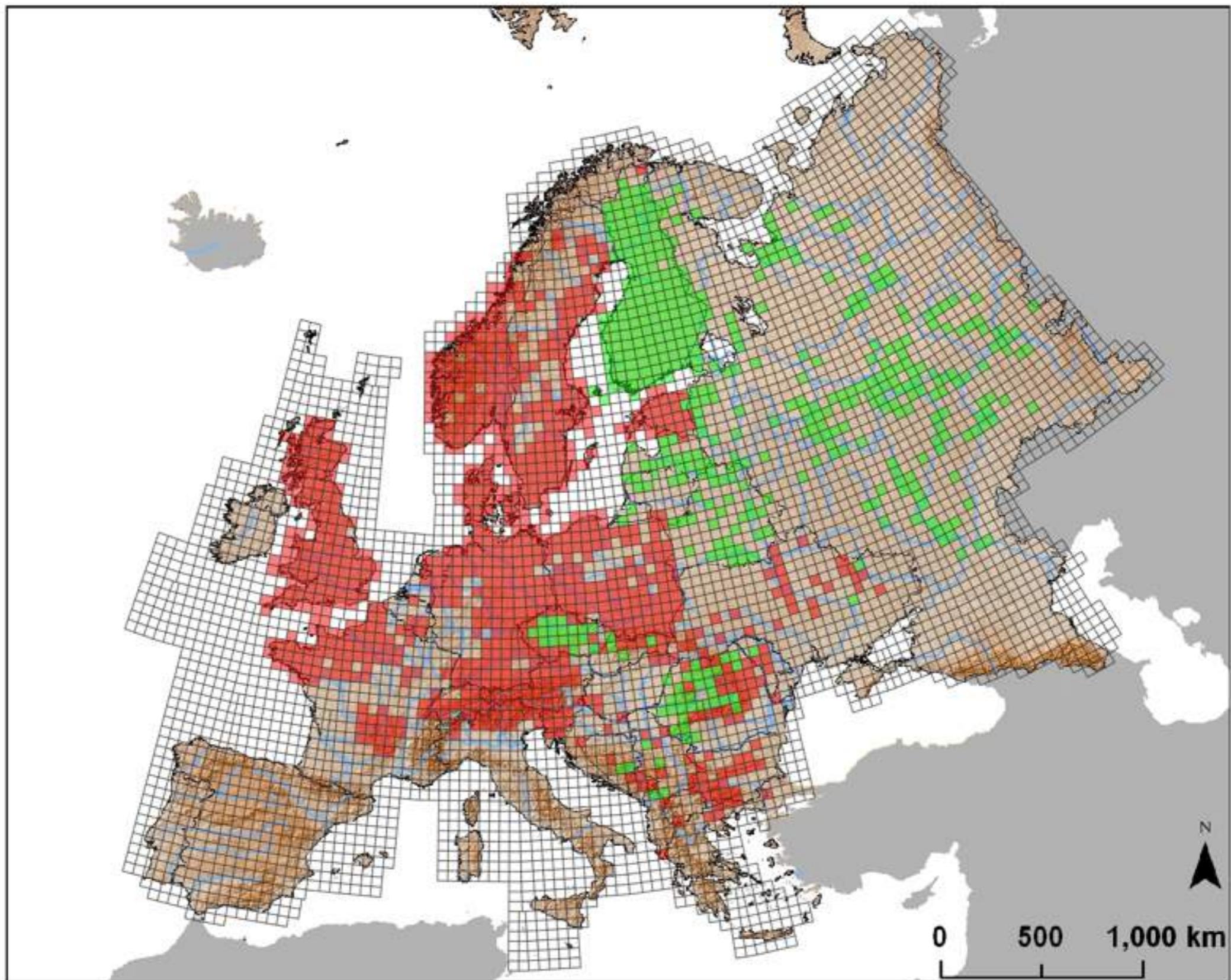




The adder (*Vipera berus*)

- small venomous snakes: 60-70 cm
- very large distribution area

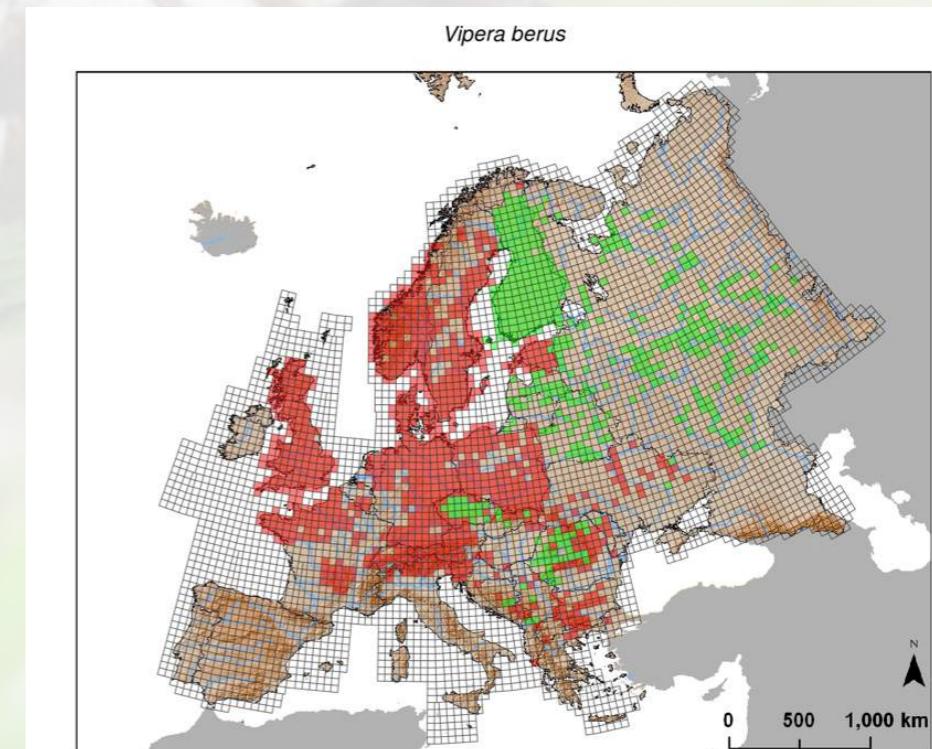
Vipera berus



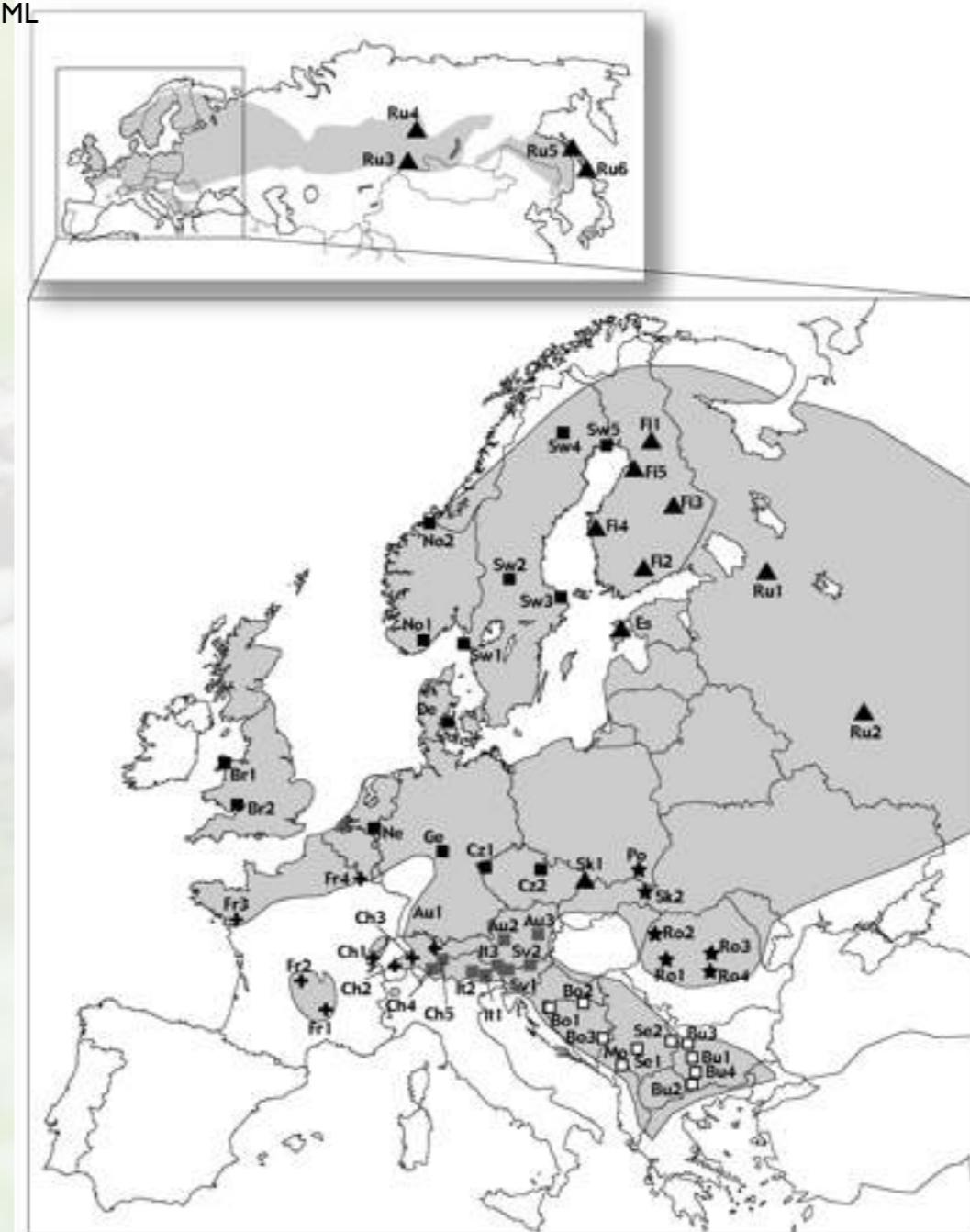
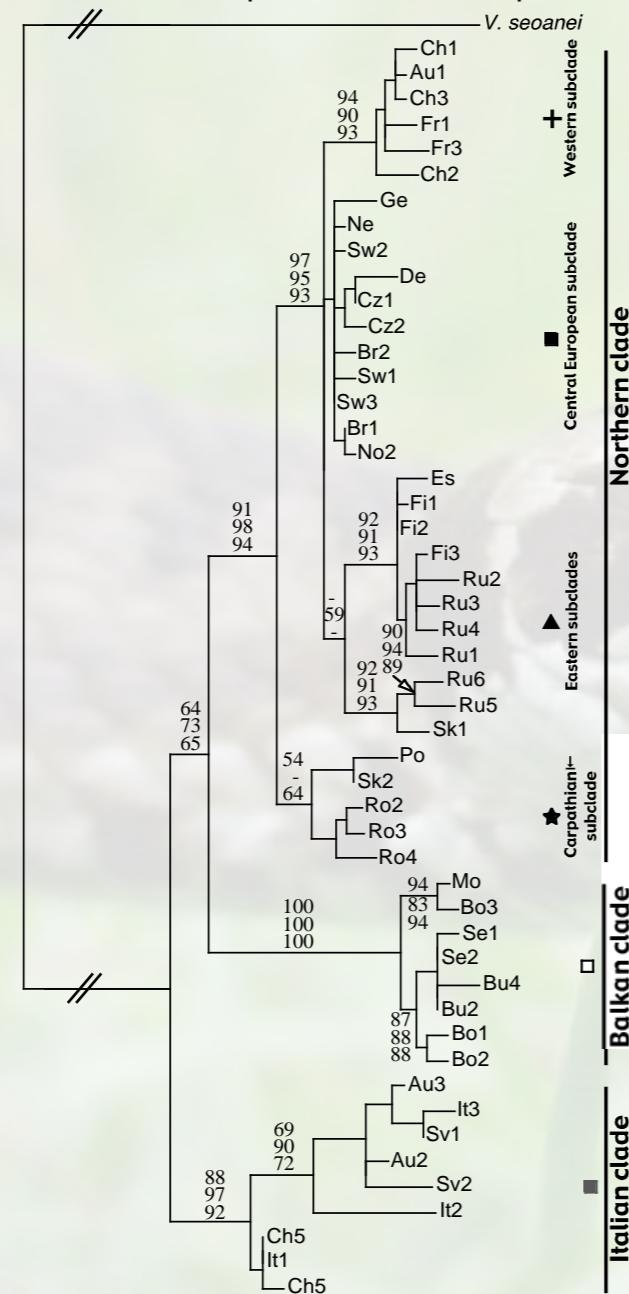
Sillero, N., J. Campos, A. Bonardi, C. Corti, R. Creemers, P.-A. Crochet, J. Crnobrnja Isailovic, M. Denoël, G. F. Ficetola, J. Gonçalves, S. Kuzmin, P. Lymberakis, P. de Pous, A. Rodríguez, R. Sindaco, J. Speybroeck, B. Toxopeus, D.R. Vieites, M. Vences (2014): Updated distribution and biogeography of amphibians and reptiles of Europe. *Amphibia-Reptilia* 35: 1-31.

The adder (*Vipera berus*)

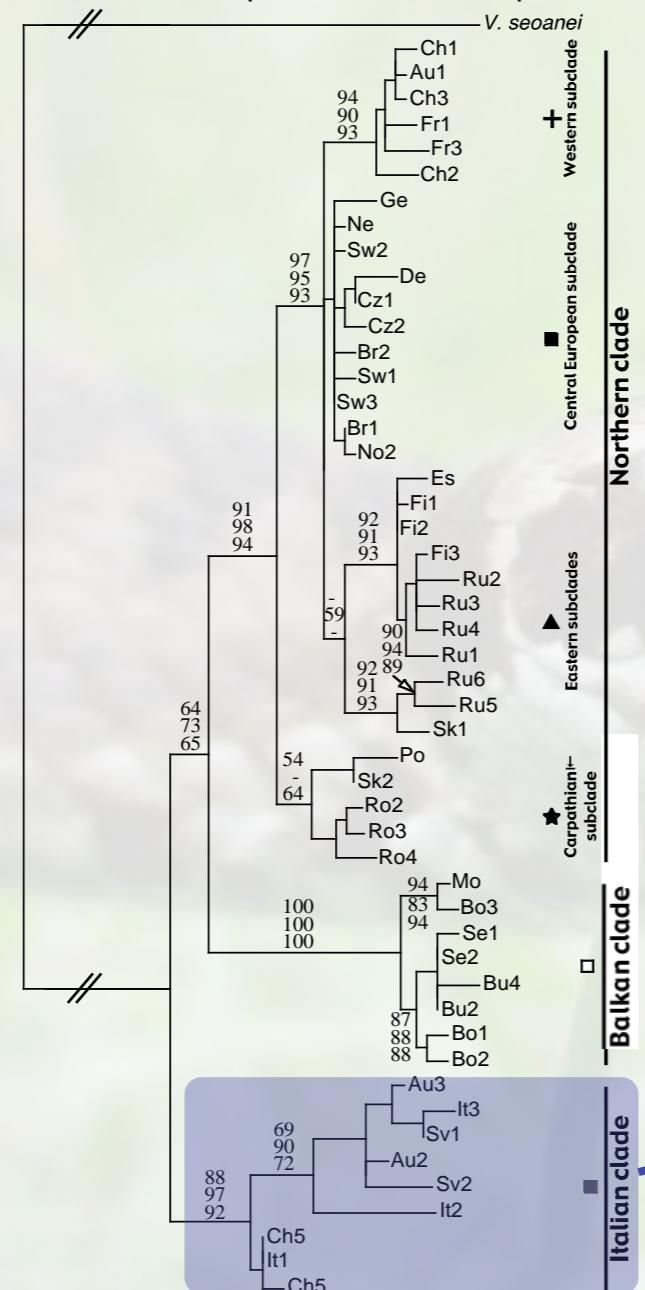
- small venomous snakes: 60-70 cm
- very large distribution area
- large tolerance to cold climate
- low dispersal abilities
- populations separated by only a few kilometres are genetically differentiated
(Ursenbacher et al. 2009)



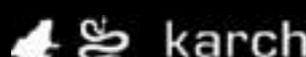
ML tree; bootstrap value for 10'000 replicates: NJ, MP, ML



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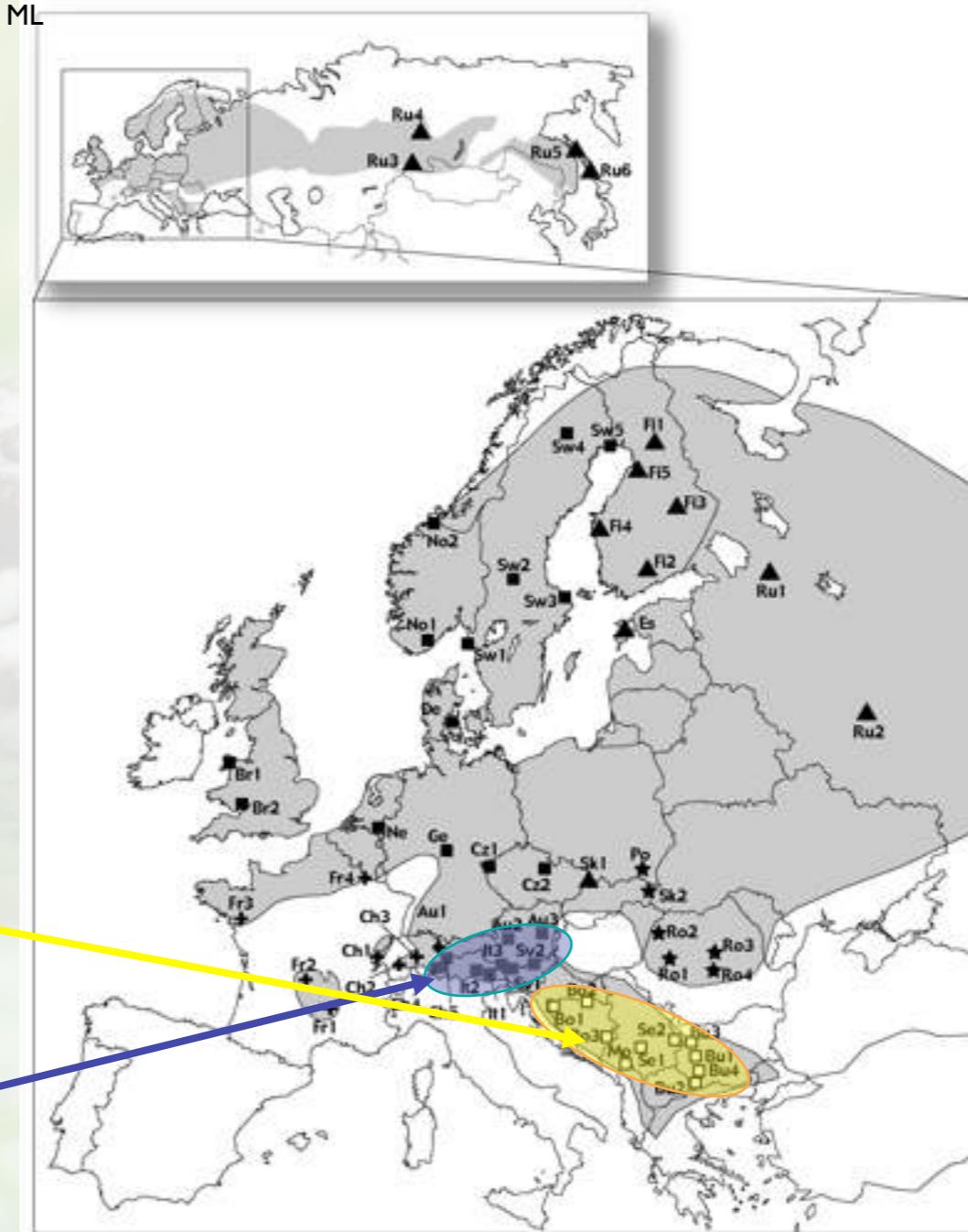
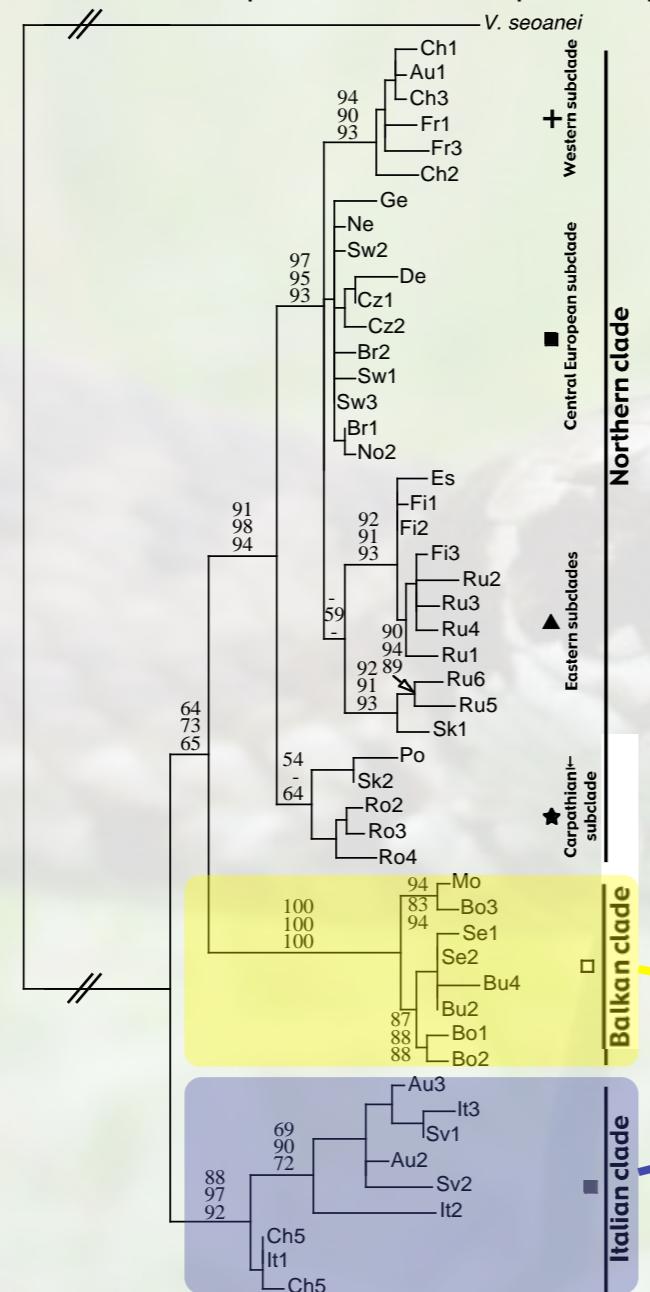


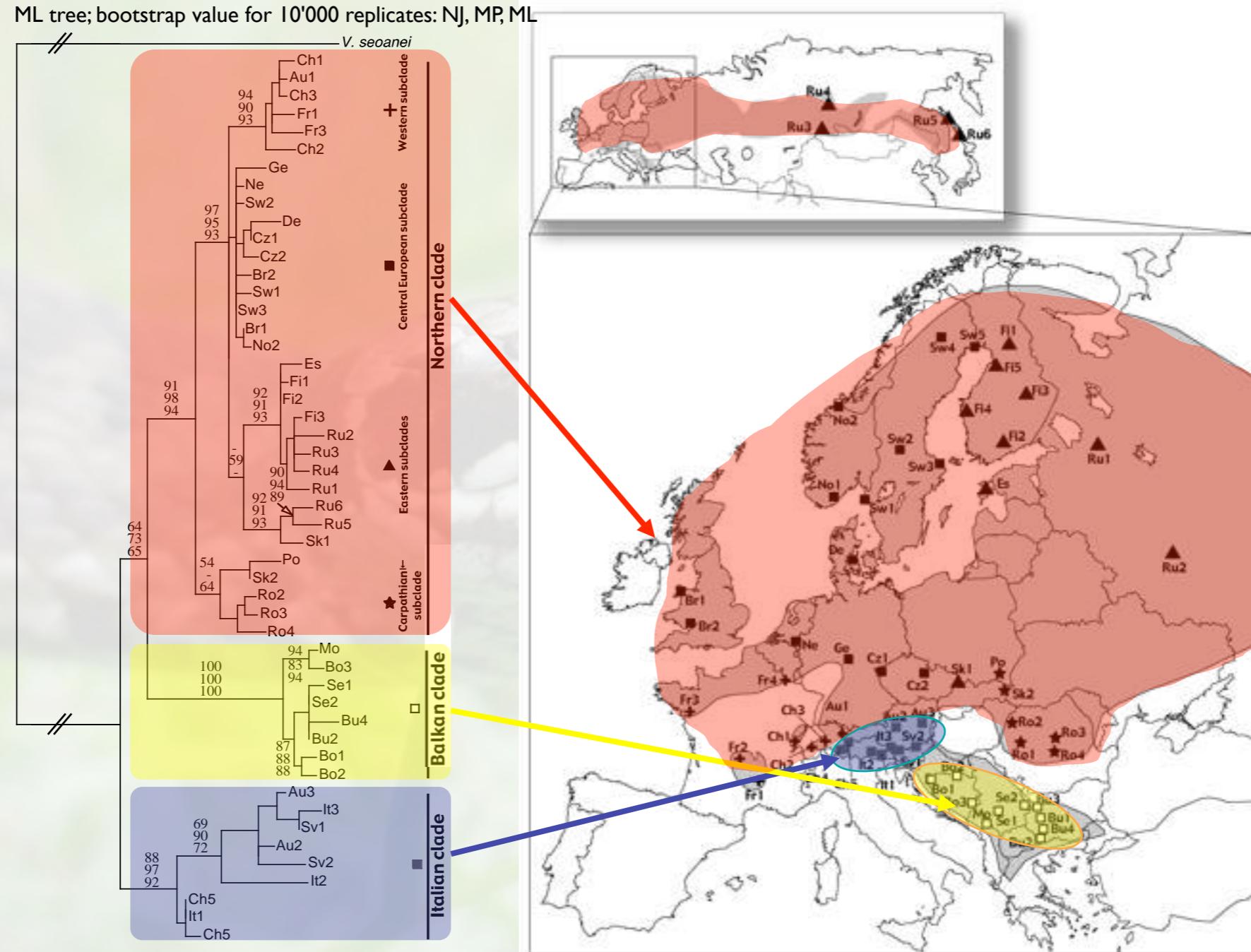
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3 Refugial areas

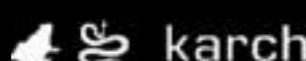
Italy

Balkan peninsula

Caucasus Mountains



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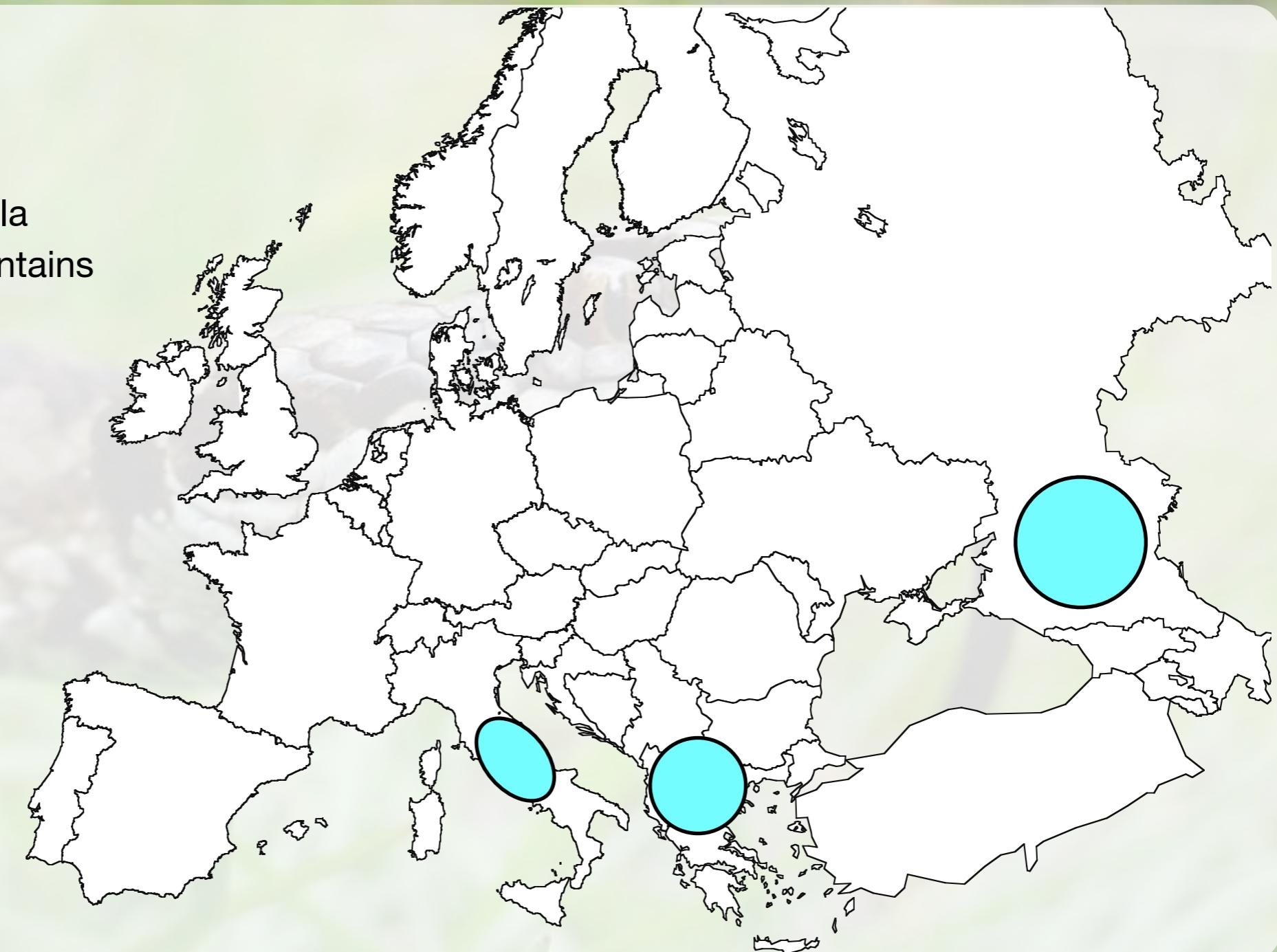
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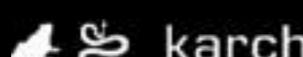
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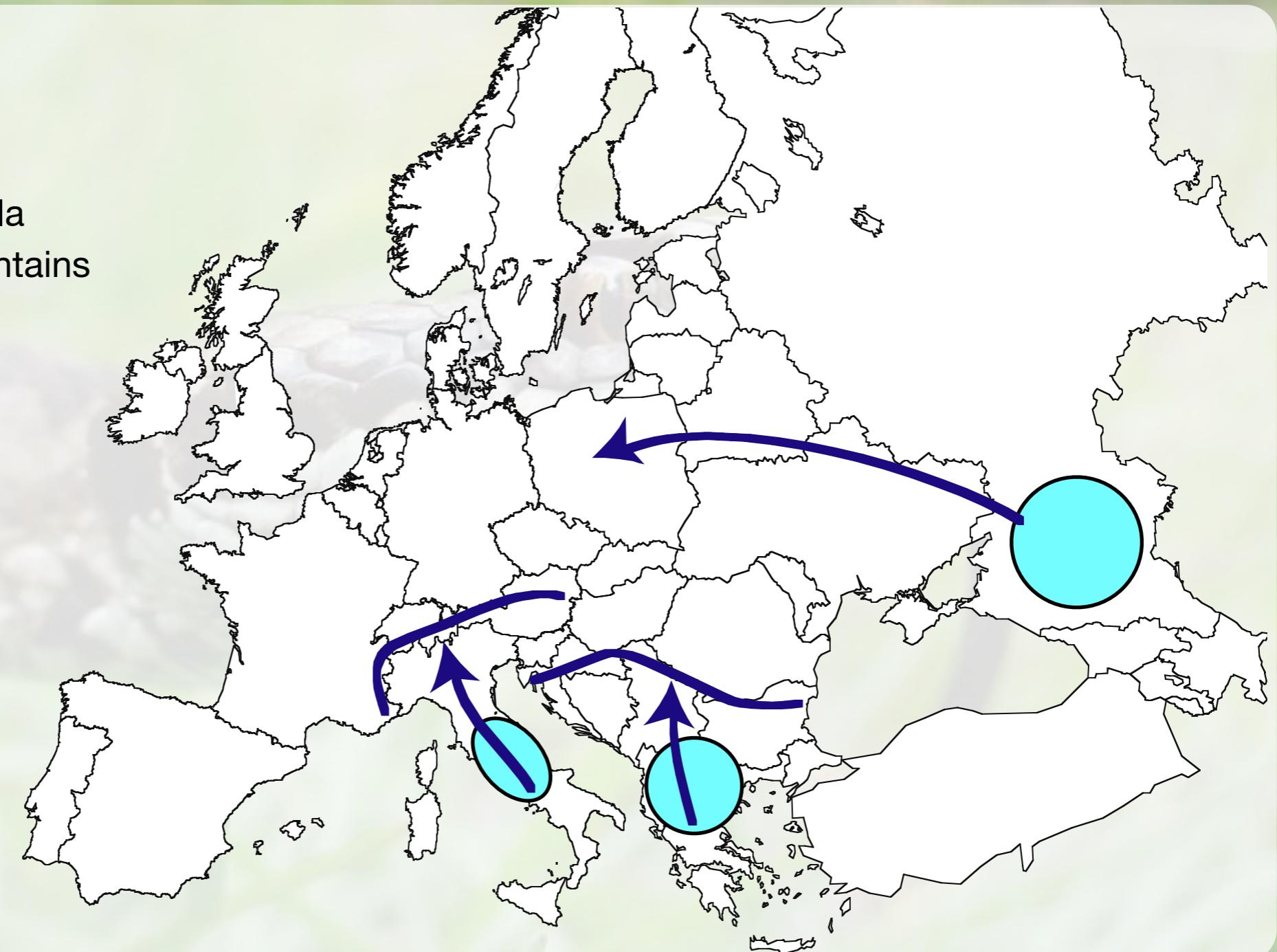
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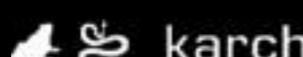
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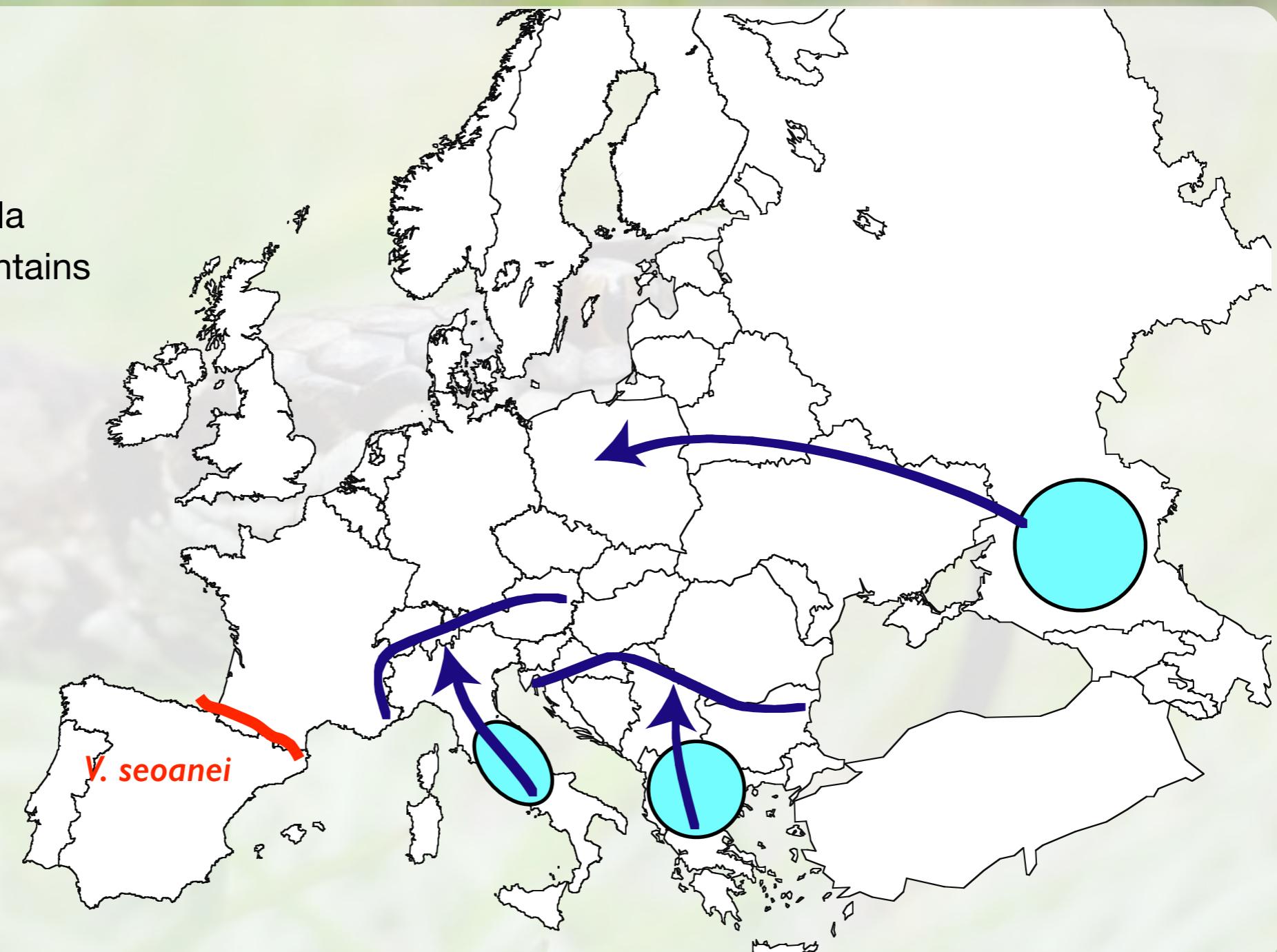
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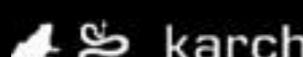
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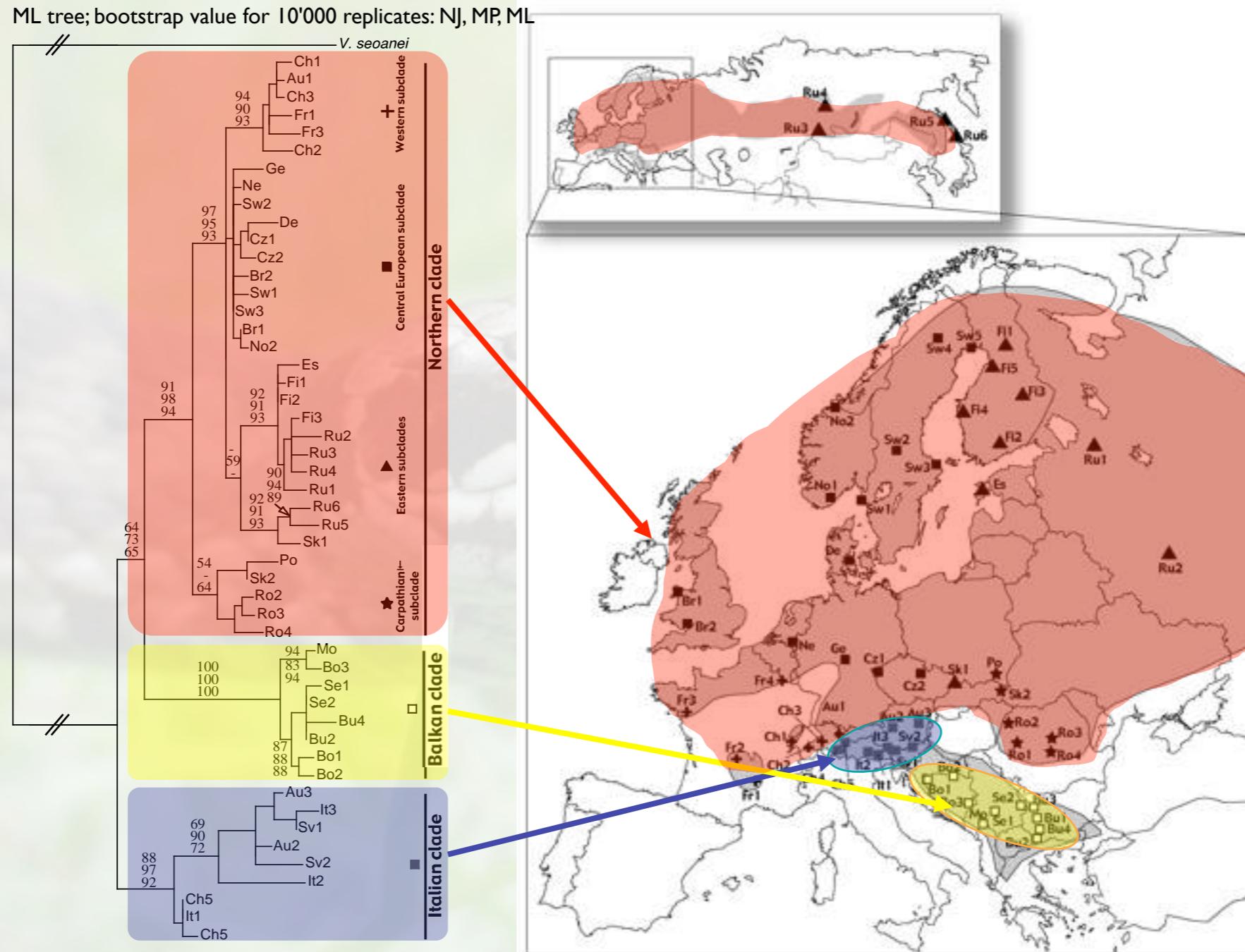
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Caucasus Mountains

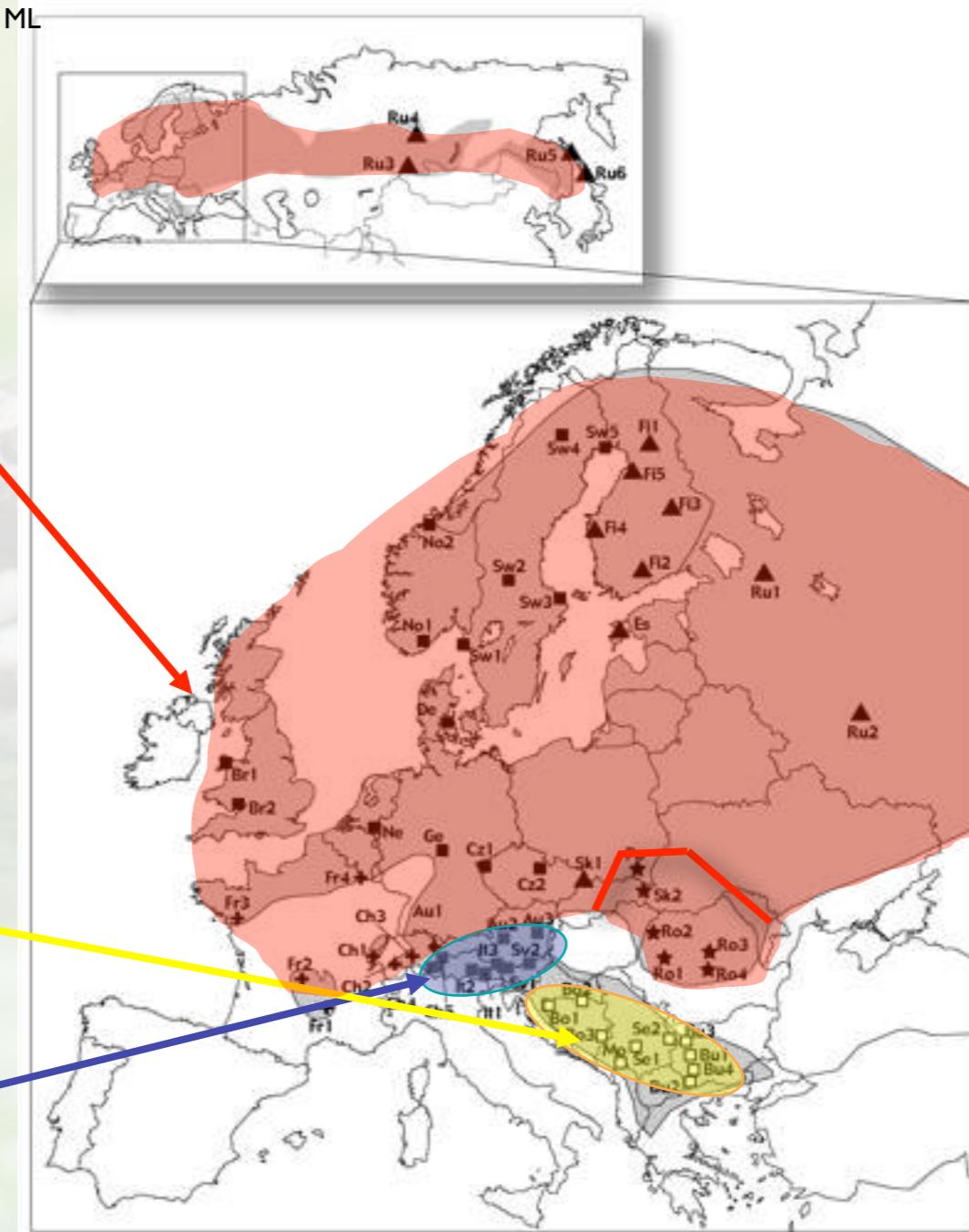
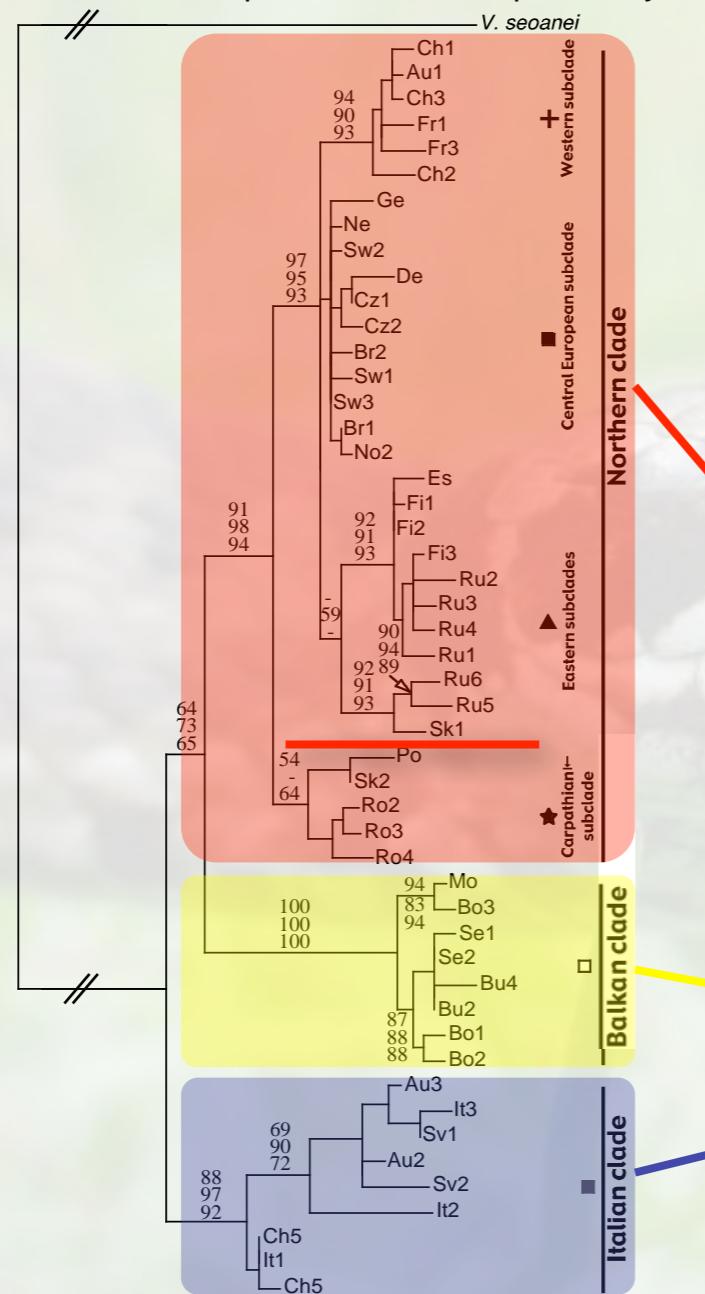


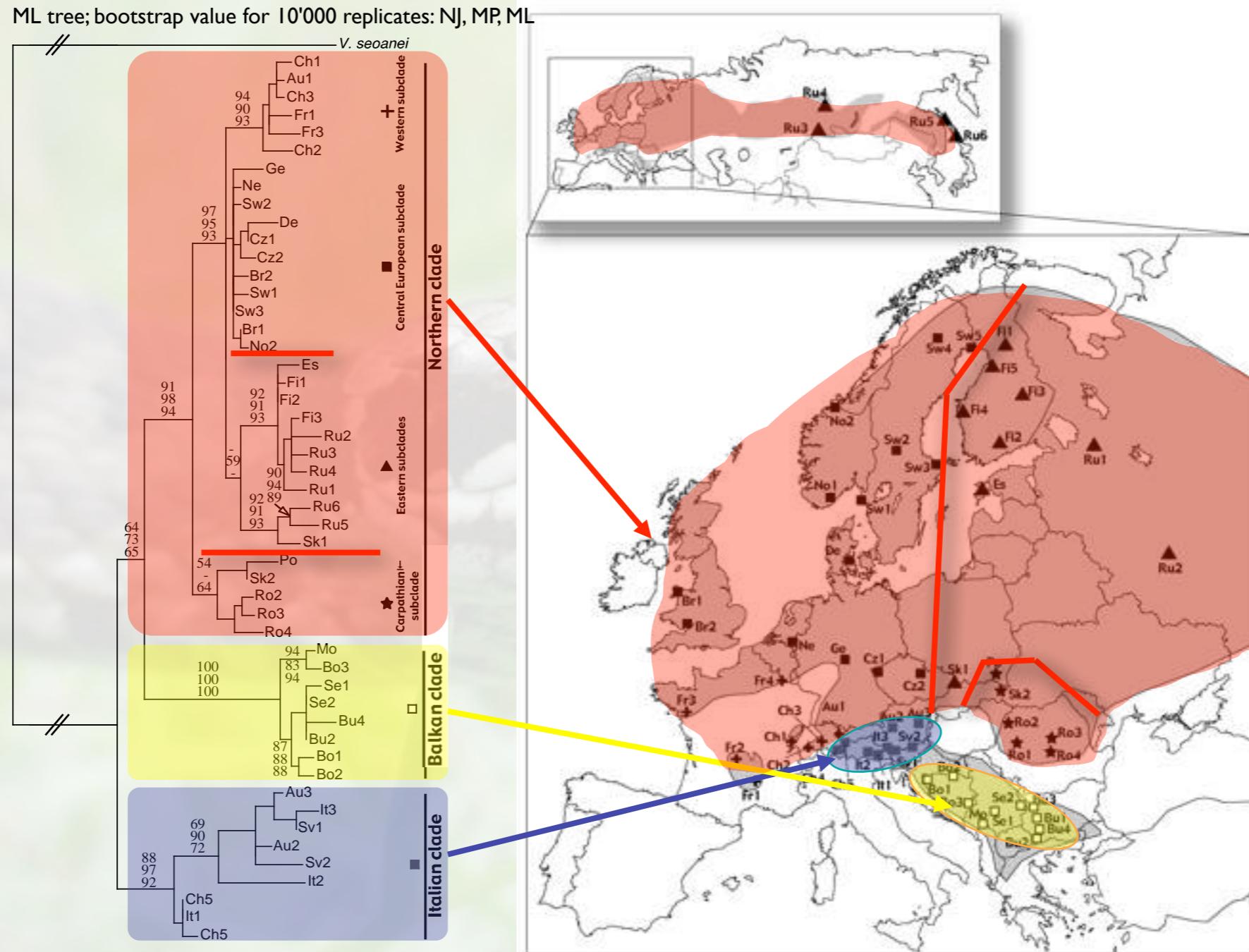
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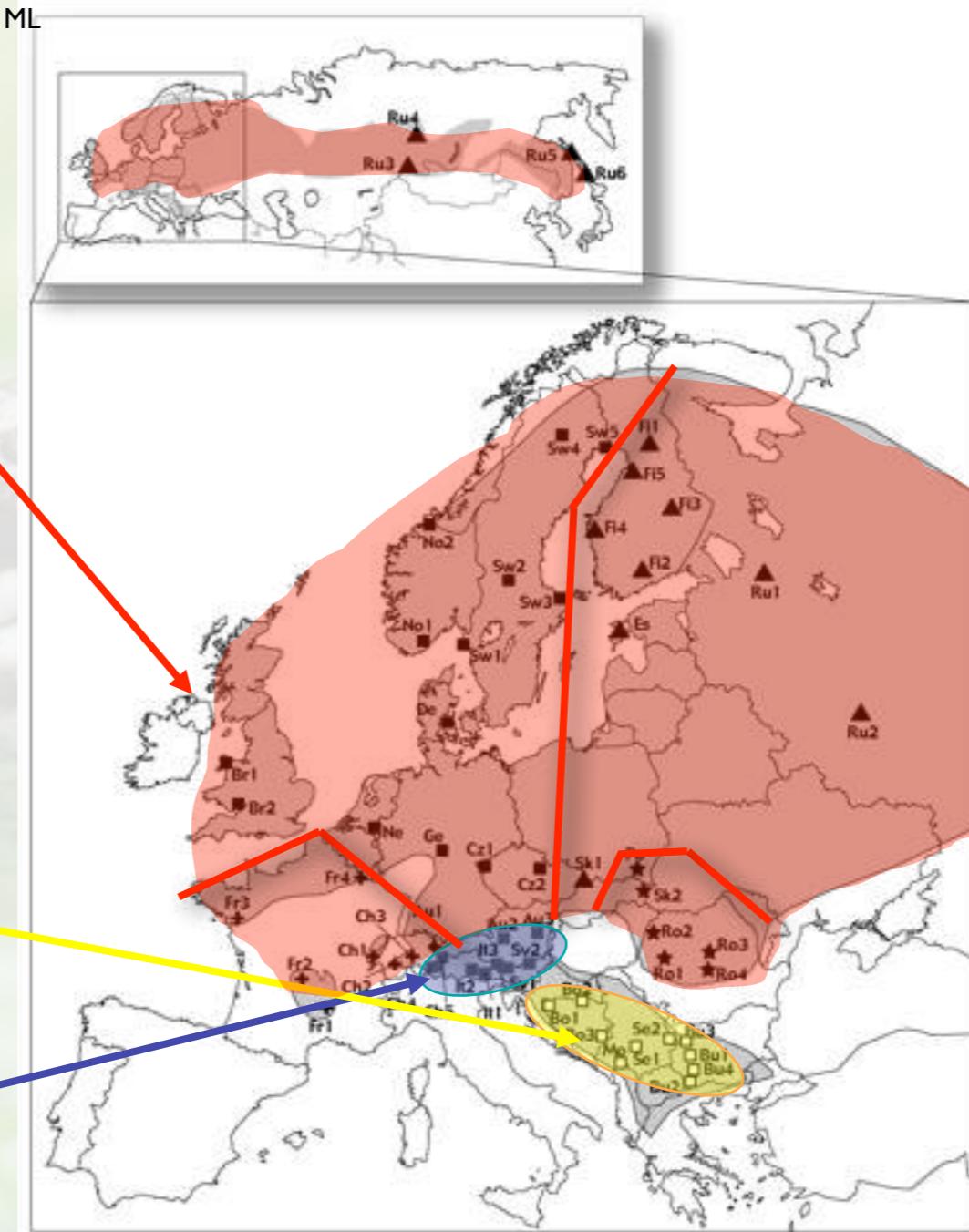
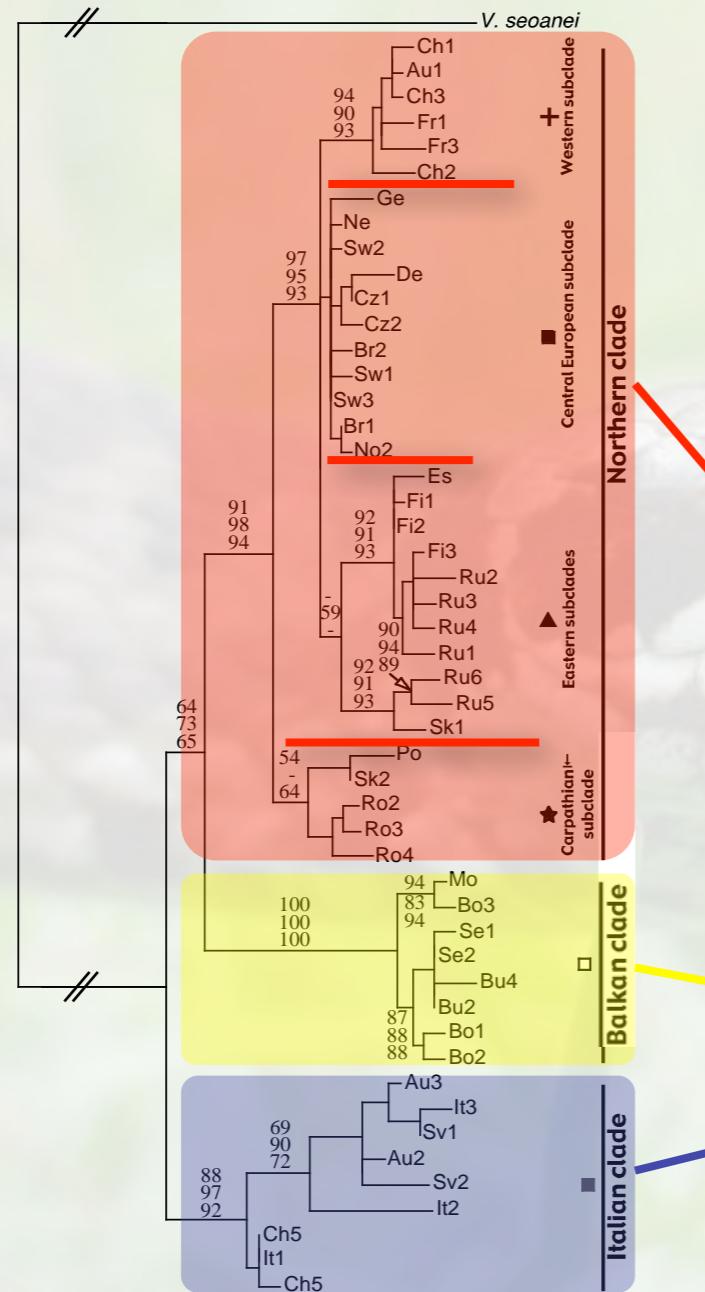


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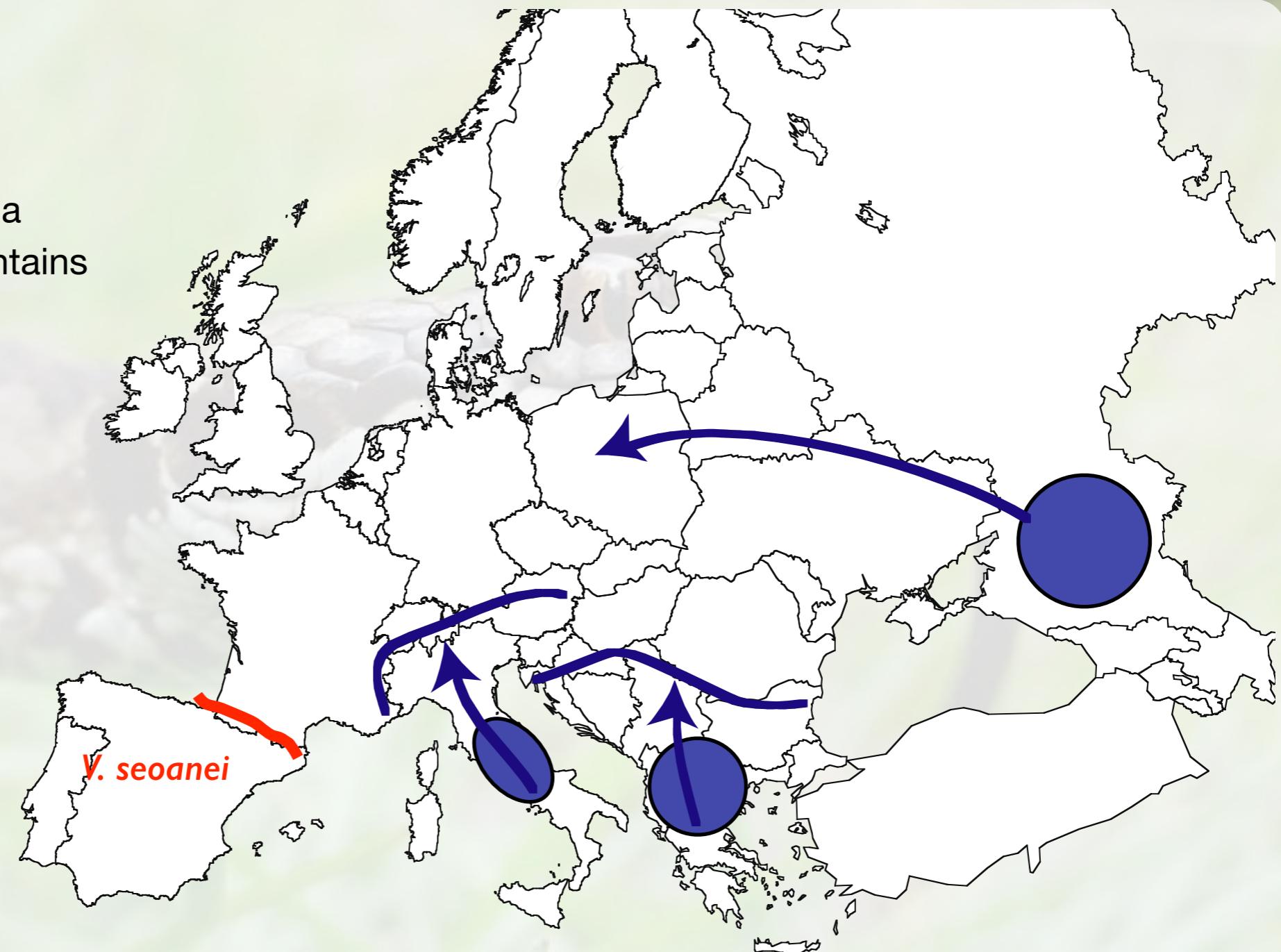


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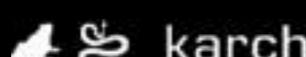
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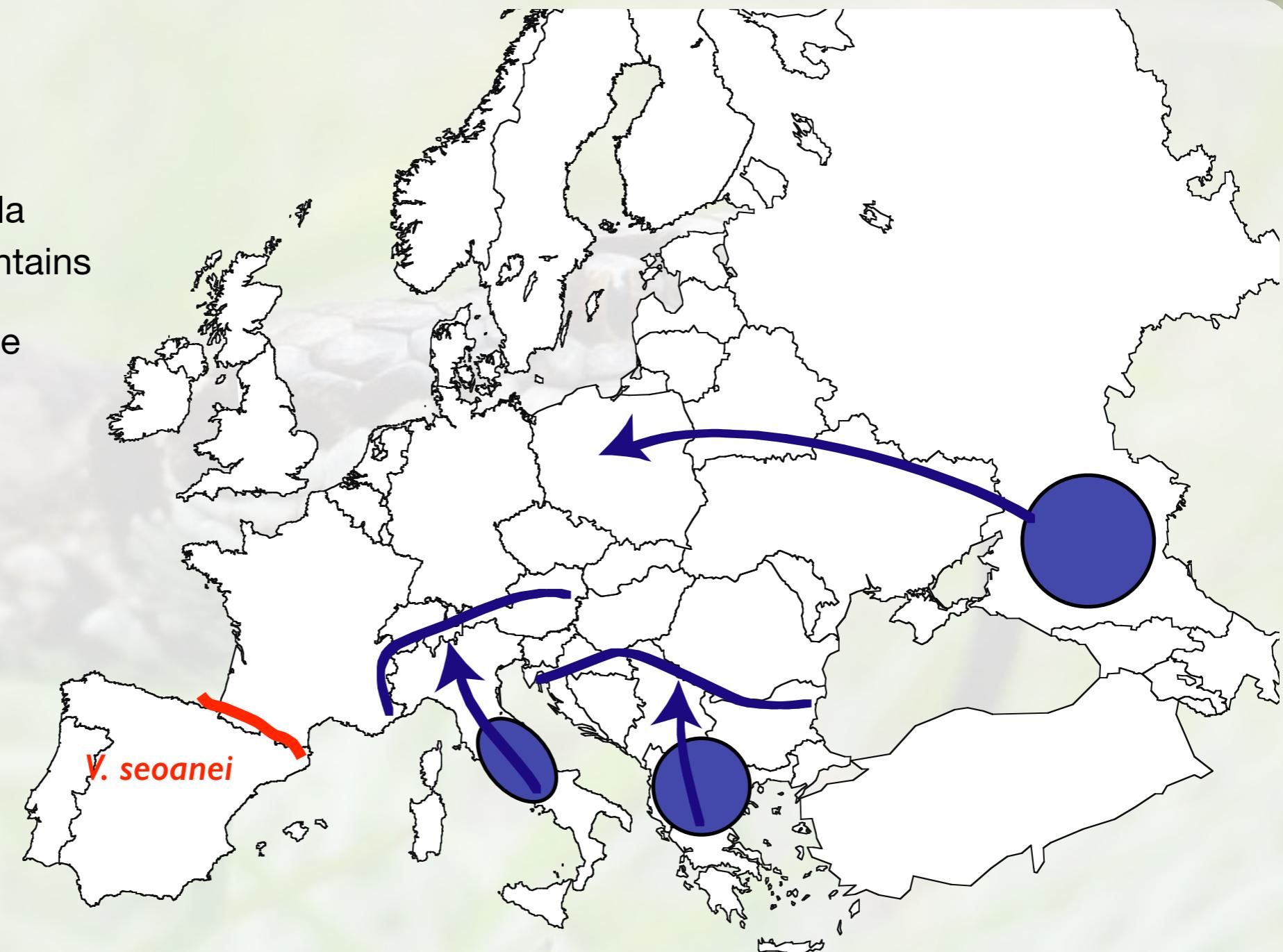
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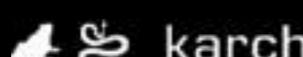
Balkan peninsula

Caucasus Mountains

Sub-structure in the
Northern Clade



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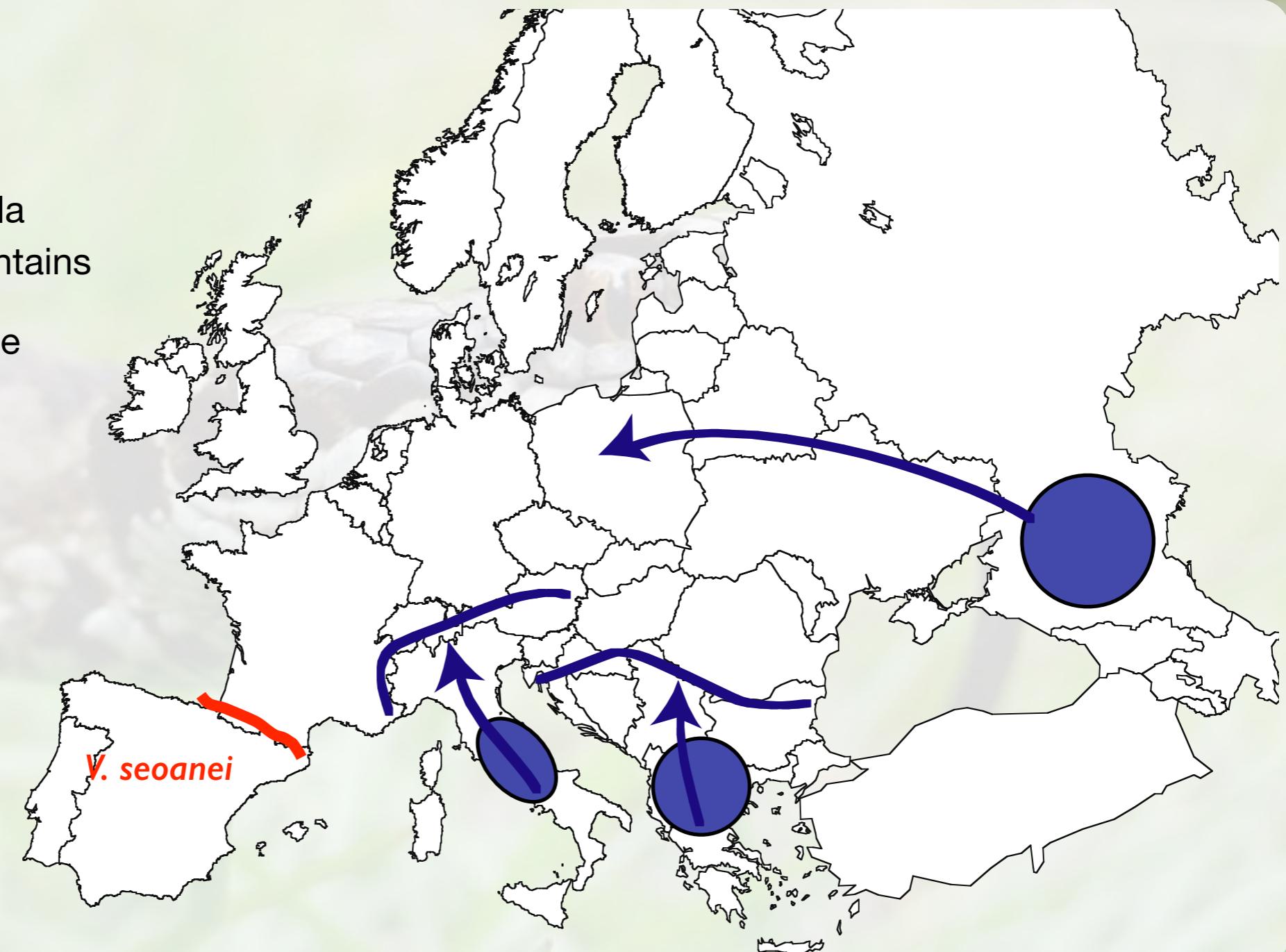
Sub-structure in the
Northern Clade

France

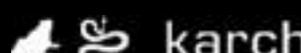
Central Europe

Romania

Russia



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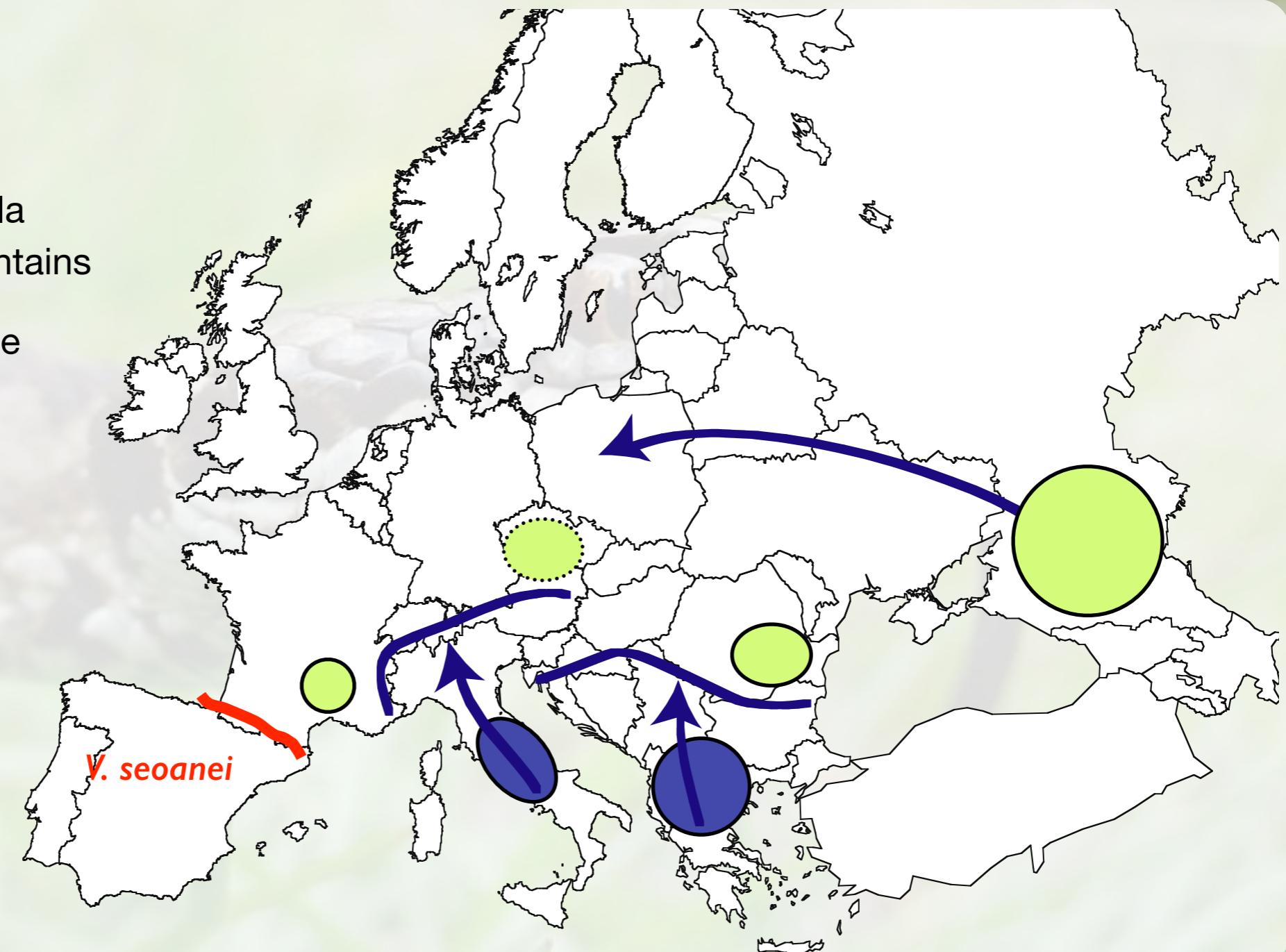
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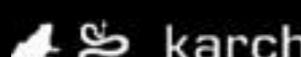
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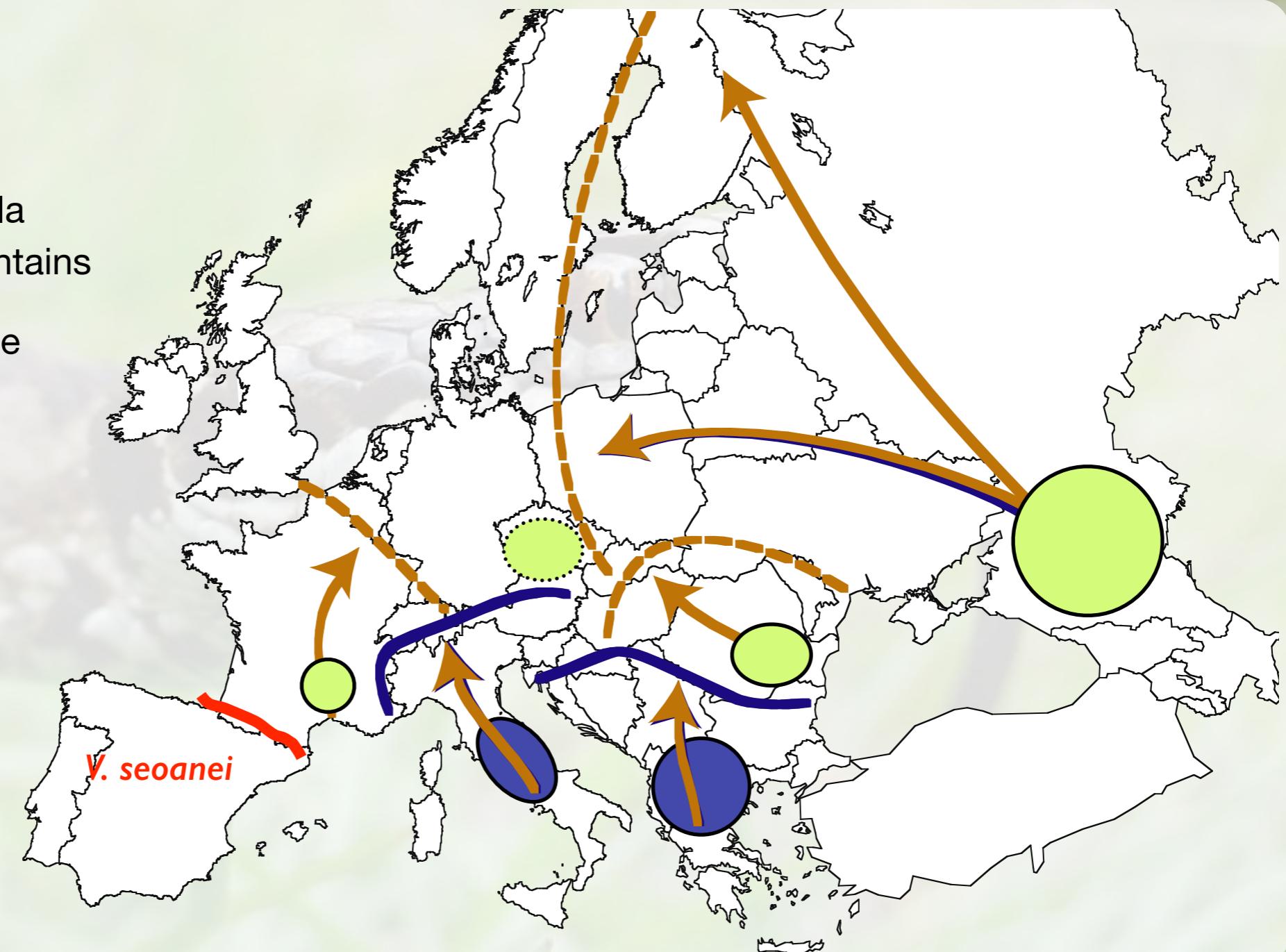
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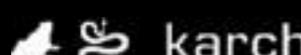
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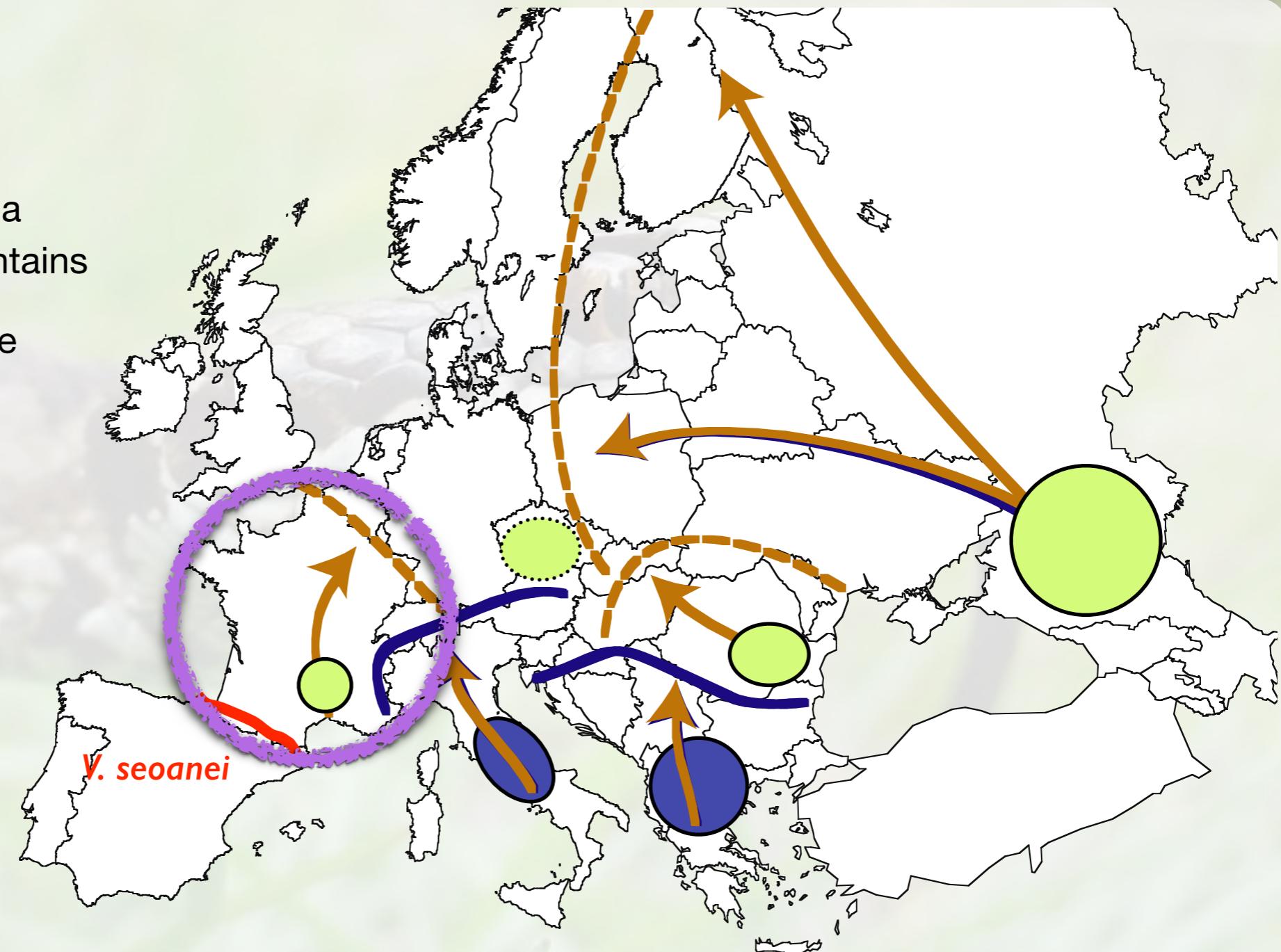
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Aims

- determine the putative glacial refugia

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- reconstruct post-glacial recolonisation routes



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Aims

- determine the putative glacial refugia
- reconstruct post-glacial recolonisation routes
- test the Central-marginal hypothesis
(populations closer to the refugia have a higher genetic diversity)



Material and Methods



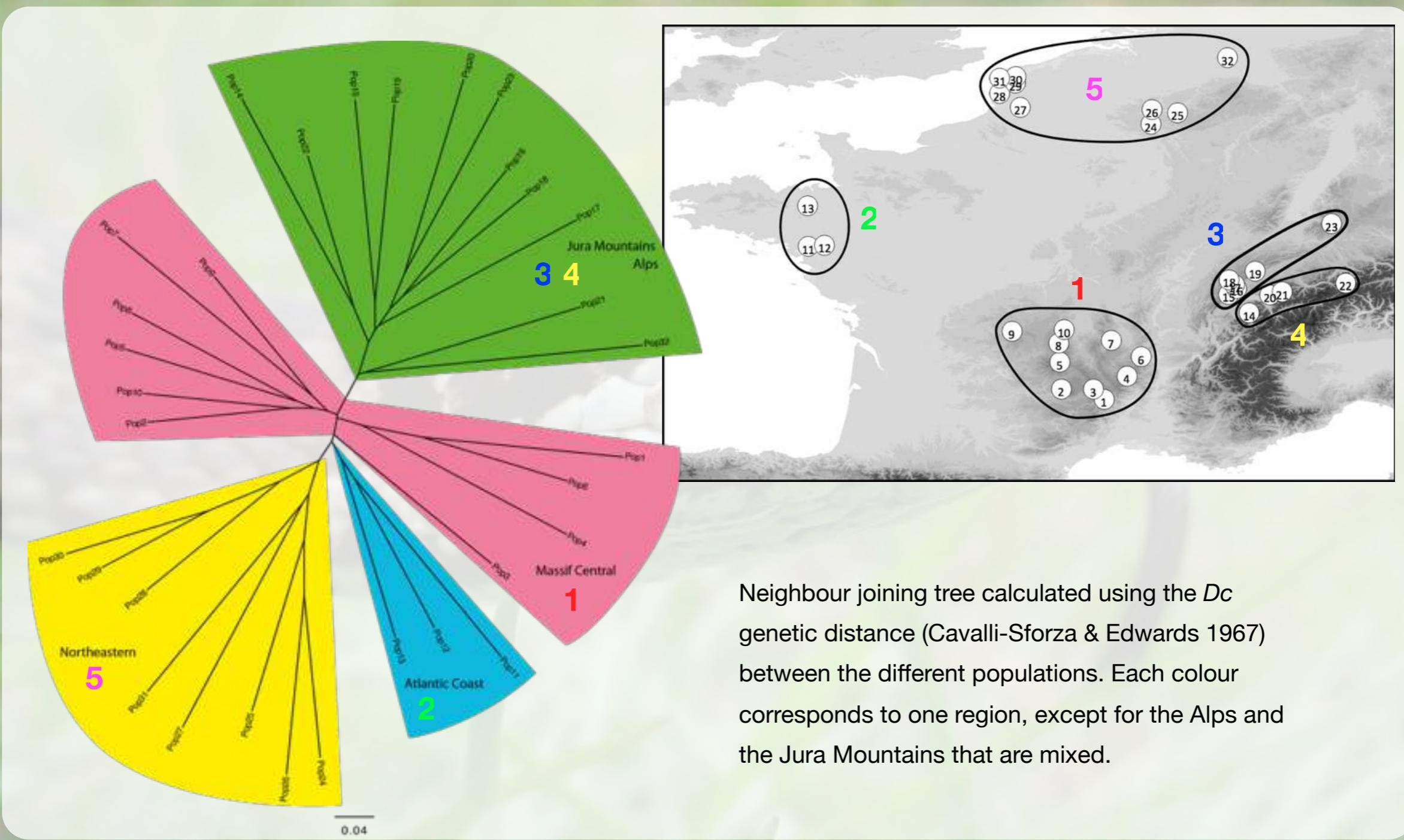
Material and Methods

- 32 populations (602 adders, between 5 and 30 ind./pop)
- 9 microsatellite markers

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- population grouping: bayesian approach (STRUCTURE),
genetic differentiation (POPULATIONS)
- testing scenarios: Approximate Bayesian Computation (DIYABC)

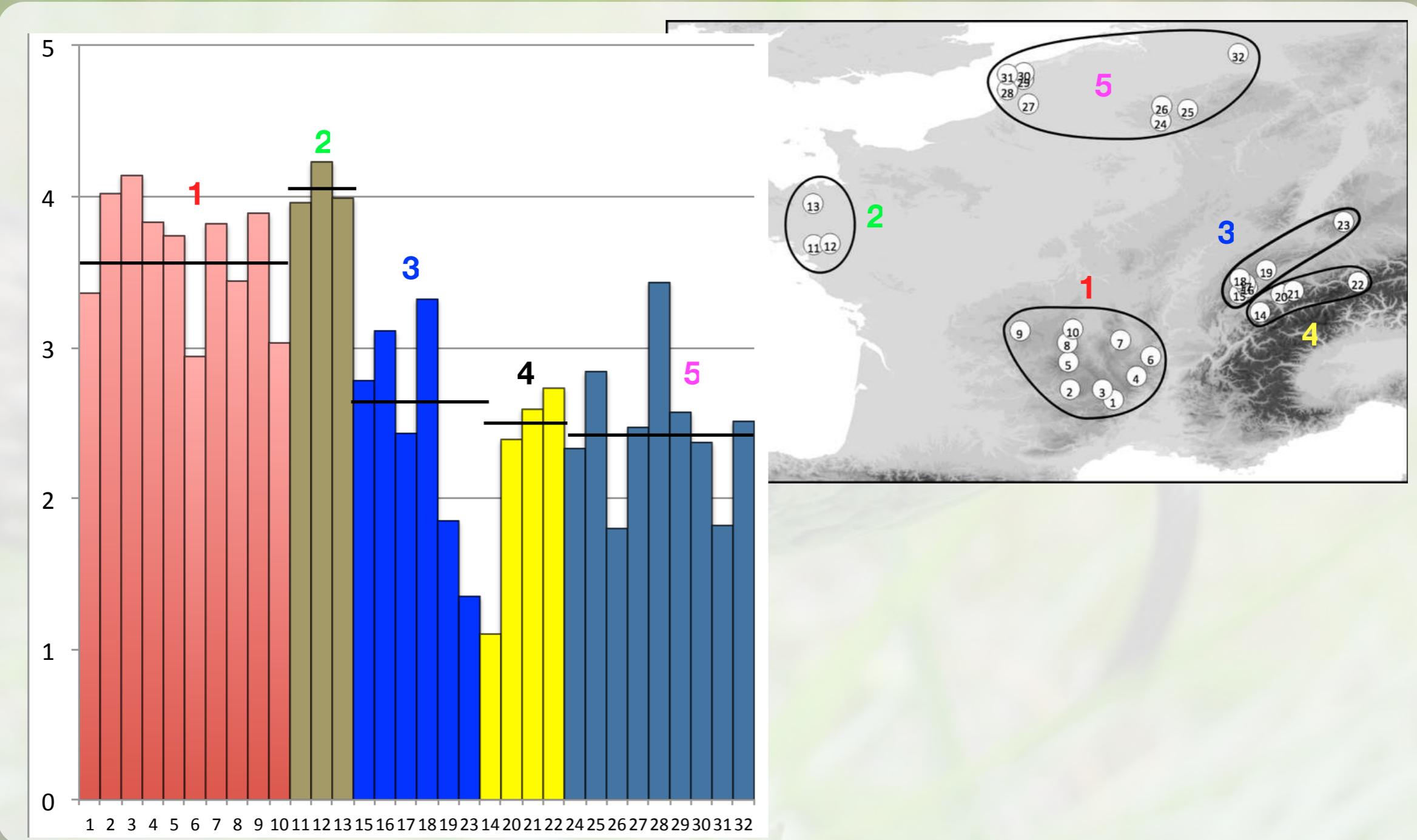
Results - genetic grouping



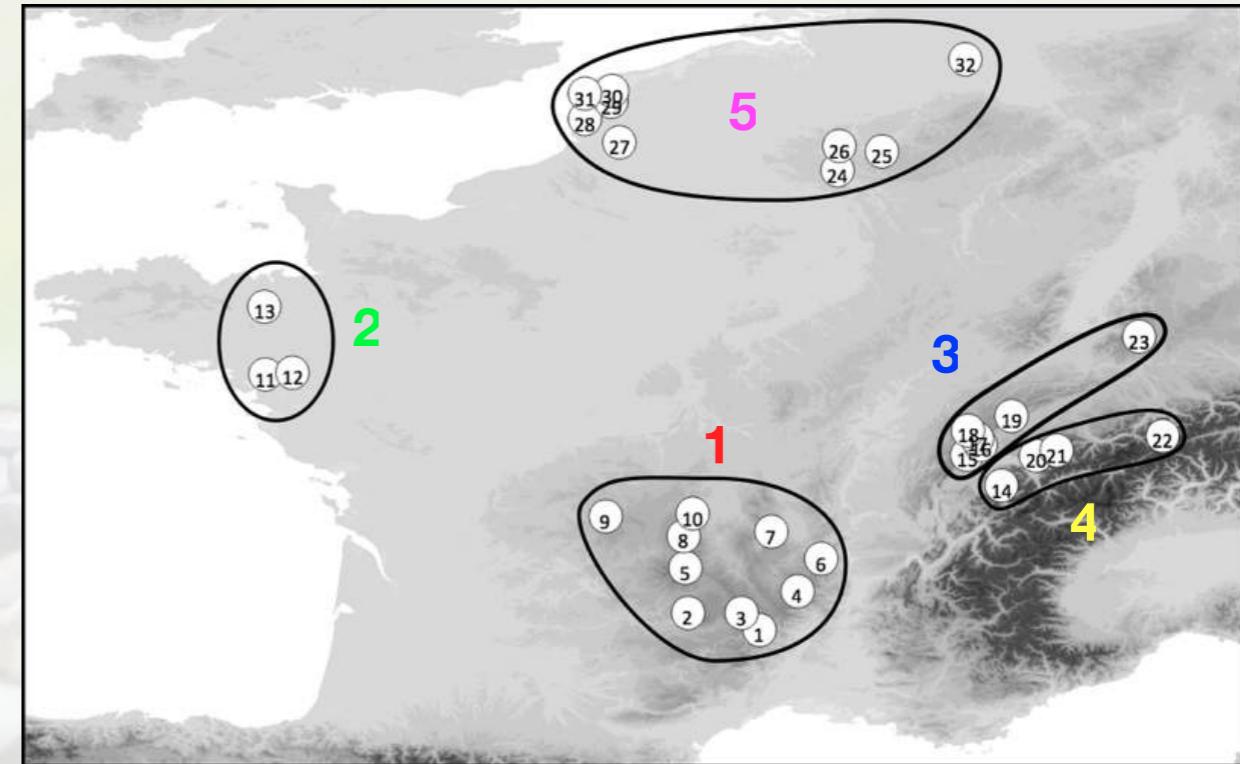
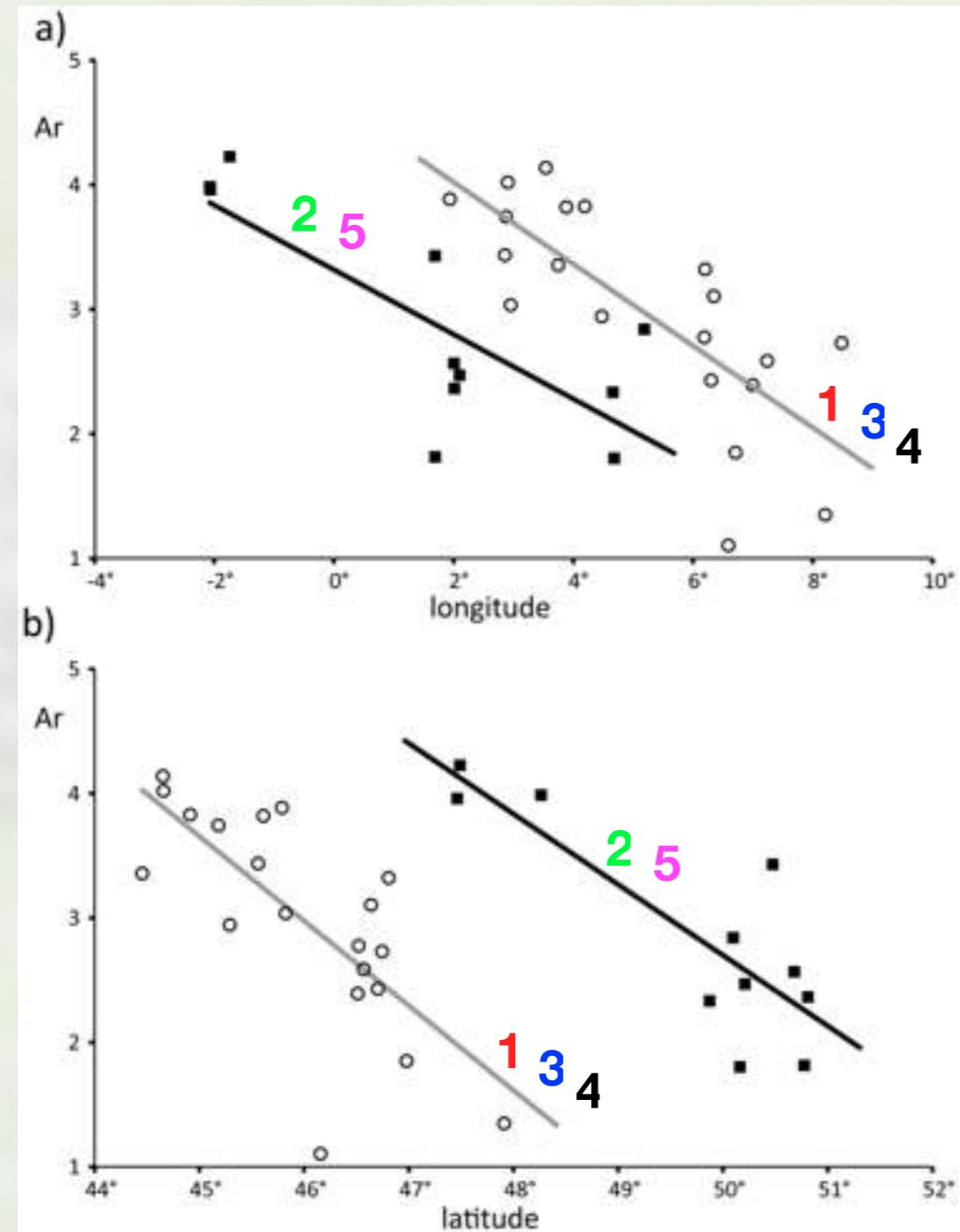
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Results - genetic diversity

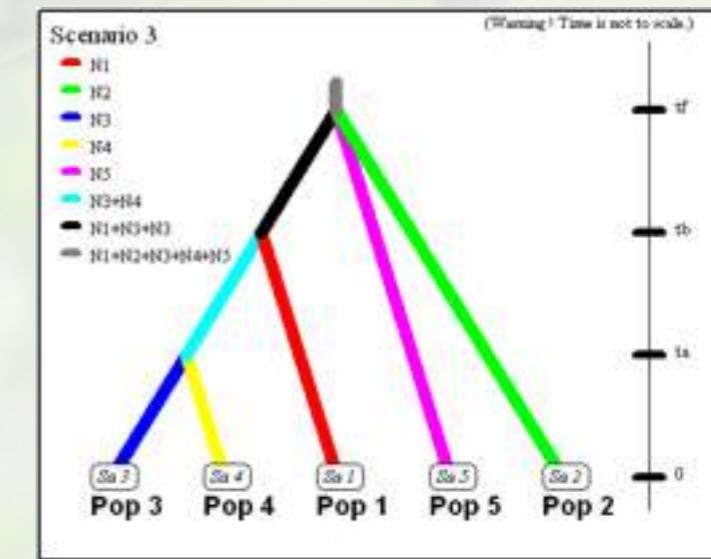
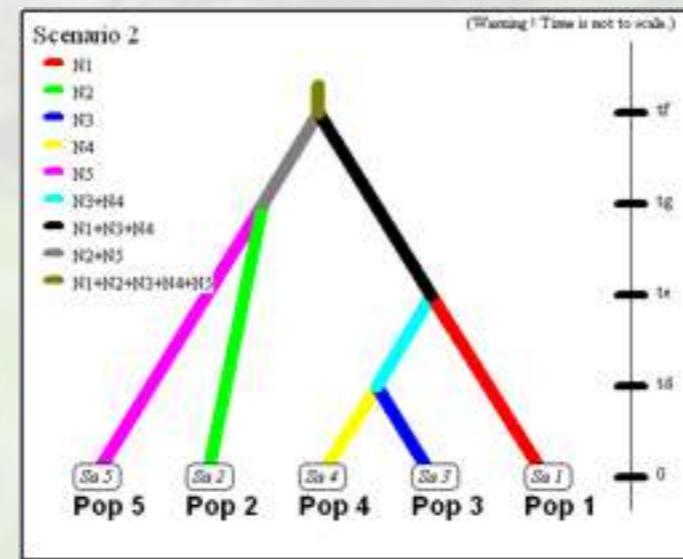
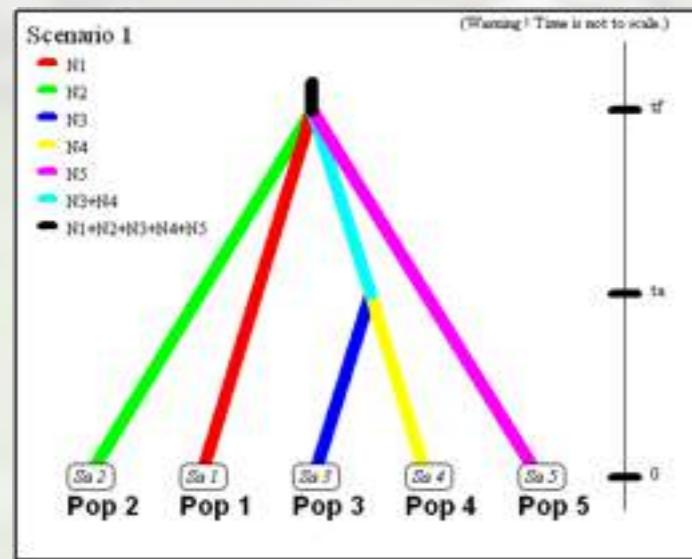
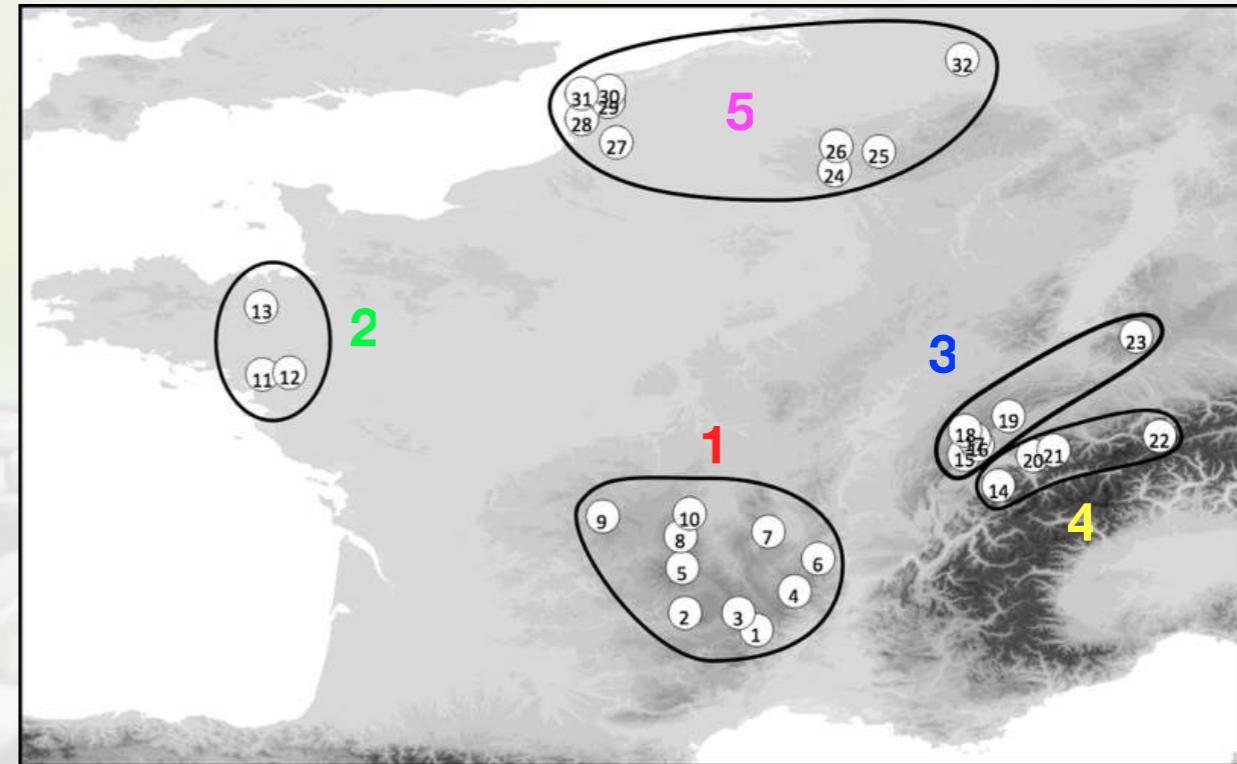
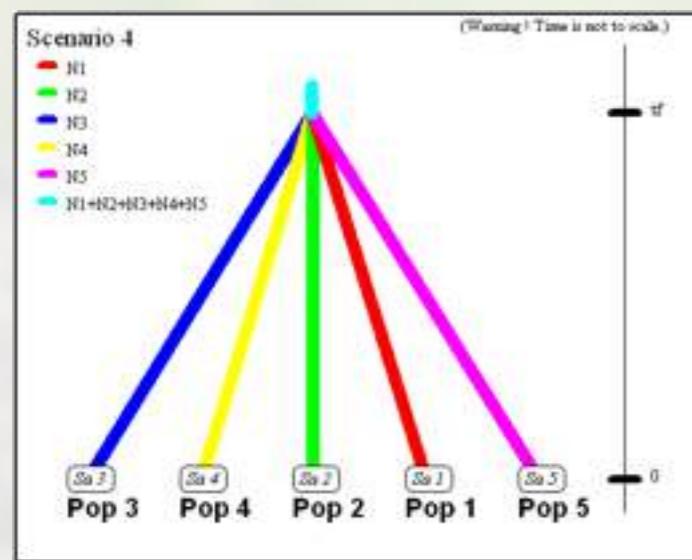


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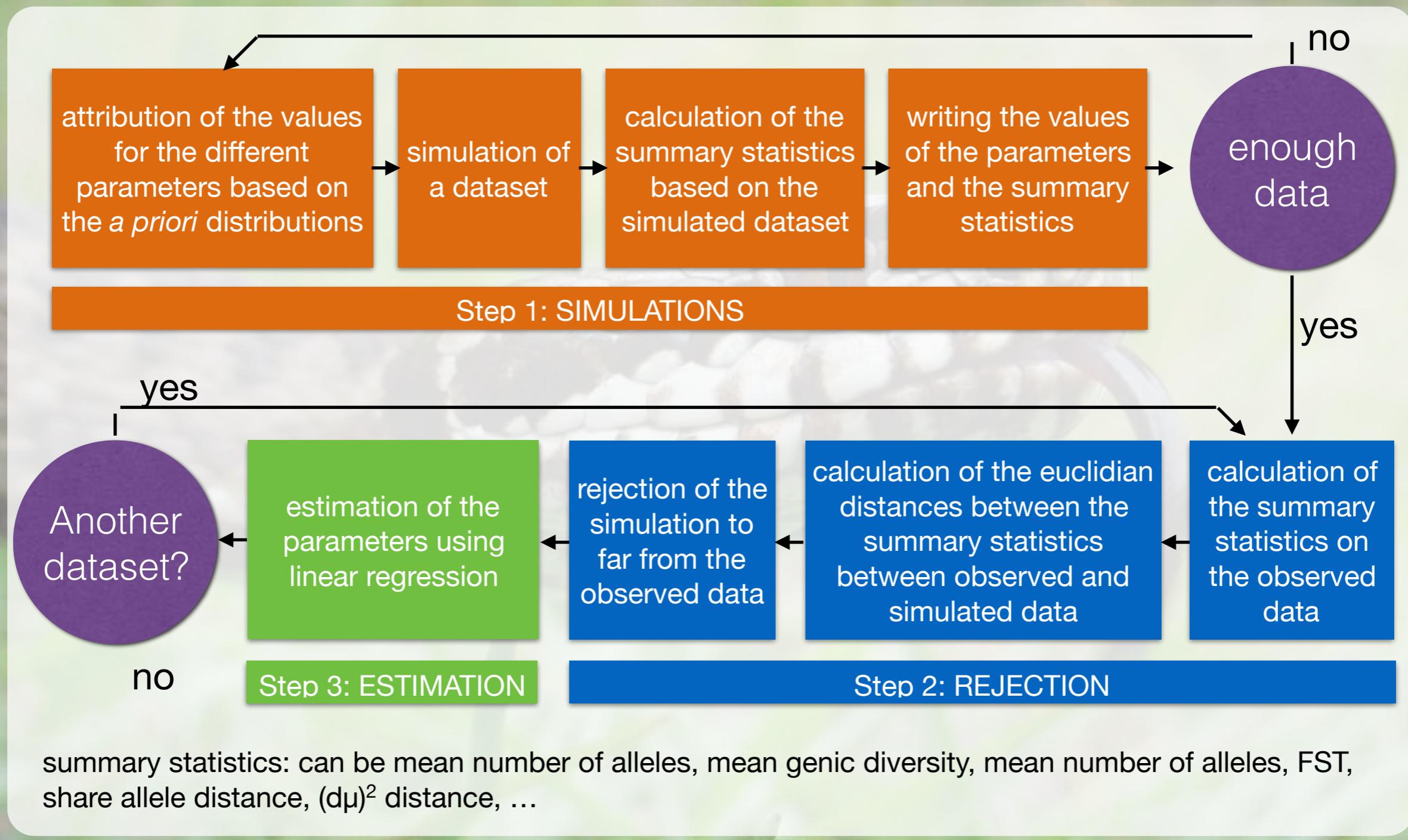


Correlations between the allelic richness (Ar) and longitude (a), latitude (b), and the distance to the putative glacial refugia (c). The solid line and plain squares are related to the Northern colonisation road (Atlantic Coast and Northeastern regions), whereas the grey line and the empty circles correspond to the central colonisation road (Massif Central, Alps and Jura Mountain regions).

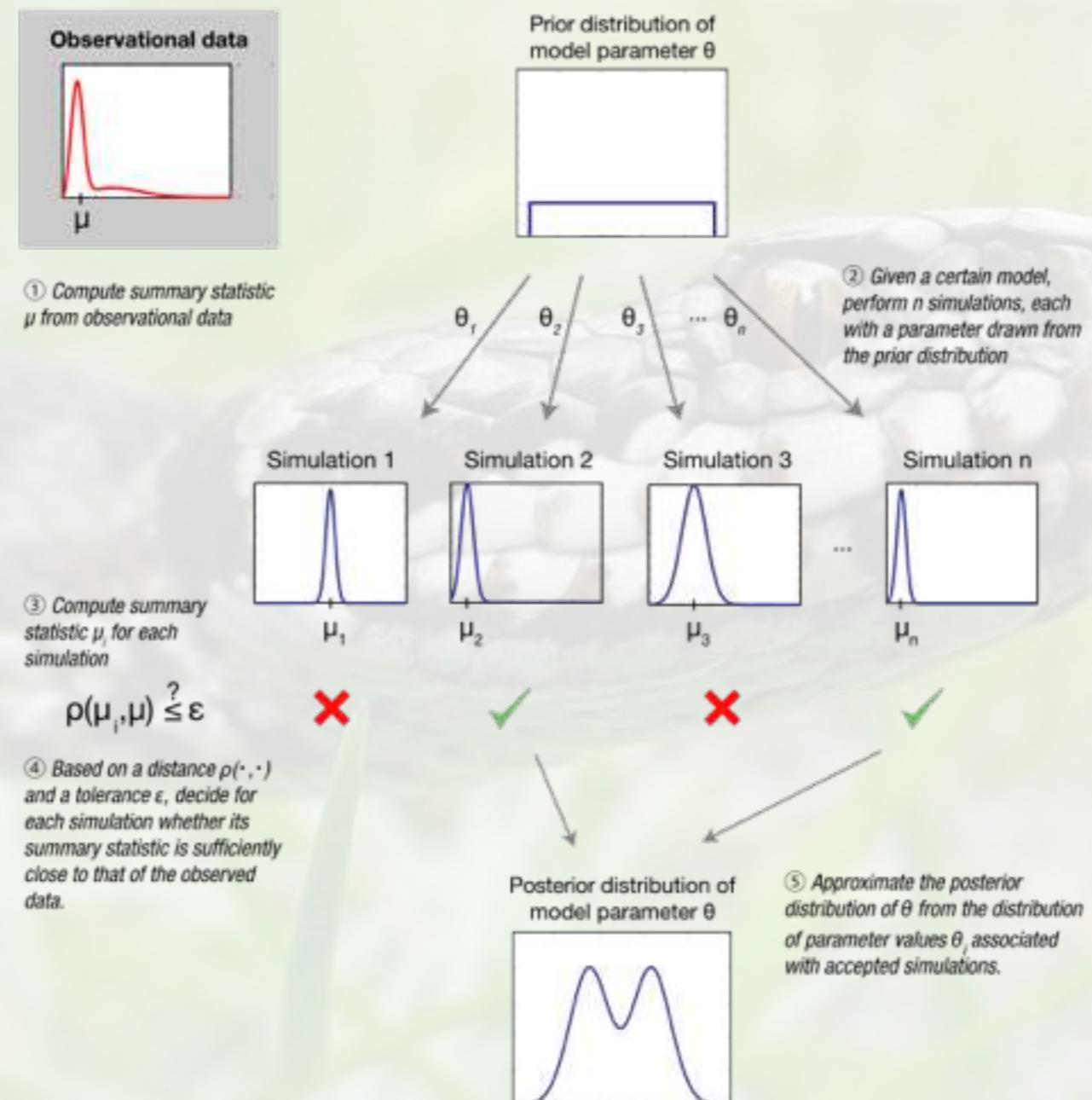
Results - ABC scenario



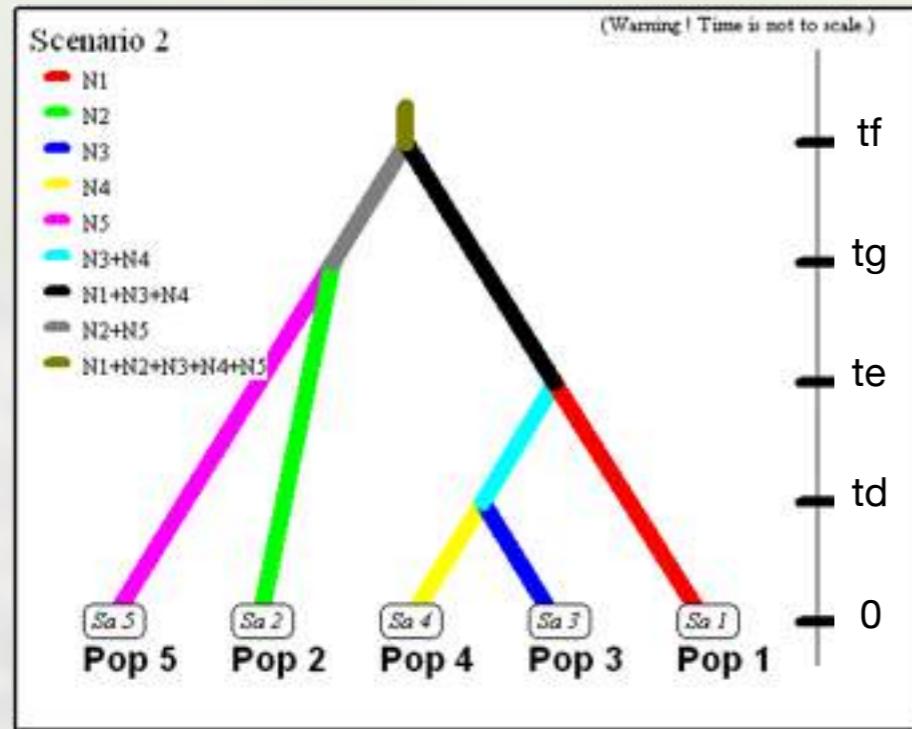
Results - ABC methodology



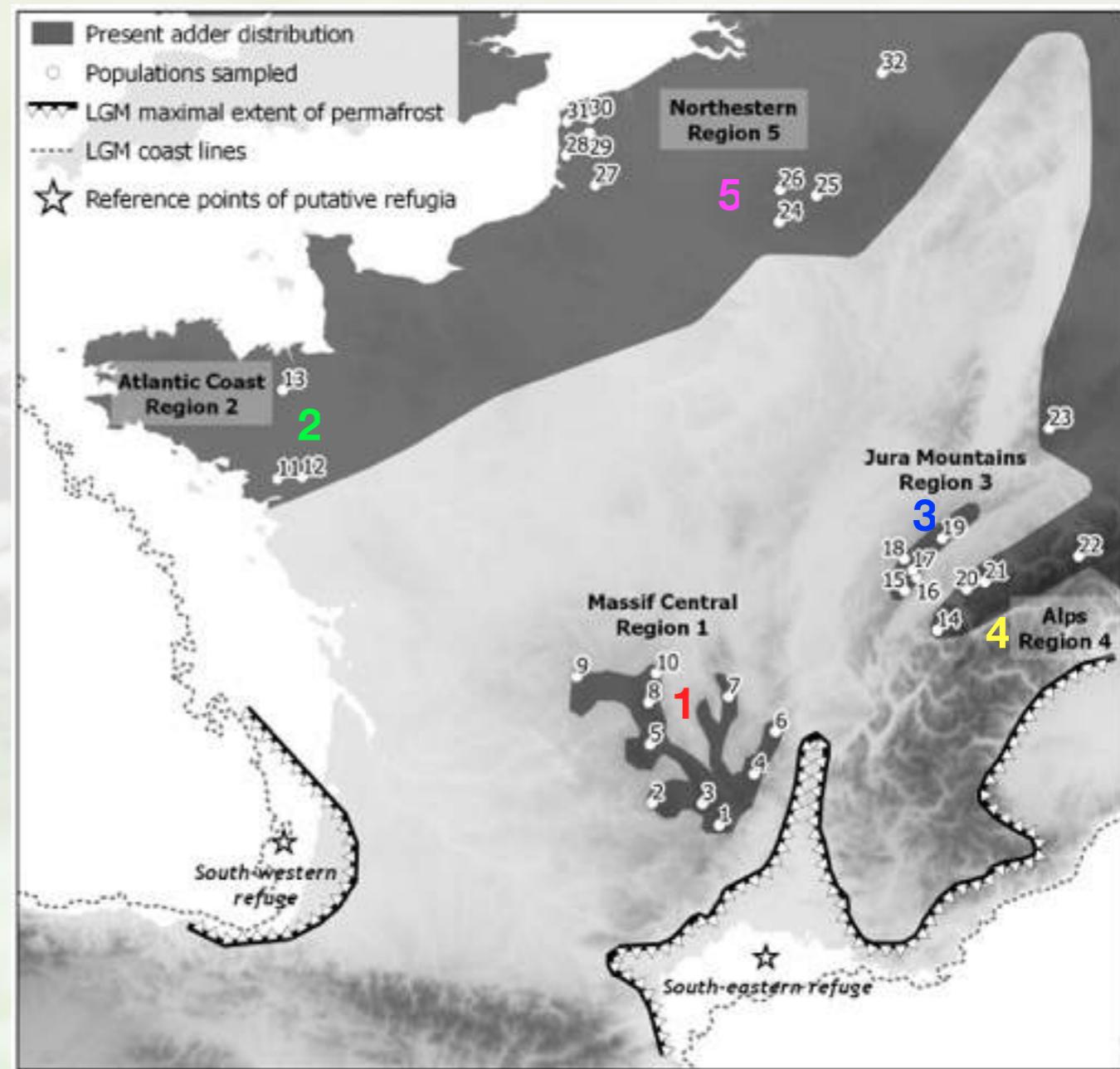
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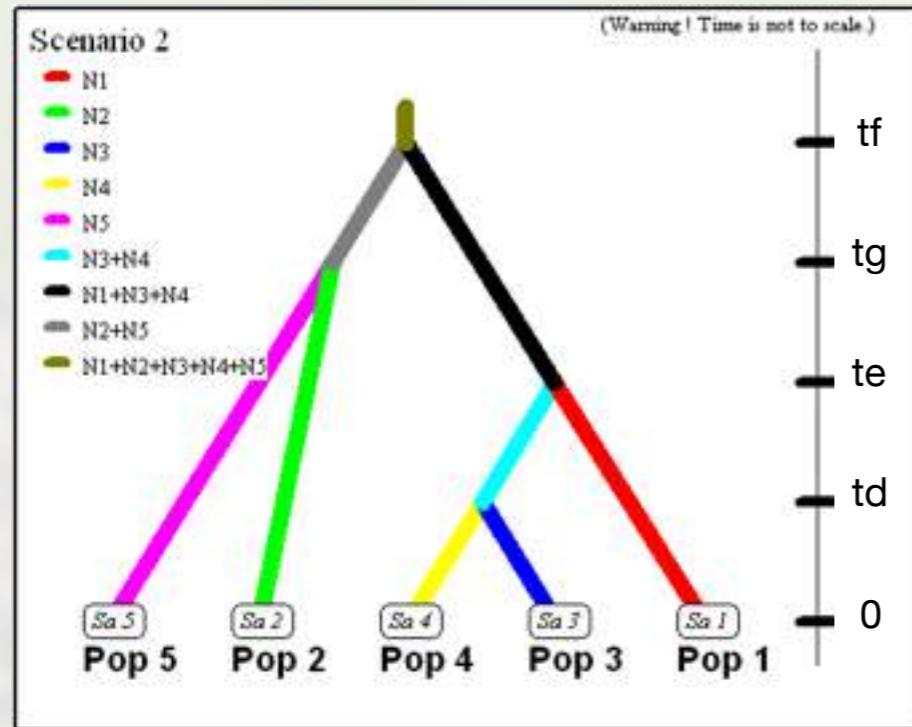
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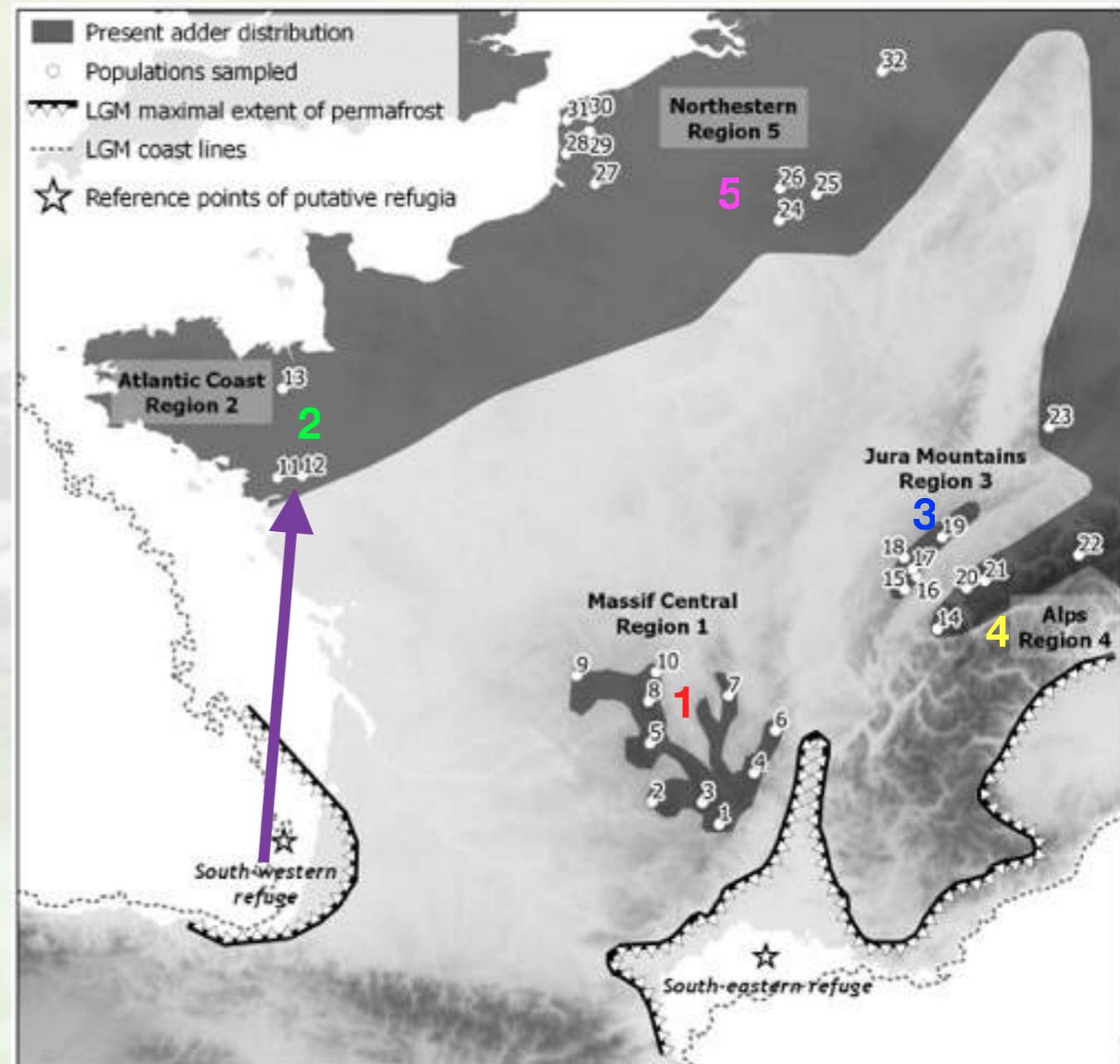
	years	95% CI
tf	29760	17,040 – 39,040
tg	18640	8,480 – 31,440
te	15440	7,136 – 25,280
td	3544	712 – 7,688



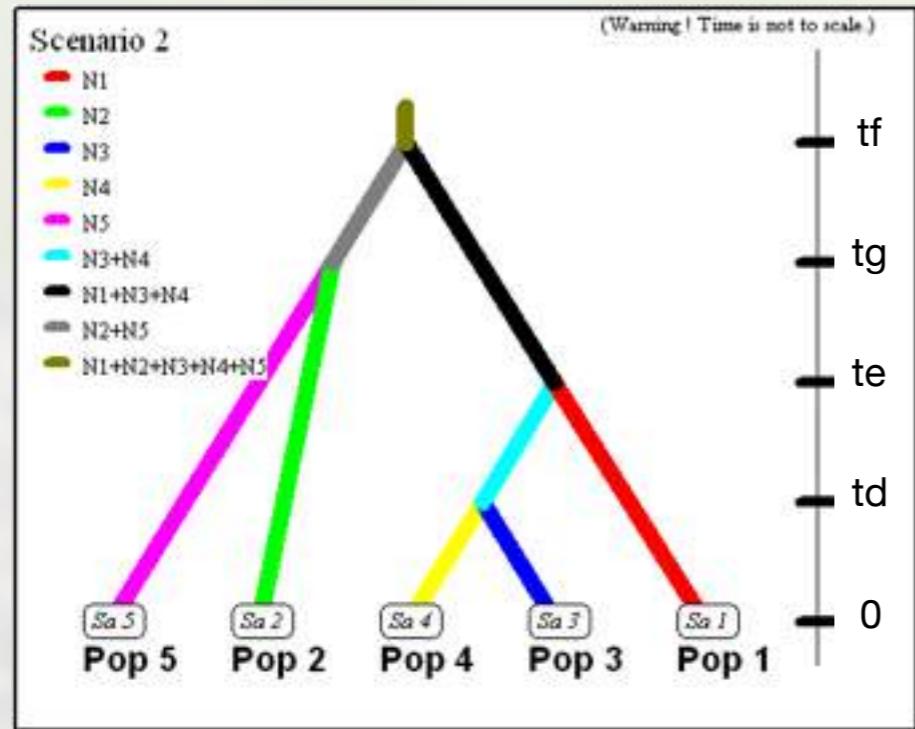
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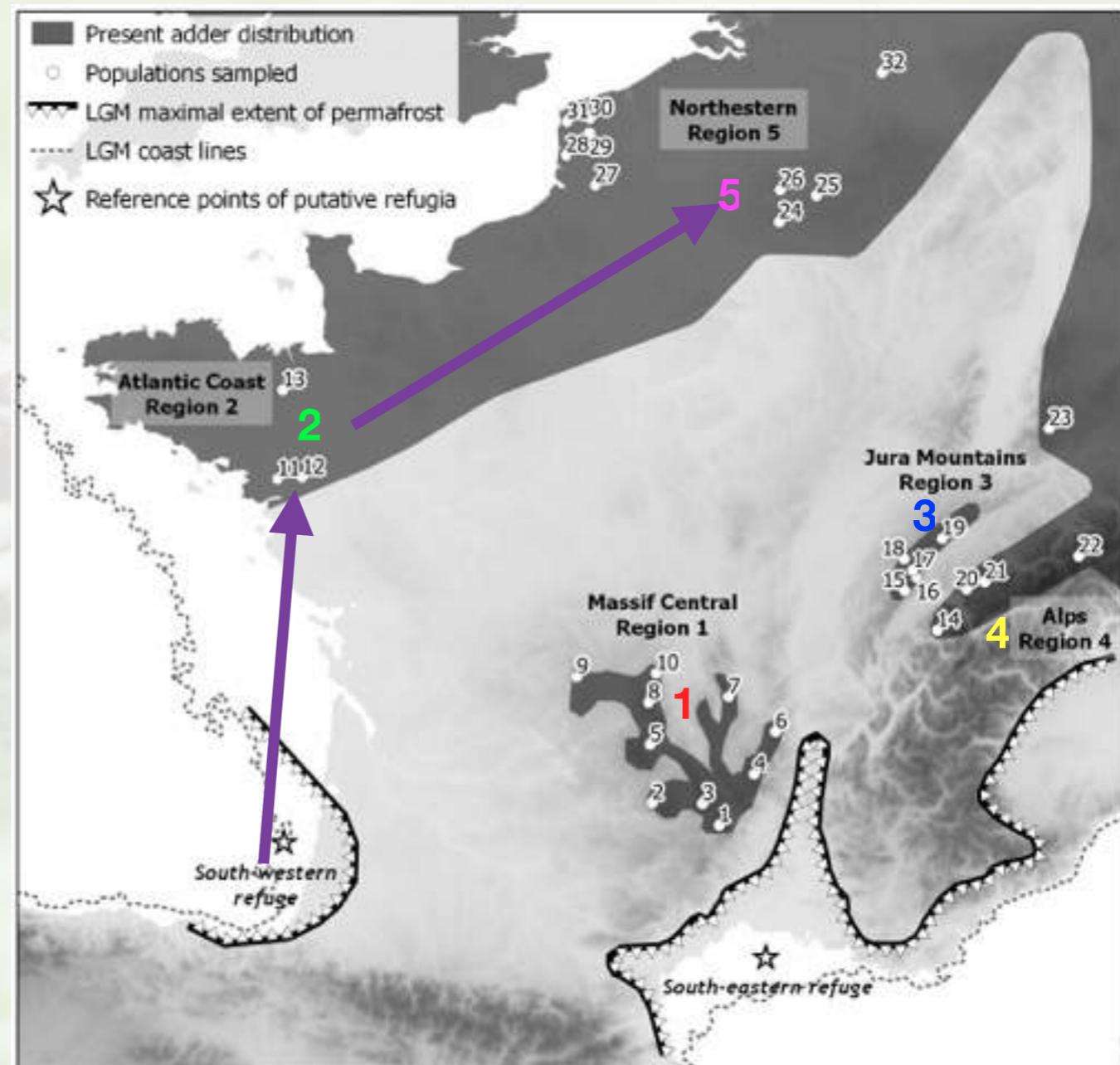
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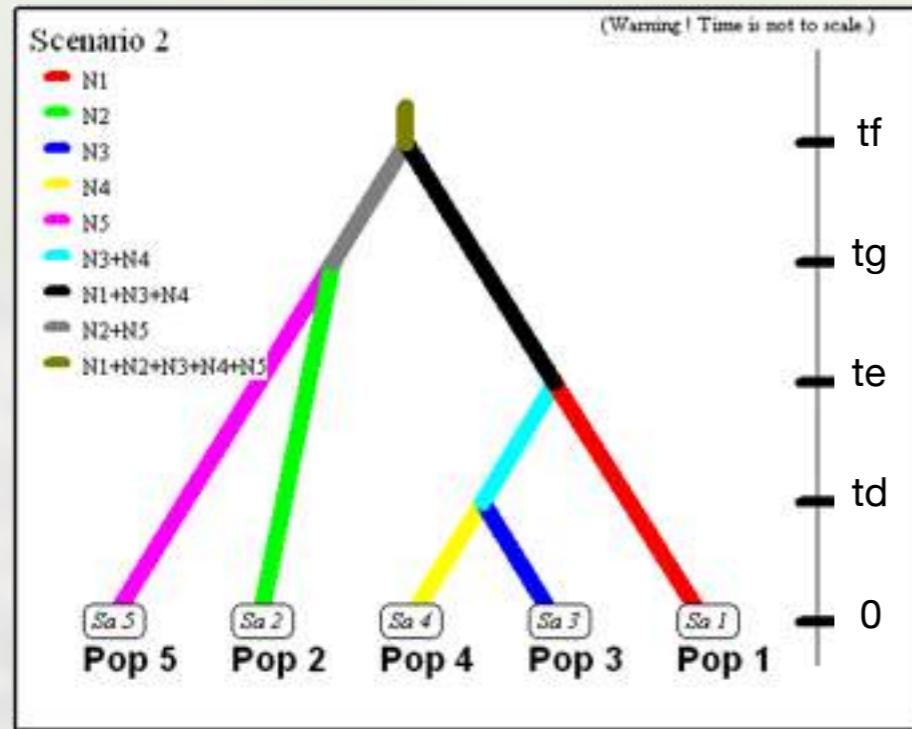
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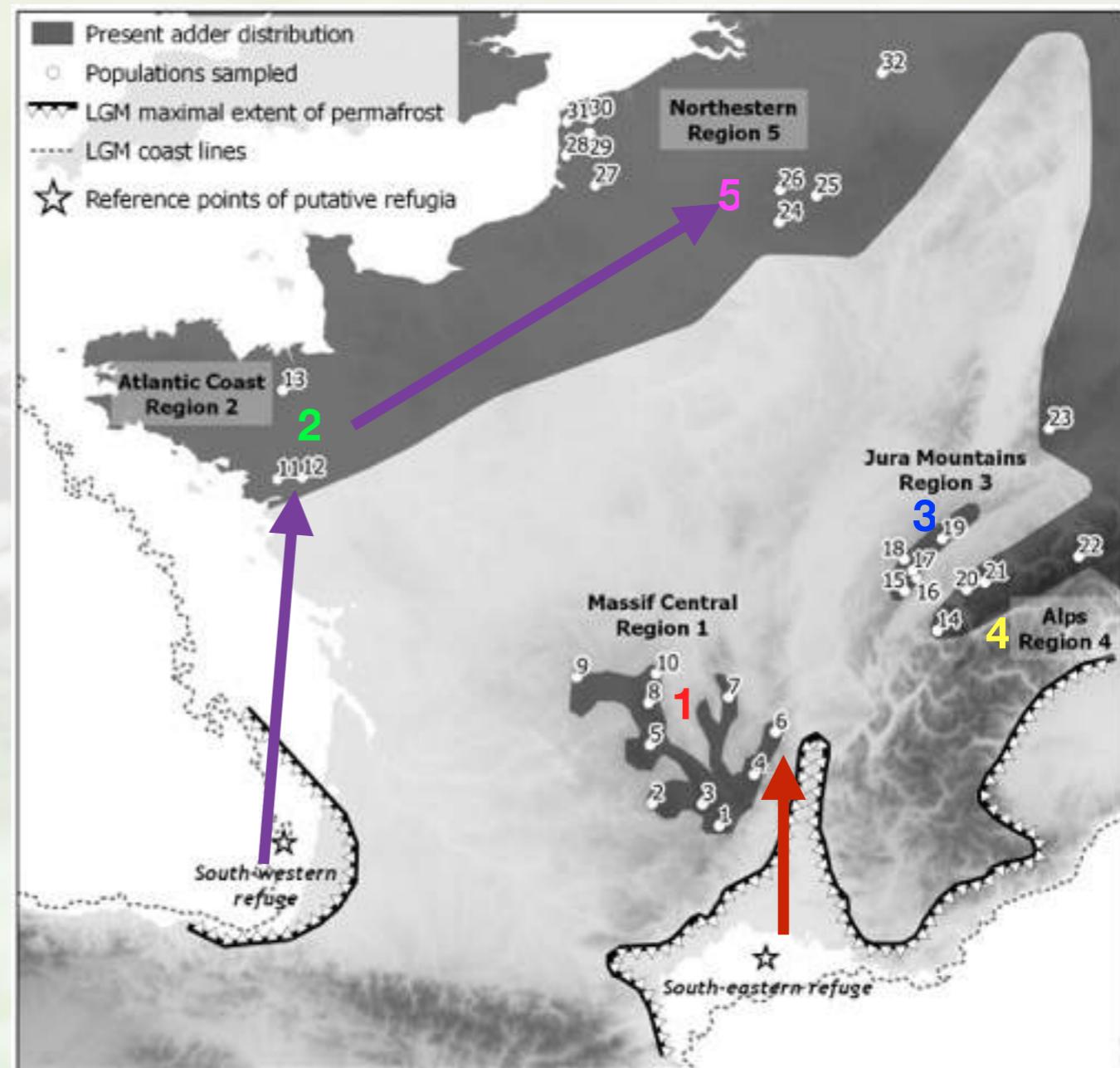
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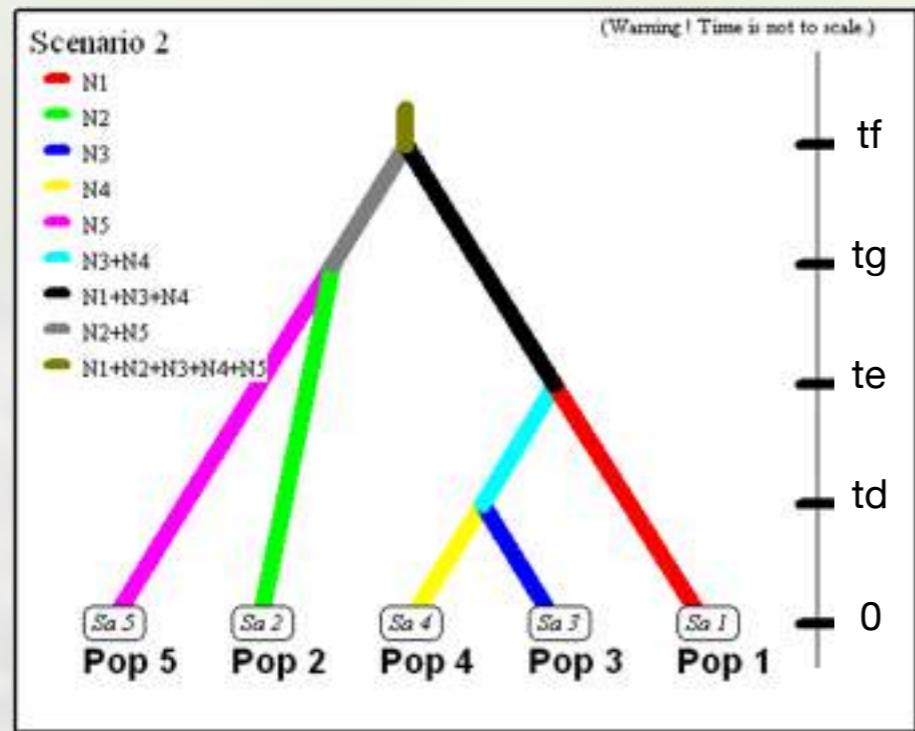
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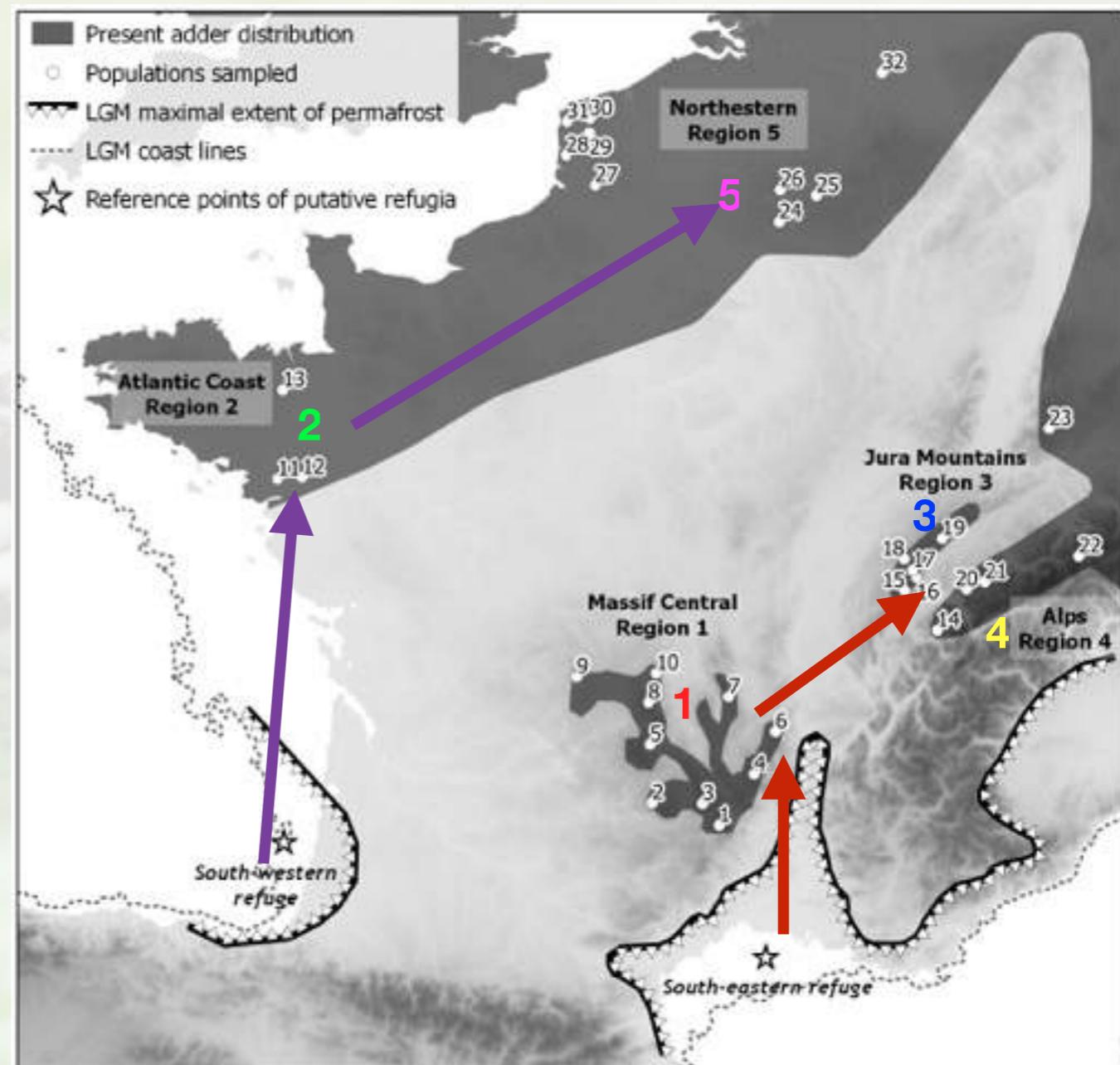
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Discussion - Central-marginal hypothesis

- reduction of the genetic diversity in northern and eastern populations
- genetic reduction \propto [distance to refugia]
- confirm the Central-marginal hypothesis



Discussion - *postglacial recolonisation*

- 2 distinctive refugia already, separated before the last LGM;
located in southern France (new location for a vertebrate)
- post glacial recolonisation:
 - direction southwestern → northeastern
 - occurred just after the LGM
 - split between the Alps and Jura Mountains very recent
- ABC: possibility to test scenario and select the most probable;
evaluation of the splits between populations



Discussion - *use of highly variable markers*

- phylogeography: mainly conducted with mtDNA or introns
- highly polymorphic markers can be of valuable interest for more recent events
- ABC:
 - can combine both kind of markers
 - testing scenario
 - timing of splits

Acknowledgements

- Sampling: M Beddek, T Durand, P Golay, E Graitson, G Guiller, P Janssen, J Legentilhomme, AJW. Lenders, G Müller, F Paysant, G Thiery, C Vanappelghem, M-A Marchand
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