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Deliverable D3.9

Distribution map of adaptive potential (climate-driven selection) for present and future climatic conditions for at least one species

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1 Summary

Forests are a key element of Europe's bio-economy sector, providing valuable ecosystem services, wood and non-wood products, and supporting ecological systems with high biodiversity. Genetically diverse wild populations of forest trees are generally more resilient (i.e., they recover faster) to biotic and abiotic disturbances because different genotypes vary in their sensitivity to environmental changes and can thus increase in frequency after major disturbances resulting in local adaptation. The typically high levels of genetic and phenotypic diversity observed in undomesticated species suggest possible rapid evolutionary responses through the action of selection on standing variation and polygenic adaptation. Thus, the level of standing genomic variation together with the existence of pre-adapted polymorphisms in the population can be used as a proxy for adaptive potential, and its assessment is crucial to guide conservation actions. In this Deliverable we provide maps for different statistics associated with adaptive potential to climate change driven by climate selection in maritime pine. Then, in a second step, we identify populations that may be less prepared to confront the genetic changes needed to match the climate they will experience in the near future.

2 Introduction

The main objective of Task 3.5 is to forecast the adaptive potential of Genetic Conservation Units in the face of climate change for three widespread forest tree species (*Pinus pinaster*, *Fagus sylvatica* and *Pinus sylvestris*) for which common garden information is available from previous projects. In D3.9 we have used last-generation modelling techniques based on both common garden and genomic data to produce maps of adaptive potential in maritime pine (*Pinus pinaster* Aiton). This DL will serve as model for the work that will be presented in D3.10 (M56), which would present the results for the three species.

Common garden data for height at 7 years old was obtained from the Bordeaux site in the CLONAPIN network. Briefly, this experiment was established based on open-pollinated seeds from 36 natural stands sampled across the natural range and covering the six previously identified gene pools, i.e., genetic groups reflecting the population genetic structure, in this species (Jaramillo-Correa et al. 2015). Collected seeds were germinated in a nursery and one seedling per open-pollinated family was selected (i.e., selected genotypes were unrelated) and vegetatively propagated by cuttings. A total of 443 genotypes (clones) belonging to 35 of the populations were used to establish the common garden in Bordeaux. This common garden consist of eight ramets per clone set in a randomized complete block design (n=3,434 trees). Genomic data was obtained from previous projects for the 443 genotypes as follows: DNA was extracted using the DNeasy 96 plant kit (QIAGEN, Germany), following the manufacturer's instructions. Then, the samples were genotyped for Single Nucleotide Polymorphisms (SNPs) using the multispecies 4TREE Axiom array (Thermo Fisher Scientific, USA). Only SNPs with high-quality scoring following the Best Practices Workflow implemented in the Axiom™ Analysis Suite v5.2 were selected and filtered by missing data (<30%), yielding a total of 10,185 SNPs.

To construct the maps, we have considered the three main components involved in the adaptive response of species to climate change (Foden et al. 2019), that is: i) the exposure, i.e., the extent to which a species/population will experience climate change across its range, ii) the sensitivity, i.e. the degree to which a species/population is affected by climate change, and iii) the adaptive capacity. As a proxy for the exposure and sensibility components, we have estimated the 'genomic offset', i.e., the decoupling between current allele frequencies at climate-adaptive loci and those predicted under future climate conditions (Fitzpatrick and Keller 2015). As a proxy of adaptive capacity, we estimated the evolvability for height, which is considered an adaptive trait in forest trees, measured in the common garden, following Rodríguez-Quilón et al. (2016) and de-Miguel et al. (2022).

Maps of adaptive potential based on genomic offset and evolvability were produced using QGIS v3.10.2. The two independent maps were compared and combined in a single framework allowing to identify populations that had at the same time higher than average genomic offset and lower than average evolvability for adaptive traits.

The results presented in this DL are part of two manuscript drafts that would be published as pre-prints at bioRxiv in early 2024:

Archambeau J, Benito-Garzón M, de-Miguel M, Changenet A, Avanzi C, Bagnoli F, Barraquand F, Marchi M, Vendramin GG, Cavers S, Perry A, González-Martínez SC. Evaluating genomic offset predictions in a highly structured forest tree. *Forthcoming.*

Theraroz A, Guadaño-Peyrot C, Archambeau J, Piotti A, Avanzi C, Pinosio S, Bagnoli F, Vendramin GG, Alía R, Grivet D, Westergren M, González-Martínez SC. The genetic consequences of population marginality: a case study in maritime pine. *Forthcoming*.

3 Results

3.1 Map of genomic offset in maritime pine

The genomic offset was estimated based on a gene-environment association analysis (GEA) as the change in genomic composition required to maintain the current gene-environment (climate) relationships under future climates (Fitzpatrick & Keller 2015; Gougherty et al. 2021). The climatic variables used to compute the genomic offset were the mean annual temperature (bio1), the isothermality (bio3), the temperature seasonality (bio4), the annual precipitation (bio12), the precipitation seasonality (bio15) and the summer heat moisture index (SHM).

To establish the current gene-environment (climate) relationships, we used two univariate methods, BAYPASS and Latent Factor Mixed Model (LFMM), and three multivariate ones, Redundancy Analysis (RDA), partial RDA and Gradient Forest (GF). Then, the genomic offset was estimated using the GF approach, which has been shown to perform best (in most cases) based on empirical validation (Lind et al. 2023; Archambeau et al. 2023), and the set of 73 candidate SNPs identified by GEA. Potential future climate for 2070 was described using the moderately alarming shared socio-economic pathway (SSP) SSP3-7.0 and five global circulation models (GCMs). As genomic offset predictions were highly correlated (Pearson's correlation coefficient >0.75), we used population averages for the five GCMs.

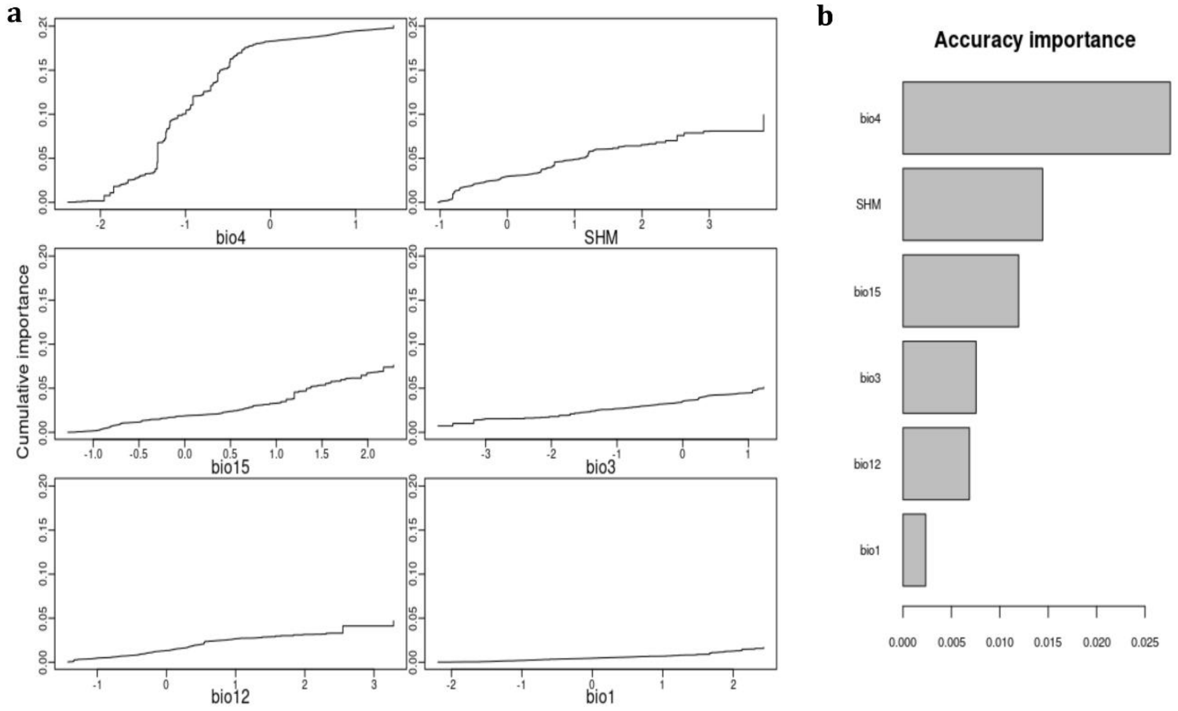

Figure 1. Genomic offset analyses; a) Turnover functions for each climate variable and the first four Moran’s eigenvectors (presented in order of importance); and b) Mean accuracy importance of each climate variable.

Temperature seasonality (bio4) was the most important predictor contributing to the genomic turnover, i.e., the turnover functions with the highest maximum height in the GF models (Figure 1). About genomic offset itself, we observed a trend towards higher values of this statistic in the western populations of maritime pine, in particular those along the Atlantic coast in the Iberian Peninsula and southern France, compared to the easternmost populations in France (Corsica) and Spain (Figure 2). Accordingly the highest genetic offset values were observed for populations in northern Spain (i.e., Asturias and Galicia, with genomic offset of ~0.080) and Aquitaine (e.g., Mimizan), and the lowest in eastern Spain (Olba, Oria and Quatretonda) and Corsica (genomic offset of ~0.015).

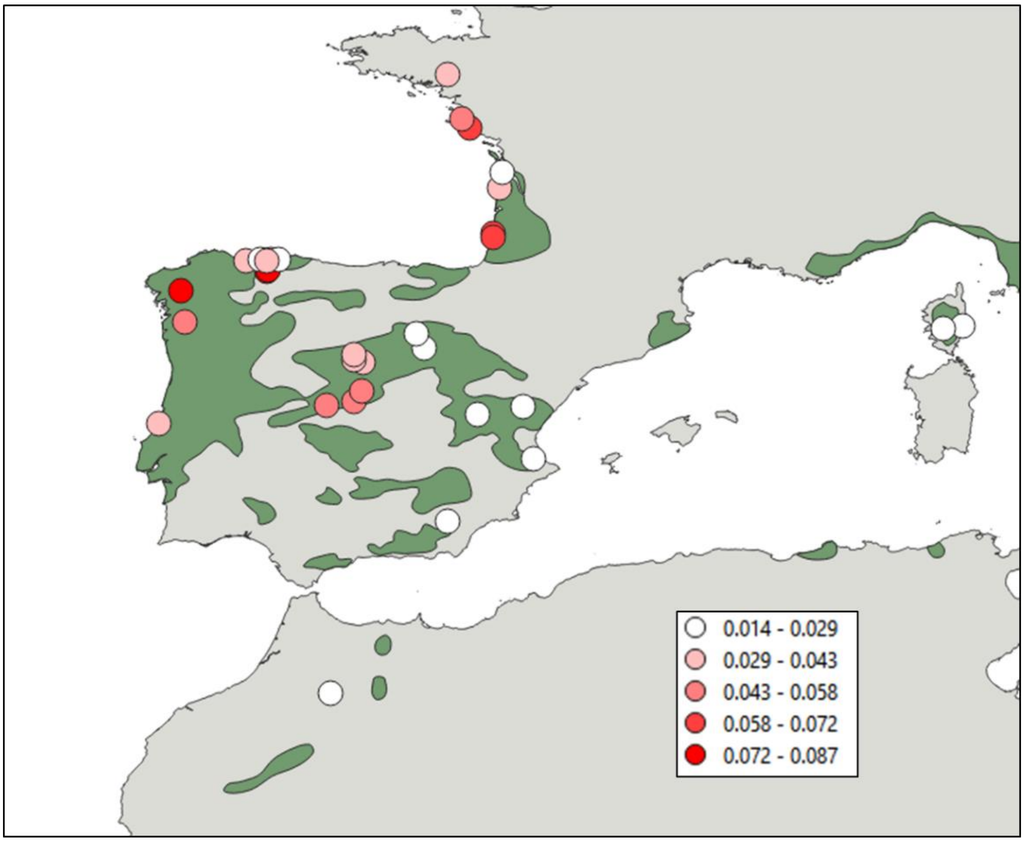

Figure 2. Genomic offset analyses; geographical distribution of genetic offset for maritime pine (darker shade indicates higher genetic offset and thus higher exposure and sensitivity to climate change).

3.2 Map of evolvability in maritime pine

Evolvability was estimated based on standard quantitative genetic analyses of common garden data, following Rodríguez-Quilón et al. (2016) and de-Miguel et al. (2022). The evolvability is defined as the additive (or clonal) genetic variance of a given trait divided by the trait mean. Interestingly, the highest evolvability values were found (mostly) in southern populations of maritime pine from central, eastern and southern Spain and Morocco, while the lowest values were found in the Atlantic populations of the species, both in the Iberian Peninsula and southern France, and Corsica (Figure 3).

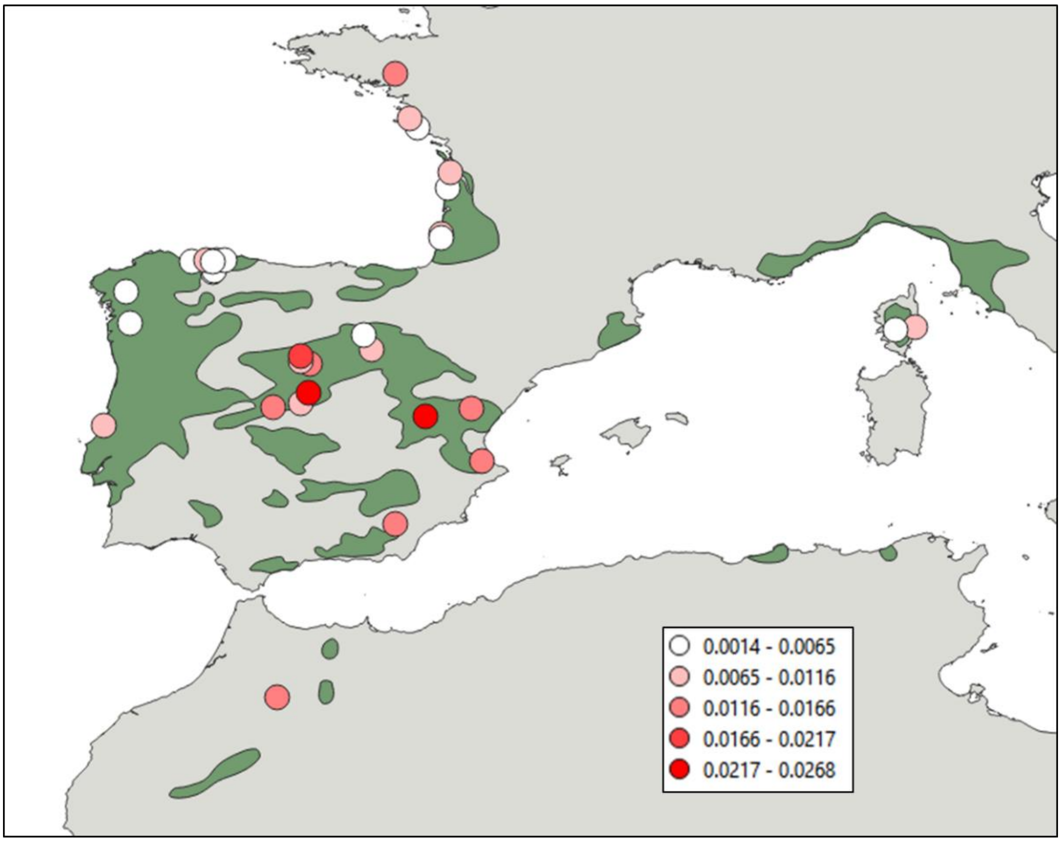

Figure 3. Evolvability; geographical variability in evolvability for maritime pine (darker shade indicates higher adaptive potential).

3.3 Identification of populations with higher vulnerability to climate change by combining genomic offset and evolvability maps

In the previous sections, we have provided maps for different components associated to the adaptive potential of maritime pine to future climates. Although combining different kind of information is not obvious, populations that have simultaneously higher than average genomic offset (i.e., those that are more exposed and sensitive to climate change) and lower than average evolvability for adaptive traits (i.e., less capacity for in situ evolution) may, overall, present higher vulnerability to climate change.

Interestingly, while some populations seems to perform poorly in both indicators (i.e., Alto de la Llama and Armayan in Asturias, northern Spain), others may have considerable potential for adaptation, brought about by standing genetic diversity, despite higher than average exposure/sensitivity to climate change (i.e., Mimizan and Olonne sur Mer in southwestern France, and Sergude in North western Spain).

4 Conclusions

Maps of adaptive potential related to climate-driven selection in maritime pine showed great variation across populations but also some consistent patterns, with population from Atlantic climates being potentially more vulnerable to climate change than those that have evolved under Mediterranean climates. This is due to both lower frequency of pre-adapted polymorphisms to future climate (i.e., higher genomic offset) and reduced genetic diversity for key quantitative traits related to adaptation (i.e., lower evolvability). Nevertheless, additional indicators and, in particular, analyses of quantitative traits related to other fitness components (notably, reproduction-related traits, which are currently unavailable) would be needed to inform adequately conservation actions.

5 Partners involved in the work

INRAE, INIA-CSIC, UKCEH, FR, GIS

6 Annexes

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