Genetic structure and gene flow analysis in the Italian wall lizard *Podarcis siculus* revealed a discordant pattern between mitochondrial and microsatellite markers in southern Italy

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INTRODUCTION

The genetic variability within a species is well known to be driven by a combination of historical process as well as more recent demographic dynamics which may lead to gene flow upon secondary contact. Recent phylogeographic studies of the Italian wall lizard *Podarcis siculus* (1,2), based on mitochondrial and nuclear genes, revealed a complex evolutionary history suggesting that long-term fragmentation and pre-LGM events such as glacial persistence were crucial in molding genetic variability in this temperate species.

TARGET SPECIES

The Italian wall lizard *Podarcis siculus* (Rafinesque-Schmaltz, 1810)

- Endemic of circum mediterrean region
- High ecological tolerance and adattability
- Strong morphological variation

AIMS

- Investigate the genetic variability and the genetic structure of *P. siculus* using 11 microsatellite loci.
- Quantify the presence of gene flow among lineages.
- Compare and discuss the results from microsatellite loci with those previously obtained using mitochondrial sequences.

MATERIALS AND METHODS

355 individuals from 113 locality of *P. siculus* from the Italian Peninsula, have been genotyped at 11 microsatellite loci.
The genetic structure has been investigated using the software STRUCTURE (3) and by calculating F-statistics indices.
To quantify the presence of gene flow among lineages we used the software migrate-n (4). The generated full parameterized model has been then tested through Bayes factor against two different models of gene flow (phylogenetic vs geographic).

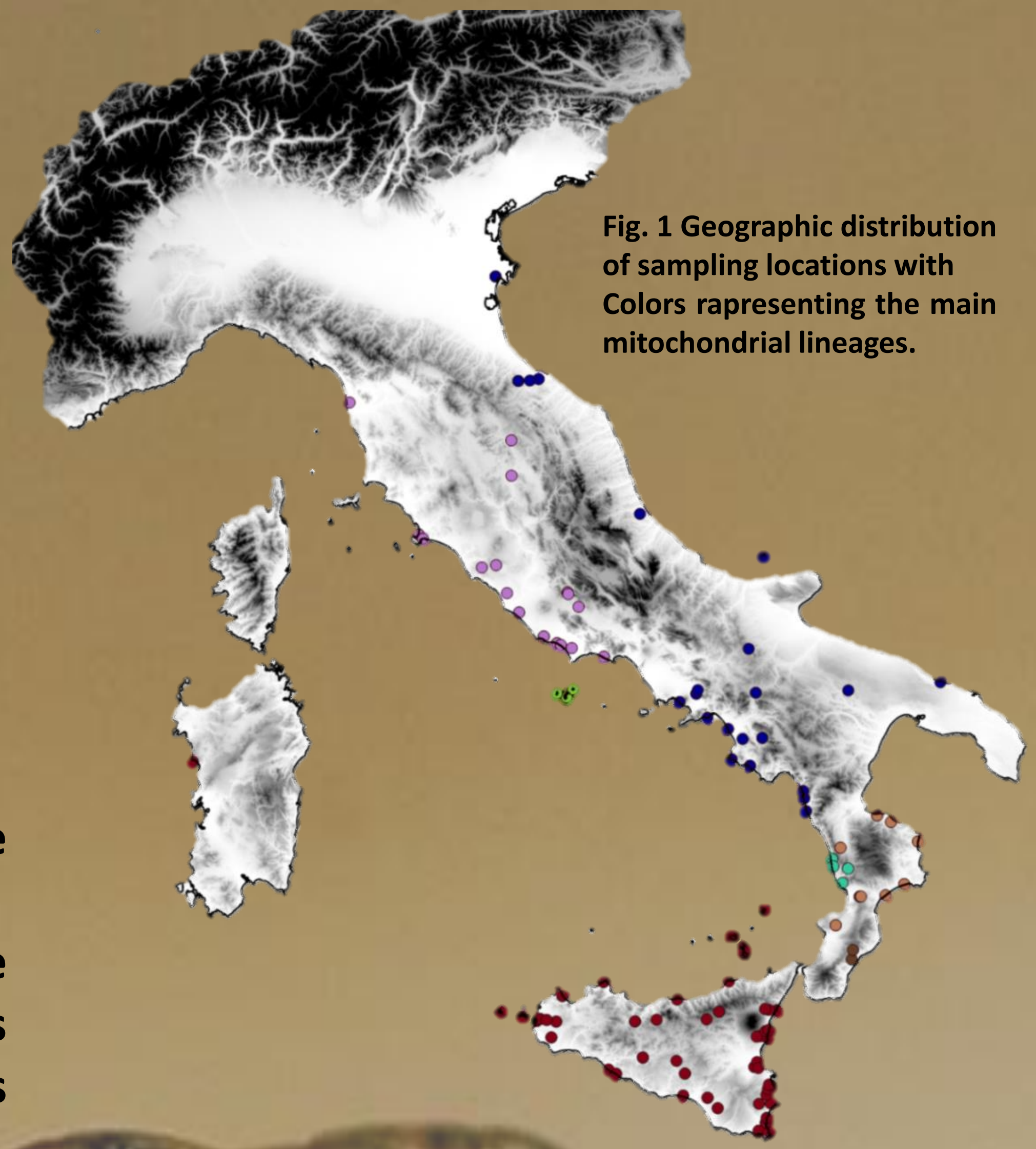

Fig. 1 Geographic distribution of sampling locations with Colors rapresenting the main mitochondrial lineages.

RESULTS

The software STRUCTURE supported the presence of five microsatellite clusters partially confirming the mitochondrial repartition in seven parapatric clades. The migrate-n analysis revealed the presence of high level gene flow among the calabrian lineages while returning low level of gene flow among the other lineages. Finally, the Bayes factor calculation indicated the geographic model of gene flow as the most reliable scenario of gene exchange.

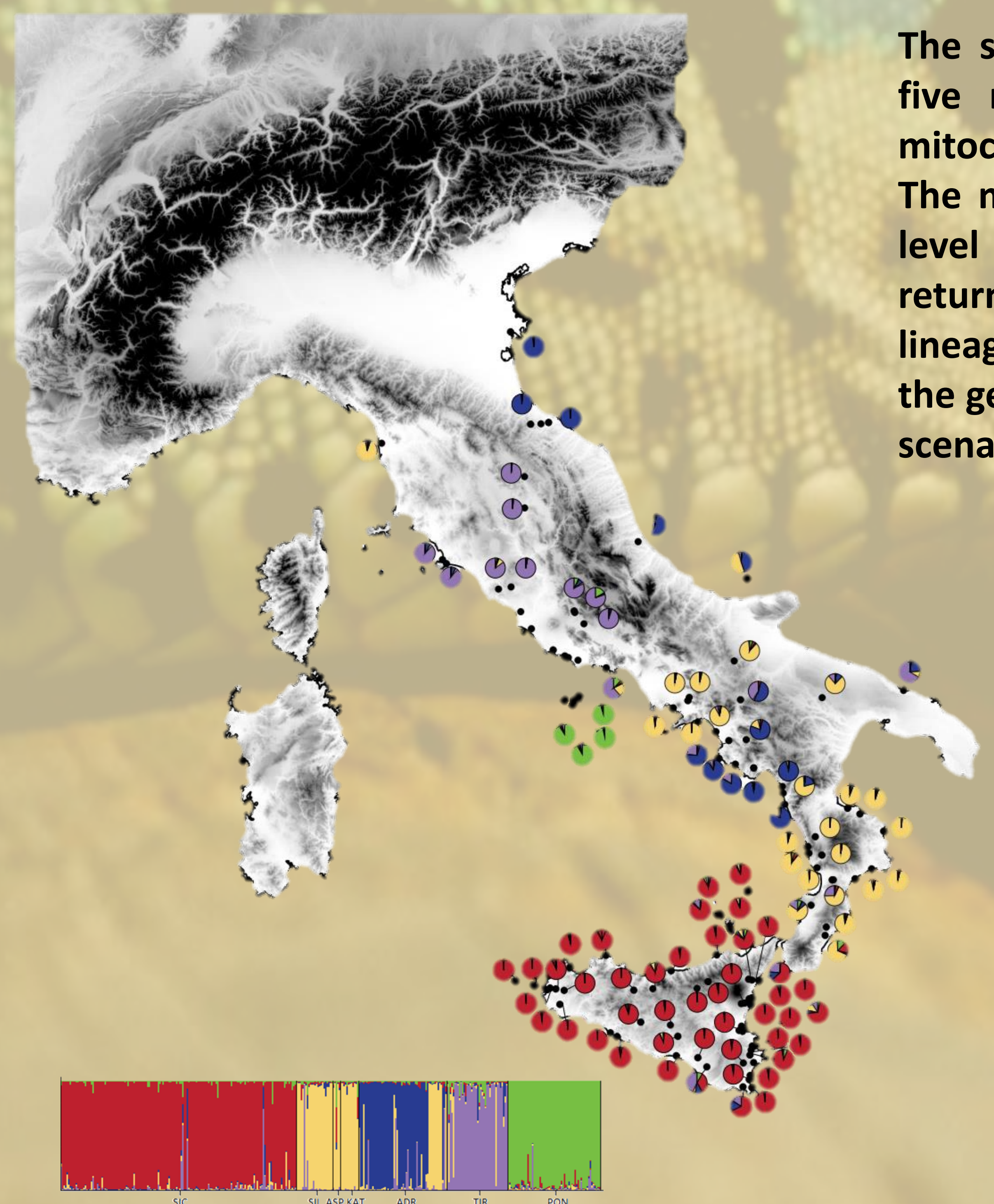

Fig.2 Genetic structure based on 11 microsatellite loci

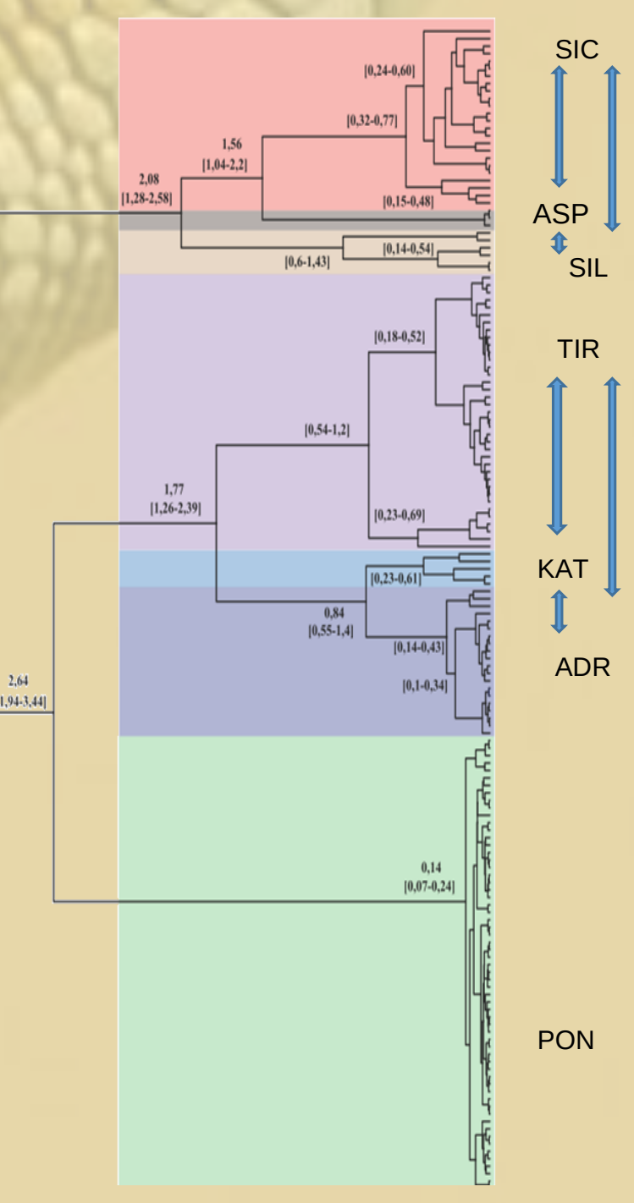

Fig. 3 Phylogenetic model

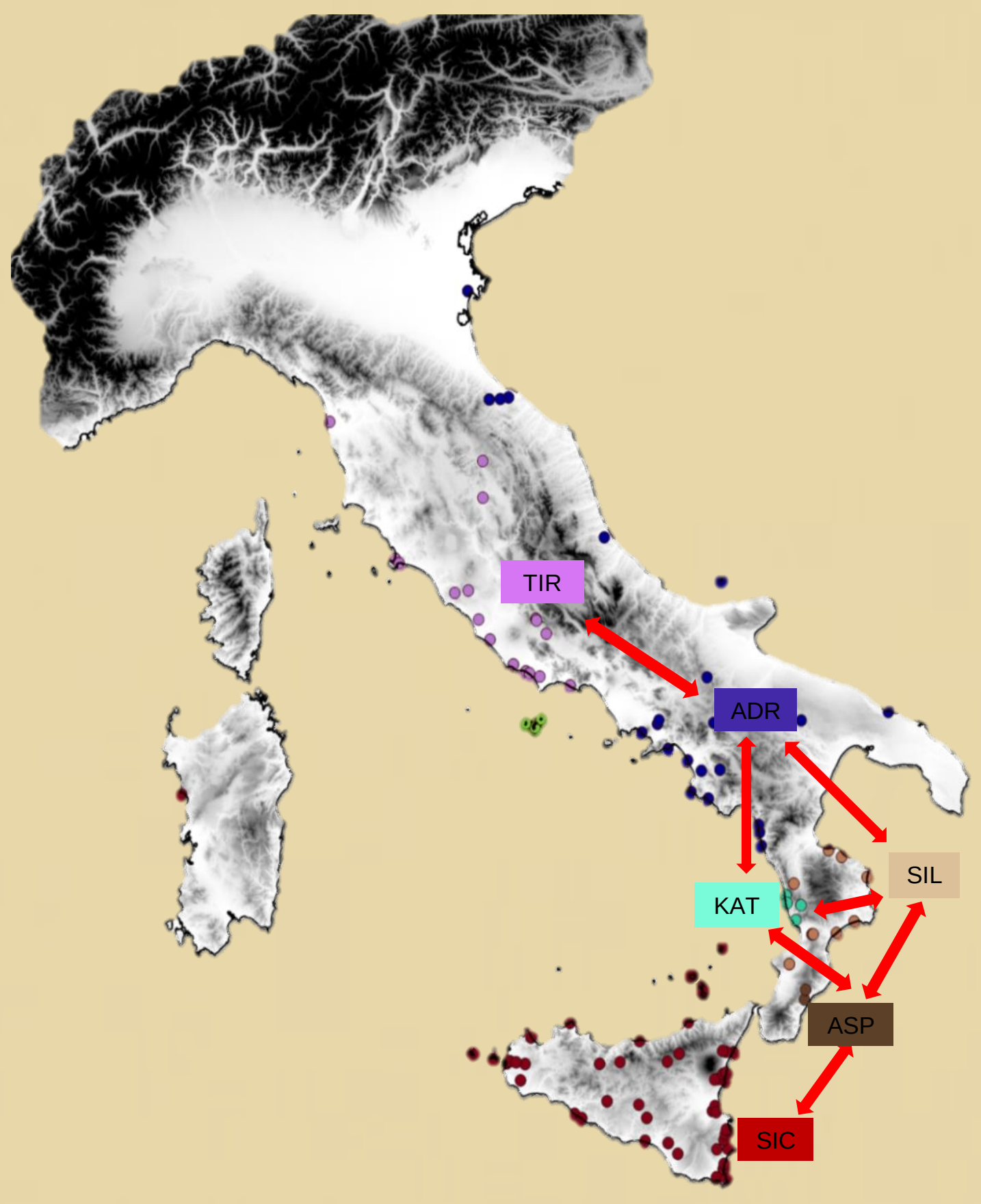

Fig. 4 Geographic model

DISCUSSION

The conforming pattern among mitochondrial and microsatellite markers detected for most of the lineages (Sicilian, Adriatic, Tyrrhenian and Pontine), underlies an active role of the principal geographic barriers in maintaining the current genetic structure.
However, the Calabrian region shows only one microsatellite cluster, rather than the three identified by mtDNA (Sila, Aspromonte, Catena costiera). Such a result was also supported by higher level of gene flow in this region, suggesting the importance of the Calabrian arc setting in promoting the formation of secondary contact zones and gene exchange among lineages.

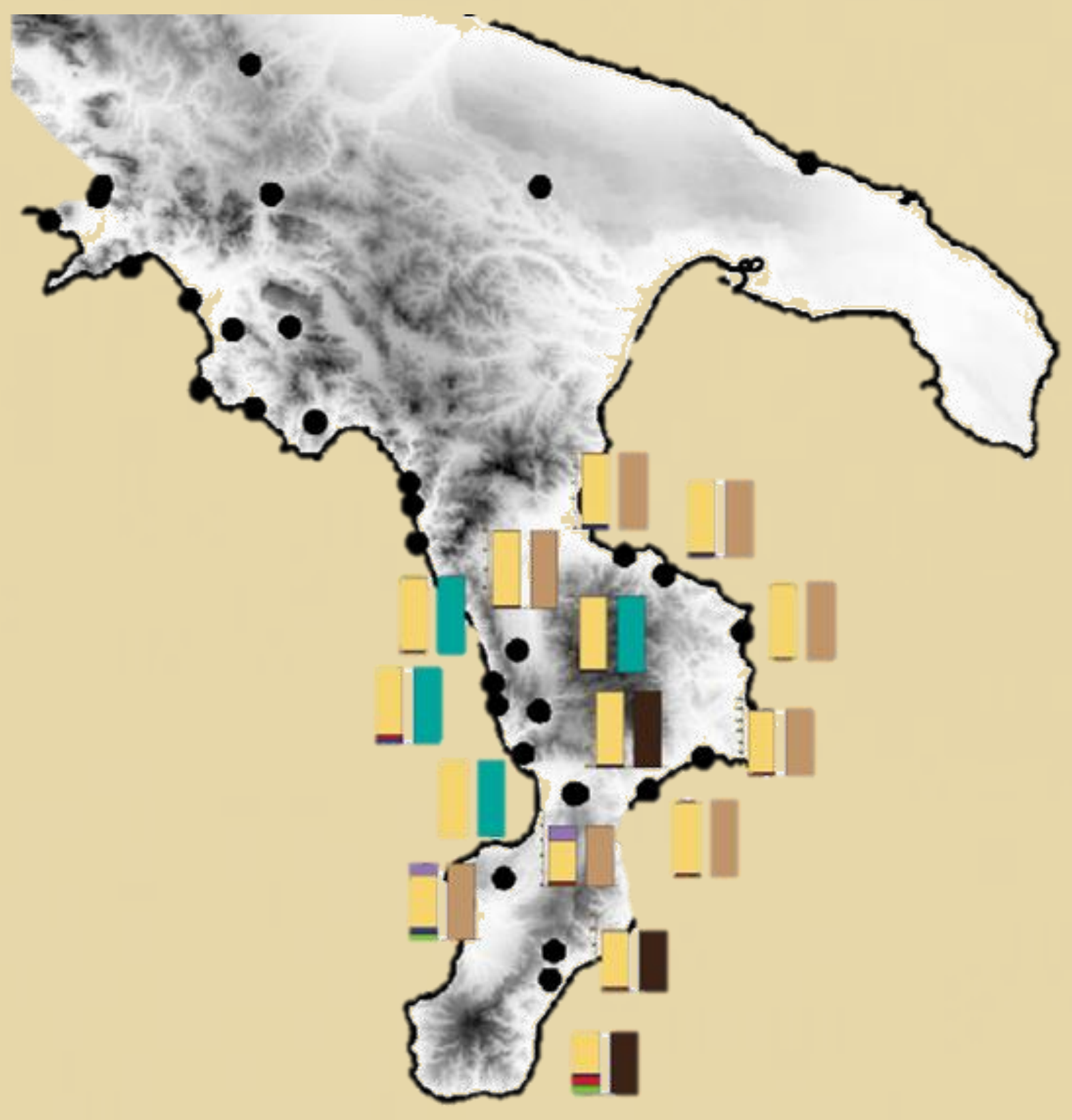

Fig. 6 Comparison of mitochondrial and microsatellite allele frequencies for each Calabrian location

CONCLUSION

- The post-glacial expansions and the formation of secondary contact areas and gene flow, at regional scale, are important aspects at least as the Pleistocene differentiation processes in ensuring the genetic diversity of a species.
- Further studies on morphological and behavioral traits would be required to shed light into the origin of the observed mito-nuclear discordance in southern Italy.

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