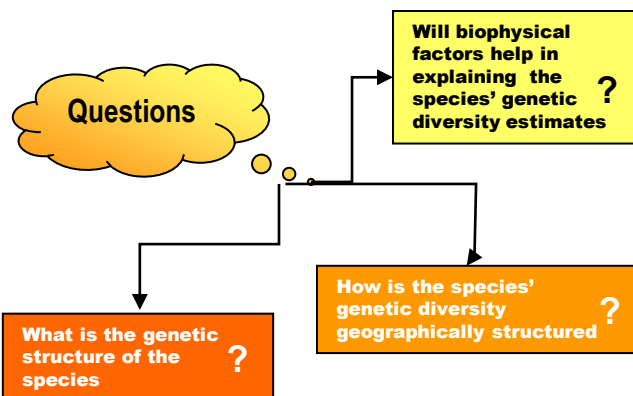


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## PURPOSE OF THE STUDY



## MATERIAL AND METHODS

- 15 natural populations (green triangles) and 30 ind./pop.
- 4 polymorphic maternally inherited cpSSRs
- Genetic differentiation among populations estimated by  $R_{ST}$  and  $G_{ST}$
- Populations clustering using a Bayesian approach: BAPS
- Biophysical and genetic diversity data were analyzed using XLSTAT to build the PCA

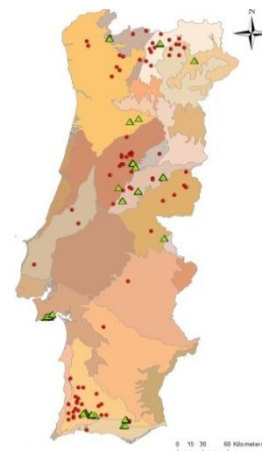


Fig. 1. Natural populations (green triangles) and natural stands recorded in the Forest Inventory 2006 (red dots).

## RESULTS

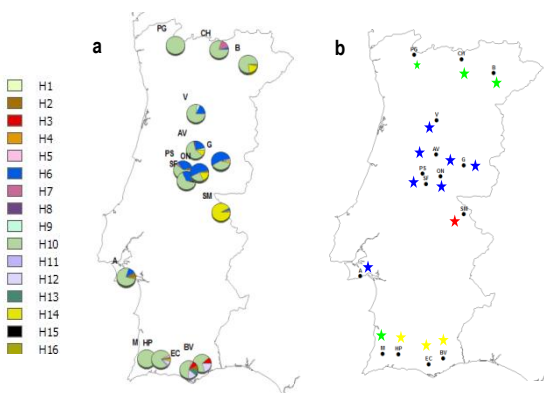


Fig 3. Distribution of 16 haplotypes in the populations (a). Populations clustering with cpSSR data using BAPS, a Bayesian approach (b).

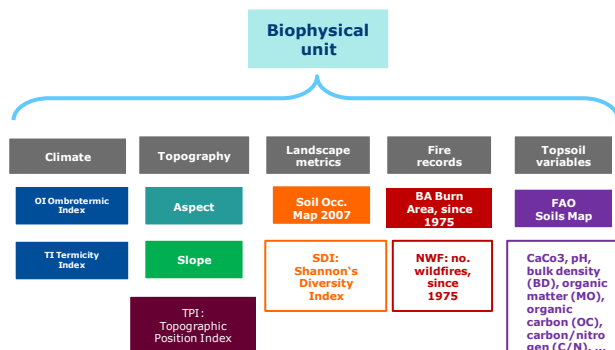


Fig. 2 Biophysical variables were studied using GIS (Geographic Information Systems) in the biophysical unit = the area spanning 1 km from each one of the 30 stand trees.

## 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.

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 H value (13%). Two other populations have probably experienced a bottleneck effect due to the impact of wildfires: PG and M. Indeed they have  $H_e=0$  and only one haplotype.

The genetic diversity estimates (H, 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.

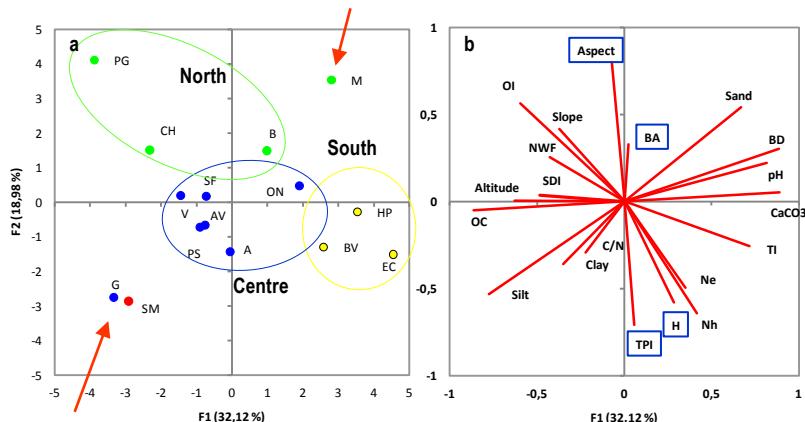


Fig 4. Principal component analysis (PCA) performed with the biophysical factors, see Fig. 2 for label details, and genetic diversity estimates (H = haplotypic diversity, Nh = no. of haplotypes, Ne = effective no. of haplotypes). The observations (populations) (a) and the variables (b). Red arrows point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

**Acknowledgements:** This work was supported by the grant from FCT PTDC/AGR-FOR/3746/2012 (Arbutus unedo plants and products quality improvement for the agro-forestry sector). Thanks to Ilaria Spanu assistance in the laboratorial analysis, also extended to Dragos Postolache that also helped us to produce the haplotypic map. Thanks are extended to Francesca Bagnoli that kindly introduced us in the data analysis with the Bayesian approach.