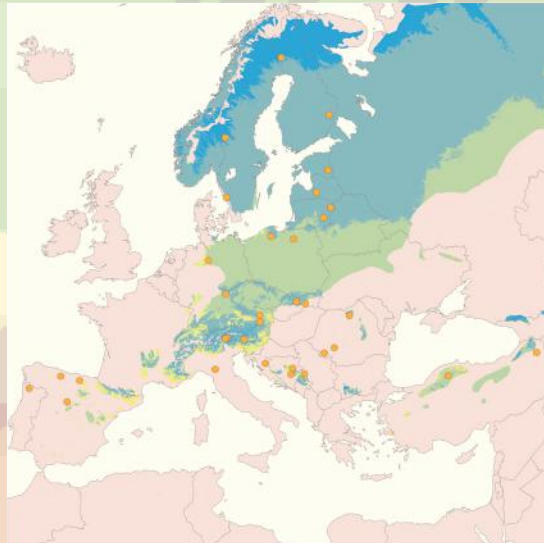
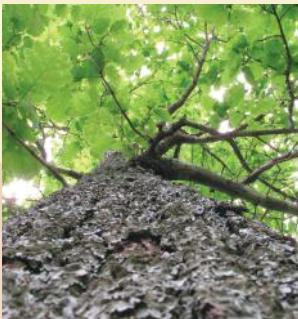




# Pan-European strategy for genetic conservation of forest trees

and establishment of a core network  
of dynamic conservation units



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**European Forest Genetic Resources Programme (EUFORGEN)** is an instrument of international cooperation promoting the conservation and appropriate use of forest genetic resources in Europe. It was established in 1994 to implement Strasbourg Resolution 2 adopted by the first Ministerial Conference of the FOREST EUROPE process, held in France in 1990. EUFORGEN also contributes to implementation of other FOREST EUROPE commitments on forest genetic resources and relevant decisions of the Convention on Biological Diversity (CBD). Furthermore, EUFORGEN contributes to the implementation of regional-level strategic priorities of the Global Plan of Action for the Conservation, Sustainable Use and Development of Forest Genetic Resources (GPA-FGR), adopted by the FAO Conference in 2013. The Programme brings together experts from its member countries to exchange information and experiences, analyse relevant policies and practices, and develop science-based strategies, tools and methods for better management of forest genetic resources. Furthermore, EUFORGEN provides inputs, as needed, to European and global assessments and serves as a platform for developing and implementing European projects. EUFORGEN is funded by the member countries and its activities are mainly carried out through working groups and workshops. The EUFORGEN Steering Committee is composed of National Coordinators nominated by the member countries. The EUFORGEN Secretariat is hosted by Bioversity International. Further information on EUFORGEN can be found at [www.euforgen.org](http://www.euforgen.org).

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## PREFACE

European forests cover 157 million hectares of land and provide a vast array of products, socio-economic benefits and ecosystem services. The distribution ranges of many European tree species extend across wide geographical areas and countries that have different forest management traditions and practices. Consequently, European forests are diverse in terms of their biological characteristics, structure, ownership patterns and uses. The biological diversity of European forests is obvious at the ecosystem and species levels, while intra-specific genetic diversity is less visible.

Genetic diversity ensures that forest trees can survive, adapt and evolve under changing environmental conditions. Genetic diversity is also needed to maintain the vitality of forests and to provide resilience to pests and diseases. Furthermore, genetic diversity is the foundation of biological diversity at species and ecosystem levels. Forest genetic resources are therefore valuable for present or future human use, and thus an invaluable asset and a corner stone of sustainable forest management.

During the past two decades, European countries have been collaborating closely at the pan-European level to promote the implementation of sustainable forest management. This means the stewardship and use of forests in a way that maintains their biodiversity, productivity, regenerative capacity, vitality and the potential to fulfil economic, social and ecological functions. In 1990, the first Ministerial Conference of the FOREST EUROPE (previously the Ministerial Conferences on the Protection of Forests in Europe) process, held in Strasbourg, France highlighted the importance of conserving forest genetic resources as part of sustainable forest management. Subsequently, the European Forest Genetic Resources Programme (EUFORGEN) was established in 1994 to coordinate pan-European collaboration on forest genetic resources as part of the FOREST EUROPE process.

EUFORGEN started its activities with pilot networks on a few model tree species and gradually it evolved into a collaborative platform focusing on broader groups of tree species and, more recently, on thematic issues. During Phase IV (2010–2014), the Programme had three objectives: (1) promote appropriate use of forest genetic resources as part of sustainable forest management to facilitate adaptation of forests and forest management to climate change; (2) develop and promote pan-European genetic conservation strategies and improve guidelines for management of gene conservation units and protected areas; and (3) collate, maintain and disseminate reliable information on forest genetic resources in Europe.

This report presents the findings and recommendations of a EUFORGEN working group that was tasked to develop a pan-European genetic conservation strategy for forest trees. The report was prepared by the working group members (the authors of this report) who held two meetings; the first was hosted by Bioversity International in Maccaresse, Italy, 2–4 November 2011, and the subsequent meeting by the Research Unit for Intensive Wood Production (CRA–PLF) of the Italian Agricultural Research Council in Casale Monferrato, Italy, 14–16 February 2012. Furthermore, the finalization of this report benefited from the discussions during the EUFORGEN workshop on conservation and monitoring of forest genetic resources that was organized in Järvenpää, Finland, 18–20 September 2012 in collaboration with the Finnish Forest Research Institute. This was a joint workshop with another EUFORGEN working group that dealt with genetic monitoring. The inputs and comments received from the workshop participants and other national experts contributing to the EUFORGEN work are gratefully acknowledged.

In particular, we acknowledge the contributions received from: Peter Zhelev Stoyanov (Bulgaria), Rumen Dobrev (Bulgaria), Alexander H. Alexandrov (Bulgaria), Josef Frýdl (Czech Republic), Petr Novotný (Czech Republic), Lars Graudal (Denmark), Mart Külvik (Estonia), Tiit Maaten (Estonia), Mari Rusanen (Finland), Pekka Vakkari (Finland), Alexis Ducouso (France), Bruno Fady (France), Heino Wolf (Germany), Ralf Kätzel (Germany), Mirko Liesebach (Germany), Bernd Degen (Germany), Celine Jolivet (Germany), Konstantinos Spanos (Greece), Aristotelis C. Papageorgiou (Greece), Filippos Aravanopoulos (Greece), Sándor Bordács (Hungary), László Nagy (Hungary), Attila Borovics (Hungary), Maria Gras (Italy), Giovanni Giuseppe Vendramin (Italy), Remigijus Bakys (Lithuania), Virgilijus Baliuckas (Lithuania), Darius Danusevicius (Lithuania), Frank Wolter (Luxembourg), Koen Kramer (the Netherlands), Tor Myking (Norway), Mari Mette Tollefsrud (Norway), Malgorzata Palucka (Poland), Iwona Szyp-Borowska (Poland), Czeslaw Koziol (Poland), Andrej Pilipovic (Serbia), Ladislav Paule (Slovakia), Dušan Gömöry (Slovakia), Gregor Bozic, Dragan Matijašic (Slovenia), Hojka Kraigher (Slovenia), Marjana Westergren (Slovenia), Alvaro Soto de Viana (Spain), Santiago C. González-Martínez (Spain), Pablo Gonzalez Goicoechea (Spain), Sanna Black-Samuelsson (Sweden), Peter Rotach (Switzerland), Andreas Rudow (Switzerland), Joan Cottrell (United Kingdom).

Special thanks to Berthold Heinze from Austria, who first came up with the concept of a ‘Common Action Plan for *Populus nigra*’ in 2001. The plan concretized his vision of concerted conservation effort of tree species in Europe transcending national interests and borders. Among others, it solicited the foundation of a network of

genetic conservation units of black poplar across its distribution range which was applicable to other species. It constitutes the basis of this strategy.

The draft report was presented to the EUFORGEN Steering Committee for further review during its 8th meeting, held in Paris, France, 27–28 November 2012. The working group then prepared a revised draft report and presented it to the Steering Committee for approval at its 9th meeting, in Tallinn, Estonia, 3–5 December 2013. The Steering Committee endorsed the approach used for developing the strategy, provided some additional minor comments, and requested the working group to finalize this report for publication.





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**ACRONYMS USED IN THE TEXT**

EUFGIS	European Information System on Forest Genetic Resources
EUFORGEN	European Forest Genetic Resources Programme
FGR	forest genetic resources
IPCC	Intergovernmental Panel on Climate Change
IUFRO	International Union of Forest Research Organizations
IUCN	International Union for Conservation of Nature
UNFCCC	United Nations Framework Convention on Climate Change

## EXECUTIVE SUMMARY

The diversity of forests, at the level of species and at the level of genetic diversity within species, is an important resource for Europe. Over the past several decades European countries have made considerable efforts to conserve the genetic diversity of tree species. According to the EUFGIS portal<sup>1</sup>, there are more than 3200 genetic conservation units which harbour more than 4000 populations of about 100 tree species. An earlier analysis of the EUFGIS information revealed significant gaps in the conservation efforts in terms of the species covered and the geographical distribution of the units within the species' ranges. Subsequently, the EUFORGEN Steering Committee established a working group to develop the pan-European genetic conservation strategy for forest trees. The process followed by the working group and its results are presented in this report.

For each pilot tree species, the strategy calls for a core network of dynamic conservation units. These units are not interconnected by geneflow, but together capture the current genetic diversity across the European continent. In addition, the working group recommends: that countries upload all outstanding data to the EUFGIS database; that progress be monitored; that resources be allocated to the EUFGIS database; that a strategy to mitigate the negative effects of climate change on forest genetic resources be developed; and that EUFORGEN continues operating through working groups.

### Methods

The working group decided to focus its attention on the conservation of adaptive genetic diversity, while recognising that neutral genetic diversity is also important. The working group selected 14 pilot tree species representing four categories, depending on their geographical distribution (wide vs restricted) and their ecology (stand-forming vs scattered). The group also created a map of eight environmental zones by amalgamating some of the zones of an earlier published environmental classification for Europe. It then sought to identify at least one conservation unit per country for each environmental zone in that country, using a set of criteria to determine the most appropriate choice of unit.

This process resulted in the identification of 1,836 dynamic conservation units, covering a total area of 205,803 ha and encompassing 2,173 tree populations. Five economically important tree species are represented by more than 200 units each, which together make up 80% of all conservation units. Other species are poorly represented.

<sup>1</sup> <http://portal.eufgis.org>

### **Genetic conservation status**

Available information on genetic diversity is variable across tree species. Distribution maps are available for all of the widely occurring species and for five less widely occurring species. For the remaining four pilot species, only rough qualitative assessments of diversity could be made using the broad genetic structure at a continental scale. Overall, the group noted a lack of information on genetic diversity within the conservation units, with uncertainty about which populations have been sampled by earlier studies. On-going projects to link various databases should make this kind of information more complete and accessible in the future.

### **Gaps in conservation efforts**

To identify gaps in existing conservation efforts, the group compared species distribution maps in each environmental zone in each country with the location of the conservation units. Any incidence of a species with no unit in an appropriate environmental zone in that country was recorded as a gap, and it was also noted when there was an information gap in the EUFGIS database.

Some countries do not yet have any genetic conservation units that meet the minimum requirements agreed for these units. Others have units but have provided either no data or only partial data to EUFGIS. Therefore, the report focuses on countries where there are no conservation units for a particular species in a particular environmental zone, as these areas can be considered a high priority for establishing new conservation units.

### **Genetic Conservation Strategy**

The working group's approach, having been tested with 14 pilot species, can be applied to all tree species in Europe. The implementation of the strategy remains the responsibility of each country, which can use the results of this report for planning and carrying out their conservation efforts. The EUFORGEN Steering Committee will promote the implementation of the strategy and monitor progress in this regard.

A particular concern is the effects of climate change on forests and the expected effects on long-lived tree species are likely to be variable, complex and difficult to predict. As a result, efforts should focus on the genetic conservation of the most vulnerable tree populations and species, for example those near the edge of their environmental limits, which often harbour high genetic diversity. Monitoring such populations should help to reveal key changes in a timely fashion, and management may then be needed to mitigate the effects of climate change.

Monitoring progress in the overall implementation of the strategy will also be necessary to ensure that it can be revised based on the progress made and future requirements.

## INTRODUCTION

During the past 20 years, European countries have made good progress in conserving their forest genetic resources. The areas managed for *in situ* and *ex situ* conservation as well as for seed production show an increasing trend since 1990 (FOREST EUROPE/UNECE/FAO, 2011). However, genetic conservation efforts are carried out for relatively few tree species. Most such efforts have concentrated on common stand-forming tree species, while many scattered – as well as several rare and endangered – tree species have received less attention. Valuable forest genetic resources are still threatened by forest fires, pests and diseases, habitat fragmentation, poor silvicultural practices and inappropriate use of forest reproductive material. Furthermore, the marginal populations of many tree species are facing new threats due to climate change.

About 10 years ago, European countries started developing so-called common action plans while collaborating through the European Forest Genetic Resources Programme (EUFORGEN). The purpose of the common action plans was to share responsibilities in conservation of forest genetic resources among the countries, and to identify gaps in these efforts at the pan-European level, taking into

account predicted climatic changes and the geographical distribution of neutral and adaptive genetic diversity of forest trees. They also aimed at promoting the implementation of genetic conservation in practice in different countries and creating pan-European networks of selected genetic conservation units for various tree species.

However, it soon became clear that countries had no common approach in establishing and managing genetic conservation units for forest trees. Moreover, due to a lack of geo-referenced and harmonized data on the units, it was difficult to reliably assess the status of genetic conservation of forest trees in Europe and to identify gaps in the existing conservation efforts across the continent. There were also different opinions among national experts regarding what should be the targeted level of genetic conservation at the pan-European level.

In 2005, the EUFGIS project (Development of a European Information System on Forest Genetic Resources) was designed to address these problems. The project received co-funding from the European Commission (DG Agriculture and Rural Development) under Council Regulation (EC) No 870/2004 on genet-

ic resources in agriculture, and it was then implemented by EUFORGEN and its member and associated countries in 2007–2011. Prior to creating the information system, consisting of a database, an intranet section and a user interface (EUFGIS Portal), the project developed pan-European minimum requirements and data standards for the genetic conservation units of forest trees. A network of national focal points in European countries was also established to provide and manage data in the information system. During the project, the first comprehensive assessment of the genetic conservation efforts was also carried out, based on the newly collected data.

The pan-European minimum requirements for the genetic conservation units are presented in a recent paper by Koskela *et al.* (2013). The minimum requirements are based on the dynamic conservation approach, i.e. long-term conservation of evolutionary processes within tree populations to maintain their adaptive potential. The units can be located in natural tree populations or plantations, which are specifically managed for genetic conservation. Each unit should have a designated status and a management plan, and contain one or more of the tree species recognized as target species for genetic conservation. The units should contain a minimum of 500, 50 or 15 reproducing individuals depending on tree species and conservation objectives. Furthermore, silvicultural interventions which are intended

to promote the genetic processes of tree populations should be allowed, and, ideally, field inventories should be carried out every 5 or 10 years to monitor regeneration and the population size.

In line with these minimum requirements, the European countries have entered data on 3,214 units and 4,061 tree populations of about 100 species into the EUFGIS Portal (as of February 2015). This demonstrates that the countries have invested a considerable amount of resources towards conserving their forest genetic resources. However, the analyses carried out at the end of the EUFGIS project confirmed that there are significant gaps in the genetic conservation efforts in terms of both species and the geographical distribution of the units. For example, 60% of the conservation units are managed for only seven tree species (*Abies alba*, *Fagus sylvatica*, *Larix decidua*, *Picea abies*, *Pinus sylvestris*, *Quercus petraea* and *Q. robur*) and there are considerable ecogeographical gaps in the conservation efforts, even for these tree species (Lefèvre *et al.*, 2013). This indicates that there is a clear need for the development of a pan-European genetic conservation strategy for forest trees (including clearly formulated and jointly agreed objectives and methodology), and for continuing the international collaboration in this area to implement such a strategy.

In September 2010, the EUFORGEN Steering Committee, including repre-

sentatives from all member countries, discussed the results of the EUFGIS project and decided to establish a working group to prepare the pan-European genetic conservation strategy. The Steering Committee formulated the following task for this working group:

1. Review the earlier work done by the EUFORGEN Networks on common action plans, including selection criteria for the most valuable conservation units.
2. Carry out the assessment of genetic conservation status for pilot species based on the EUFGIS data.
3. Carry out a review of the knowledge on the genetic diversity of the species.
4. Select the most valuable units (in conservation terms) from the pan-European perspective.
5. Identify gaps in the network of conservation units to improve the long-term sustainability.
6. Develop strategies at the level of groups of species.
7. Prepare a draft report.

The working group recognized that it is important to conserve both adaptive and neutral genetic diversity of forest trees, but decided to give priority to adaptive

diversity. Consequently, the pan-European conservation strategy presented in this report aims at conserving the adaptive diversity of forest trees throughout their distribution ranges. It is proposed that a climatic zoning of Europe will be used as a proxy for characterizing adaptive diversity conserved in the genetic conservation units across the continent. Subsequently, gaps in the conservation efforts have been identified based on the country borders and climatic zones within each country. Furthermore, the working group applied a systematic approach to select the most valuable genetic conservation units at the pan-European level for the establishment of a core network of dynamic conservation units for pilot tree species. The selection was done using the EUFGIS database and each core network should ultimately cover all countries and climatic zones within the distribution range of a given species. For testing this approach, the working group used 14 pilot tree species representing stand-forming and scattered species with both wide and limited distribution ranges.

The following sections present in detail the findings and recommendations of the working group.





## OBJECTIVES OF THE GENETIC CONSERVATION STRATEGY

### What do we propose to conserve and why

The overall goal of the pan-European conservation strategy is to maintain the adaptive and neutral genetic diversity of forest trees. This goal can be met by applying the dynamic conservation approach across tree species' distribution ranges in Europe (only the 46 countries larger than 100 km<sup>2</sup> were considered during the preparation of this strategy: Albania, Andorra, Armenia, Austria, Azerbaijan, Belarus, Belgium, Bosnia and Herzegovina, Bulgaria, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, FYR Macedonia, Georgia, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Liechtenstein, Lithuania, Luxembourg, Malta, Moldova, Montenegro, The Netherlands, Norway, Poland, Portugal, Romania, Russia, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Turkey, Ukraine, and United Kingdom). Regional collaboration through EUFORGEN plays a crucial role in promoting the implementation of the strategy and in monitoring the progress made.

The establishment of a core network of dynamic conservation units supports the implementation of the strategy and it aims to identify those conservation units within each tree species' distribu-

tion range that will most effectively capture the current genetic diversity of the species at the pan-European level. The word "network" in this context refers to a network of units identified on a map; it does not mean that the tree populations should be inter-connected through gene flow. The word "core" means the minimum set of units considered necessary for this purpose at the pan-European level. The core network operates at the range-wide level and it is not intended to replace national conservation networks or override national conservation priorities.

### Targeted level of genetic conservation at the pan-European level

Forest trees have long generation cycles and retain the capacity to adapt to changing (local) conditions through evolutionary processes such as gene flow and natural selection. Maintaining the adaptive diversity of forest tree populations is thus the key objective of genetic conservation as it provides the raw material for the evolutionary processes to act on. Changing climate conditions are predicted to affect the distribution ranges of many European tree species and may also lead to loss of genetic diversity. Local adaptation, genetic diversity and phenotypic

plasticity will all influence the severity of these effects on the survival of tree populations in different locations and species distribution. To ensure the adaptability of tree populations in the future, efforts should be made to conserve a sizeable amount of the adaptive genetic variation that currently exists in European tree populations.

The working group defined the targeted level of genetic conservation based on the country borders and environmental zones. This approach is in line with the Convention on Biological Diversity and FOREST EUROPE commitments, i.e. each country is responsible for managing bio-

logical diversity and forest sustainability within its territory. In addition, it is reasonable to assume that tree populations growing within a given environmental zone are adapted to the prevailing local conditions. The working group therefore considered that by including one conservation unit per country and per environmental zone an adequate amount of adaptive diversity would be captured within the distribution range of each species. The working group developed its draft report based on the environmental zones of Europe as identified by Metzger *et al.* (2005) and then prepared the final report based on the new environmental stratification developed by Metzger *et al.* (2013).

## METHODS

### Selection of pilot tree species

The working group selected pilot tree species to test the underlying concept of the proposed conservation strategy. This was done based on the data entered into the EUFGIS database, i.e. the number of genetic conservation units established for a given tree species in Europe. The selected pilot species were grouped on the basis of their geographical distribution (wide or restricted distribution) and ecological appearance (stand-forming or scattered). Thus, four broad ecological categories of species were identified: (1) widely distributed and stand-forming; (2) widely distributed but scattered; (3) restricted distribution but locally common; and (4) restricted distribution and locally scattered. Furthermore, the pilot tree species were selected based on the availability of range-wide information on genetic diversity within the distribution ranges.

### Selection and ranking of conservation units for the establishment of the core network

No perfect method is available for assessing the geographical distribution of adaptive diversity within tree species at the European scale. This diversity is shaped by several factors, such as geomorphology, colonization source, soil

and human activities (Graudal, Kjaer and Canger, 1995) as well as vegetation types (Bohn, Zazanashvili and Nakhutsrishvili, 2007; Olson *et al.*, 2001). However, climate, both at the local and regional scale, is recognized as a major driving force for adaptation of tree populations. Therefore, the working group decided for practical reasons to use the environmental zoning of Europe (Metzger *et al.*, 2005; 2013) as a proxy for the core network for sampling the adaptive diversity found in the genetic conservation units across the continent. The sampling procedure is therefore based on available pan-European climatic zoning. It was decided not to take into account the intensity of the predicted changes in climate at this stage, although the working group recognized that some of the selected units may remain within the species' climatic envelope whereas others may not.

The working group first tested the environmental zoning of Europe published by Metzger *et al.* (2005). This paper only presented the environmental zones as far east as 32°E, leaving large parts of the pan-European region (Ukraine, Russia, Turkey and the Caucasus) uncovered. For these parts, the working group therefore used the pan-European

environmental zoning prepared by Metzger *et al.* (unpublished) for the Intergovernmental Panel on Climate Change (IPCC), which is based on the same statistical methods. The combined environmental zoning included 17 zones (Arctic, Icelandic, Boreal, Nemoral, Atlantic North, Atlantic Central, Lusitanian, Continental, Pannonian, Anatolian, Mediterranean Mountains, Mediterranean North, Mediterranean South, Black Sea, Alpine North, Alpine South and Eastern Mountains) (Metzger *et al.*, unpublished). The environmental zoning was considered to be an appropriate approach for developing the strategy, but in the case of some countries, the zoning based on Metzger *et al.* (2005) was somewhat different from the observed climatic conditions. The working group consulted M.J. Metzger about these problems and he recommended to use a new environmental zoning of Europe which was developed as part of a global analysis of ecological and environmental data (Metzger *et al.*, 2013). Following this, the working group decided also to test the newer environmental zoning.

The global environmental stratification (Metzger *et al.*, 2013) consists of 125 strata, which have been aggregated into 18 global environmental zones, of which only 14 zones occur in Europe. It has a relatively high spatial resolution (30 arcsec, equivalent to 0.86 km<sup>2</sup> at the equator). The strat-

ification is based on six classes of growing degree-days describing temperature conditions (extremely cold, cold, cool temperate, warm temperate, hot and extremely hot) and six classes of an aridity index (arid, zeric, dry, mesic, moist and wet). This environmental stratification for Europe is presented in Figure 1.

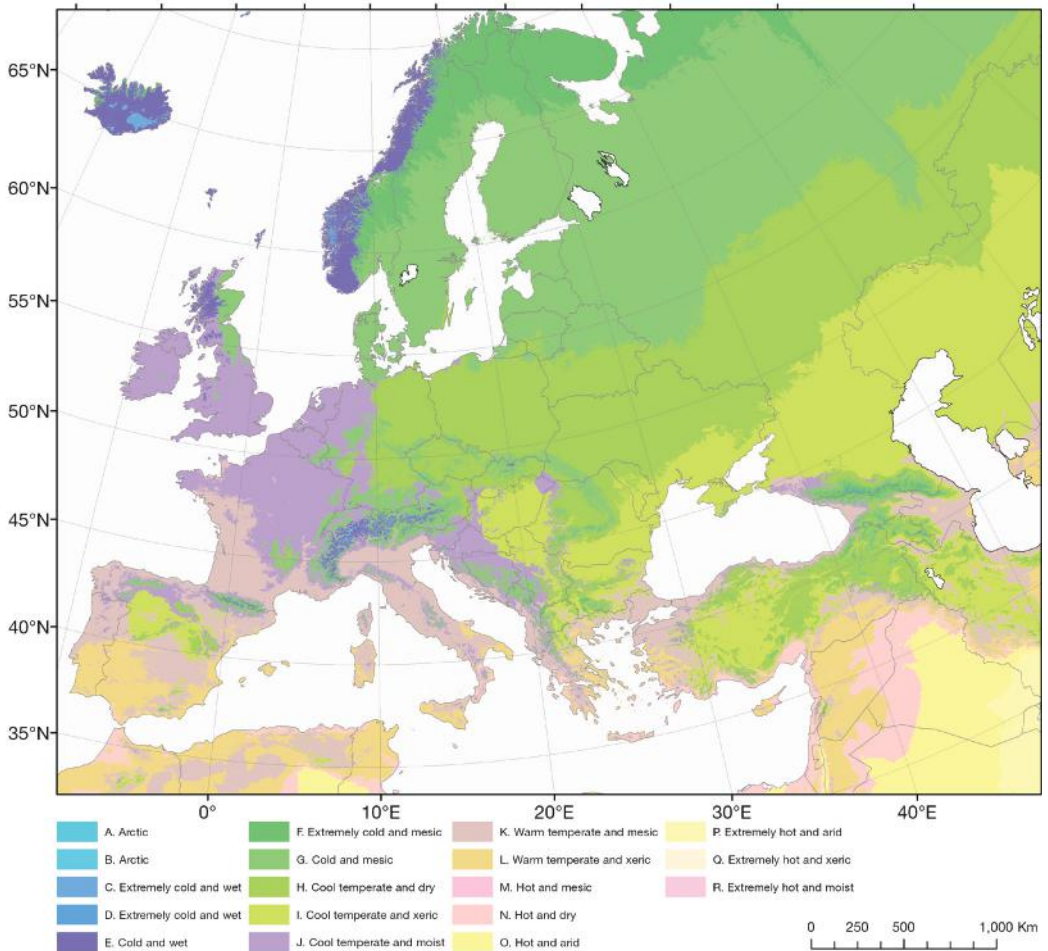
The working group concluded that the global environmental stratification with 14 zones in Europe, as presented by Metzger *et al.* (2013), is too detailed for the purpose of developing the pan-European genetic conservation strategy for forest trees. The five classes of temperature occurring in Europe (extremely cold, cold, cool, warm and hot) were kept as presented by Metzger *et al.* (2013), with the exception of the Arctic areas, which were merged into the extremely cold areas. To make it reflect the broader-scale adaptation of forest trees, the working group decided to aggregate the four classes of the aridity index occurring in Europe (xeric, dry, mesic and moist) into two classes (dry and moist). The modified aggregation resulted in a total of eight environmental zones for Europe (see Figure 2). In the legend of Figure 2, the letters show how the original zones of Metzger *et al.* (2013) were aggregated into the new ones by the working group.

The distribution ranges of the pilot tree species were then divided into smaller areas following the country × zone approach using the eight aggregated envi-

ronmental zones. All conservation units of the pilot species were then assigned to these areas based on their location. In cases where there were more than one unit per the “country × zone” area in the database, the unit for the core network was selected using the following process and criteria:

Eliminate before ranking:

- all *ex situ* units; and
- all the units with the origin of material indicated as “introduced” (but keep unknown and autochthonous).

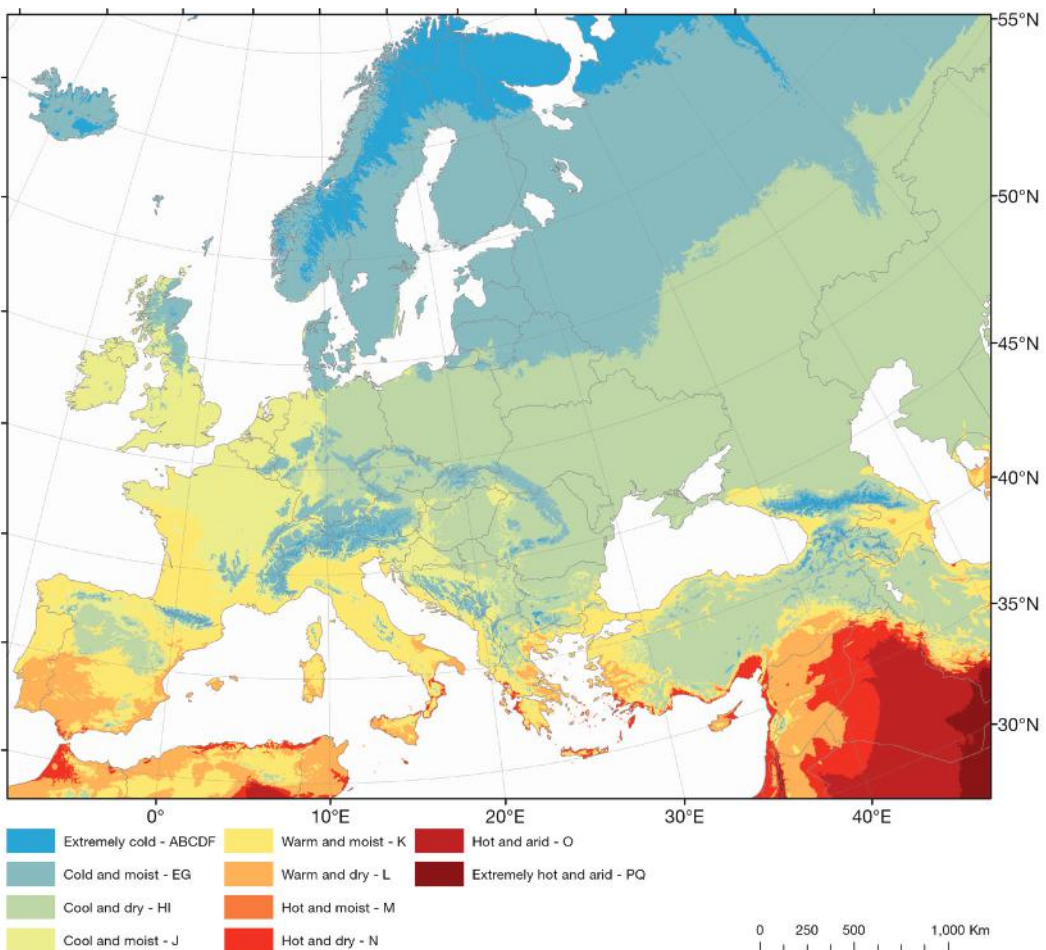


**Figure 1.** Environmental zoning of Europe (Metzger *et al.*, 2013).

Ranking based on a synthesis of:

- number of reproducing trees (larger numbers are preferred);
- ownership (public preferred except if population is too small);
- management (prefer the ones where management interventions are allowed);
- area within the unit where the species occurs (larger areas are preferred); and
- other relevant factors?

If there were still more than one unit available after applying these criteria, the working group made the selection of the core unit on the basis of expert judgement.



**Figure 2.** Aggregated environmental zoning of Europe (based on Metzger *et al.*, 2013).



The EUFORGEN National Coordinators and the EUFGIS National Focal Points will later be asked to comment on the selection of the units in their country and they will have an opportunity to propose changes to the selection of the core units. While doing this, they should also keep in mind that it should be possible to collect seed or other reproductive material from the core units for research and production purposes.

Furthermore, additional conservation units covering migration routes, refugial areas and contact zones can be selected for the core network, where this information is available. In the case of marginal or scattered tree populations and rare or endangered tree species, it is recommended that duplicates within each “country × zone” area should be included.

Following the discussions at the workshop held in Järvenpää, Finland, in September 2012, it was recommended that the units for genetic monitoring should be chosen from the core network of the conservation units. However, due to particular criteria for the selection of units for genetic monitoring, such as accessibility, additional units could be suggested and added to the core network for this purpose.

### **Assessment of genetic conservation status of the pilot tree species**

An overall assessment of the genetic conservation status of the pilot tree species was done based on the information available in the EUFGIS Portal. A more comprehensive

assessment of dynamic genetic conservation efforts was recently carried out as part of the EUFGIS project (see Lefèvre *et al.*, 2013). As part of the conservation assessment, the working group also considered available information on distribution of neutral genetic diversity in the pilot species. In the case of *Abies alba*, *Fagus sylvatica*, *Fraxinus excelsior*, *Picea abies*, *Pinus brutia/halepensis*, *Pinus cembra*, *Pinus sylvestris*, *Populus nigra* and *Quercus petraea*, the availability of genetic diversity maps enables assessment of the distribution of genetic diversity to guide the selection of additional units. In the case of the other species (*Pinus nigra*, *Populus tremula*, *Sorbus torminalis*, *Castanea sativa*), only a qualitative and broad-scale analysis can be carried out by comparing the distribution of the conservation units and the broad genetic structure found at the continental scale.

### **Identification of gaps in dynamic conservation efforts**

Gaps in the existing conservation efforts were identified. In the case of adaptive diversity, the gaps were identified by overlaying the species distribution ranges with the environmental zones (see Section ‘Selection and ranking of conservation units’ above) occurring in each country and the location of the conservation units. Lists of environmental zones per country and per pilot species were then developed based on the “country × zone” approach. If no conservation unit existed within a given “country × zone” area, it was recorded as a gap.





## RESULTS

### Selected pilot tree species

The working group selected a total of 14 pilot tree species (Table 1).

**Table 1.** Pilot tree species

<b>Widely distributed and stand-forming species</b>
<i>Abies alba</i>
<i>Fagus sylvatica</i>
<i>Picea abies</i>
<i>Pinus brutia</i>
<i>Pinus halepensis</i>
<i>Pinus nigra</i>
<i>Pinus sylvestris</i>
<i>Quercus petraea</i>
<b>Widely distributed and scattered species</b>
<i>Fraxinus excelsior</i>
<i>Populus nigra</i>
<i>Populus tremula</i>
<i>Sorbus torminalis</i>
<b>Restricted-distribution and locally common species</b>
<i>Castanea sativa</i>
<b>Restricted-distribution and locally scattered species</b>
<i>Pinus cembra</i>

For all selected pilot tree species, the distribution maps have been compiled on the basis of existing literature and other information sources during the earlier EUFORGEN work. EUFORGEN Technical Guidelines for genetic conservation

and use are also available for the selected species. The distribution maps are available on the EUFORGEN website ([www.euforgen.org/distribution\\_maps.html](http://www.euforgen.org/distribution_maps.html)).

### Tentative units for the establishment of the core network

A summary of the conservation units, the total number of country × zones, and the number of tentatively selected units are presented in Table 2. The location of the units within the distribution ranges of the pilot species are shown in Annex 1. The maps also show the environmental zones within the distribution ranges.

As explained on page 7, a total of 38 *ex situ* units were excluded from the conservation assessment and the establishment of the core networks (*Castanea sativa* (1), *Fraxinus excelsior* (2), *Picea abies* (1), *Pinus brutia* (2), *Pinus cembra* (1), *Pinus halepensis* (1), *Pinus nigra* (15), *Pinus sylvestris* (11), *Quercus petraea* (4)), and 16 units with the origin of material indicated as “introduced” (i.e. *Abies alba* (2), *Fagus sylvatica* (1), *Fraxinus excelsior* (1), *Picea abies* (4), *Pinus nigra* (3), *Pinus sylvestris* (5)).

### Assessment of genetic conservation status of the pilot tree species

There are 1836 units conserving the pilot species *in situ*, covering a total of 205,803 ha and harbouring 2,173 tree populations. At the pan-European level, the conservation efforts are highly variable among the pilot tree species (Table 2). Some species have extensive coverage. Five species (*Abies alba*, *Fagus sylvatica*, *Picea abies*, *Pinus sylvestris* and *Quercus petraea*) are conserved in more than 200 units each and together these units represent 80% of all conservation units (1,747) established for the pilot species. However, other species are less well covered. In most of the 2,173 tree populations, management is allowed (Table 4).

### Assessment of available genetic data on selected pilot tree species

There is a variety of coverage levels in the genetic diversity studies currently available for the pilot tree species. In the case of *Abies alba*, *Fagus sylvatica*, *Fraxinus excelsior*, *Picea abies*, *Pinus brutia/halepensis*, *Pinus cembra*, *Pinus sylvestris*, *Populus nigra* and *Quercus petraea*, the availability of genetic diversity maps enables assessment of the range-wide distribution of genetic diversity to guide the selection of additional units for the core network. In the case of the other species (*Pinus nigra*, *Populus tremula*, *Sorbus torminalis* and *Castanea sativa*), only a qualitative and broad-scale analysis can be carried out by comparing the

**Table 2.** Total number of units and country × zones, and the number of tentatively selected units for the core networks of the pilot tree species

Species	Total number of units	No. of country × zone in distribution range <sup>(1)</sup>	Number of tentatively selected units
<b>Widely distributed and stand-forming species</b>			
<i>Abies alba</i>	297	69	30
<i>Fagus sylvatica</i>	471	102	39
<i>Picea abies</i>	447	75	39
<i>Pinus brutia</i>	60	19	5
<i>Pinus halepensis</i>	24	18	4
<i>Pinus nigra</i>	109	61	23
<i>Pinus sylvestris</i>	285	97	33
<i>Quercus petraea</i>	247	125	34
<b>Widely distributed and scattered species</b>			
<i>Fraxinus excelsior</i>	83	147	25
<i>Populus nigra</i>	29	149	12
<i>Populus tremula</i>	30	140	6
<i>Sorbus torminalis</i>	30	124	13
<b>Restricted-distribution – locally common species</b>			
<i>Castanea sativa</i>	14	84	8
<b>Restricted-distribution – locally scattered species</b>			
<i>Pinus cembra</i>	47	24	7

Notes: (1) Areas smaller than 50 km<sup>2</sup> were not included for the species with restricted distribution. For widely distributed species, the threshold was 100 km<sup>2</sup>.

distribution of the conservation units and the broad genetic structure found at the continental scale.

There is a lack of information on genetic diversity within the conservation units. It is not known exactly which conservation populations have been sampled by the previous or ongoing genetic diversity studies in Europe. The ongoing linking of the

EUFGIS and (GD)<sup>2</sup> (GeoReferenced Database of Genetic Diversity; <http://gd2.pierroton.inra.fr>) databases by the FORGER project ([www.fp7-forger.eu](http://www.fp7-forger.eu)) will be useful for more detailed analysis of how many conservation units have been sampled by the earlier studies and how many other tree populations have been sampled in the vicinity of the units ([http://portal.eufgis.org/search/#search\\_gd2](http://portal.eufgis.org/search/#search_gd2)).

**Table 3.** Total number of conservation units and the number of units per conservation objectives in the pilot tree species

Species	To maintain genetic diversity in large tree populations			To conserve specific adaptive phenotypic traits in marginal or scattered tree populations				To conserve rare or endangered tree species with populations consisting of a low number of individuals				Total units
	No. of reproducing trees			No. of reproducing trees				No. of reproducing trees				
	Units	>5001	501-5000	Units	>5001	501-5000	51-500	Units	501-5000	51-500	15-50	
<b>Widely distributed and stand-forming species</b>												
<i>Abies alba</i>	253	63	190	28		6	22	16		10	6	297
<i>Fagus sylvatica</i>	423	149	274	42	4	6	32	6		6		471
<i>Picea abies</i>	417	199	218	28	1	5	22	2	1	1		447
<i>Pinus brutia</i>	58	55	3	1		1		1			1	60
<i>Pinus halepensis</i>	24	1	23	0				0				24
<i>Pinus nigra</i>	92	41	51	14		4	10	3	1	1	1	109
<i>Pinus sylvestris</i>	251	73	178	33	1	3	29	1		1		285
<i>Quercus petraea</i>	220	71	149	22		1	21	3		2	1	247
<b>Widely distributed and scattered species</b>												
<i>Fraxinus excelsior</i>	35	3	32	39	2	4	33	9	1	6	2	83
<i>Populus nigra</i>	3		3	6		2	4	20	1	9	10	29
<i>Populus tremula</i>	12	4	8	16				16	2	2		30
<i>Sorbus torminalis</i>	1		1	12				12	17	1	6	30
<b>Restricted-distribution – locally common species</b>												
<i>Castanea sativa</i>	10	2	8	3				3	1		1	14
<b>Restricted-distribution – locally scattered species</b>												
<i>Pinus cembra</i>	37	3	34	7	1	3	3	3	1	1	1	47

**Table 4.** Characterization of the 2,173 populations according to the level of management allowed

Species	Conservation by active intervention carried out	Minimal intervention allowed	No intervention allowed	No Information	Total no. of Units
<b>Widely distributed and stand-forming species</b>					
<i>Abies alba</i>	178	107	7	5	297
<i>Fagus sylvatica</i>	215	219	19	18	471
<i>Picea abies</i>	207	189	49	2	447
<i>Pinus brutia</i>	2	57	1		60
<i>Pinus halepensis</i>	22			2	24
<i>Pinus nigra</i>	46	49	3	11	109
<i>Pinus sylvestris</i>	138	124	14	9	285
<i>Quercus petraea</i>	108	111	5	23	247
<b>Widely distributed and scattered species</b>					
<i>Fraxinus excelsior</i>	40	8	20	15	83
<i>Populus nigra</i>	11	7	3	8	29
<i>Populus tremula</i>	4	5	4	17	30
<i>Sorbus torminalis</i>	14	10	2	4	30
<b>Restricted distribution – locally common species</b>					
<i>Castanea sativa</i>	7	2	5		14
<b>Restricted distribution – locally scattered species</b>					
<i>Pinus cembra</i>	13	21	13		47

**Table 5.** A list of large-scale or range-wide genetic studies undertaken for the pilot trees species. The list only includes studies done using neutral genetic markers.

Species	Data availability	Reference	Markers
<b>Widely distributed and stand-forming species</b>			
<i>Picea abies</i>	Yes	Tollefsrud <i>et al.</i> , 2008; Vendramin <i>et al.</i> , 2000	mtDNA; cpDNA
<i>Pinus sylvestris</i>	Yes	Cheddadi <i>et al.</i> , 2006	mtDNA
<i>Abies alba</i>	Yes	Liepert, Bialozyt and Ziegenhagen, 2002; Ziegenhagen <i>et al.</i> , 2005	mtDNA; cpDNA
<i>Fagus sylvatica</i>	Yes	Magri <i>et al.</i> , 2006	SSR and isozyme
<i>Quercus petraea</i>	Yes	Petit <i>et al.</i> , 2002	cpDNA
<b>Widely distributed and scattered species</b>			
<i>Fraxinus excelsior</i>	Yes	Heuertz <i>et al.</i> , 2004	cpDNA
<i>Pinus nigra</i>	Yes	Afzal-Raffii and Dodd, 2007	cpSSR
<i>Populus tremula</i>	Yes	de Carvalho <i>et al.</i> , 2010; Fussi, Lexer and Heinze, 2010	SSR, cpDNA
<i>Populus nigra</i>	Yes	Cottrell <i>et al.</i> , 2005	cp DNA
<i>Sorbus torminalis</i>	Yes	Demesure <i>et al.</i> , 2000; Angelone <i>et al.</i> , 2007	Isozymes, cpDNA
<b>Restricted-distribution locally common species</b>			
<i>Castanea sativa</i>	Yes	Fineschi <i>et al.</i> , 2000	cp DNA
<b>Restricted-distribution locally scattered species</b>			
<i>Pinus cembra</i>	Yes	Teodosiu and Pärnuta, 2007; Gugerli <i>et al.</i> , 2001; Höhn <i>et al.</i> , 2009	Isozymes, mtDNA, cpDNA

## Identification of gaps

The gap analyses were done for the 46 pan-European region countries. The number of environmental zones in each country are: Albania (5), Andorra (2), Armenia (4), Austria (4), Azerbaijan (6), Belarus (2), Belgium (2), Bosnia and Herzegovina (5), Bulgaria (5), Croatia (5), Cyprus (3), Czech Republic (3), Denmark (3), Estonia (1), Finland (2), France (5), FYR Macedonia (5), Georgia (5), Germany (4), Greece (7), Hungary (3), Iceland (2), Ireland (2), Italy (7), Latvia (1), Liechtenstein (2), Lithuania (2), Luxembourg (2), Malta (1), Moldova (1), Montenegro (4), The Netherlands (1), Norway (3), Poland (4), Portugal (5), Romania (4), Russia (5), Serbia (5), Slovakia (4), Slovenia (5), Spain (7), Sweden (3), Switzerland (4), Turkey (7), Ukraine (4), and United Kingdom (3). The pan-European region was divided into a total of 174 country × zones (>100 km<sup>2</sup>) units.

While developing the lists of country × zones for the pilot tree species, areas smaller than 50 km<sup>2</sup> were not considered for the species with restricted-distribution. The threshold for the widely distributed species was 100 km<sup>2</sup>. The reason is that the species distribution maps were developed at the pan-European scale and therefore their spatial resolution does not allow, in many cases, reliable analysis of species occurrence at a local scale within a country.

The working group identified four types of gaps: (1) countries with no units;

(2) countries have units but no data (or only partial data) are provided to the EUFGIS Portal; (3) country × zones without units; and (4) gaps in conserved neutral genetic diversity, i.e. no units in certain sub-regions. There is one more type of gap, which the study does not address however: certain species, e.g. riparian species such as *Populus nigra*, do not occur everywhere in a given distribution range, because they depend on specific ecological circumstances. These are in fact not real gaps.

For the first type of gap (countries with no units), the United Kingdom, for example, has indicated that the country does not yet have any conservation units that meet the minimum requirements. The second type of gap (country with units that lack data) consists of countries that have units (e.g. Belarus, Georgia, Germany and Ukraine) but which have entered either no data or, for various reasons, only part of their data, into the EUFGIS database.

Regarding the third type of gap (country × zone without units), it was possible to develop a detailed overview of the country × zones with no conservation units for the pilot species. These gaps are summarized in Table 6 and visualized in maps in Annex 1. This study is predominantly about this type of gap.

The fourth type of gap (relating to neutral genetic diversity) also reflects the overall gaps in conservation efforts.

In several pilot species (e.g. *Populus nigra*, *Fraxinus excelsior*, *Sorbus torminalis*), there are considerable gaps in conservation efforts within their distribution ranges.

Furthermore, in some species, the gaps are found in certain subregions where they occur marginally (e.g. *Quercus petraea* in northern Europe).

**Table 6.** Number of country × zone areas, countries and zones with and without genetic conservation units within the distribution ranges of the pilot tree species

Species	Countries <sup>(2)</sup>			Environmental zones			Country × env. zone		
	Total <sup>(3)</sup>	With units	Without units	Total <sup>(4)</sup>	With units	Without units	Total <sup>(5)</sup>	With units	Without units
<b>Widely distributed and stand-forming species</b>									
<i>Abies alba</i>	20	14	6	5	5	0	69	31	38
<i>Fagus sylvatica</i>	31	19	12	5	5	0	102	39	63
<i>Picea abies</i>	26	19	7	5	5	0	75	39	36
<i>Pinus brutia</i>	6	2	4	6	4	2	19	5	14
<i>Pinus halepensis</i>	5	3	2	6	3	3	18	4	14
<i>Pinus nigra</i>	15	12	3	7	4	3	61	23	38
<i>Pinus sylvestris</i>	33	17	16	6	4	2	97	33	64
<i>Quercus petraea</i>	36	23	13	7	4	3	125	34	91
<b>Widely distributed and scattered species</b>									
<i>Fraxinus excelsior</i>	41	17	24	7	3	4	147	25	122
<i>Populus nigra</i>	38	9	29	7	4	3	149	12	137
<i>Populus tremula</i>	41	5	36	6	3	3	140	6	134
<i>Sorbus torminalis</i>	32	10	22	7	4	4	124	13	111
<b>Restricted-distribution – locally common species</b>									
<i>Castanea sativa</i>	25	5	20	7	3	4	84	8	76
<b>Restricted-distribution – locally scattered species</b>									
<i>Pinus cembra</i>	9	4	5	5	2	3	24	7	17

NOTES: (2) Of the 46 countries included in the pan-European region – see the list on page 5; (3) The countries were included when the occurrence of the species within the country × environmental zones exceeded the thresholds (>50 km<sup>2</sup> for species with restricted distribution, and 100 km<sup>2</sup> for widely distributed species); (4) Occurrence of the species within the environmental zones exceeding the threshold (>50 km<sup>2</sup> or 100 km<sup>2</sup>). (5) Occurrence of the species within the country × environmental zones exceeding the threshold (>50 km<sup>2</sup> or 100 km<sup>2</sup>).

## IMPLEMENTATION OF THE PAN-EUROPEAN GENETIC CONSERVATION STRATEGY

The strategy outlined in this report provides a concept for defining the targeted (minimum) level of genetic conservation for forest trees at the pan-European level. The concept has been tested with the pilot species but the approach is applicable to all tree species in Europe. The report also presents the criteria for selecting dynamic conservation units for the core network, which represents the minimum level of genetic conservation considered necessary at the pan-European level. In addition, the report identifies gaps in the current conservation efforts of the pilot species, for further action. The implementation of the strategy remains the responsibility of each country. Countries are expected to give special attention to the management of the units selected for the European core networks. Furthermore, countries should try to establish new units in the areas identified as gaps in this report. The pan-European strategy thus helps countries in planning and implementing their conservation work. The role of the EUFORGEN Steering Committee is to promote the implementation of the strategy, identify additional units for the core network once countries have established new ones to fill the gaps, and monitor the progress made.

Following the minimum requirements for the dynamic conservation units, static *ex situ* collections are not accepted into the core network. However, we recognize that they complement the implementation of the pan-European strategy and such collections should be established if this is the only way to conserve specific genetic diversity in living material. Usually, there is no need for duplicating selected units in each country × zone. For marginal or scattered tree populations and for rare or endangered species, however, it is recommended that countries identify duplicate units, when possible, as a backup within each environmental zone. This action will also remain a national responsibility. The following sections discuss additional issues related to the implementation of the pan-European conservation strategy.

### Climate change

The pan-European core network of dynamic conservation units can help to mitigate the negative effects of climate change. Climate change has been shown to be responsible for significant changes in phenology of tree populations, such as budburst (Menzel *et al.*, 2006). However, the effects of climate change



on long-lived tree species are likely to be variable, complex and difficult to predict. For example, competition with other species and potential influx of new pests and diseases are of major concern. Due to climate change, it may be necessary to: (1) predict the most vulnerable populations and species; (2) monitor the impact of climate change on the units; and (3) actively manage the units to mitigate the negative effects of climate change.

As it is impossible to predict all the effects of climate change, only a subset of likely effects can be mitigated for. Therefore, efforts should be made to identify the most vulnerable tree populations and species. These are likely to be those on the edge of distribution ranges or living at the environmental limits of a species. In particular, southern European tree populations are likely to be affected most by increases in temperature, and these populations often harbour high genetic diversity as they are found in areas of glacial refugia (Hampe and Petit, 2005). However, the response of these populations to climate change depends on species-specific requirements and adaptation potential of each population. Information from provenance tests and climate change models can be used for assessing the predicted impacts of range shifts for individual units and the core network.

It is crucial to know what is happening within the units as a result of climate

change and this makes field inventories a key activity. Such monitoring can reveal changes in species composition or in the occurrence of particular indicator species and competitors of target species. However, this type of monitoring is a long-term process and there are still many knowledge gaps concerning the impacts of climate change. Recent reports suggest that further research is needed to increase our understanding of the potential impacts of climate change on forest trees, such as studies on growth rhythm and climate change (Savolainen *et al.*, 2007) and changes in genetic composition and evolutionary change of tree populations over time (Kremer, 2007).

Active management of the units may be necessary to mitigate the effects of change. Management may focus on improving growth and reproduction *in situ*, as well as reducing competition between target species and other plants (including invasive plant species) and shortening regeneration time. It could also include *ex situ* measures, such as moving populations from vulnerable locations to more suitable areas or creating a multiple population breeding system (MPBS) as recommended by Eriksson, Namkoong and Roberds (1993).

### Monitoring progress

Monitoring of the progress made in implementing the pan-European strategy is necessary to demonstrate achievements and to obtain information for the

revision of the strategy. This also supports the management of the core network of the conservation units. The progress made by the countries needs to be evaluated frequently to verify which gaps have been filled and to detect any problems or constraints. For this purpose, various indicators could be used, such as calculating “gap filling” ratios (i.e. number of gaps filled per number of gaps to be filled) or the overall completion status of the core networks (number of country × zones with units compared with the total number of country × zones within the distribution ranges). Subsequently, EUFORGEN could develop annual or bi-annual summary reports per species and per country.

### **Revision of the strategy**

Once the core networks of the dynamic conservation units have been established for the pilot species, they need to be updated in the future. The strategy is based on information that was available in the EUFGIS Portal on 16 February 2015. At that time, the database contained information on the units in

31 countries. Some countries that have agreed to participate by nominating a national focal point, have not yet entered their data into the database. It is also possible that additional countries will join EUFGIS at a later date. The EUFGIS Portal must therefore be viewed as a dynamic, evolving database so that data on new units can be entered into the system as they become available. Some of these later entries might also be incorporated into the core conservation networks.

The global environmental zoning (Metzger *et al.*, 2013) was used by the working group for developing an aggregated climatic zoning of Europe to simplify the zoning. In addition, the list of species selected as pilot species for the strategy may be expanded. Thus, an updating procedure will have to be agreed on how to make future changes to the core networks. This would be the duty of the EUFORGEN Steering Committee. The EUFORGEN Secretariat could then perform the updating as a part of the maintenance of the EUFGIS Portal.



**RECOMMENDATIONS**

The working group recommends that:

1. All countries are strongly requested to finalize their work and upload the data on their units to the EUFGIS database.
2. Monitoring of progress must be continued at the European level.
3. Adequate resources should be allocated for the future maintenance and development of the EUFGIS database. This database is crucial for the implementation of the pan-European strategy for genetic conservation of forest tree species.
4. A strategy should be developed for mitigating the negative effects of climate change. This should include identification of vulnerable species or populations, identification of potential climate change indicators and threats, and a review of possible active management measures.
5. Within EUFORGEN, the use of the working group approach should be continued and interaction between relevant working groups should be facilitated as relevant and needed.



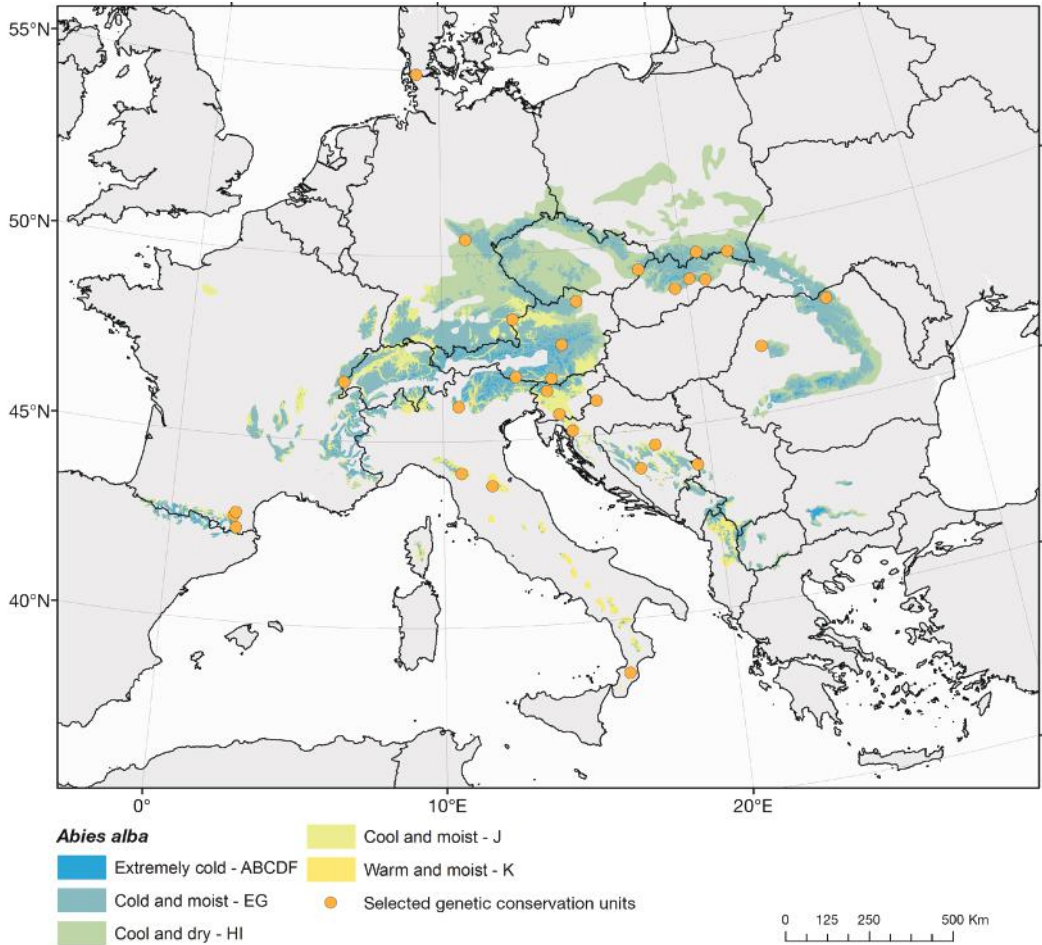
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## ANNEX 1. LOCATION OF SELECTED GENETIC CONSERVATION UNITS AND ENVIRONMENTAL ZONES<sup>1</sup> WITHIN THE DISTRIBUTION RANGES OF FOURTEEN PILOT TREE SPECIES.

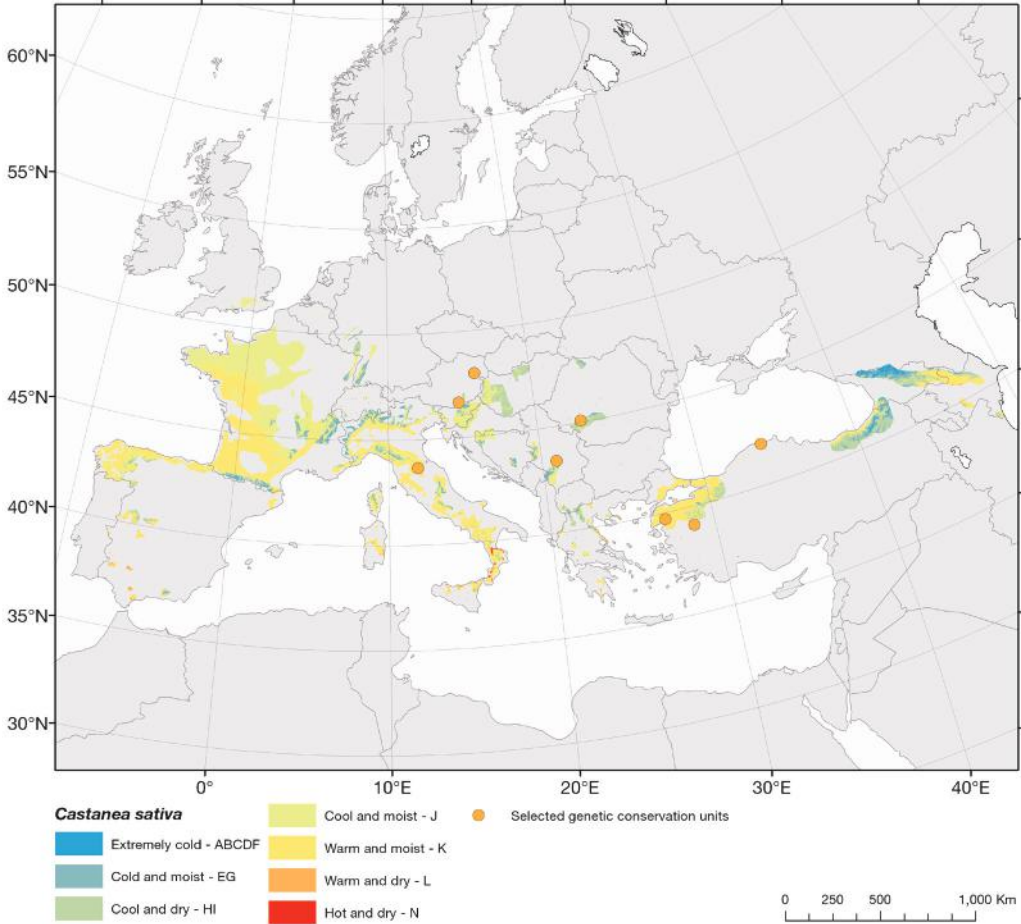
### *Abies alba*

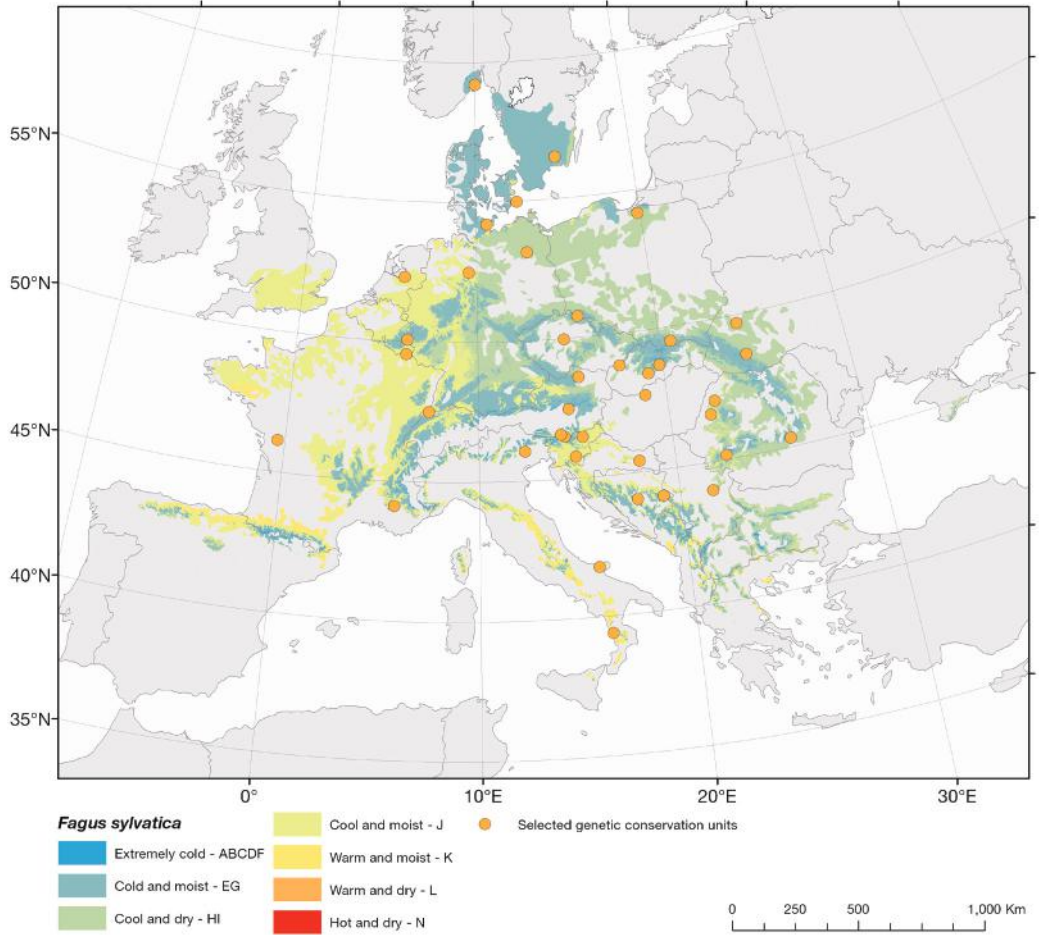


<sup>1</sup> Aggregated environmental zoning of Europe (based on Metzger *et al.*, 2013).

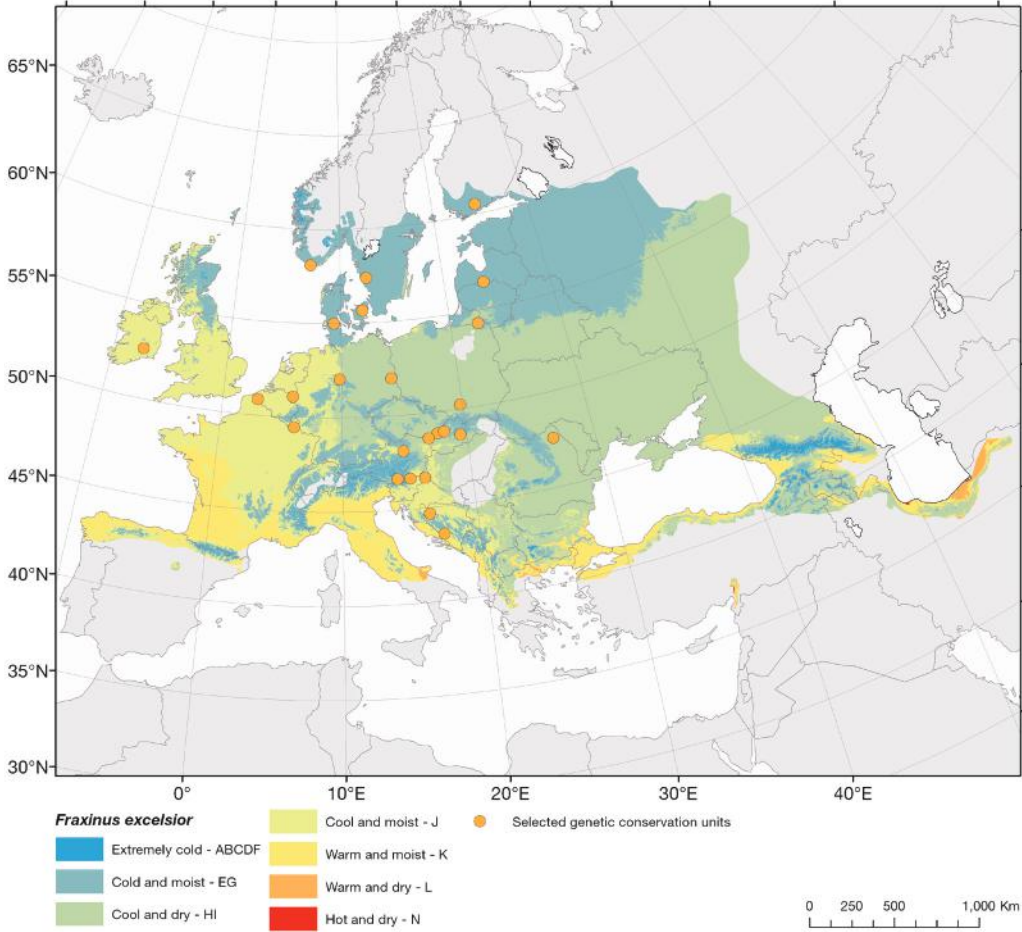


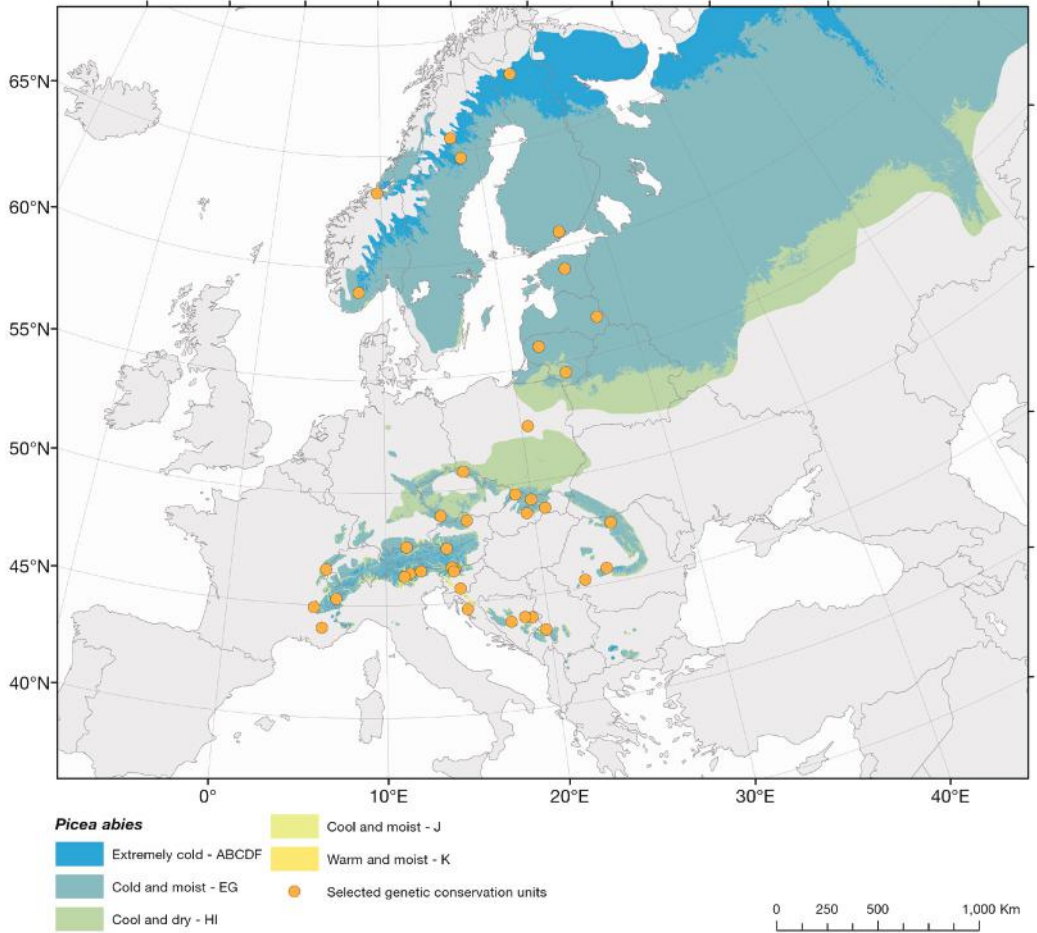
*Castanea sativa*



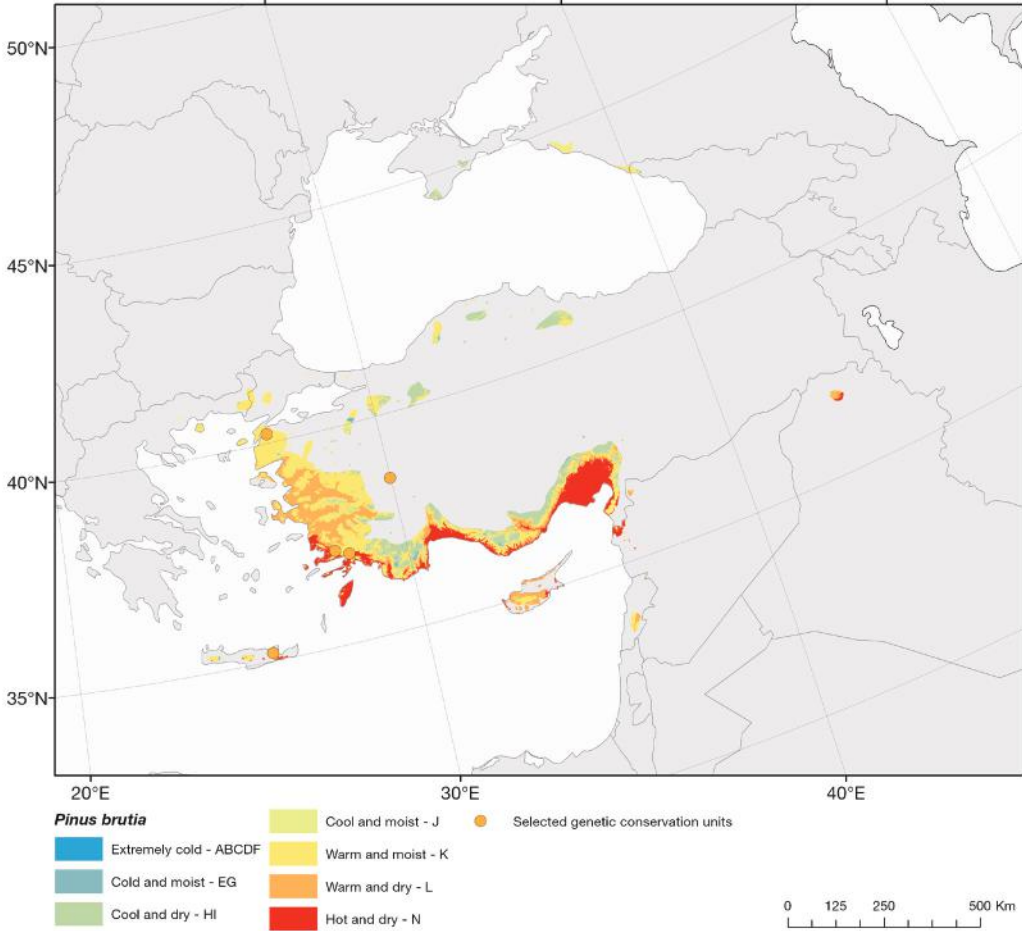
*Fagus sylvatica*

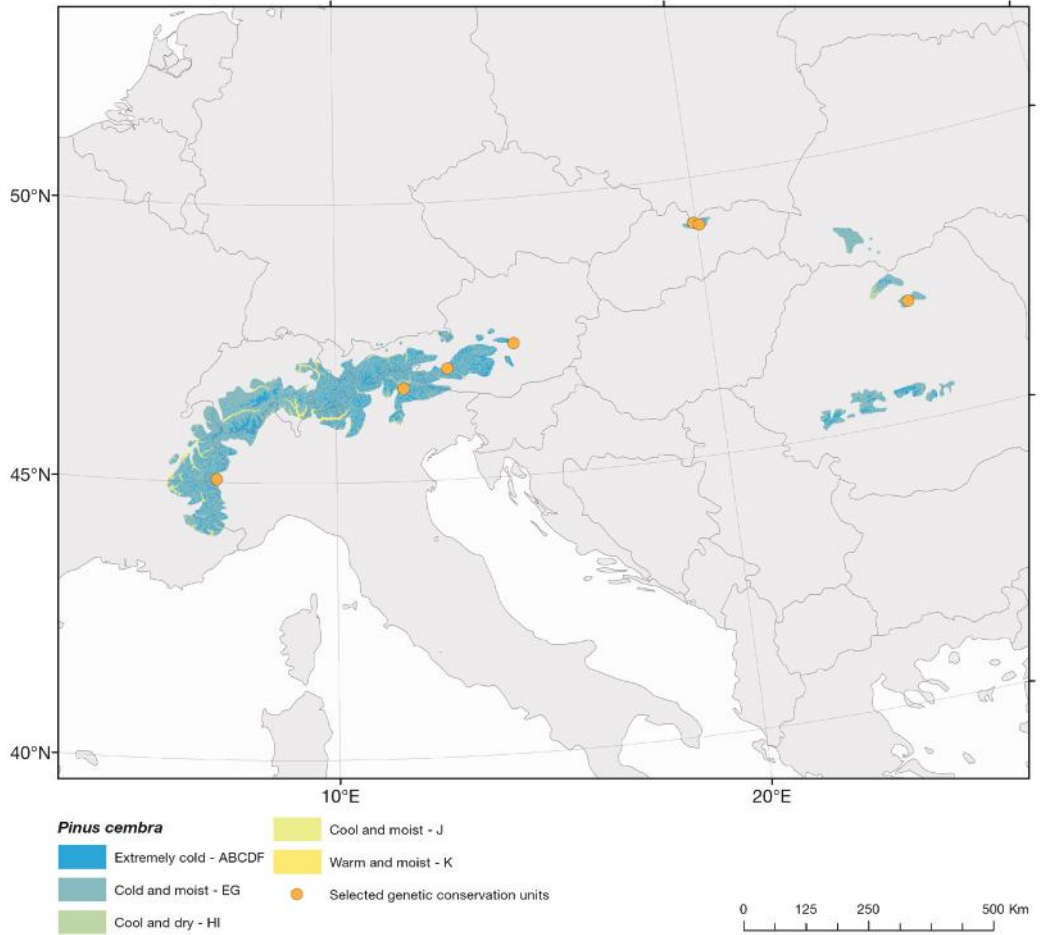
*Fraxinus excelsior*



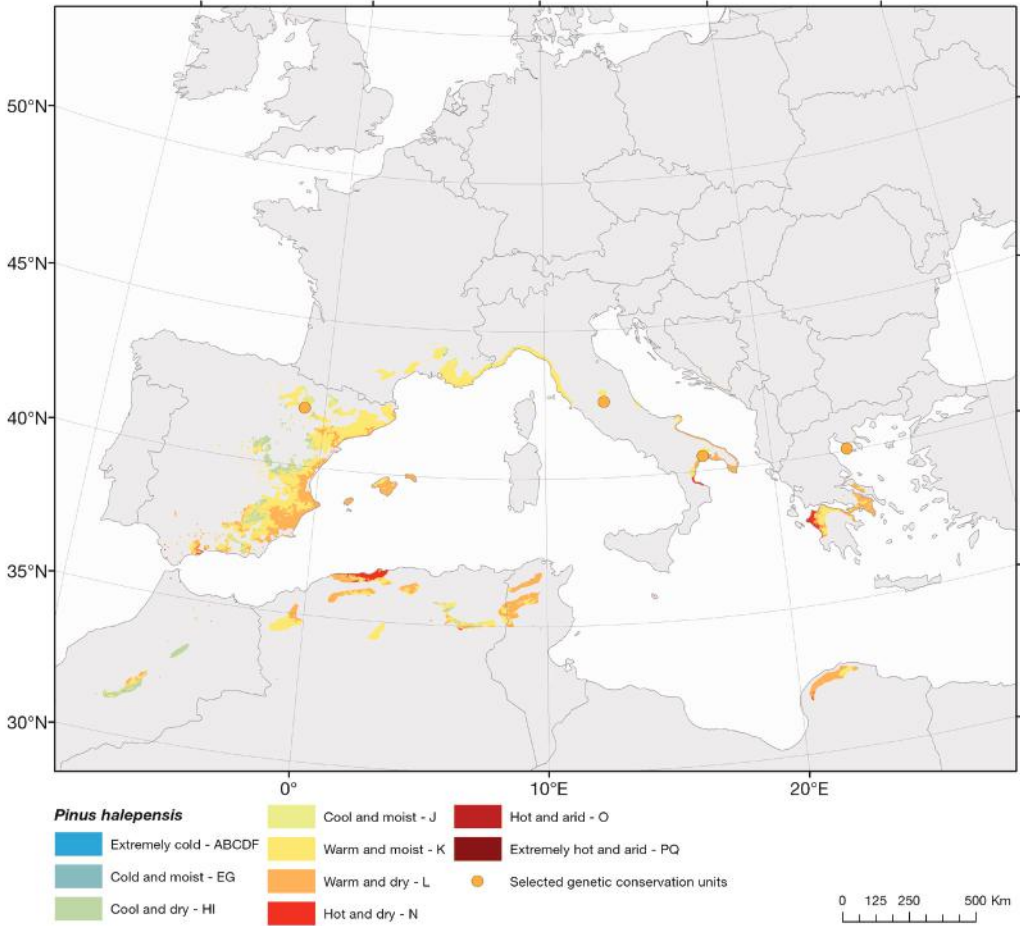
*Picea abies*

*Pinus brutia*

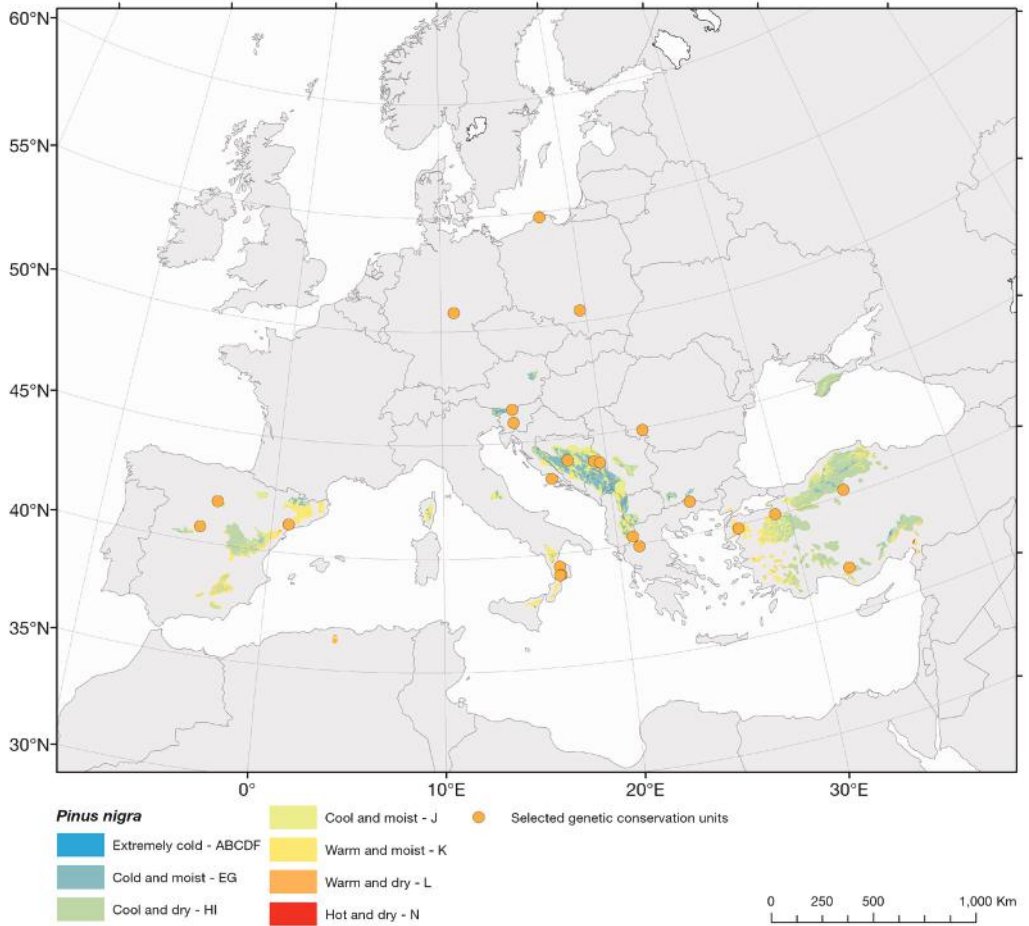


*Pinus cembra*

*Pinus halepensis*

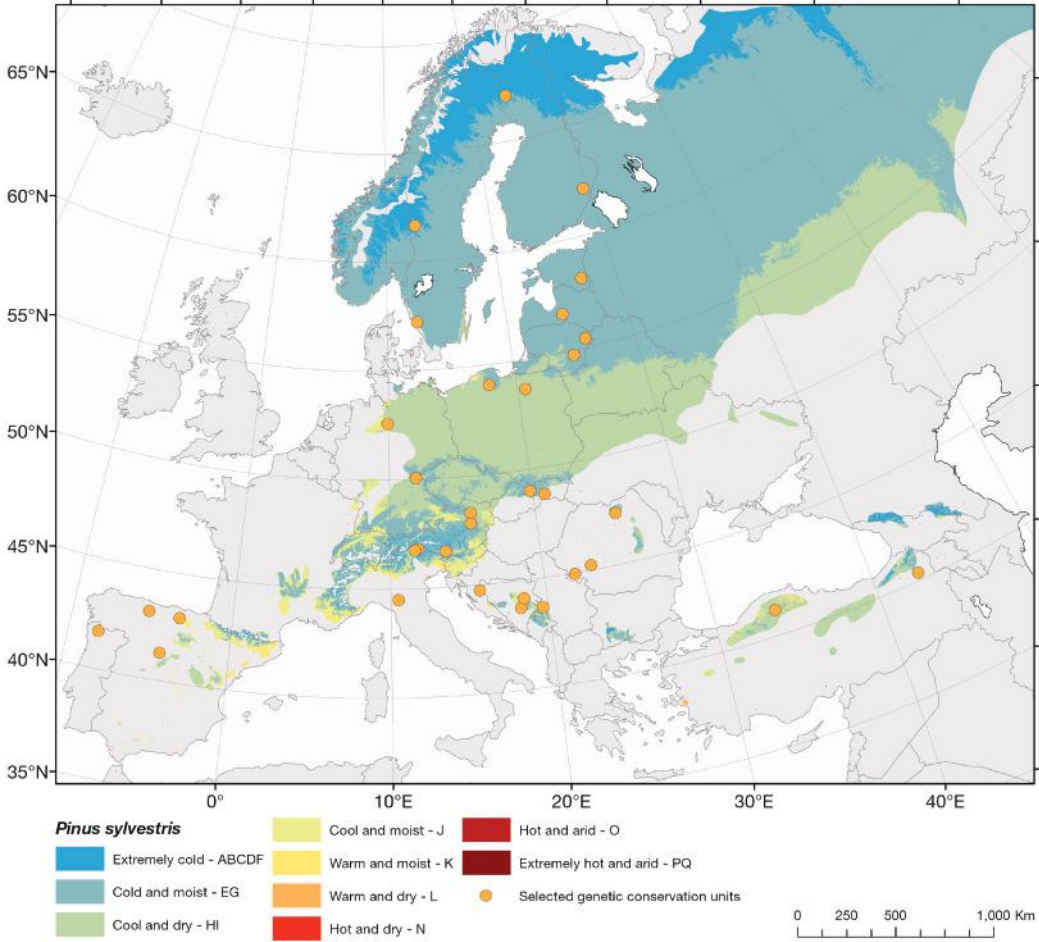


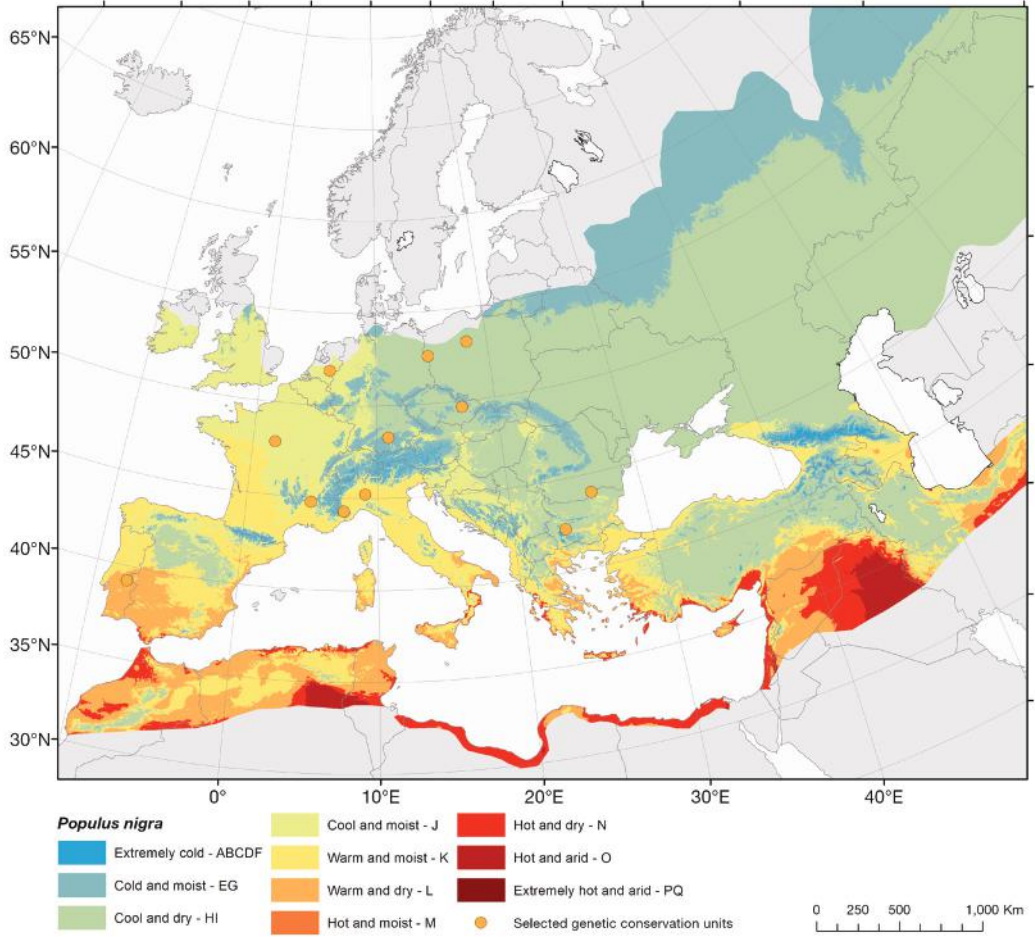


*Pinus nigra*

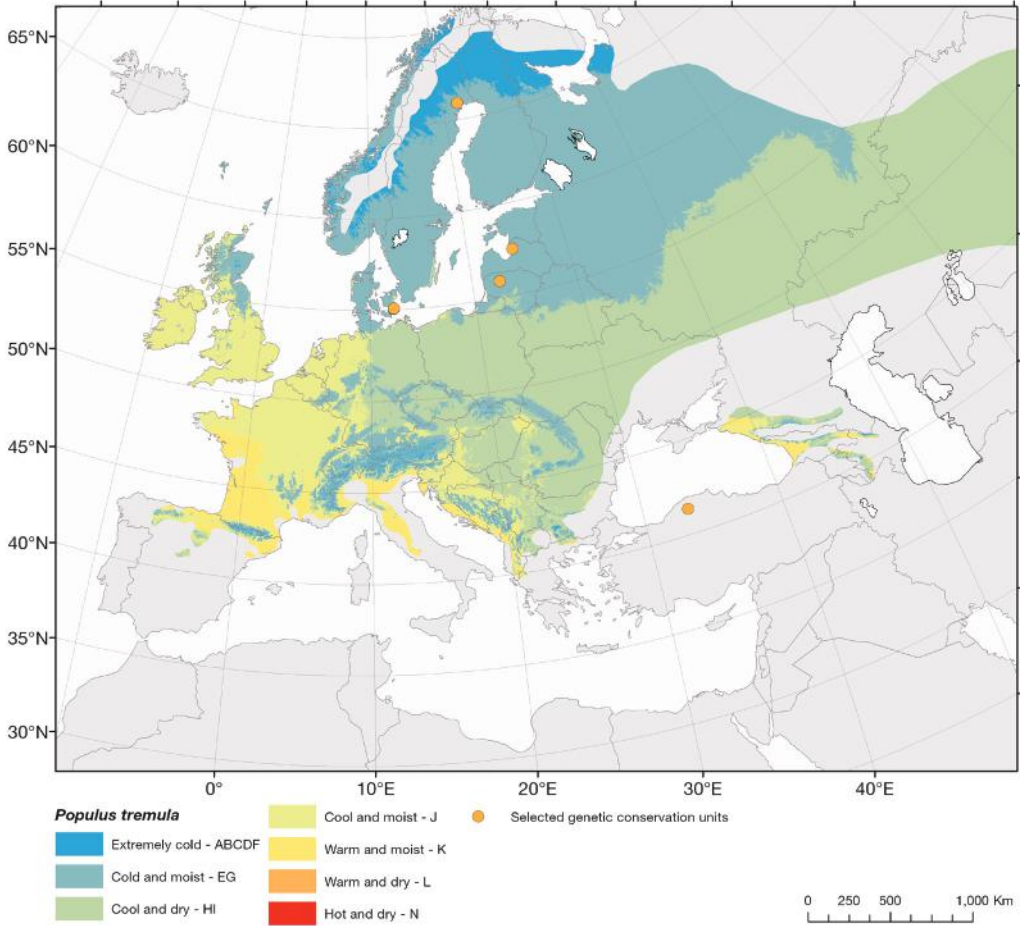


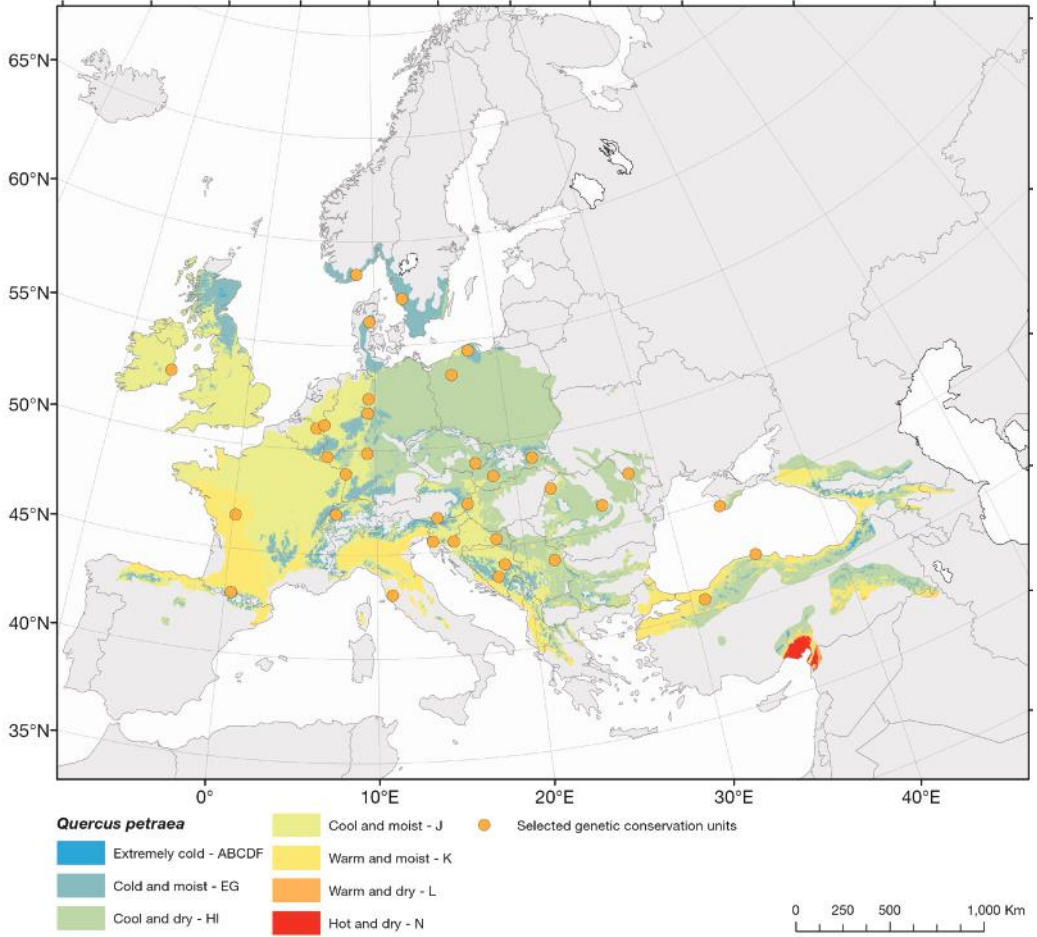
*Pinus sylvestris*



*Populus nigra*

*Populus tremula*



*Quercus petraea*

*Sorbus torminalis*

