Differential introgression between two Iberian *Podarcis* lizards

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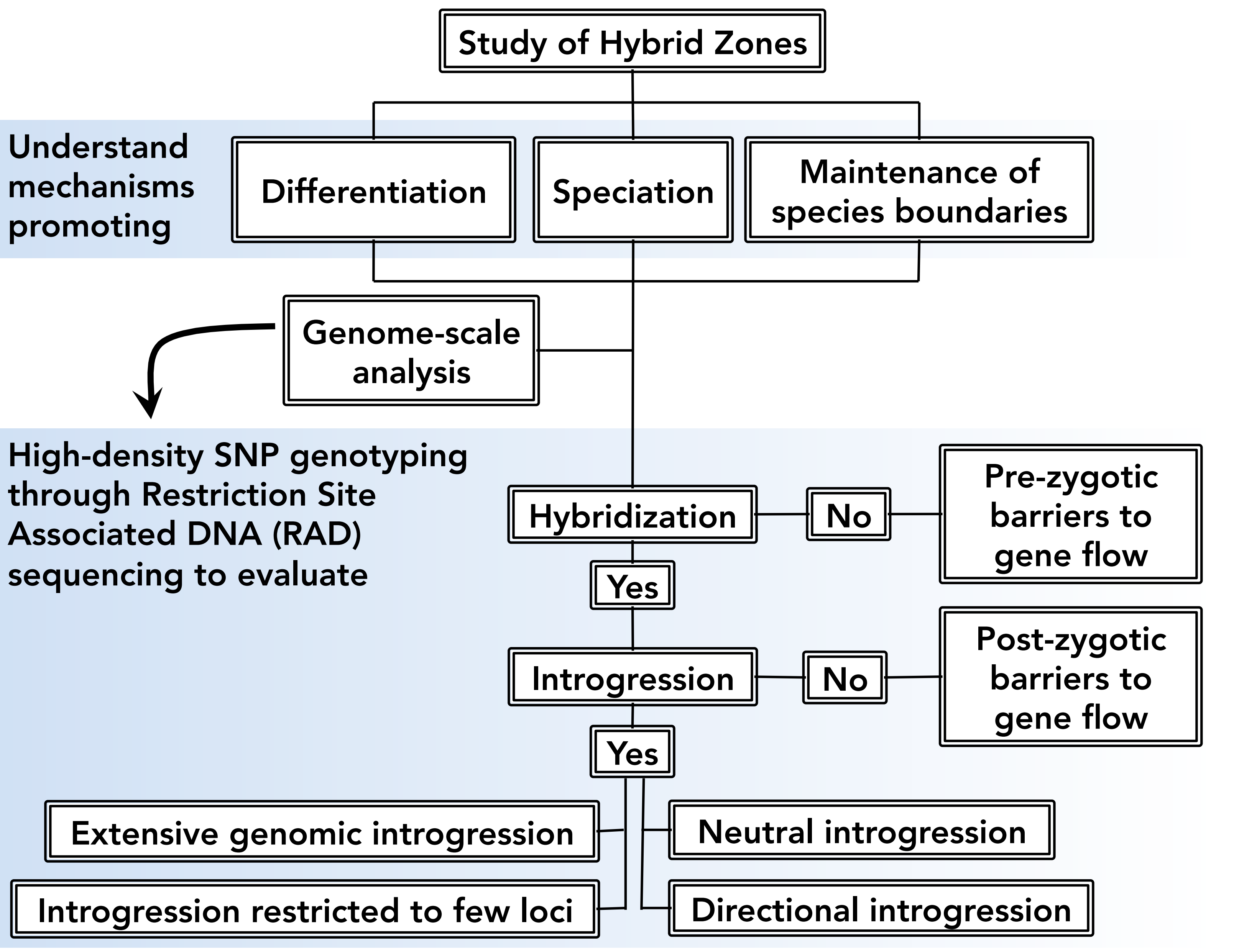
Background Information

- A narrow hybrid zone (HZ) is known between *Podarcis bocagei* (Pb) and *P. carbonelli* (Pc).
- Previous studies in this HZ show low hybridization, limited introgression for nearby populations, evidence for a bimodal hybrid zone [1,2] and no intermediate morphology [1,3,4].
- Few loci were used (<22).



Study of Hybrid Zones

Understand mechanisms promoting

Differentiation

Speciation

Maintenance of species boundaries

Genome-scale analysis

High-density SNP genotyping through Restriction Site Associated DNA (RAD) sequencing to evaluate

Hybridization – No – Pre-zygotic barriers to gene flow

Yes

Introgression – No – Post-zygotic barriers to gene flow

Yes

Extensive genomic introgression

Introgression restricted to few loci

Neutral introgression

Directional introgression

Objectives

- Are results similar to previous studies?
- Is hybridization introgressive?
- Similar introgression across genome?
- Which is the direction of introgression?
- Which kinds of selection are present?

Sampling and SNP data

- Double digestion RAD library construction with 330 individuals.
- Complete dataset with 6905 loci after demultiplexing and filtering.
- "Disgnostic" dataset with 2300 loci with frequency >0.8 in one parental and <0.2 in other.

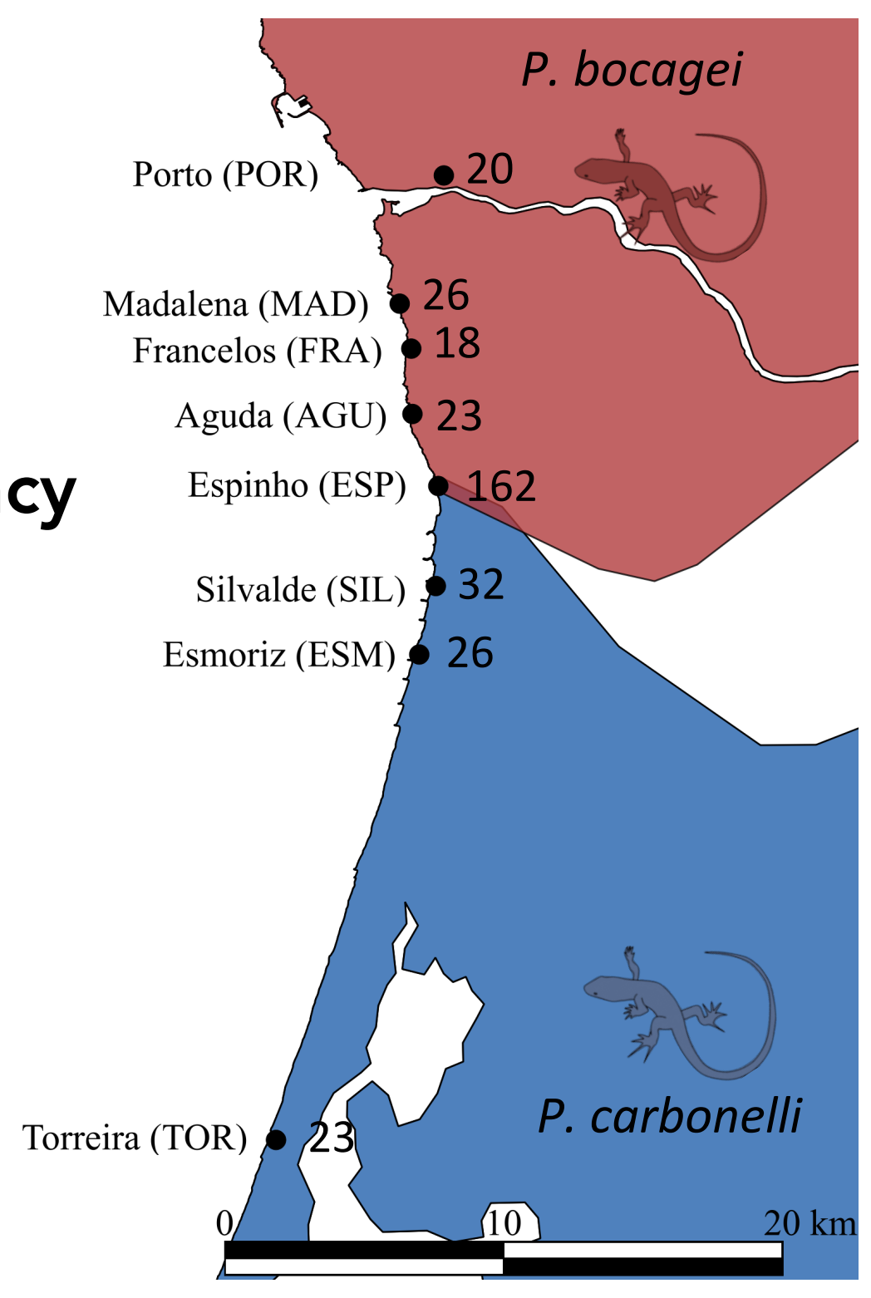
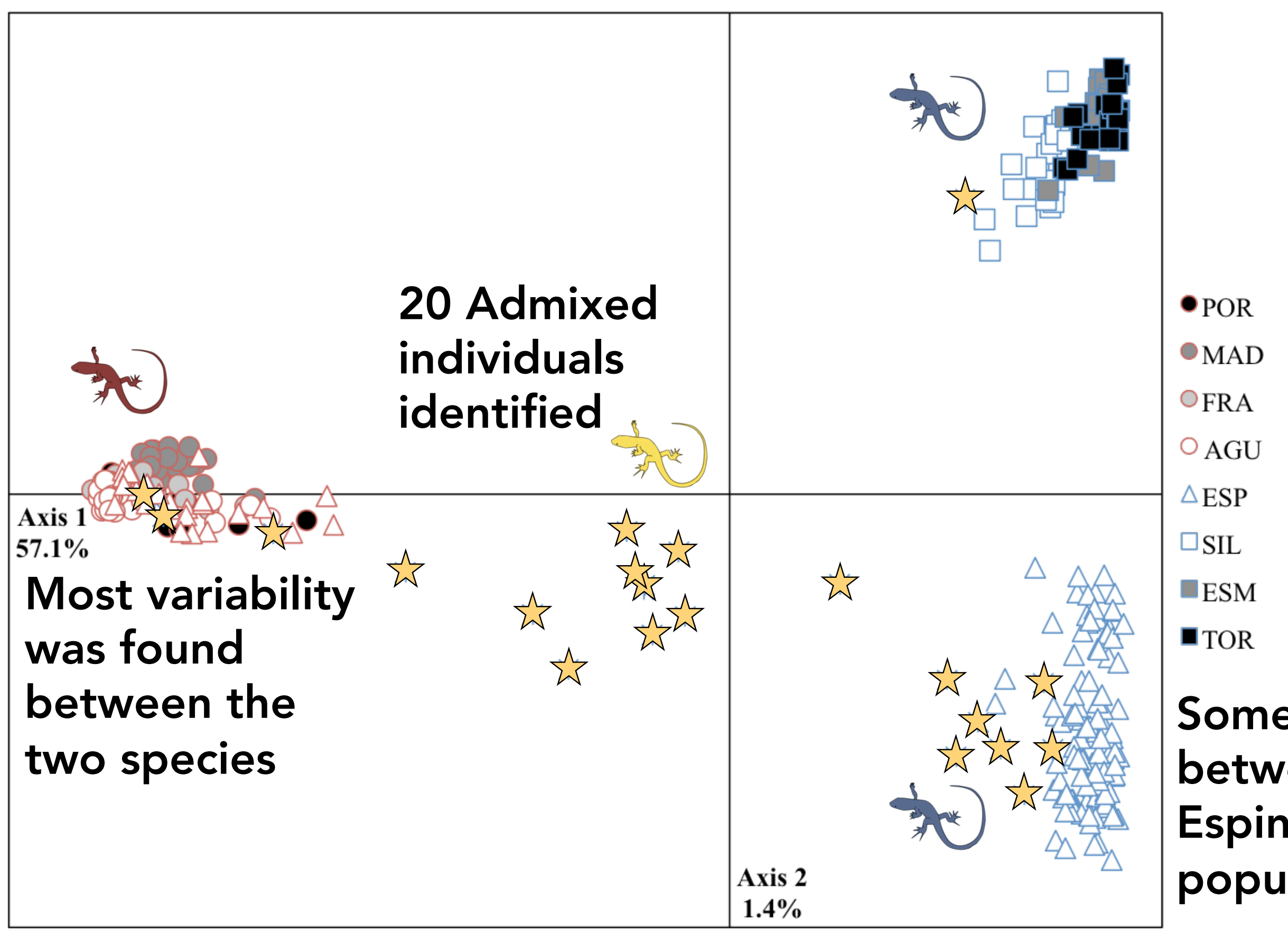


Fig. 1 – Species distribution in the study area and sampling location along the north-south transept with number of samples for each one.

Structure of the contact zone



20 Admixed individuals identified

Most variability was found between the two species

Some variability between Pc from Espinho and other Pc populations

Fig. 2 - Principal Component Analysis of 6906 SNP variation in the 330 individuals calculated with ADEGENET[5] R package. Circles represent individuals from populations north of the contact zone, triangles correspond to the individuals from the contact zone, squares identify the individuals from populations south of the contact zone and stars represent the admixed individuals identified with BAPS[6]. Population acronyms as in Fig. 1.

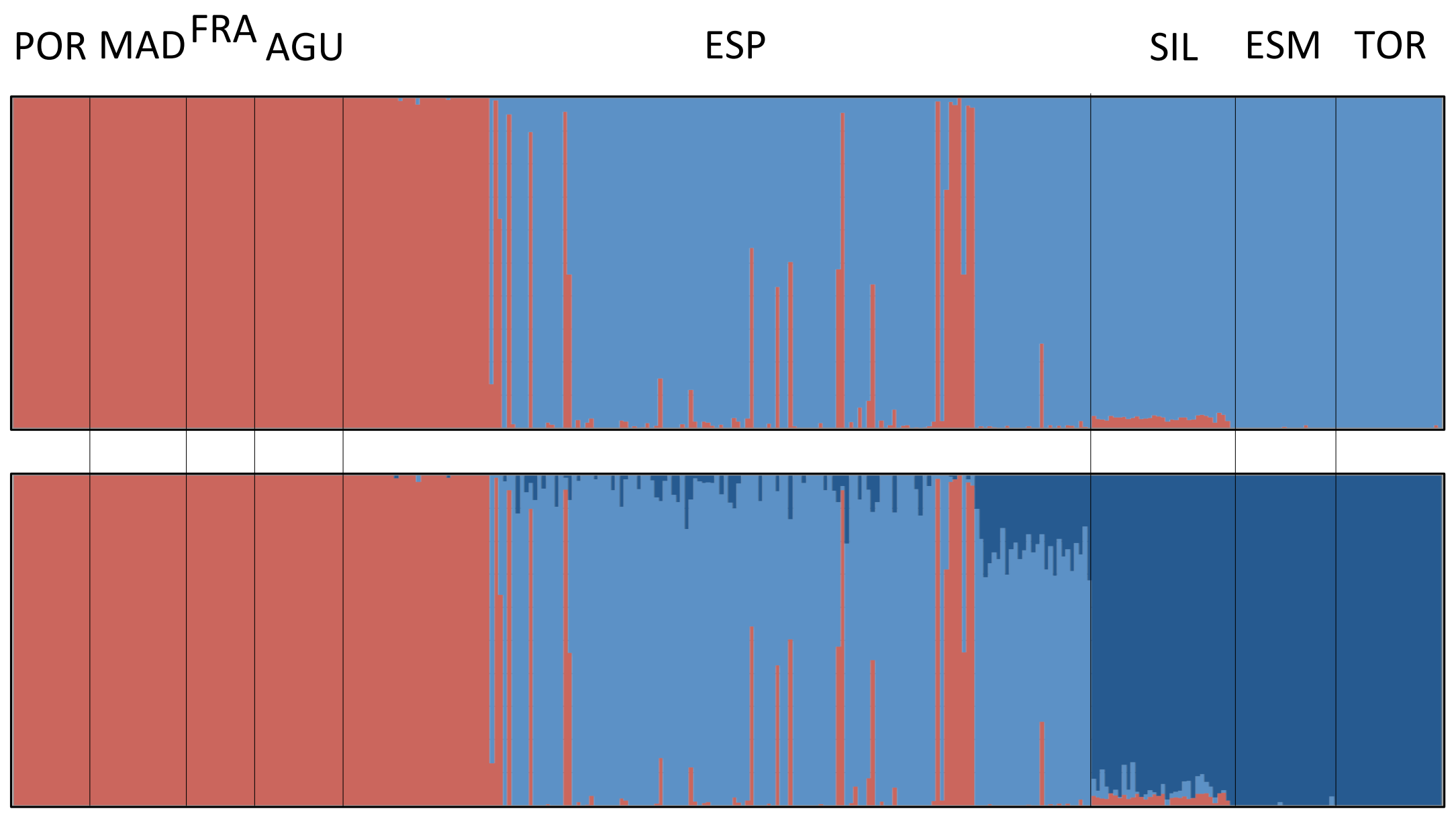
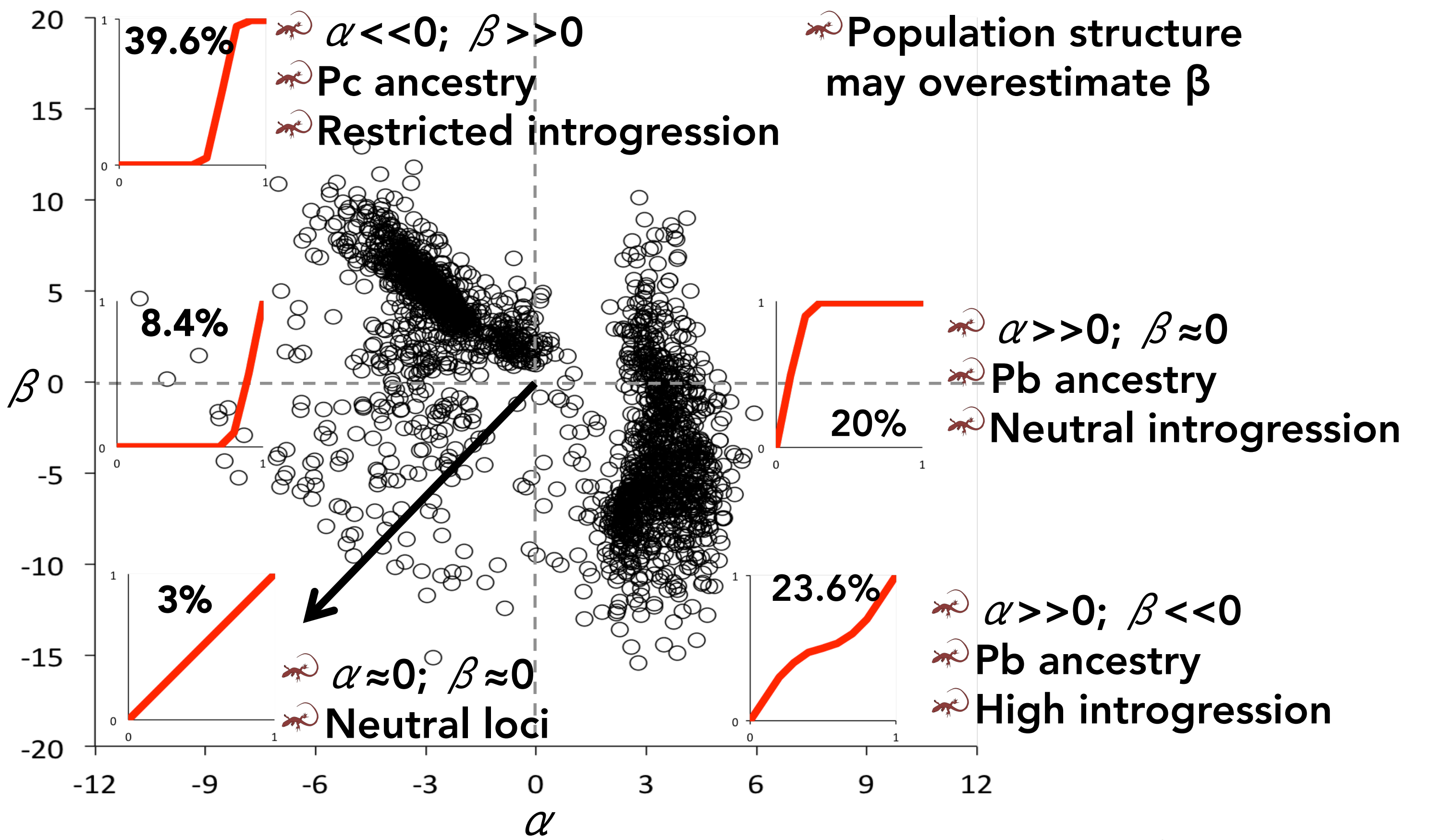


Fig. 3 - Results from individual multilocus genotype clustering computed with ADMIXTURE[7] for the 6905 loci. Similar results were obtained for both datasets and with BAPS. Each individual is represented by a vertical line proportionally partitioned into the K colored segments. Top chart represents K=2 and bottom chart K=3. Population acronyms as in Fig. 1.

Introgression

- Genomic cline parameters α: cline center (probability of ancestry); and β: introgression rate.
- Pb ancestry (α>>0) for 1031 loci (44.8%); Pc ancestry (PbA, α<<0) for 1148 loci (49.9%); 101 loci (4.4%) with no specific ancestry ($\alpha \approx 0$).
- 960 loci (41.7%) shown restricted introgression (β>>0), 619 loci (26.9%) with increased introgression (β<<0) and 721 loci (31.3%) followed the neutral expectations ($\beta \approx 0$).
- No outlier loci were detected for both α and β.



- α<<0; β>>0
- Pc ancestry
- Restricted introgression

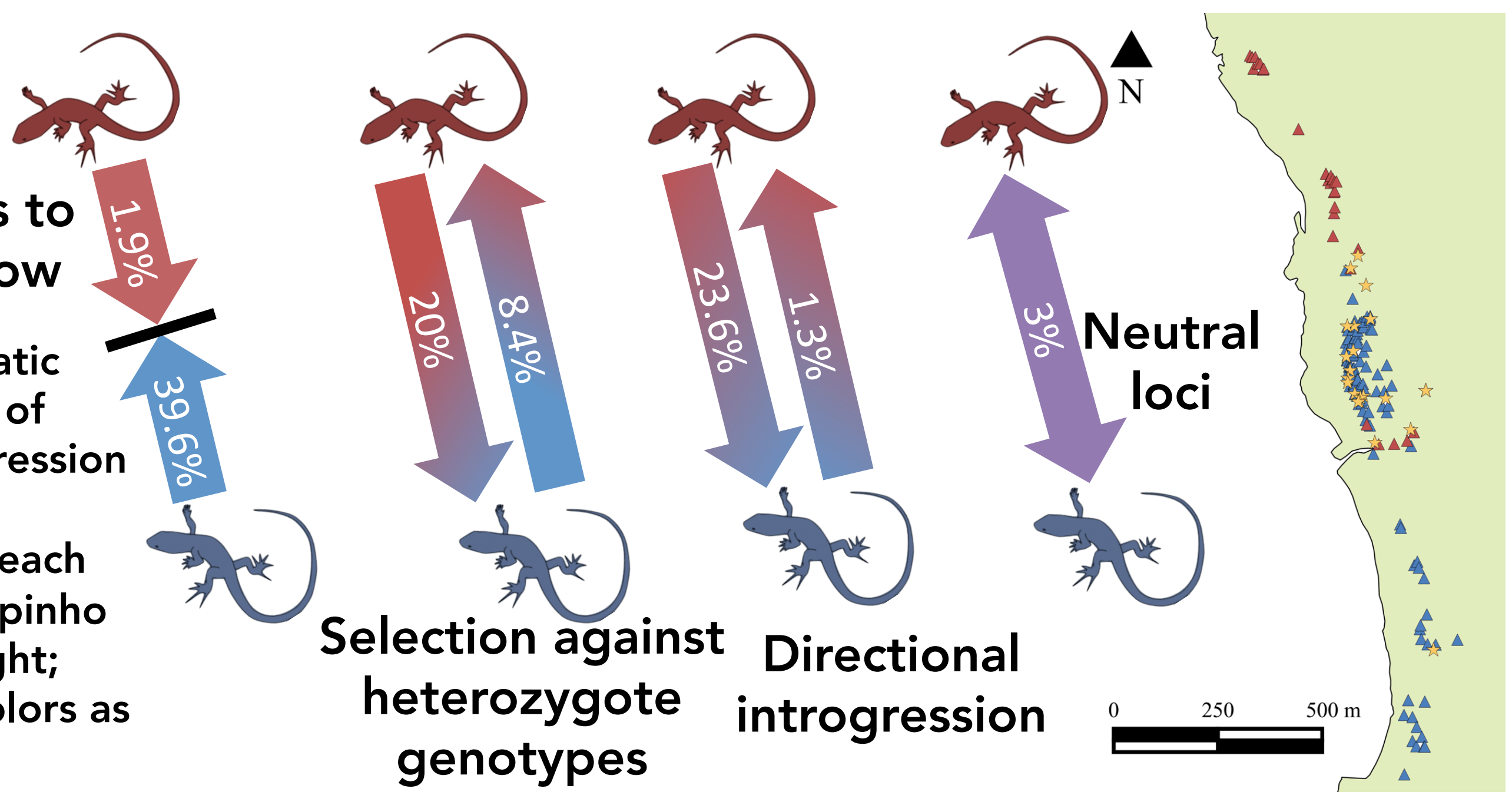
- Population structure may overestimate β

- α>>0; $\beta \approx 0$
- Pb ancestry
- Neutral introgression

- $\alpha \approx 0$; $\beta \approx 0$
- Neutral loci

- α>>0; β<<0
- Pb ancestry
- High introgression

Fig. 4 – Variable introgression between Pb and Pc based on α and β computed with BGC[8]. Each circle represents one of the 2300 loci. Main genomic clines representative of loci in the corresponding region of the $\alpha - \beta$ parameter space are shown in red.



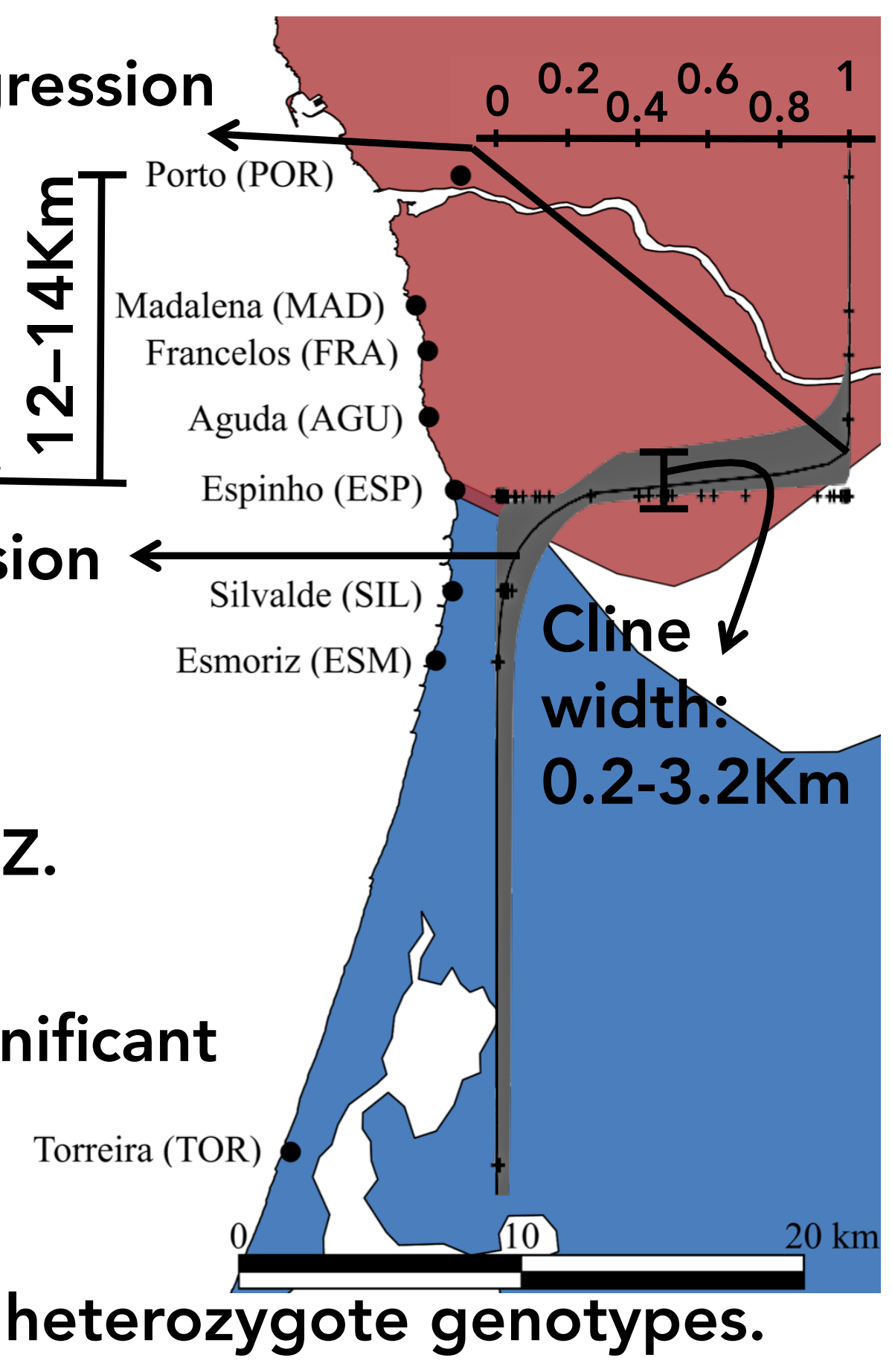
Barriers to gene flow

Selection against heterozygote genotypes

Directional introgression

Neutral loci

Fig. 5 – Schematic representation of variable introgression (arrows) and distribution of each individual in Espinho (map on the right; symbols and colors as Fig. 2).



Almost no introgression tail to north

Cline center

0.08–3.2Km introgression tail to south

Cline width: 0.2-3.2Km

Fig. 6 – Species distribution map with HZAR[9] geographic cline represented. ADMIXTURE assignments for both SNP dataset were used as hybrid index (HI) leading to similar results. Top bar represents HI.

Main Conclusions

- Are results similar to previous studies?
  Yes: Bimodal HZ; No: Structure detected in HZ.
- Is hybridization introgressive? Yes.
- Similar introgression across genome? No; Significant nr of loci involved in reproductive isolation.
- Direction of introgression? Mostly Pb ➔ Pc.
- Kinds of selection present? Selection against heterozygote genotypes.

Ongoing Work

- Estimate geographic cline for each loci to compare with genomic clines.

Literature cited

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Host institutions

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