

ARTICLE

SHORT COMMUNICATION

The Spanish Network of Genetic Conservation Units: a cooperative tool for the conservation and sustainable use of forest genetic resources under a changing environment

Red Nacional de unidades de conservación genética: una herramienta cooperativa para la conservación y el uso sostenible de los recursos genéticos forestales bajo un ambiente cambiante

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Abstract: *Aim of study:* Genetic diversity is essential for forest resilience in the context of climate change. With the aim of preserving the intraspecific genetic variation and the evolutionary dynamics of the main forest tree species throughout their distribution range, Spain is establishing a National Network of Genetic Conservation Units. *Area of study:* Genetic conservation units are selected across Spain according to the distribution range of each species, initially using national-scale regions of provenance to identify populations adapted to distinct local environmental conditions. *Material and methods:* The existing proposal consist of 298 *in situ* genetic conservation units (plus 32 backup units) involving 20 forest tree species (out of 62 species in total). The establishment of this National Network requires an important effort of coordination involving actors at the regional, national and international level, fieldwork, data analyses and monitoring. *Main results:* Thanks to an integrative workflow and an active collaboration among all actors involved, the implementation of the National Network of Genetic Conservation Units is thriving, with an essential effort in the characterization of the units (both genetically and in terms of their threats and conservation value). *Research highlights:* The characterization of the genetic conservation units aims to make scientifically-based decisions for prioritizing forest populations in conservation and sustainable management programs.

Keywords: forest genetic resources; genetic diversity; *in situ* conservation; National Register and Catalogue of genetic conservation units.

Resumen: *Objetivo del estudio:* La diversidad genética es un pilar fundamental para la resiliencia de los bosques en un contexto de cambio climático. Con el objetivo de preservar la variación genética intraespecífica y el potencial evolutivo de las especies forestales principales en toda su área de distribución, España está creando una Red Nacional de Unidades de Conservación Genética. *Área del estudio:* Las unidades de conservación genética se seleccionan por toda España en función del área de distribución de cada especie, utilizando inicialmente las regiones de procedencia a escala nacional con el fin de identificar poblaciones adaptadas a distintas condiciones ambientales. *Material y métodos:* La propuesta actual incluye 298 unidades de conservación genética *in situ* (más 32 de respaldo) para 20 especies forestales (de un total de 62 especies). El establecimiento de esta Red Nacional requiere un esfuerzo importante de coordinación entre actores regionales, nacionales e internacionales, trabajo de campo, análisis de datos y monitoreo. *Resultados principales:* Gracias a un flujo de trabajo integrado y a la colaboración activa entre todos los actores involucrados, el establecimiento de la Red Nacional de Unidades de Conservación Genética está prosperando, con un esfuerzo esencial en la caracterización de las unidades (tanto a nivel genético como en relación con sus amenazas y su valor de conservación). *Aspectos destacados de la investigación:* La caracterización de las unidades de conservación genética tiene como objetivo tomar decisiones con base científica a la hora de priorizar las poblaciones forestales en los programas de conservación y gestión sostenible.

Palabras clave: conservación *in situ*; diversidad genética; recursos genéticos forestales; Registro y Catálogo nacionales de unidades de conservación genética.

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Supplementary information ↓

1. INTRODUCTION

Conserving biodiversity is key for ecosystem resilience and functions that are increasingly threatened by environmental change and anthropogenic stressors. The Convention on Biological Diversity (1992) recognizes that biological diversity, at all levels of organization -genes, species, ecosystems- have an

intrinsic value and sustains the life systems of the biosphere. Although genetic diversity is essential for the evolution and adaptation of forest populations, it has not been a priority until recently (Hoban et al., 2020; Laikre et al., 2020). This also applies to Mediterranean forests according to the new Mediterranean Forest Research Agenda 2030 (Bou Dagher-Kharrat et al., 2022; Fady et al., 2022). The Mediterranean basin is a unique area for the long-term conservation of genetic and taxonomic diversity due to extensive environmental change processes that operate in this region. It represents a significant reservoir of unique genetic diversity favourable to the evolutionary processes of Mediterranean plant species (Médail & Diadema, 2009). Understanding the amount, distribution and functional significance of genetic variation in natural populations is critical to implement genetic conservation strategies. Technological advances are allowing to address a wider range of these factors on an unprecedented scale, e.g., genetic *versus* genomic conservation (Allendorf et al., 2010; Chano et al., 2025). Moreover, methodological advances are permitting the integration of key components of forests characteristics to pursue relevant conservation strategies, namely linking patterns of genetic variation to environmental conditions and adaptive responses (Flanagan et al., 2018; Rellstab et al., 2021; Miryeganeh & Armitage, 2024).

The management and conservation of species require a political commitment from the whole community. In this context, a coordinated initiative was launched in the 1990s with the aim of promoting the protection and sustainable management of European forests. Established in 1994, the European Forest Genetic Resources Programme (EUFORGEN), focuses specifically on the characterization, conservation and management of forest genetic resources, taking evolutionary processes into account. To maximize the effectiveness of these initiatives, a National Network of *in situ* genetic conservation units (GCU) has been set up according to the pan-European minimum requirements (Koskela et al., 2013; De Vries et al., 2015). The information on GCU is stored in the European Information System on Forest Genetic Resources (EUFGIS, <http://portal.eufgis.org>), a platform supporting countries in their conservation efforts (Lefèvre et al., 2013).

An *in situ* genetic conservation unit is a natural population constituted by a group of individuals of one or more tree species that occupies a defined geographical area and is genetically isolated, to a certain degree, from other different groups. There are currently 3,520 GCU registered in 37 countries and for 118 species across Europe. Originally, the units were selected to cover environmental zones, which were used as a proxy for adaptive genetic variation (selecting at least one unit per zone; De Vries et al., 2015), without prior genetic knowledge, a costly information available for few species. With the evolution of technologies, genotyping is becoming more accessible, and European countries have started to characterize GCU with the aim of incorporating the evolutionary history of populations for several ecologically and economically important forest trees species. This effort has been possible through several European projects aiming at conserving and managing forest genetic resources: project B4EST (European Union Horizon, 2020a), project GenRes Bridge (European Union Horizon, 2020b), project GenTree (European Union Horizon, 2020c) and particularly project FORGENIUS (European Union Horizon, 2020d), which upgraded EUFGIS with the aim of improving access to forest genetic resources information and services for end-users.

Spain approved the national regulation Royal Decree 159/2022, (BOE, 2022) on the conservation and sustainable use of forest genetic resources and wild flora, following the recommendations of the EUFORGEN program and the Spanish strategy for the conservation and sustainable use of forest genetic resources (Jimenez et al., 2009). This regulation establishes the planning, coordination and collaboration instruments for both *in situ* and *ex situ* conservation of the forest genetic resources. The tool for *in situ* conservation is the implementation of the National Network of GCU. This National Network requires the coordination among actors at the regional, national and international levels. Several actions have been taken for its implementation (García del Barrio et al., 2018). In the present work, we outline the concept, development and implementation of this Spanish Network of GCU under a context of high species diversity and a complex regulatory framework including different levels and actors. We provide perspectives and recommendations for the conservation and sustainable use of forest genetic resources.

2. MATERIAL AND METHODS

The actors involved in the implementation of the National Network of GCUs include the authorities responsible for the registration and approval of GCUs. The Ministry for the Ecological Transition and the Demographic Challenge (MITECO) is responsible for the general roadmap, the coordination at the national level, the management of the National Register and Catalogue and reporting to the EUFORGEN program. The 17 Spanish regional governments are responsible for the approval of GCUs. The National Committee of Forest Genetic Resources is coordinating all these authorities. Other actors are involved at different stages of the implementation of the network, including forest owners, companies and administrative entities involved in forest management and forest genetic resources. Two organizations assist the MITECO, in the scientific implementation, characterization of the units, and promoting the dissemination of the network (ICIFOR-INIA-CSIC and TRAGSA). In addition, other research centers and universities assist the regional governments. To facilitate the interaction among all these actors, a workflow has been established, which is detailed below and summarized in the Figure 1a.

2.1. Requirements for *in situ* genetic conservation units

Units must be native population with a sufficient size to ensure reproduction, providing added value to the network, with a buffer zone and natural regeneration (BOE, 2022). The units were selected to cover the distribution of tree species according to their regions of provenance (Figure 1b; Alía *et al.*, 2009). The regions of provenance are areas with populations of similar ecological, phenotypical or genetic characteristics (DOCE, 1999), and are used to identify populations adapted to distinct local environmental conditions. The selection of units in a given region of provenance has been prioritized based on the existence of genetic data, or the prior declaration by the Regional Governments of seed sources (plant material of autochthonous origin), and preferentially located on public land property. These characteristics will facilitate their future management.

2.2. Characterization of the GCUs

The selected units are phenotypically and genetically characterized to confirm their representativeness within the network. For each unit, we selected, marked and georeferenced 25 trees, measured their diameter and collected some leaves for the genetic analyses. The choice of molecular markers follows the European strategy to ensure compatibility of results across the full distribution of a species. Single Nucleotide Polymorphisms (SNPs) for several forest tree species have been developed in previous European projects (B4EST and FORGENIUS) and are available to the public for the 20 species included in the network.

After each field visit and sampling, a report is prepared describing whether the unit meets the minimum requirements set by national regulations, as well as the access to the unit, the contact information of local authorities, and a description of the population. The report also includes management guidelines that address potential threats and provide recommendations for the long-term genetic conservation of the unit. These guidelines are integrated into the owners' forest management plans or other territorial management plans, such as those for protected areas or species.

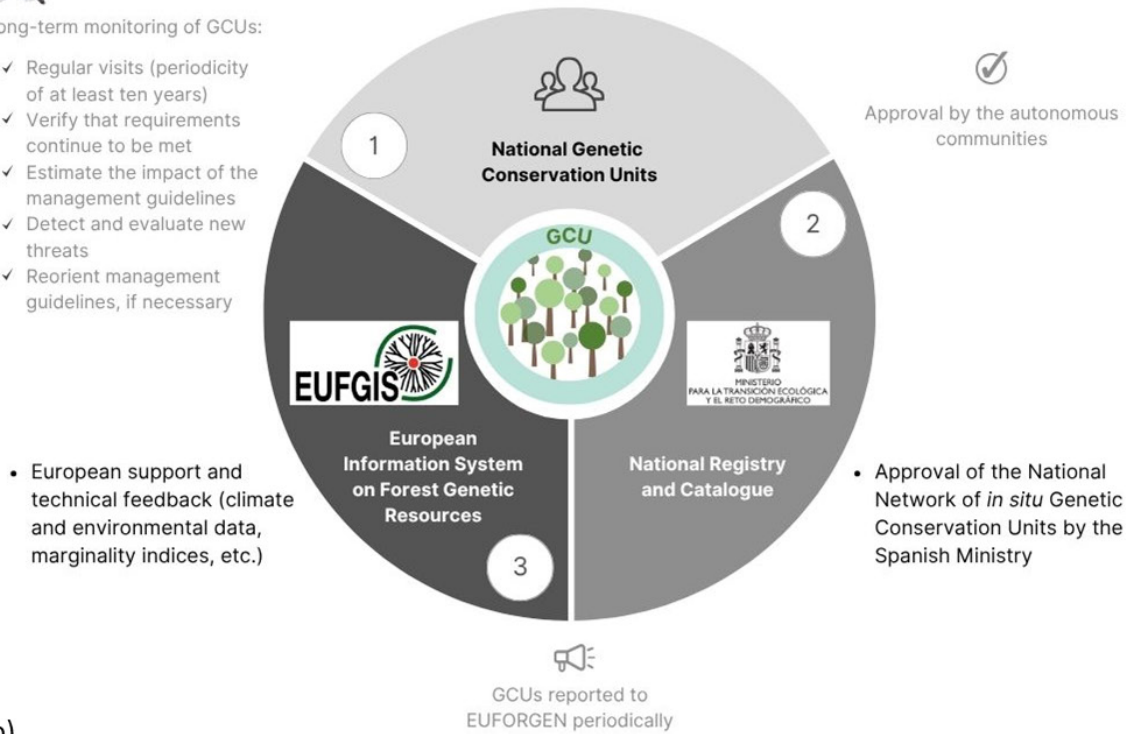
(a)



Long-term monitoring of GCU:

- ✓ Regular visits (periodicity of at least ten years)
- ✓ Verify that requirements continue to be met
- ✓ Estimate the impact of the management guidelines
- ✓ Detect and evaluate new threats
- ✓ Reorient management guidelines, if necessary

- Verify requirements according to the National Regulation
- Genetic characterization
- Management recommendations



(b)

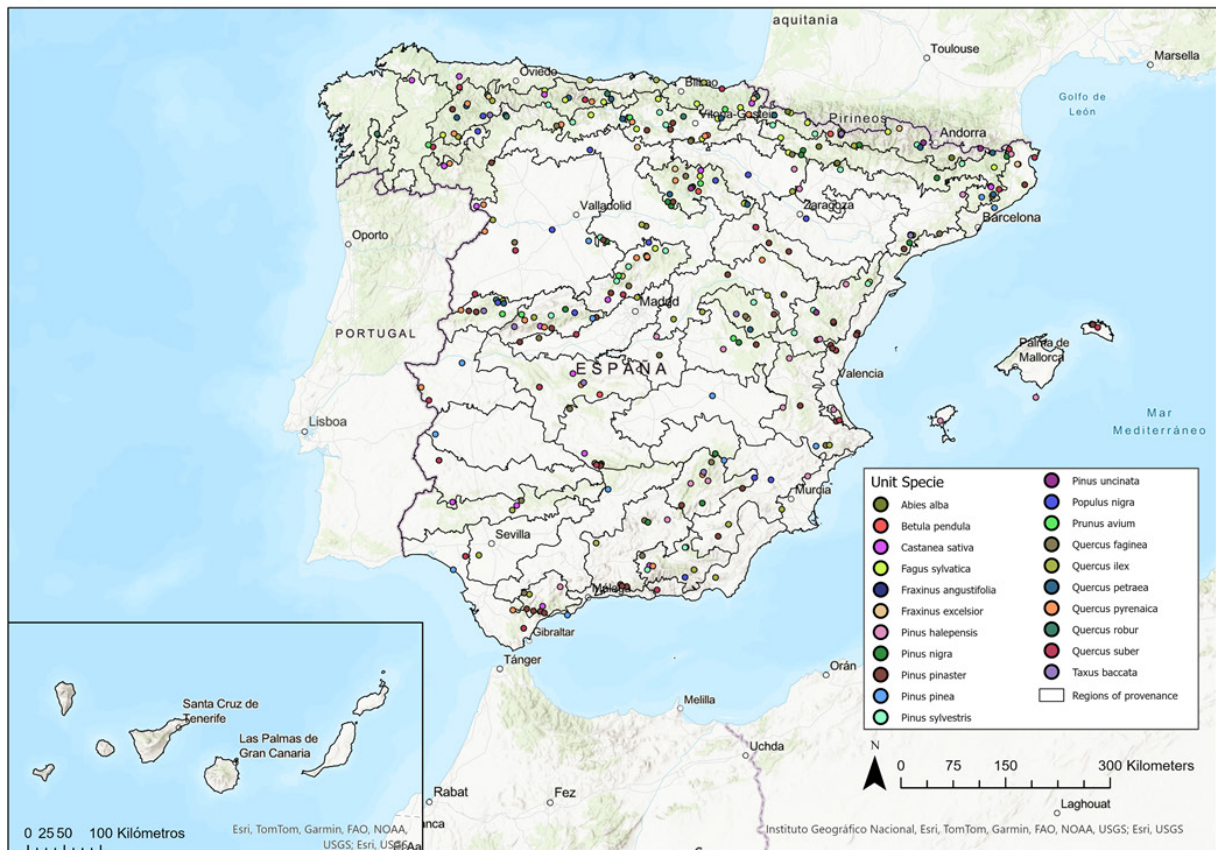


Figure 1. (a) Summary of actions for the implementation of the National Network of Genetic Conservation Units; (b) the National Network of Genetic Conservation Units, showing the 330 GCU's (circles) for the 20 species, along with the unified regions of provenance (black lines).
[Click here to see the proposed units in the GIS Viewer.](#)

2.3. Approval by the regional and national authorities

Each Regional Government reviews the proposal of the *in situ* GCUs. After the units are validated, the MITECO includes them in the National Register and Catalogue. Monitoring of the units is foreseen by regular visits, at least every ten years, to verify that their requirements continue to be met. These visits allow assessing the impact of the management guidelines, detecting and evaluating new threats and reorienting management guidelines if needed.

2.4. Uploading the information in a GIS Viewer

Information on *in situ* GCUs is integrated in a user-friendly GIS Viewer (Auñón, 2024), which is updated periodically. This platform includes the previously described GCU reports along with other relevant information, including current and future potential threats (based on Mauri *et al.*, 2022 for future climatic conditions and on Estadística General de Incendios Forestales-EGIF, Ministerio para la Transición Ecológica y el Reto Demográfico, 2025 for fire occurrence), whether the population is marginal or peripheral (as in Alía *et al.*, 2009) and whether the unit is designated as a natural protected area and/or a basic material for the production of forest reproductive material.

2.5. Incorporation of the national units in EUFGIS and monitoring

Approved *in situ* GCUs are reported to EUFORGEN periodically, through the national focal point, and they are integrated in the EUFGIS portal.

3. RESULTS AND DISCUSSION

Currently, the proposed Spanish Network of *in situ* genetic conservation units includes 298 units for 20 forest tree species (8 conifers and 12 broadleaves) (Figure 1b), while in the long term the aim is to define GCUs for 62 species (15 conifers and 47 broadleaves, see annex I of Royal Decree, 159/2022, BOE, 2022).

Several statistics provide a general characterization of the *in situ* genetic conservation network (Table 1). The number of GCUs varies greatly across species (from 4 to 40), mainly linked to the extent of the distribution of species. Some species have units spanning all their regions of provenance (*Fagus sylvatica* L., *Pinus pinaster* Ait., *Pinus pinea* L. and *Pinus uncinata* Mill.), while others cover only a small portion of their regions of provenance because their distribution is difficult to define (e.g., *Betula pendula*, *Populus nigra* and *Prunus avium* have less than 30% of their regions of provenance represented by GCUs). Another relevant statistic concerns the number of units defined as basic material (for production of reproductive material according to the EU regulation), which is rather high across species, with a mean of 68%. This proportion reflects the association of basic material with areas of differentiated ecological, phenotypic and genetic characteristics, where the species grows in favourable conditions and with sufficient individuals to ensure reproduction (as a drawback, this selection prevents sampling other areas of interest for the species). It is also noteworthy that the percentage of units located in natural protected areas varies from 16 to 86% (mean 50%). There are some pending issues related to the identification of the gaps in the network, to a more exhaustive analysis of the threats, and to the implementation of conservation approaches integrating area-based and species-based approaches (Heywood, 2019).

Table 1. Main characteristics of the 298 units forming the Spanish Network of Genetic Conservation Units (plus 32 backup units) (downloadable here from the GIS Viewer)

Species	GCU	Area (km)	% RP	% BM	% Protected	% Marginality threat	% Climatic threat	% Fire threat
<i>Abies alba</i>	6	583.25	100	33.3	50	50	33.3	16.7
<i>Betula pendula</i>	4	354.11	20	25	25	25	25	0
<i>Castanea sativa</i>	17	1295.11	40.5	70.6	52.9	29.4	35.3	5.9
<i>Fagus sylvatica</i>	24	3037.61	100	83.3	66.7	8.3	79.2	12.5
<i>Fraxinus excelsior</i>	10	275.40	52.9	40	50	30	40	10
<i>Pinus halepensis</i>	19	1943.60	95	63.2	15.8	10.5	63.2	15.8
<i>Pinus nigra</i>	16	1645.24	92.9	68.8	43.8	37.5	87.5	6.3
<i>Pinus pinaster</i>	41	4297.05	96.4	70	32.5	22.5	70	5
<i>Pinus pinea</i>	12	1795.69	100	66.7	41.7	41.7	33.3	0
<i>Pinus sylvestris</i>	22	3664.50	100	54.5	59.1	27.3	27.3	0
<i>Pinus uncinata</i>	7	691.06	100	71.4	28.6	57.1	NA	0
<i>Populus nigra</i>	13	476.98	28.3	69.2	38.5	7.7	30.8	7.7
<i>Prunus avium</i>	10	374.26	30.3	80	60	30	30	20
<i>Quercus faginea</i>	20	1902.26	76.9	90	70	20	45	0
<i>Quercus ilex</i>	27	2000.27	96.4	48.1	59.3	37	51.9	7.4
<i>Quercus petraea</i>	16	1204.83	92.9	56.3	56.3	31.3	75	12.5
<i>Quercus pyrenaica</i>	25	2202.05	82.1	80	60	24	56	8
<i>Quercus robur</i>	7	788.49	50	100	85.7	14.3	71.4	14.3
<i>Quercus suber</i>	22	2118.01	76.9	85.0	35	55	55	5
<i>Taxus baccata</i>	12	1659.31	46.2	58.3	75	8.3	25	8.3

GCU: number of proposed GCU; Area: area in km of the polygon corresponding to each GCU; %RP: percentage of proposed GCU corresponding to region of provenance; %BM: percentage of proposed GCU corresponding to basic material; % Protected: percentage of proposed GCU corresponding to protected natural area; % Marginality: percentage of GCU with geographic marginality threats; % Climatic: percentage of GCU with climatic threats; % Fire: percentage of GCU with fire threats; NA: not available.

Different threats were evaluated for each genetic conservation unit, including the percentage of units considered geographically marginal or peripheral (small, isolated stands, far from their biological optimum, as defined in Alía et al., 2009) across the species distribution (from 8 to 57%). These populations should be identified, since the Spanish plan for conservation of forest genetic resources establish some specific actions to preserve them. The percentage of units threatened by future climatic conditions is provided (based on Mauri et al., 2022), with values ranging from 25 to 88%. This information is essential for identifying the gaps in *ex situ* conservation, and developing the activities for the National Forest and Wild Flora Germplasm Bank. Finally, fire threats are also reported, though the percentage of units where the number of fires increased moderately to highly (above 23%) in the past years (between 1996-2005 and 2006-2015; (Estadística General de Incendios Forestales-EGIF,

Ministerio para la Transición Ecológica y el Reto Demográfico, 2025) in the municipality. Overall, the main pressure threatening the genetic conservation units is linked to climate change (52% of the units), followed by their marginality status (27% of the units), and the threat by forest fires (7% of the units).

The characterization of the genetic conservation units provides scientifically-based information for prioritizing populations in conservation programs. Integrating genetic information can inform many central issues in conservation, such as estimating population size, their uniqueness, structure, connectivity and demography, detecting hybridization, admixture or inbreeding, describing kin relationship, identifying adaptive variation that enable populations to adapt and persist to environmental change, and understanding the factors that affect this potential (Hohenlohe *et al.*, 2021).

As an illustration is the example of the genetic variation across the Spanish Network of *in situ* GCUs of maritime pine, *P. pinaster* (modified from Theraroz *et al.*, 2024; Figure 2). The spatial genetic structure shows ten distinct gene pools, with populations showing some degree of genetic admixture with nearby gene pools, suggesting historical or contemporary gene flow. The 29 genotyped units cover 24 of the 28 regions of provenance of the species, which constitutes an almost complete coverage allowing to conserve the minimum level of genetic diversity necessary to ensure the evolutionary potential of this forest tree species. The spatial genetic pattern of maritime pine reflects both the past demography history of the populations and their local adaptation (Jaramillo-Correa *et al.*, 2015; Ramírez-Valiente *et al.*, 2022). Therefore, regions of provenance with similar genetic characteristics may not necessarily respond identically to future selection pressures, and their adaptive potential should be contemplated before grouping them together (Rodríguez-Quilón *et al.*, 2016). Additionally, we should be cautious when using reproductive material in the proximity of the units, as previous studies have shown the risk of introgression (Robledo-Arnuncio *et al.*, 2009).

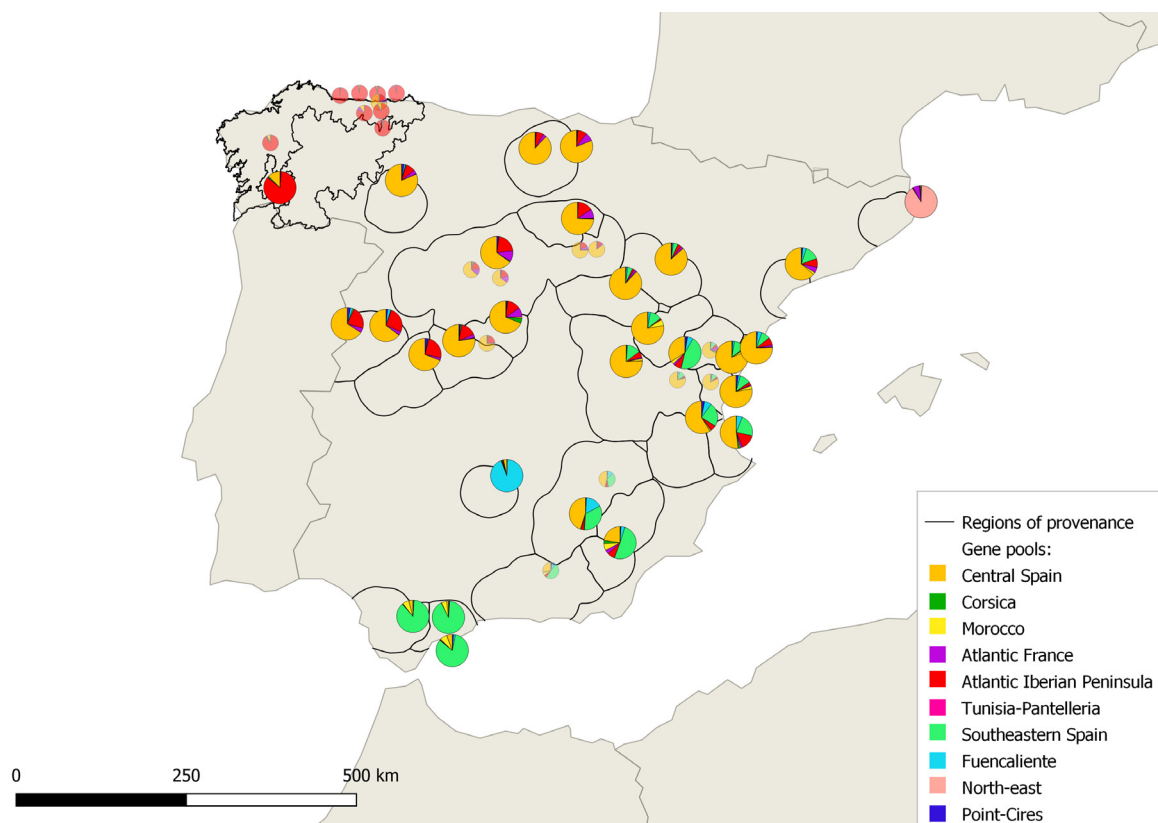


Figure 2. Gene pools in *Pinus pinaster* (modified from Theraroz *et al.*, 2024). Pie charts colours depict membership proportions of each genetic group ($K = 10$) for each studied population (circles), while black lines represent the 24 regions of provenance. Both genotyped GCUs (29 large circles) and other populations (19 small semi-transparent circles) are represented to provide a more complete picture of the spatial genetic variation.

Besides its central role in conservation, the Spanish Network of *in situ* Genetic Conservation Units also constitutes a highly relevant reference material that will allow testing whether proposed basic material can be of autochthonous origin, and differentiated at the national and European levels (e.g., [Olsson et al., 2025](#); [Degen et al., 2022](#); [Peery et al., 2022](#)). Knowledge of genetic diversity will also be very useful to ongoing breeding activities by guiding the choice of genetically diverse populations to be integrated into programs that are usually based on few selected traits of interest, resulting in a limited genetic background ([Olsson et al., 2023](#)).

Supplementary information ↑

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Supplementary material

Not applicable.

Data availability

The genetic data of *P. pinaster* that support the findings of this study were obtained from Theraroz et al., 2024, available at <https://doi.org/10.57745/SPUDQQ>

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Authorship contribution statement

Marta Callejas-Díaz: Conceptualization, Data curation, Formal analysis, Methodology, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing.

Francisco J. Auñón: Data curation, Methodology, Software, Writing – review & editing.

Sanna Olsson: Data curation, Formal analysis, Investigation, Methodology, Validation, Visualization, Writing – review & editing.

M. Regina Chambel: Data curation, Methodology, Writing – review & editing.

Diana Barba: Data curation, Methodology, Writing – review & editing.

Eduardo Notivol: Data curation, Methodology, Software, Writing – review & editing.

José M. García del Barrio: Data curation, Formal analysis, Investigation, Methodology, Writing – review & editing.

Felipe Pérez: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Writing – review & editing.

Delphine Grivet: Conceptualization, Data curation, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing.

Competing interests

The authors have declared that no competing interests exist.

Statement on the use of Artificial Intelligence

Not applicable.

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