

Proposal of a network of conservation units of forest genetic resources in Spain. The importance of GENTREE sampling points as network nodes.



Genetics to the rescue
Managing forests sustainably in a changing world

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Background/Objectives

A proposal for the selection and characterization of a set of genetic conservation units (CUs) that meet the objective of preserving the genetic variability of the populations of main forest species has been recently developed in Spain. To this end, and taking into account the recommendations of the EUFORGEN program, we intend to establish the axes on which research on the dynamic evolution of populations and their adaptation to climate change will be developed, focusing the efforts in the network of CUs.

Material and Methods

We have used the delimitations by climatic typology both at European (European Environmental Zones, Metzger et al 20012) and Spanish level (Provenance Regions, Alía et al, 2009) as a proxy to establish areas with distinguishable populations for possible local adaptation, and therefore establish the minimum number of CUs to be located.

Populations with existing genetic information should be proposed as the main source to designate CUs (molecular, provenance or progeny tests). In the absence of such information, populations with phenotypic information (selected stands, GenTree pops) have been selected. Finally and as the last option, we have considered those populations of which there is evidence of their reproductive capacity as they were designated as base materials. In the Provenance Regions where there are no populations that meet any of the three requirements indicated, no CUs have been proposed.

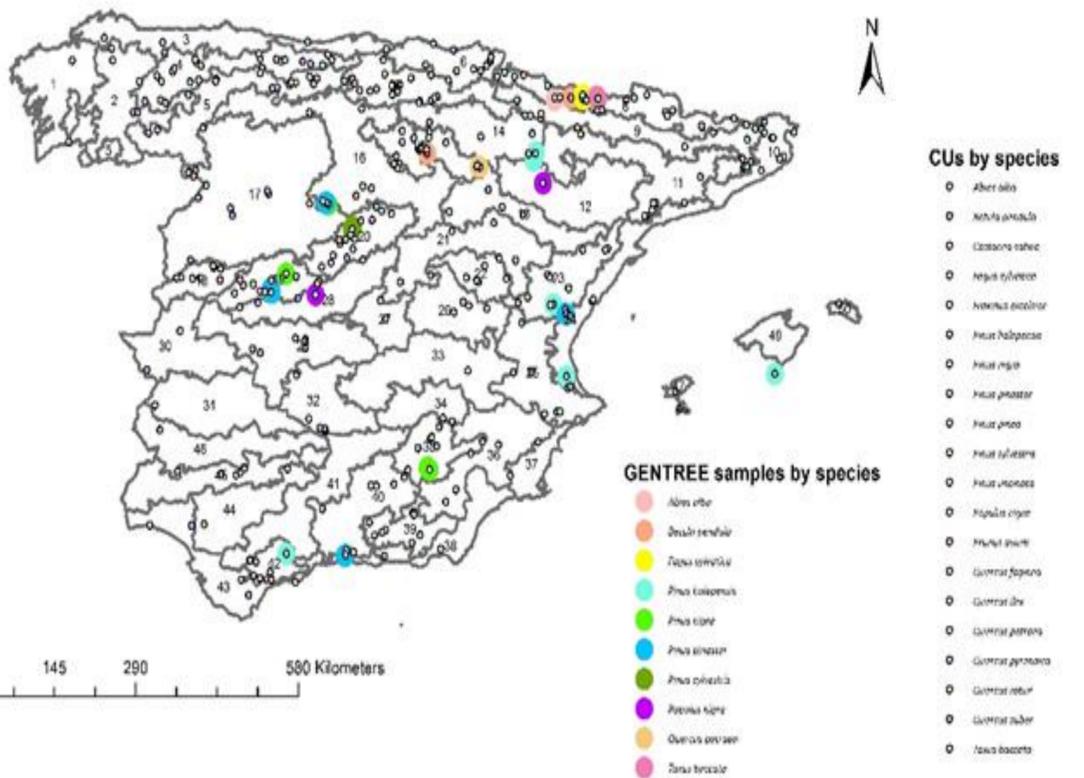


Figure 1. Spanish CUs by species and GENTREE samples by species (see figure legend) located in the Spanish Procurement Regions (grey contour) named by its number.

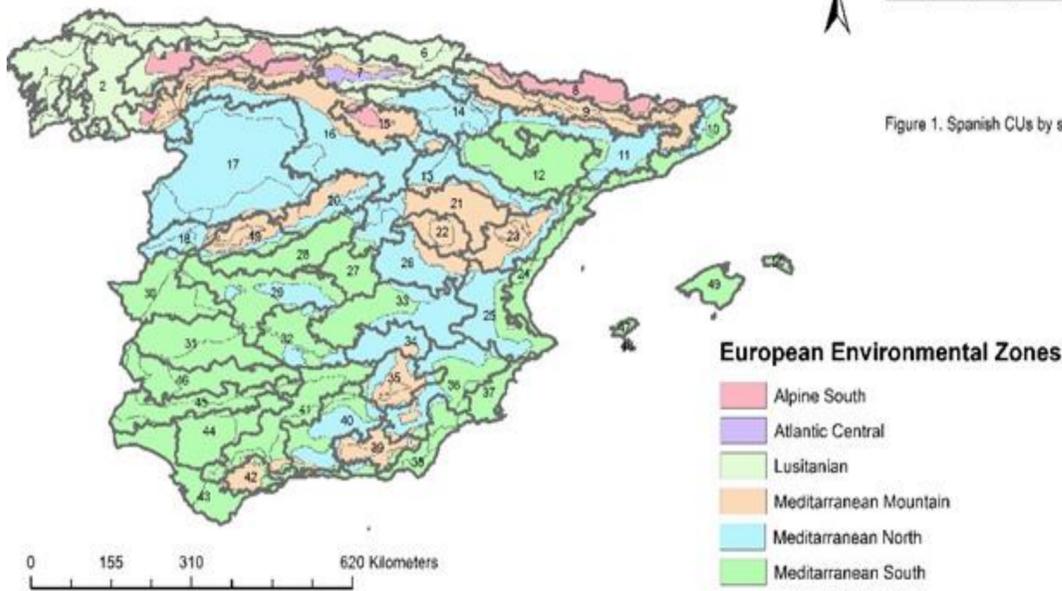


Figure 2. Spatial relationship between European Environmental Zones (coloured polygons) including subzones (thin black lines) and the Spanish Procurement Regions (gray contour) named by its number.

Conclusions

The proposed Spanish Genetic Conservation Units Network included most of the actual knowledge relative to populations of the 20 initial species studied, and focalized further research on nodes related with species sampled in the GENTREE project. We think that this a cost effective procedure for gather geographically significant information in order to understand the performance of the main species to the new environmental conditions upcoming.



Gentree sampling point. Trees sampled for *Betula pendula*

Results

A total of 357 CUs have been selected for 20 species (Figure 1). Of these CUs, 23 correspond to populations of 10 species sampled in the GenTree project, which represents only 6.5% of the total. The rest of the populations have been selected based on the availability of genetic information (diversity calculated from different molecular markers), 115 or 32.2% of the total, being part of the first EUFGIS listing because their phenotypic characteristics or their status as marginal/ threatened populations, 31 or 8.7% of the total, or having been previously designated as a source of forest reproductive material, 188 or the remaining 52.6. This does not imply an exhaustive designation of a CU by species and Provenance Region (or Procurement Region) (Figure 2), as the 50 Procurement Region are clearly corresponsive with the most extensive European environmental zones (6) and sub-zones (33). This lets think us that the representativeness achieved with the CUs actually designated is enough.

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References

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