

OPPORTUNITIES TO IMPROVE GENETIC CONSERVATION OF FOUR IMPORTANT EUROPEAN TREE SPECIES

PROJECT BRIEF

FORGER

TOWARDS THE SUSTAINABLE
MANAGEMENT OF FOREST GENETIC
RESOURCES IN EUROPE

Forest genetic resources (FGR) form the base for adaptation of European forests to future environmental conditions and societal demands. Genetic diversity, i.e. diversity within-species, allows a species to evolve over time and in space and plays a key role for both the long-term survival of a species and the stability of forest ecosystems. It is thereby a fundamental and critical part of biodiversity.

Forest genetic resources (FGR) are defined as genetic material of forest trees that is of actual or potential value for future generations. Genetic resources are embedded in forest reproductive material such as seeds, seedlings or other propagules.

Genetic conservation is defined as any maintenance of genetic diversity (*in situ* or *ex situ*) to secure the future utilization of the genetic resources. *In situ* conservation is a measure taken to conserve tree populations in their natural environment or in the environment where they have developed their distinctive properties. Usually, this refers to designated genetic reserves where the genetic adaptability of forest tree species is maintained by natural processes. Conversely, the *ex situ* conservation of genetic resources entails all measures including the removal of various kinds of genetic material (DNA, pollen, seeds, whole trees, populations), their storage in gene banks or in clonal archives or so-called *ex situ* gene reserves, as long as the resource is considered valuable.



Beech forest, Central Appennines, Italy (photo E. Hermanowicz)



Figure 1



Figure 2

FGR *in situ* conservation often aims at a dynamic preservation of genetic resources through the safeguarding of the biological mechanisms that maintain genetic diversity. In general, FGR conservation is a multifaceted issue including risk assessment and valuation of genetic resources, identification of target species on social, ecological and economic grounds, identification of individuals and populations, collecting and evaluating samples, genetic monitoring and *in situ* and *ex situ* maintenance. The challenge for an effective conservation is to cover a representative sample of appropriate tree populations and to evaluate what amount of the gene pool is conserved. Past decades have shown an immense progress in detecting patterns of genetic diversity, due to fast technological advances. However, despite extensive research efforts supported by the EU, the picture of the current distribution of genetic diversity, of even the most important forest tree species, is still incomplete.

BACKGROUND

Much of the data on genetic diversity of economically important forest tree species in Europe is gathered in the GeoReferenced Database of Genetic Diversity (*GD*²). This database, constructed and curated by the EVOLTREE network of excellence (<http://www.evoltree.eu/>), compiles all genetic surveys that have been published and documented so far in European forest tree species. Recently, European countries completed an extensive inventory of standardized geo-referenced information on genetic conservation units, and the tree species occurring within these units, as part of the EUFGIS project (Establishment of a European Information System on Forest Genetic Resources; <http://portal.eufgis.org>), implemented under the framework of the European Forest Genetic Resource Programme (EUFORGEN; www.euforgen.org). The data on these units for 100 tree species, across 34 countries, is available through the EUFGIS portal.

Figure 1: Location of the EUFGIS genetic conservation units for *Fagus sylvatica*. The light green areas indicate the distribution of *Fagus sylvatica* in Europe. The dots represent the location of the genetic conservation units included in the EUFGIS portal at the time of publication of this leaflet. New units are progressively included.

Figure 2: Location of all *GD*² sites where a characterization of genetic diversity for *Fagus sylvatica* has been carried out.

Figure 3: Distribution of the 5 climatic factors with the highest correlation with genetic diversity. Green bars indicate the variation of climatic variables across the whole geographic distribution of *Fagus sylvatica*; yellow bars indicate the variation of climatic variables within the genetic conservation units. A mismatch between the two bars for each variable indicates a gap in the representativeness of the network of genetic conservation units.

The process of inclusion of existing genetic conservation units in the EUFGIS portal is still in progress and the database is being progressively updated. However, the EUFGIS database does not include any information on genetic diversity. Therefore, one of the main aims of the FORGER project was to link the observations performed on genetic diversity, available in the *GD*² database, and the general information on genetic conservation units, available in the EUFGIS database. The linked databases would provide stakeholders with a genetic characterization of the FGR currently conserved at pan-European level in the genetic conservation units.

Another objective of FORGER was to identify gaps in current FGR conservation efforts, in particular for the following species: *Fagus sylvatica*, *Quercus spp.*, *Pinus sylvestris* and *Picea abies*. An analysis was carried out to determine to what extent the genetic conservation units cover the diversity of climatic conditions found within the range of each of the 4 selected species. This approach enables us to identify conservation gaps, i.e. those parts in a species range that are insufficiently covered by the genetic conservation units network.

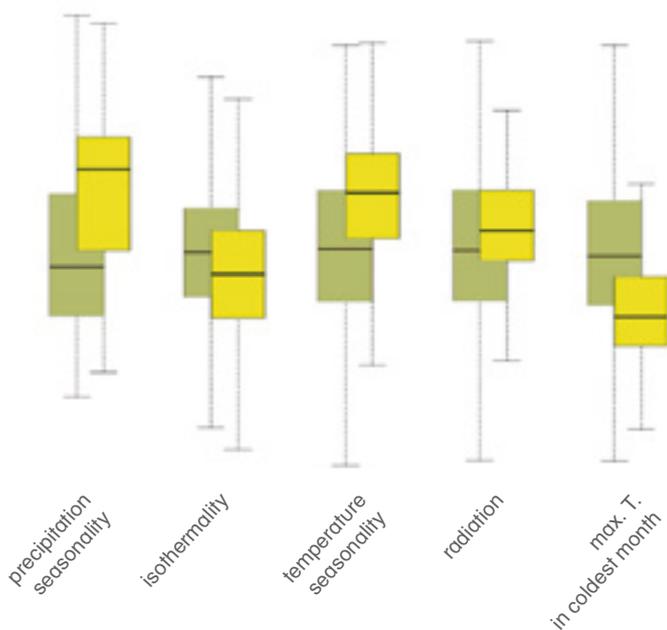


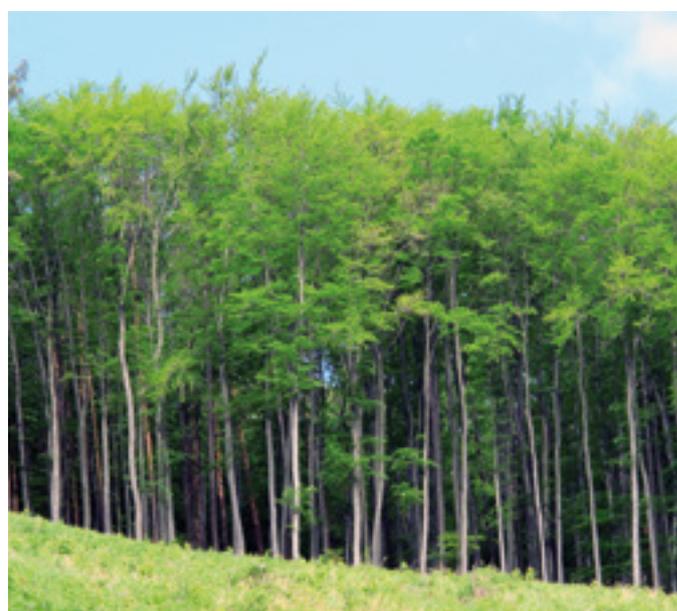
Figure 3

- Variation of 5 climatic variables across the range of *Fagus sylvatica*.
- Variation of 5 climatic variables across the genetic conservation units of *Fagus sylvatica* included in the EUFGIS portal at the time of publication of this leaflet.

MAIN RESULTS

A main finding that emerged after linking the GD² and EUFGIS databases was that few measurements of genetic diversity are available from within the genetic conservation units (see Figure 1 with 2). Currently no definitive conclusions can be drawn on the characterization of the FGR included within the genetic conservation units at a pan-European level, but a comparison was carried out between the positioning of the genetic conservation units relative to the full width of variation of climatic conditions found across the spatial distribution of the main four species investigated. This comparison enabled the identification of conservation gaps, i.e. of locations where the species examined occur in climatic conditions that are distinct from the climatic conditions found within the genetic conservation units (see in Figures 1-3 the example of *Fagus sylvatica*). It should be noted that climatic factors do not causally explain the distribution of genetic diversity over Europe, but are partly associated with it. The main gradients in climatic factors over Europe (mainly from south to north) coincide with the patterns of colonization by tree species from the refugia in the south of Europe, since the ice age.

A third aspect that emerged was that the genetic markers available to characterize the genetic diversity of tree species were not associated with the adaptive properties of trees. Adaptive markers would be extremely useful in guiding practical forest management, but have only recently started to become available for some species.



Beech stand in a genetic conservation unit, West Hungary (photo M. Bozzano).

FINAL CONSIDERATIONS

- More research is necessary to genetically characterize the genetic conservation units, with intensification of genetic studies in areas within or adjacent to existing genetic conservation units.
- The representativeness of the genetic conservation units should be further assessed, both at country and pan-European level, once the information on the genetic conservation units has been completed updated.. It is recommended that genetic conservation units are evenly distributed across the 'climatic range' of a species, rather than evenly distributed across the geographic space. This means that:
 - ▶ in cases where considerable changes over short distances are found in an important climatic factor, the genetic conservation units should be located in sites that appropriately cover the deep climatic gradient.
 - ▶ the current positioning of the genetic conservation units could be biased to one side of the climate range, when compared to the full range of climatic conditions found across a species' distribution (see the case of *Fagus sylvatica* in Figure 3).
- Genetic conservation units should be located in hotspots of genetic diversity, across the geographic distribution of the species, particularly in areas with fragmented forests.
- It is recommended that research on genetic diversity of adaptive traits be strengthened, in particular within the genetic conservation units, and that the information be made available for practical forest management.



Beech forest, Central Appennines, Italy (photo E. Hermanowicz)

This brief presents recommendations that are based on the findings of the final report of the project to be published in 2016.

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