

Science for Environment Policy

Conserving the genetic diversity of Europe's forests

Conserving genetic diversity is vital to allow populations to adapt in the face of changing conditions. A new study, assessing the conservation of genetic diversity of trees across Europe, has identified areas for improvement that could help maintain the genetic diversity of Europe's forests.

Without a diverse gene pool, whole populations of animals and plants may be unable to adapt to new diseases or a changing climate, potentially leading to their extinction. In order to prevent such problems the EC Council Regulation No. 870/2004 established a community programme to promote genetic diversity and sustainable use of genetic resources in agriculture¹. Following on from this, the [EUFGIS](#) (Establishment of a European Information System on Genetic Resources in Agriculture) project developed pan-European requirements for genetic conservation units of tree species², typically located in forests managed for multiple use, protected areas and seed stands.

Data from 31 countries is stored in the EUFGIS Portal database. The researchers report that these countries conserve 86 indigenous tree species across a network of 1967 separate conservation units. Seven species are conserved in 100 or more conservation units while 15 are only conserved in one. In general, the researchers found that most conservation units target large tree populations (more than 500 reproducing trees) rather than those that are small or rare.

The study revealed that countries use two different approaches in designing their conservation strategies. A total of 17 followed the single species approach, targeting only one species in each conservation unit, and 14 followed a site-orientated approach by designating conservation units for multiple species. In around three quarters of conservation units, there was just one target species. The researchers recommend combining the two conservation approaches - the species-oriented strategy for priority species, and the site-oriented strategy to ensure a wider coverage of tree species at the pan-European level.

The authors used 'gap analysis' to assess the conservation status of 11 tree species. Gap analysis assesses how well a conservation network is achieving its aims, for example, by identifying species and populations that are not adequately represented. Silver fir, European beech, Scots pine and sessile oak were conserved in the highest numbers of conservation units - between 195 and 349 sites each - although only in between a half to a third of the countries. By contrast, black poplar, wild service tree and white elm were less well conserved - between 10 and 13 units each. By looking at genetic information for six species, the researchers found that certain lineages, i.e. genetically distinct groups within single species, were underrepresented in the conservation network. One particular lineage of common ash was absent altogether. Researchers also examined 'gaps' in conserved diversity across Europe. In the Mediterranean, for example, species such as black poplar and wild service tree were missing, suggesting that genetic conservation efforts should be increased in this region.

The results also show that most genetic conservation efforts in Europe are focused on economically valuable species. The authors suggest that, in order to preserve diversity, minimum numbers of conservation units should be defined for species that currently have low economic value but may be useful in future.



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1. <http://ec.europa.eu/agriculture/genetic-resources/>
2. Koskela, J., Lefèvre, F., Schueler, S., et al. (2013). Translating conservation genetics into management: Pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity. *Biological Conservation*, 157:39-49.
3. <http://www.euforgen.org/>
4. <http://www.foresteurope.org/>