



LIFE baccata, Preserving and restoring the yew forests of the Cantabrian Mountain chain | LIFE15 NAT/ES/000790 | 2016-2020

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Conservation of the genetic diversity of yew

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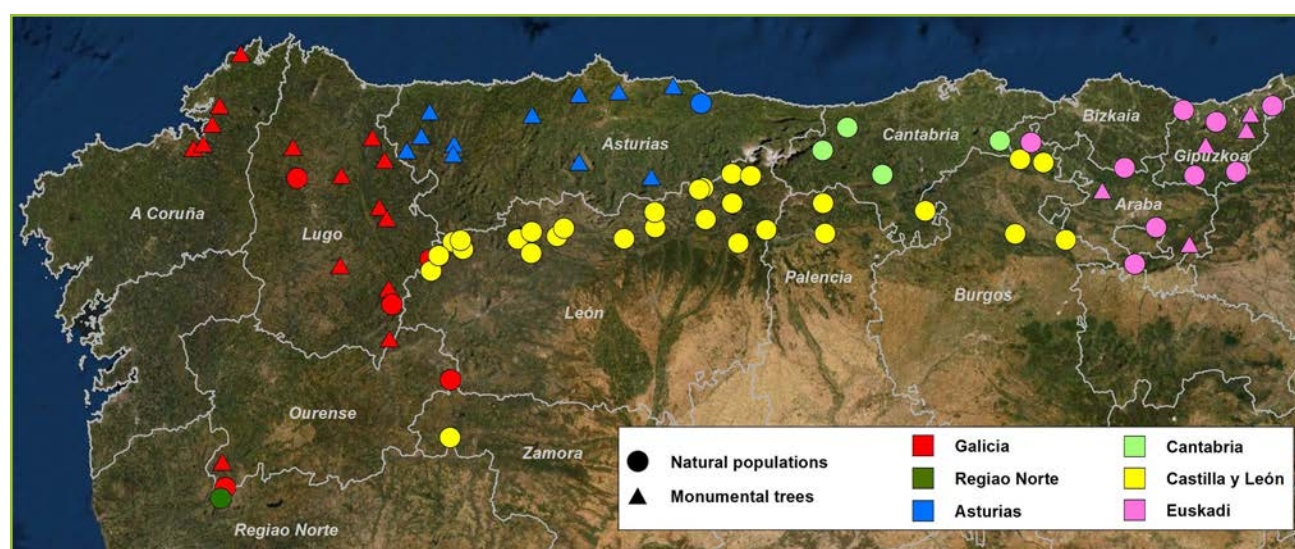


ADMINISTRACIONES COLABORADORAS



Conservation of the genetic diversity of yew (*Taxus baccata*) in the Cantabrian–Atlantic area within the framework of the LIFE BACCATA project

LIFE BACCATA project aims to improve the conservation status of yew woods in the Atlantic Biogeographical Region of the Iberian Peninsula. The characterization of the genetic variability of main yew populations in this region represents a transversal action of the project that involves several Spanish (Galicia, Asturias, Castilla y León, Cantabria, Euskadi) and Portuguese (Regiao Norte) regions. It will be very helpful as an important basis for the actions to be carried out in yew forest genetic resources conservation program. Genetic diversity is the basis of the adaptive potential of species and is key to rational and sustainable forest management. Genetic diversity contributes to guaranteeing the future and viability of yew woods, especially in a context such as the current climate change.



Phase 1. Genetic sampling of yew populations and unique trees

Collection and conservation of genetic samples

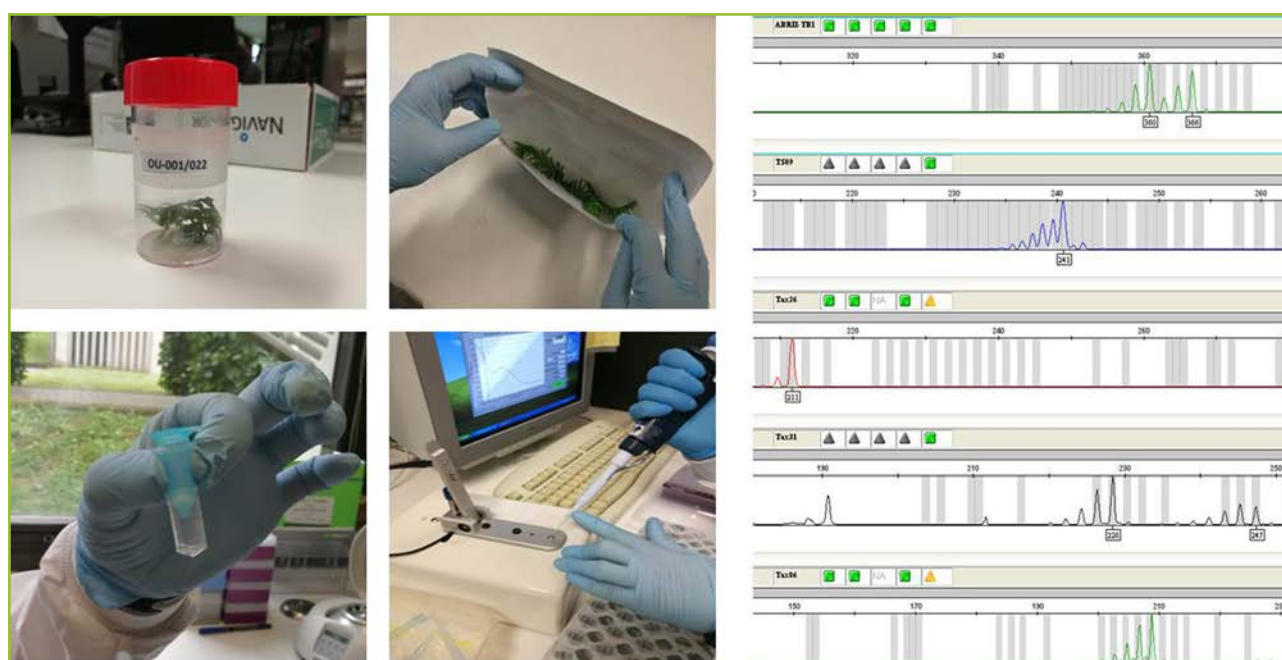
The project analysed 80 population locations in Northern Iberian Peninsula, from western areas in Northern Portugal, Galicia, Asturias and Castilla y León regions, to the easternmost ones in the Basque Country, including 49 natural populations into 30 Natura 2000 special areas for conservation (SAC). An average of 20–30 trees per population were sampled, as well as a selection of 31 monumental protected tree sites (most of them designated as Natural Monuments, Historic Sites, or their inclusion in singular tree catalogues), which persist as remains of ancient natural populations or as symbolic trees in relevant places (churches, cemeteries, monasteries, gardens, etc.). A small sample of fresh leaves was collected for each tree, being sent to the Genetics Laboratory at the Lugo Campus of the University of Santiago de Compostela (USC), where the analysis of genetic data has been carried out. Once they were analysed, IBADER at Lugo Campus has proceeded to preserve the tissue and DNA bank of all the samples collected at Lugo's herbarium, useful for future studies.



Genetic data analysis

To detect genetic variability in yew, nine informative microsatellite DNA (SSR) markers were analysed using PCR and automatic sequencer techniques at USC Genetics Laboratory. All genetic variants were identified by SSR marker and individual, generating a database of yew genetic profiles (genotypes) in the Atlantic Biogeographical Region, as a basis of the following population analyses:

- Genetic diversity and kinship, to assess genetic status, identify signs of genetic erosion and degree of inbreeding in populations
- Genetic structuring to identify genetically differentiated populations and groups
- Integration of LIFE BACCATA project within previous yew studies in the Iberian Peninsula, standardizing a genotypic database with more than 2,700 yews from 126 populations from six Iberian biogeographical regions.
- Genetic characterization of monumental yews with respect to natural reference populations, to trace the most likely genetic similarity as a source of origin.



Genotipos multilocus

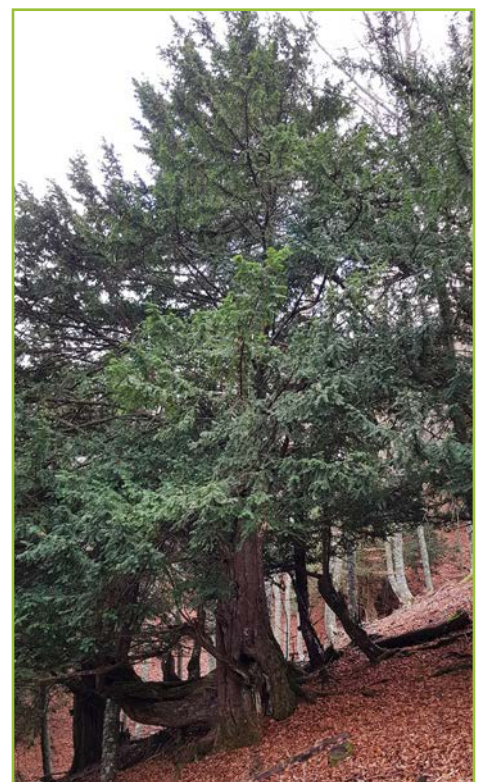
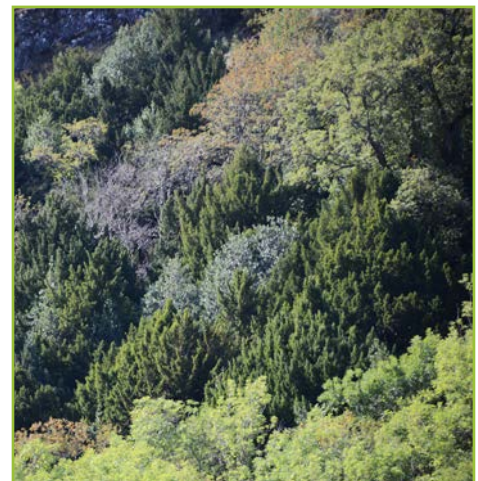
"DNA barcoding": "Código Barras genético"

ID	Tax23	Tax23	Tax36	Tax36	Tax60	Tax60	Tax92	Tax92	ABRII-TB1	ABRII-TB1	TS09	TS09	Tax26	Tax26	Tax31	Tax31	Tax86	Tax86
AR001_001	176	176	176	186	103	130	217	217	349	351	240	240	239	239	203	228	154	207
AR001_002	176	176	159	159	130	154	166	217	366	368	244	254	239	280	228	257	154	209
GI001_006	155	176	176	186	159	159	166	209	353	366	234	240	233	284	203	232	154	186
GI001_007	155	176	164	176	103	103	205	275	349	349	223	248	265	290	203	255	211	211
LE_014_011	155	155	204	231	103	103	166	205	338	360	216	222	211	284	228	228	154	154
LE_014_012	155	176	186	231	103	111	217	217	360	368	216	220	280	284	203	257	186	209

Phase 2. Genetic characterization of yew populations from Cantabrian–Atlantic area of the Iberian Northwest in LIFE BACCATA project

The results of the extensive sampling carried out confirm a high diversity of yew genetic resources in the Iberian Atlantic Region, representing an important source of genetic variation of the species. Some populations showed high genetic variability and low kinship, signs of a larger population size and connectivity throughout the LIFE BACCATA area (for example, Devesa da Escrita and Devesa da Rogueira in Lugo province, La Seita and Monte Teixedo in León province, Sierra de Aralar in Guipúzcoa province). Other populations showed less genetic diversity and greater kinship, indicative of isolation, such as Altide (Lugo), Casaio (Ourense), Boca de Huérgano (León), Sarón (Burgos) or Tosande (Palencia). Some of these sites represent locally differentiated genetic characteristics into the Atlantic Biogeographic Region.

The analysis of genetic grouping between populations showed evidence of structuring at different spatial scales, probably associated with the combination of effects of climatic fluctuations of the historical past with a more recent human impact. On a global scale, a differentiation of the easternmost samples from the Cantabrian–Basque Mountains was observed, with signs of greater historical connectivity in the western areas. On a regional scale, genetic differences were identified between biogeographical groups, associated with processes of change and dispersion in the evolutionary history of the species, including the Galician interior depression, the Galaico Leonés massif, the Naviano–Ancarenses Mountains, the Cantabrian Range and the Basque Mountains. On a local scale, an important component of local structuring was detected, reflecting low connectivity between populations, characteristic



of southern ranges of distribution of this species. Small, isolated populations, sometimes with significant kinship, can be affected by different limiting factors in seed dispersal and pollination, such as the unequal proportion of female and male trees per population, or the restriction of fruit-eating animals.

The genetic data obtained has provided key information to support conservation actions for this species associated with protected habitats in the Atlantic Biogeographical Region of the Iberian Peninsula. Based on the delimitation of genetic conservation units at global, regional and local levels, management guidelines have been established in each region, as they are responsible for forest management, but highlighting the importance of inter-regional coordination in shared biogeographical groups for conservation of yew genetic resources from a global point of view in the Atlantic Region.

Phase 3. Genetic guidelines to support the conservation actions of yew woods in the Atlantic Biogeographical Region of the Iberian Peninsula

Maintaining genetic diversity and structure, and the evolutionary potential of populations, is crucial in a conservation program. The evaluation of yew genetic resources in LIFE BACCATA targeted areas has provided information and criteria as a basis to guide conservation actions, both in situ (in their natural habitat) and ex situ (for example, seed and clonal banks).

Assistance in management based on genetic conservation units is useful for prioritizing key resources, due to their representative value of genetic diversity and/or their genetic specificity. At a regional level, a contribution of all biogeographic groups to total variability was observed, with notable values of diversity in the eastern zone and of differentiation throughout the entire Atlantic biogeographical area. At a local level, the contribution of each population to total genetic diversity and differentiation was estimated as an indicator of conservation. Maximizing the maintenance of population genetic diversity is highly relevant taking into account the evidence of the local adaptation of the yew to climatic factors, such as temperature.

Genetic criteria support the actions to improve the habitats associated with yew in the Atlantic Biogeographic Region, in close collaboration between researchers and administrations involved in environmental management. The conservation of yew in its natural habitats related to populations with high genetic variability is a priority, as well as a higher census and connectivity in more stable environmental conditions for the species. In smaller and more isolated populations, with greater kinship within the population, reinforcement actions can be assessed from genetically similar neighbouring populations.

To implement actions for improving the area of occupation and recruitment, it is important to take into account the gene pool of the donor and recipient populations involved. Collecting the genetic diversity harboured in ex situ conservation collections, including singular and monumental yews, has implications for its management to improve connectivity, minimizing the risk of hybridization with genetically differentiated populations.

Genetic indicators are very relevant for planning the different conservation actions in selected populations, such as the opening of the canopy to regulate competition for other tree species, the control of herbivorous fauna or the application of preventive measures to protect the ecological system. The execution of the actions of the LIFE BACCATA project seeks to strengthen the conservation of these protected habitats.



Phase 4. Genetic characterization of monumental yews

Singular or monumental yews, many of them protected by their values and remarkable characteristics (such as size, age or location), represent resources of environmental and cultural value, but their historical records are not always properly known. In LIFE BACCATA project, the genetic profile of different singular yews was characterized, with respect to the reference population database from the studied area.

Most of the singular or monumental yews were genetically assigned to natural populations in the same biogeographic area, sometimes to very close ones, such as Cereixido Yew (Lugo), suggesting their origin or transfer from older populations distributed in Courel Range. In other cases the allocation was ambiguous, being able to assign it to different populations, which is partly explained by the complex genetic structure in different groupings at global and regional level.

The allocation to very distant populations could be explained in cases of trees transferred from their original site to unique remote locations in gardens, cemeteries, churches, etc. However,



it seems more likely that most of them came from nearby woodlands, currently persisting as remains of ancient natural populations (already disappeared) that were more widely distributed and genetically related to the current ones in the same area.

It should be borne in mind that not all possible populations of origin have been sampled, some currently extinct, such as in western coastal areas of the Cantabrian–Atlantic area. Genetic data improves knowledge about the population dynamics of yew woods as well as of singular yews, being also a fundamental tool in the implementation of conservation programs for the species and the natural habitats where it is present.

