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Information and services for end-Users**

Deliverable D3.8

Estimation of GCUs adaptability (quantitative genetics linking trait proxy and genomics) for the remaining species

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1 Summary

The ultimate goal of WP3 is to forecast the adaptability of forest genetic resources. One approach employed to reach that goal is to use quantitative-genetic theory (Task 3.4), combined with the measurements of adaptive traits to predict the adaptability of the genetic conservation units (GCUs). This approach requires the integration of adaptive traits (both "soft" and "hard" traits, that is, those that are more and less driven by plasticity caused by environmental conditions, respectively), together with genomic (to control for relatedness among individuals) and environmental (to control for site heterogeneity) data. We present here the advances for the two GCUs (500 adults and 250 progenies each) of *Pinus pinaster* (FRA00051 and ITA00019), *Fagus sylvatica* (FRA00045 and SVN00047) and *Pinus sylvestris* (FIN00001 and GBR00001). The three datasets are available for all species and allowed to produce preliminary estimates of the heritability of individual traits and selection gradients in natural populations.

2 Introduction

To be able to use quantitative genetic model to predict the GCUs adaptability, three main datasets are needed, which were produced via different technologies and partners (see D3.2): adaptive traits produced in WP2 (hard traits) and WP3 (soft traits), genomic data produced in WP4 and environmental data produced in WP3 via unmanned aerial vehicle.

Following a similar methodology used in D3.7 for *Populus nigra*, here we describe the advances in producing and processing the three datasets for the three remaining species. It is important to stress that ALL datasets are now available and curated for all four species. Partners are in the process of integrating them into complex estimates, namely, selection gradient (i.e. the relationship between fitness and phenotypic traits), and heritability of the traits (i.e. how much phenotypic variance is genetically determined and heritable).

3 Results

Pinus pinaster

Primary Datasets

The three datasets (phenotypic, genomic, and environmental) are available and curated:

- Genomic data: 8,761 SNPs
- Phenotypic data: 5 traits measured in situ (height, DBH, height at the start of the crown, crown area, and wood density)
- Environmental data: out of the 13 environmental variables acquired with UAV, competition index and fine-scale soil moisture index, from a Digital Terrain Model were used to estimate the adaptive indices.

Derived Datasets

- Estimation of individual fitness from genomic data and UAV datasets are available and described in details in the M36 Scientific Report.
- Estimation of the kinship matrix (genetic relationship among individuals) is available.

- Estimation of NIRS-proxies from NIRS datasets measured in WP3 and phenotypic traits measured in WP2 (P50, P12, Gmin and SLA) are available and described in details in the M36 Scientific Report.

Selection gradients

Generalized models with covariates including competition index, spatial autocorrelation of fitness and environmental data were used to calibrate selection gradients in *Pinus pinaster*. Details are provided in the M36 Scientific Report and in D3.5.

While strong selection gradients were found for DBH (see Figure 1), favouring trees with bigger trunks no significant selection gradient was found for the other phenotypic traits. Covariates showed different effects on realized fecundity depending on the methods.

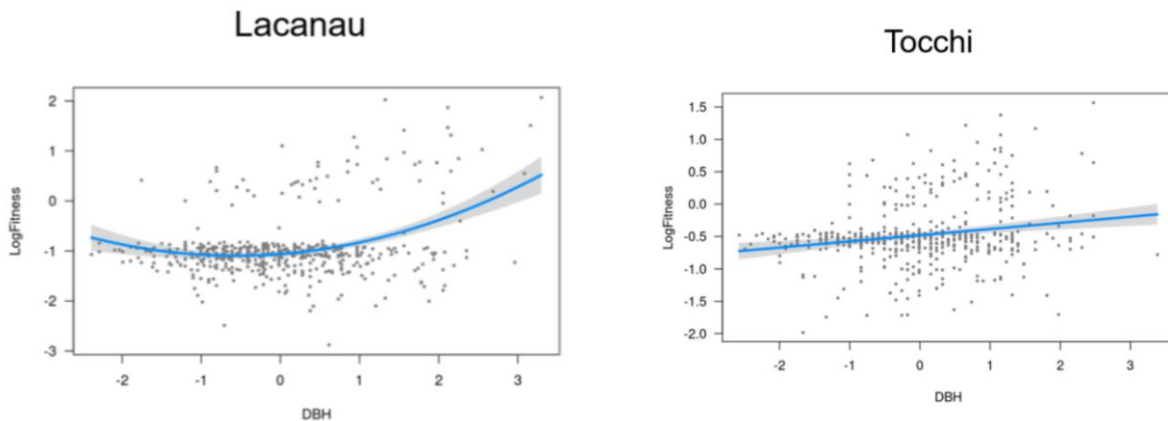


Figure 1: Significant selection gradients for DBH in two *Pinus pinaster* GCUs.

Heritability

Once phenotypic traits are available, and their relationship with fitness is estimated (through selection gradients), it is crucial to estimate how much phenotypic variance is genetically determined and heritable and able to respond to natural selection (i.e. heritability).

We used Bayesian statistical models to estimate trait heritability. These models include phenotypic traits, environmental variables at individual level (accounts for the micro-environmental effect on the phenotype), spatial splines with the location of the individuals (accounts for spatial autocorrelation), genetic relations among individuals, and error term. (Table 1). Details are provided in the M48 Scientific Report.

Table 1. Heritability estimates and [confidence interval] for nine traits in the *Pinus pinaster* GCUs integrating no covariates (null model), covariates for environmental variation and spatial autocorrelation (full model).

Pinus pinaster

Trait	FRA00051		ITA00019	
	Null model	Full model	Null model	Full model
<i>Tree height</i>	0.176 [0.002-0.438]	0.142 [0.001-0.410]	0.468 [0.282-0.659]	0.033 [0.000-0.159]
<i>Diameter at breast height (DBH)</i>	0.237 [0.005-0.521]	0.287 [0.017-0.561]	0.119 [0.000-0.373]	0.136 [0.001-0.396]
<i>Slenderness index</i>				

	0.163 [0.001-0.455]	0.140 [0.000-0.421]	0.145 [0.001-0.402]	0.069 [0.000-0.270]
<i>Crown area</i>				
	0.061 [0.000-0.253]	0.132 [0.000-0.434]	0.055 [0.000-0.213]	0.051 [0.000-0.200]
<i>Wood density</i>				
	0.254 [0.008-0.528]	0.206 [0.002-0.486]	0.246 [0.018-0.508]	0.105 [0.000-0.382]
<i>Number of cones</i>				
	0.167 [0.002-0.438]	0.148 [0.001-0.431]	0.232 [0.018-0.483]	0.199 [0.005-0.456]
<i>P50</i>				
	0.290 [0.017-0.571]	0.355 [0.040-0.638]	0.270 [0.083-0.483]	0.271 [0.070-0.497]
<i>P12</i>				
	0.120 [0.000-0.390]	0.158 [0.000-0.488]	0.286 [0.092-0.504]	0.229 [0.027-0.468]
<i>Specific leaf area (SLA)</i>				
	0.214 [0.004-0.483]	0.168 [0.001-0.452]	0.446 [0.248-0.634]	0.362 [0.136-0.580]

Heritability estimates for the studied traits fall within the range of values for forest trees. However, as seen in Table 1, including co-variables to account for environmental variation in the models changes the heritability estimates, which are expected to be more realistic and conservative when employing the full model. These output highlight the need to perform these approaches in natural populations to be able to forecast the adaptive potential of populations.

Output of *Pinus pinaster* are the subject of a scientific article that will be sent for publication at the beginning of 2026.

Fagus sylvatica

Primary Datasets

The three datasets (phenotypic, genomic, and environmental) are available and curated.

- Genomic data: 44,423 and 49,938 high quality SNPs were detected for FRA00045 and SVN00047, respectively.
- Phenotypic data: 3 traits measured in situ (height, crown area, and wood density)
- Environmental data: a set of 13 continuous variables was processed to characterize the environmental conditions of each GCU, grouped into three main categories: solar energy, hydrology, and terrain morphometry.
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Derived Datasets

- Estimation of individual fitness from genomic data and UAV datasets are available and described in D3.6.
- Estimation of kinship matrix (genetic relationship among individuals) is available.
- Estimation of NIRS-proxies from NIRS datasets measured in WP3 and phenotypic traits measured in WP2 (capacitance, wood density, P50 and P88) is available (Figure 2).

Fagus sylvatica - short cores

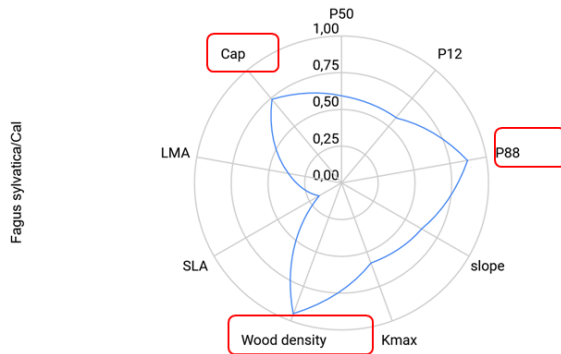


Figure 2: radar chart showing phenotypic prediction of the 10 individual phenotypic traits tested for their correlation with NIRS in *Fagus sylvatica*.

Selection gradients & Heritabilities

A preliminary estimate of selection gradients for NIRS-derived traits is available and described in D3.6. No trait showed a significant effect on male and female fecundity, in neither of the two GCUs. Final estimates of heritabilities and selection gradients will be made available by the end of April 2026.

Pinus sylvestris

Primary Datasets

The three datasets (phenotypic, genomic, and environmental) are available and curated.

- Genomic data
 - o FIN00001, 750 samples at 45,899 'best and recommended' SNPs. No samples removed as outliers.
 - o GBR00001, 749 samples at 45,813 'best and recommended' SNPs. No samples removed as outliers.
- Phenotypic data: 3 traits measured in situ (height, crown area, and wood density)
- Environmental data: a set of 13 continuous variables was processed to characterize the environmental conditions of each GCU, grouped into three main categories: solar energy, hydrology, and terrain morphometry.

Derived Datasets

- Estimation of individual fitness from genomic data and UAV datasets are available and described in D3.6.
- Estimation of kinship matrix (genetic relationship among individuals) is available.
- Estimation of NIRS-proxies from NIRS datasets measured in WP3 and phenotypic traits measured in WP2 (Kmax, lma, sla and tlp) is available (Figure 3).

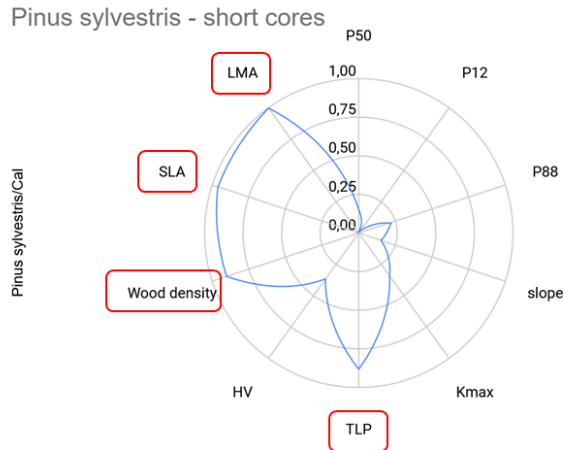


Figure 3: radar chart showing phenotypic prediction of the 10 individual phenotypic traits tested for their correlation with NIRS in *Pinus sylvestris*.

Selection gradients & Heritabilities

A preliminary estimate of selection gradients for NIRS-derived traits is available and described in D3.6. The only trait showing a significant, positive effect on (male) fecundity was turgor loss point in GBR00001 GCU. Final estimates of heritabilities and selection gradients will be made available by the end of April 2026.

Deviation from the original timeline. In this Deliverable we present the complete primary and derived datasets for the 2 GCUs of *Pinus pinaster*, *Fagus sylvatica* and *Pinus sylvestris*, while those for *Populus nigra* are also available and described in the M48 Scientific Report. Delays in data production have been linked to various reasons including, bad field conditions for UAV flights in the case of *P. sylvestris* and technological challenges for *Fagus sylvatica* genotyping. To mitigate for these delays, we opted to work on two species in parallel (*Pinus pinaster* and *Populus nigra*) to develop the methodologies.

4 Conclusions

NIRS enabled us to predict multiple functional and hydraulic traits across four key species, using only small wood cores. The quantitative genetic approaches (integrating genetic, NIRS-proxies traits, and UAV-measured environmental data) applied to natural populations (rather than common garden experiments) proved to be feasible. Now that all curated datasets and preliminary estimated of heritabilities and selection gradients are available, we expect to have the final indices of adaptability during the first quarter of 2026.

5 Partners involved in the work

GIS, UKCEH, FR, INIA-CSIC, INRAE, CREAM, CNR, UMR

6 Annexes

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