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Genetic Structure of an Endangered Species, the Hermann's Tortoise (*Testudo hermanni hermanni*), in Western Europe Revealed by Microsatellites : Implications for Conservation



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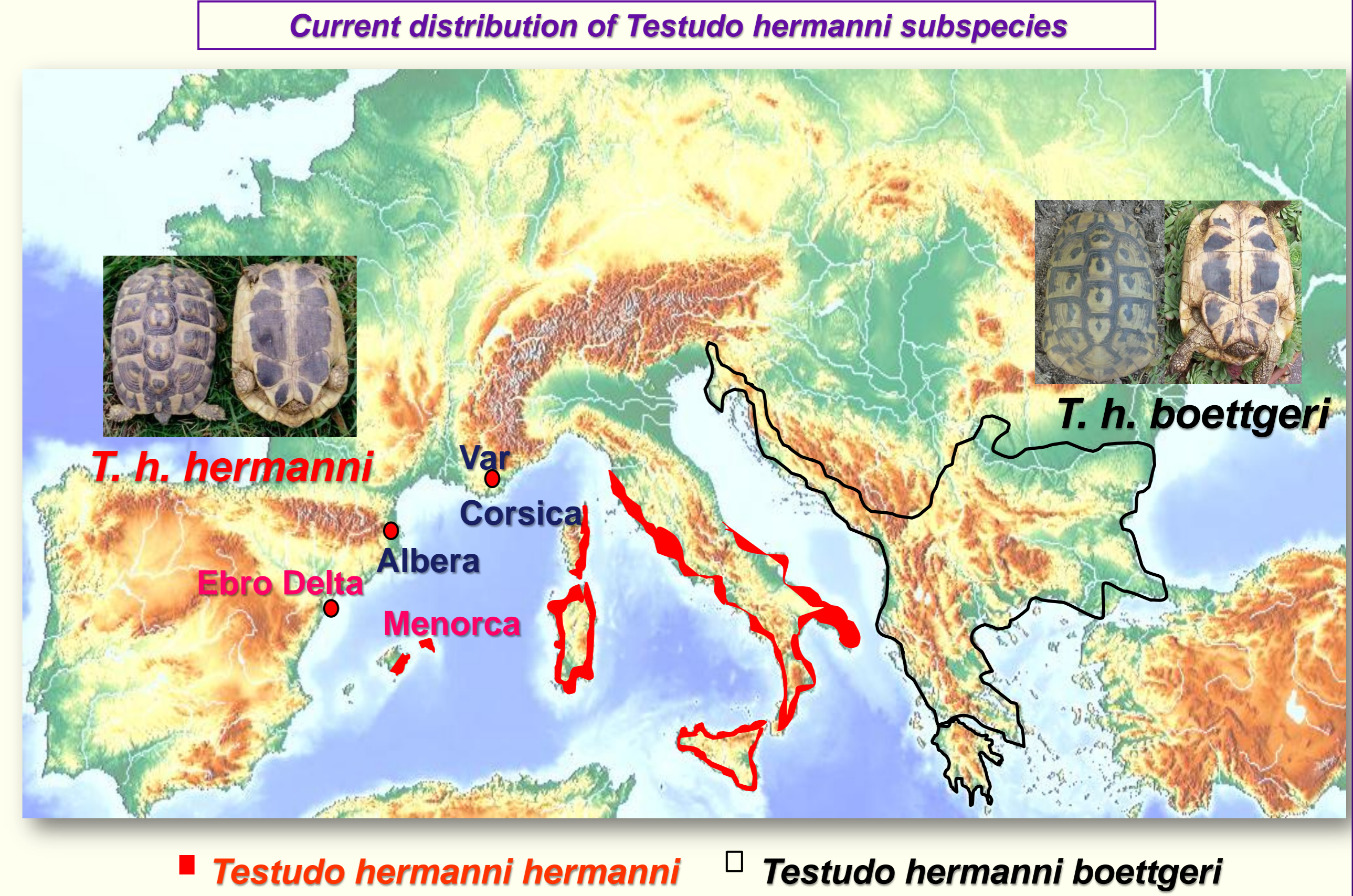
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1. Scientific context

❖ The Hermann's tortoise *Testudo hermanni* is endemic to southern Europe. It's vulnerable and highly threatened by human activity (habitat destruction, poaching, etc.).

❖ Two subspecies (see distribution map) were defined by morphology and genetically confirmed on the basis of the cytochrome b sequences.

❖ 19 microsatellite loci, obtained by pyrosequencing, were used to better understand the structure of several Hermann's tortoise populations in the occidental Mediterranean basin.

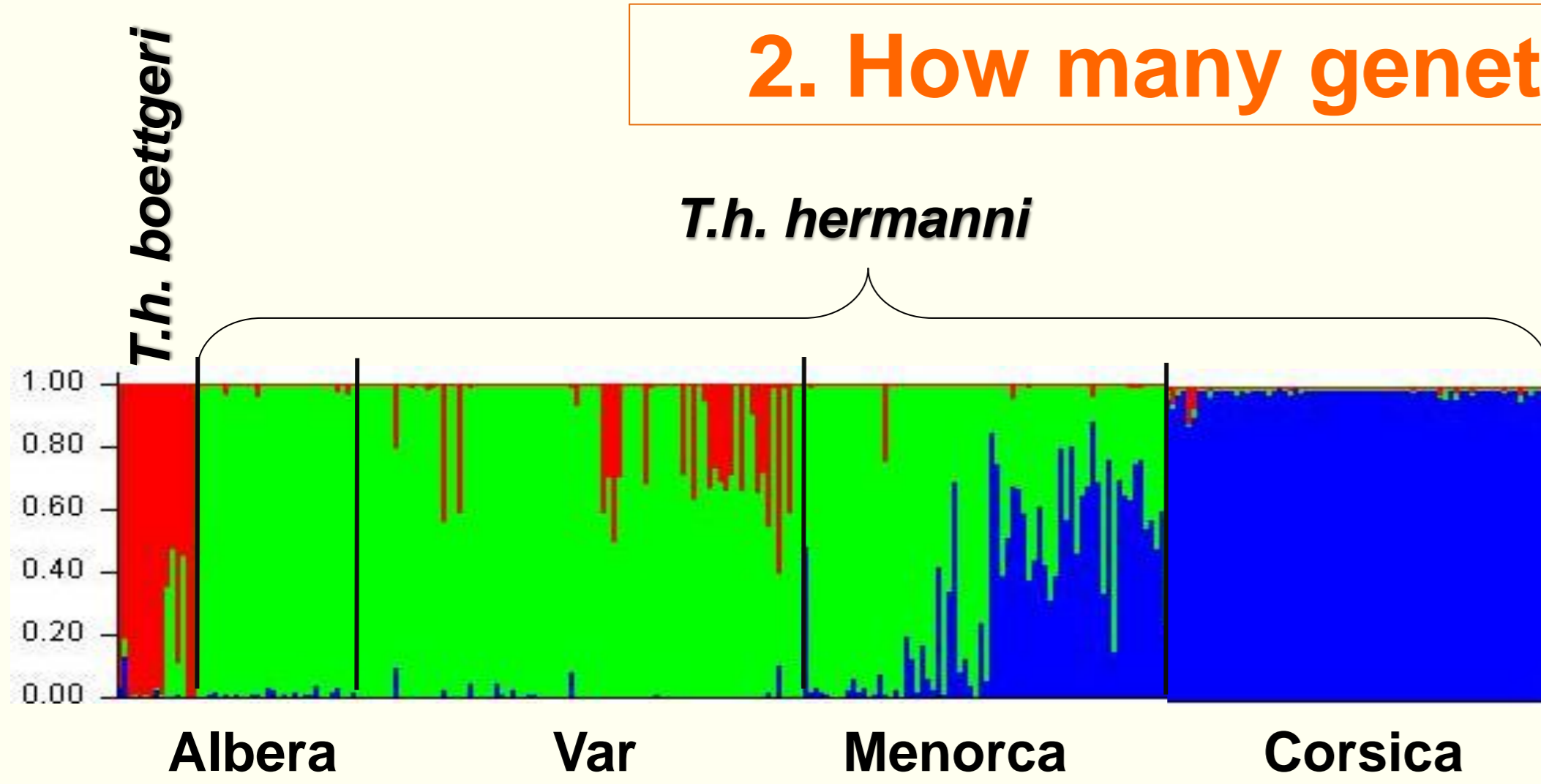


Our study focused on the genetic structure and diversity of the western subspecies

Testudo hermanni hermanni populations from five geographic regions:

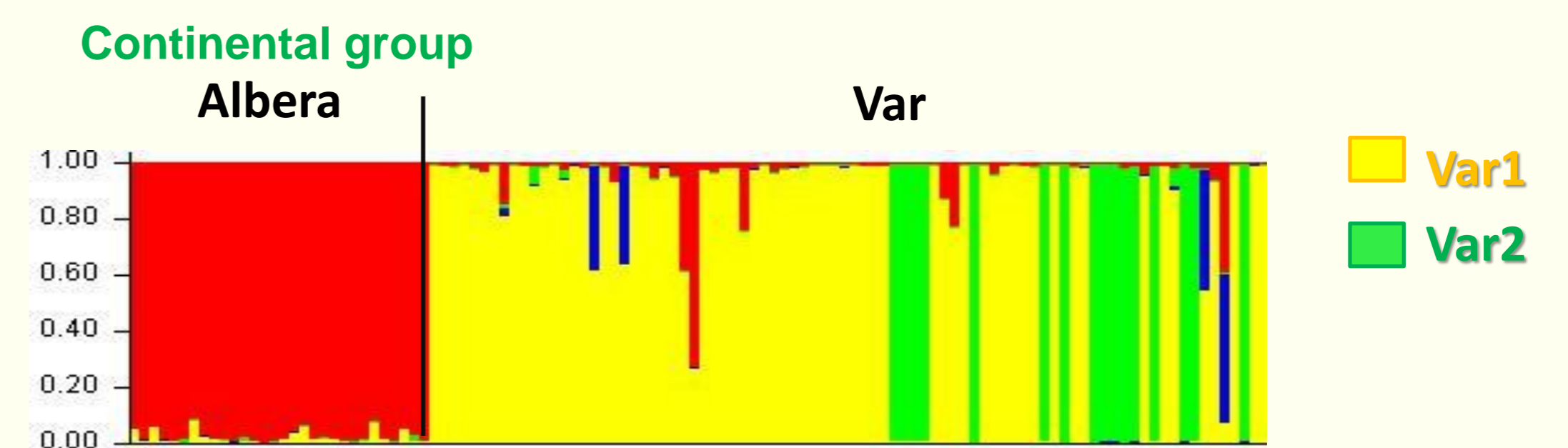
Three native populations : Var, Albera and Corsica / Two introduced populations : Menorca and Ebro Delta

2. How many genetic groups within the *Testudo hermanni* complex?

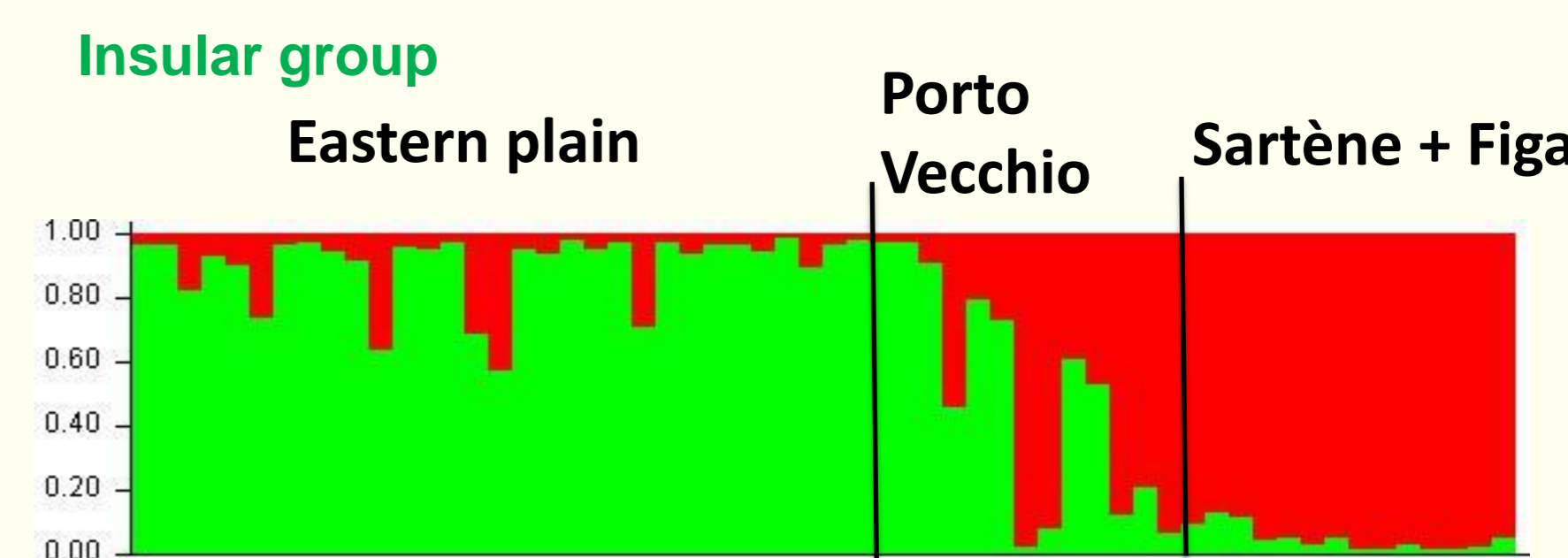


❖ Bayesian individual assignment approach implemented in STRUCTURE clearly distinguished the two subspecies *T. h. hermanni* and *T. h. boettgeri*. Two groups are also evidenced within *T. h. hermanni*: One continental group : Var, Albera, Menorca and one insular group : Corsica, Menorca and Ebro Delta

❖ The analysis revealed that several individuals from the Var (in green and red) are introgressed by alleles of the *T. h. boettgeri* subspecies

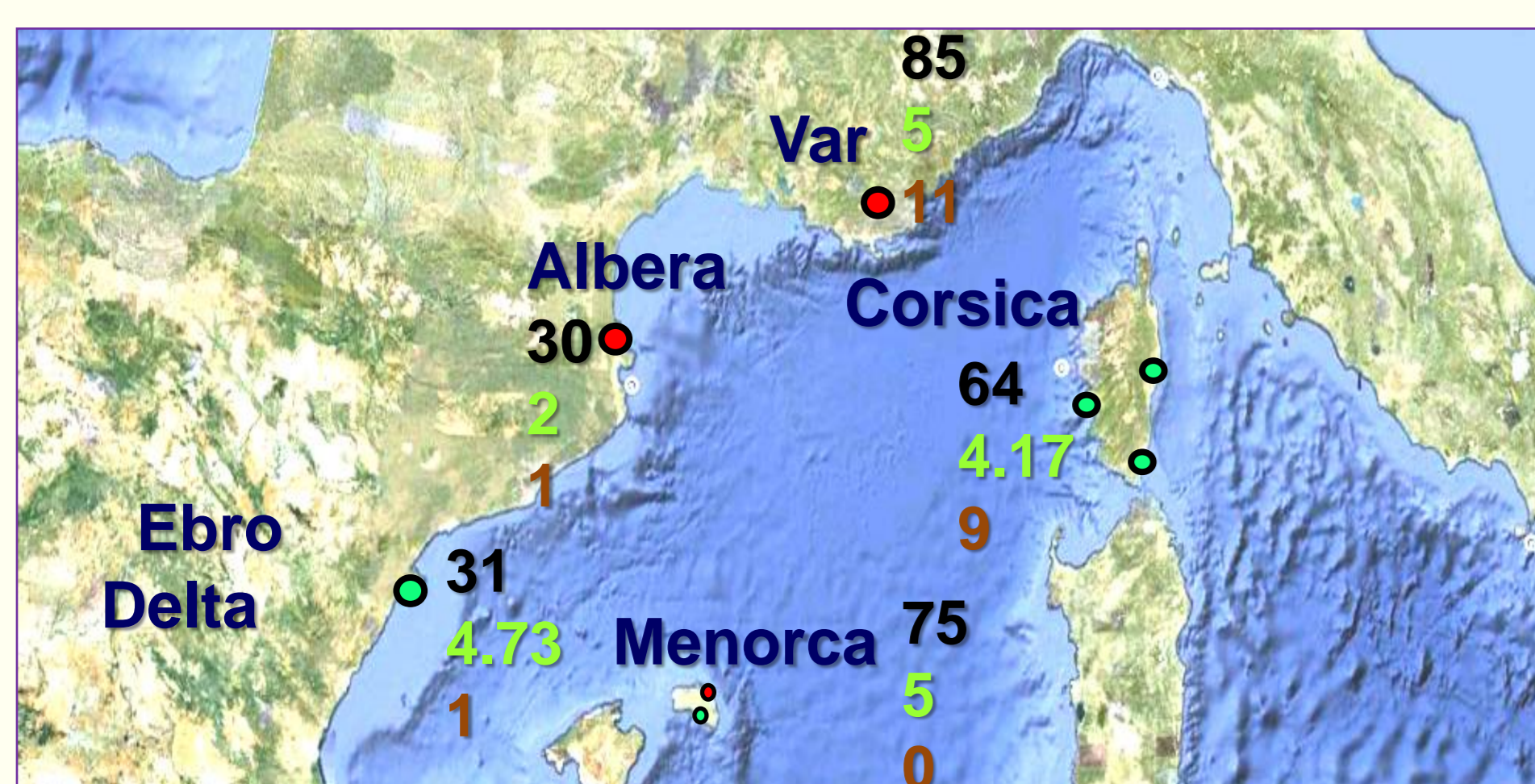


❖ The Albera population appeared to be homogeneous, whereas in the Var, the analysis revealed the existence of two genetic entities



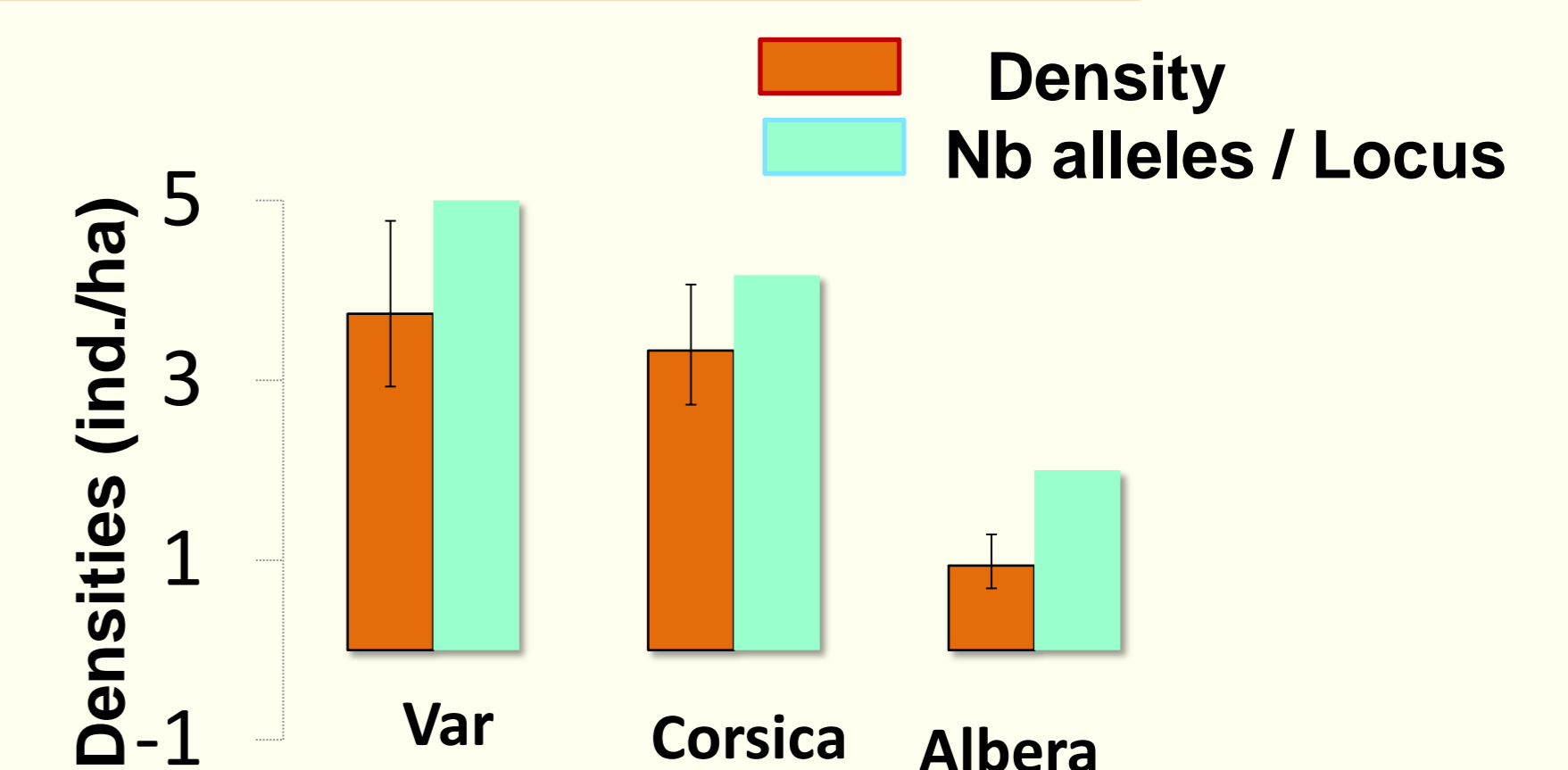
❖ A sub-population structure in two groups was also evidenced for Corsican population

3. What is the level of genetic diversity of *T. hermanni hermanni*'s populations ?



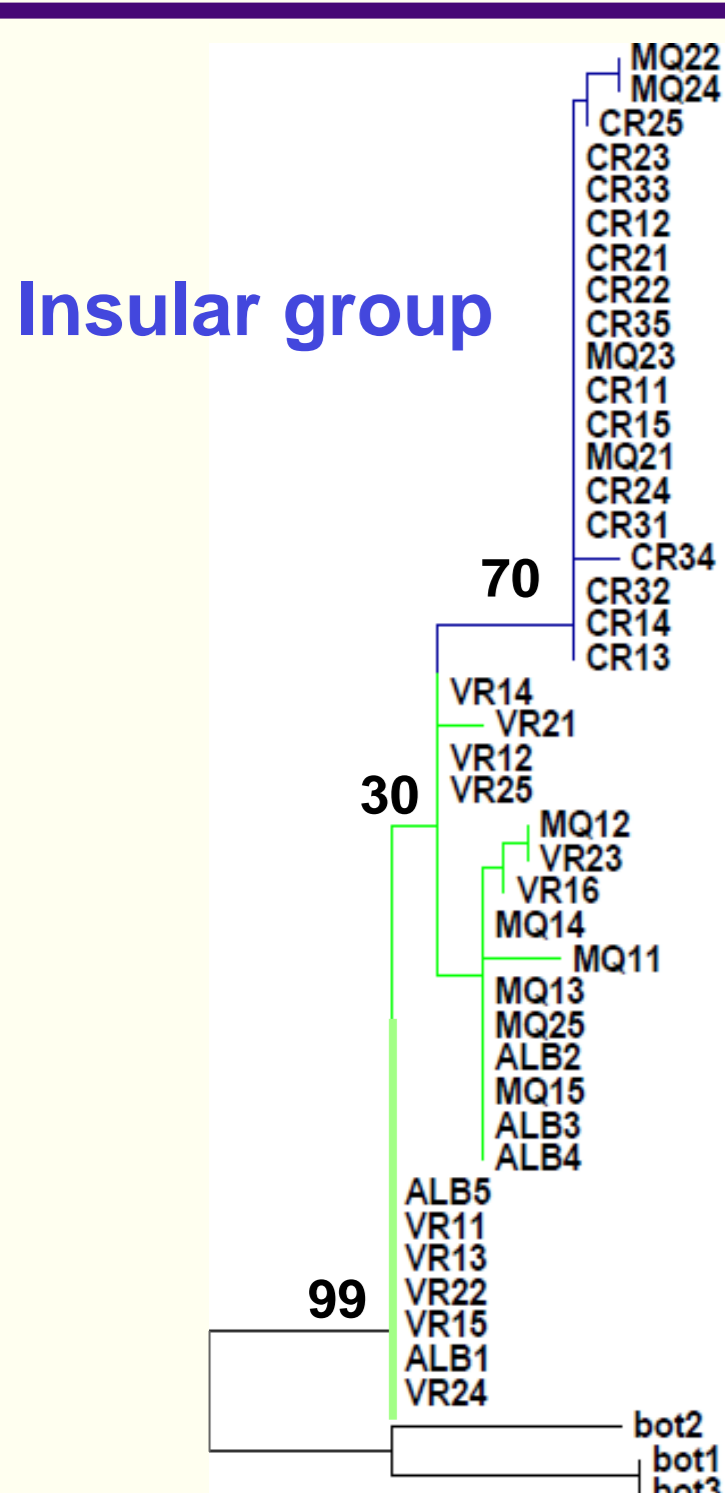
❖ Allelic richness is similar between introduced (Menorca, Ebro delta) and autochthonous (Albera, Var) populations.

❖ The number of private alleles is important for the populations of the Var and Corsica but low for other populations (Albera, Ebro Delta, Menorca).



❖ The Albera population displayed some signs of decline : a weak density and a low allelic richness.

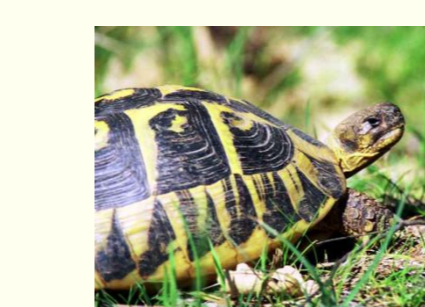
4. Phylogenetic analysis



phylogram based on the concatenation (3462bp) of two mitochondrial (cytochrome b and ND4) and one nuclear (R35) genes. Numbers at nodes represent, bootstrap proportion obtained in Maximum Likelihood (PhyML).

Autochthonous continental and insular populations are included in two separate and strongly supported clades whereas individuals from Menorca and Ebro delta are found in the two groups.

5. Conclusion and Perspectives



❖ The subspecies *T. h. hermanni* appeared structured in two major lineages that are evidenced both by mitochondrial (sequences) and nuclear (microsatellites) markers. One group includes continental populations (Var, Albera) and the second one is insular (Corsica) whereas the two lineages are found on the Menorca island. This result will have to be confirmed in including samples from Italy (continent, Sardinia and Sicily).

❖ Interestingly, our results indicate that introduced populations (Menorca, Ebro delta) do not show a significant reduction of variability (excepted the number of private alleles). On the other hand, the Albera population shows a significant decrease in genetic diversity and thus likely a reduced ability of adaptation.

❖ Concerning conservation issues, our results indicate that each autochthonous population (Albera, Var, Corsica) constitutes at least one original conservation units. However, more samples have to be analyzed to better defined subpopulations and their genetic relatedness to make possible reintroduction programs.