Application of biophysical factors and molecular markers to explain spatial genetic structure in strawberry tree using GIS tools

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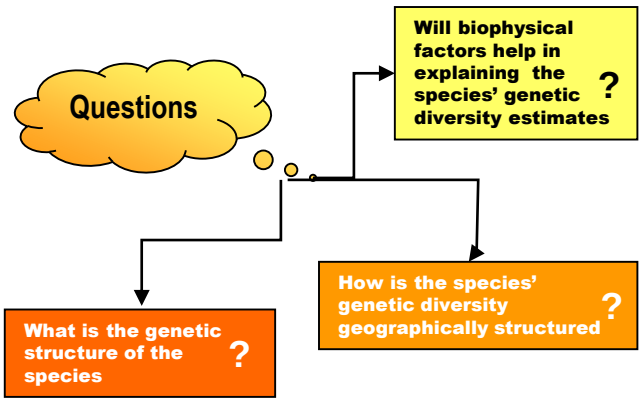
PURPOSE OF THE STUDY



MATERIAL AND METHODS

- 15 natural populations ▲ and 30 ind./pop.
- 4 maternally inherited cpSSRs
- Genetic differentiation among populations estimated by R_{ST} and G_{ST}
- Populations clustering using a Bayesian approach and stand coordinates: BAPS
- Biophysical and genetic diversity data were analyzed using XLSTAT to built the PCA

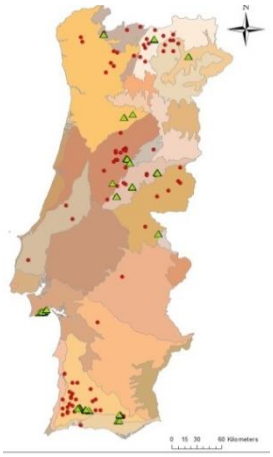


Fig. 1. Natural populations (green triangles) and natural stands recorded in the Forest Inventory 2006 (red dots).

RESULTS

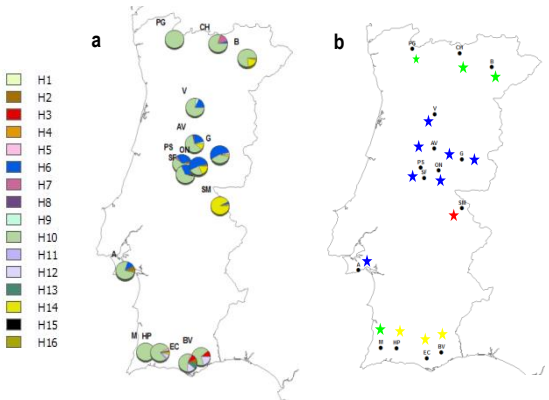


Fig 3. Distribution of 16 haplotypes in populations. The numbers indicate the code of the haplotype (a). Populations clustering with cpSSR data and stands coordinates using BAPS, a Bayesian approach (b).

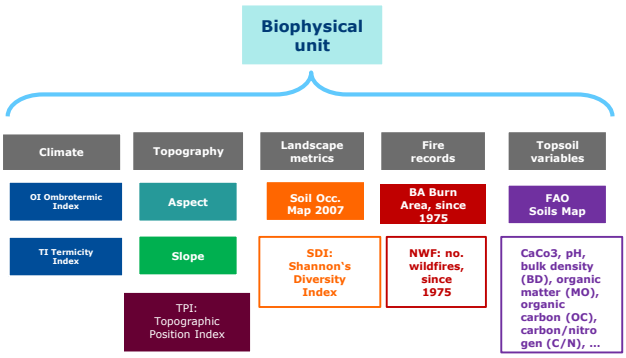


Fig. 2 Biophysical variables were studied using GIS (Geographic Information Systems) in the biophysical unit = the area spanning 1 km from each one of the 30 stand trees.

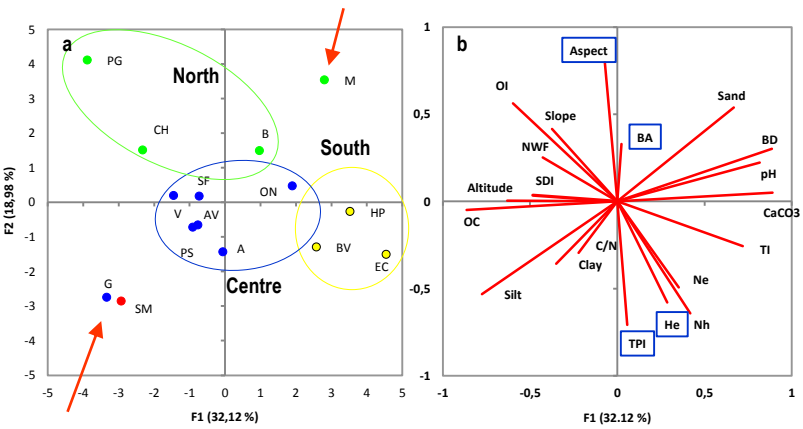


Fig 4. Principal component analysis (PCA) performed with the biophysical factors, see Fig. 2 for label details, and genetic diversity estimates (He = haplotypic diversity, Nh = no. of haplotypes, Ne = effective no. of haplotypes). The observations (populations) (a) and the variables (b). Red arrows point at putative outliers. The total of the variance explained with F1 and F2 is 51,1%.

TAKE HOME

A high among population differentiation was observed (G_{ST}=28.8%) and even a stronger R_{ST} (54.8%) value was found, indicating a strong geographical structure, due, probably, to low gene flow through pollen.

A clear clustering in 3 groups was untangled by the Bayesian analysis (Fig 3b) and also supported both by the distribution of the haplotypes (Fig. 3a) and the PCA observations' projection (Fig. 4a): the Northern, the Central and the Southern populations

One outlier is clear in Fig 3b with a red star: the SM population, with an haplotypic pattern clearly different from all the others (Fig 3a), and a low He value (13%). Two other populations have probably experienced a bottleneck effect due to the impact of wildfires: PG and M. Indeed they have He=0 and only one haplotype.

The genetic diversity estimates (He, Nh and Ne) are inversely correlated to the burn area (BA) and the Aspect, though the former is only partially explained by the 2nd factor (Fig 4b), and directly correlated with the TPI (a rugosity index). Future work will include the use of nuclear microsatellites to improve the power to identify the factors that are responsible for the observed spatial structuring of species' genetic diversity.

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