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

Will biophysical factors help in explaining the species’ genetic diversity estimates?

How is the species’ genetic diversity geographically structured?

What is the genetic structure of the species?

RESULTS

Biophysical unit

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

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%) 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 (15%). 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 (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.

MATERIAL AND METHODS

- 15 natural populations 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

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