Ref. Ares(2025)11426344 - 19/12/2025

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Deliverable D3.10

Distribution map of adaptive potential (climate-driven selection) for present and future climatic conditions for the remaining species

Planned delivery date (as in DoA): 31/11/2025 (M59)

Actual submission date: 19/12/2025 (M60)

Workpackage: WP3

Workpackage leader: INIA-CSIC

Deliverable leader: UKCEH

Version: 1.0

Project funded by the European Commission within the Horizon 2020 Programme	
Dissemination Level	
PU Public	**PU**
CI Classified, as referred to Commission Decision 2001/844/EC	
CO Confidential, only for members of the consortium (including the Commission Services)	

Research and Innovation action: GA no. 862221

Start date of the project: January 1st, 2021

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1 Summary

Genomic offset methods offer a potential rapid evaluation method for identifying populations at elevated risk from climate changes. However substantial uncertainties underlying the genome-environment association, statistical approaches, and climate change forecasting means extensive testing is needed. Here, we tested a range of genomic offset approaches for two important European tree species.

2 Introduction: genomic offset in two European trees

European Beech (*Fagus sylvatica*) and Scots pine (*Pinus sylvestris*) are two of Europe's most economically and ecologically important tree species. Both are major timber species as well as having significant remaining natural populations in which they are the defining species of the ecosystem. Climate changes pose a substantial threat to both species but outcomes are likely to vary widely by population as both species occupy large, environmentally heterogeneous geographic ranges. Although genetic diversity may provide a degree of resilience to change, where environmental shifts are substantial or populations possess particular genetic characteristics they may be at elevated levels of risk. For more effective conservation, there is an urgent need to develop the capability for rapid assessment and forecasting of the degree of risk posed to populations by different climate change scenarios.

Genomic offset approaches offer a potential means to undertake such assessments. A wide range of approaches has quickly developed as interest in the method has grown. Here we evaluated, for European beech and Scots pine, the effectiveness of a set of GO approaches, under a range of different climate scenarios. The comparison also allows testing of the dependency of the method on spatial scale and environmental range, as we tested beech across its western European range, whilst Scots pine was evaluated across its Scottish range. The former crosses a wide range of environments, with a degree of isolation by distance shaping genetic structure (Buiteveld et al 2007, Postolache et al 2021); latter constitutes a steep environmental gradient with little to no genetic structure (Wachowiak et al 2013). We present the approaches taken, summarised outcomes and basic conclusions on the efficacy of the methods and of the implications for each species.

2.1 European beech

2.1.1 Methods

Fifty-one populations of *Fagus sylvatica* were included in the analysis. Fourteen were sampled within FORGENIUS WP4 (excluding the Turkish GCU, which was found to belong to *Fagus orientalis*), and thirty-seven within WP3. These were sampled in a common garden in Slovenia, planted as part of the 1998 series of COST Action E52 beech common garden trials. This common garden was also phenotyped at tree age 28 years using internal resources. Based on the results of the admixture analysis, the number of ancestral genetic clusters used for the analyses was four (K = 4).

The initial genomic dataset, comprising 104,066 variants across 1,228 individuals, was filtered for allele balance (between 0.2 and 0.8), missing data (30% per SNPs and individuals; remaining missing data were imputed using the most common genotype within each main gene pool identified by admixture analysis), and minor allele count below twice the number of individuals in the smallest population prior to filtering. This resulted in a final dataset of 21,529 SNPs across 1,177 individuals from 51 populations, which was used in downstream analysis.

The genomic offset was estimated based on a gene–environment association (GEA) analysis 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 mean annual temperature (bio1), mean diurnal range (bio2), temperature seasonality (bio4), mean temperature of the driest quarter (bio9), annual precipitation (bio12), precipitation seasonality (bio15), and summer heat moisture index (SHM).

To establish current gene–environment (climate) relationships, we used two univariate methods, BAYPASS and Latent Factor Mixed Model (LFMM), and three multivariate methods: Redundancy Analysis (RDA), partial RDA (pRDA), and Gradient Forest (GF). Genomic offset was then estimated using the GF, RDA, and pRDA approaches, which have been shown to perform best based on empirical validation with data from the Slovenian common garden (Fig. 1). Two sets of SNPs were used for genomic offset estimations: a set of 292 candidate SNPs (identified by at least two GEA methods with more conservative (MC) thresholds), and a set of 292 SNPs randomly selected from the full set of SNPs, excluding those identified by at least one GEA method, with the same size. Potential future climate for 2070 was described using the moderately alarming shared socio-economic pathway (SSP) SSP3-7.0.

2.1.2 Results

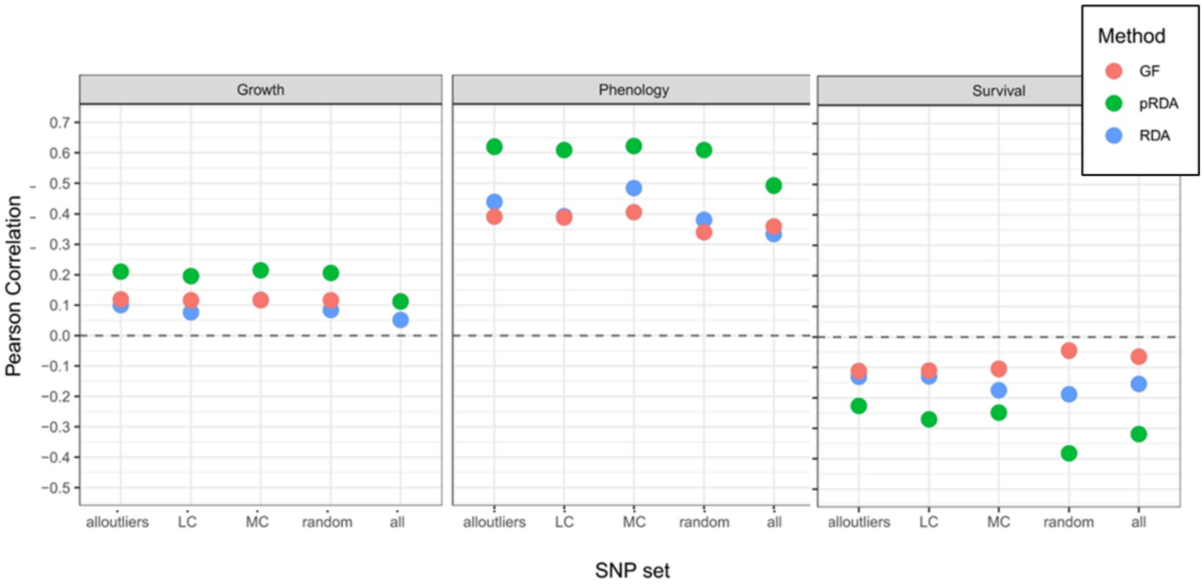

Figure 1: Pearson’s correlations between the genomic offset models and the fitness proxies (growth, phenology and survival) assessed under common garden conditions. Genomic offset was calculated for each population as the Euclidean distance between the predicted optimal genomic composition in the climate of origin of the population and that of the common garden.

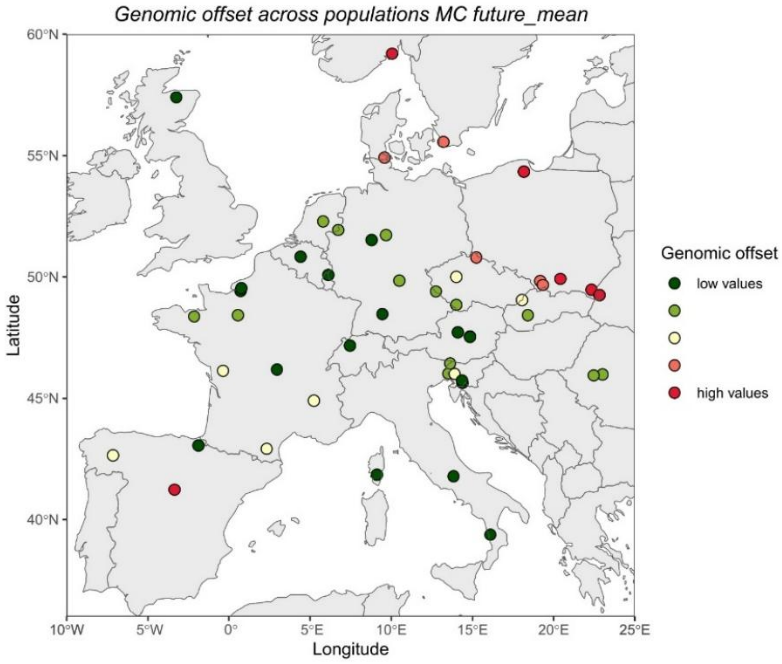

Figure 2: Genomic offset predictions for the RDA model using the set of 292 candidate SNPs identified by at least two GEA methods. Genomic offset predictions were standardised to range from zero (low - green) to one (high - red) and categorised into five classes.

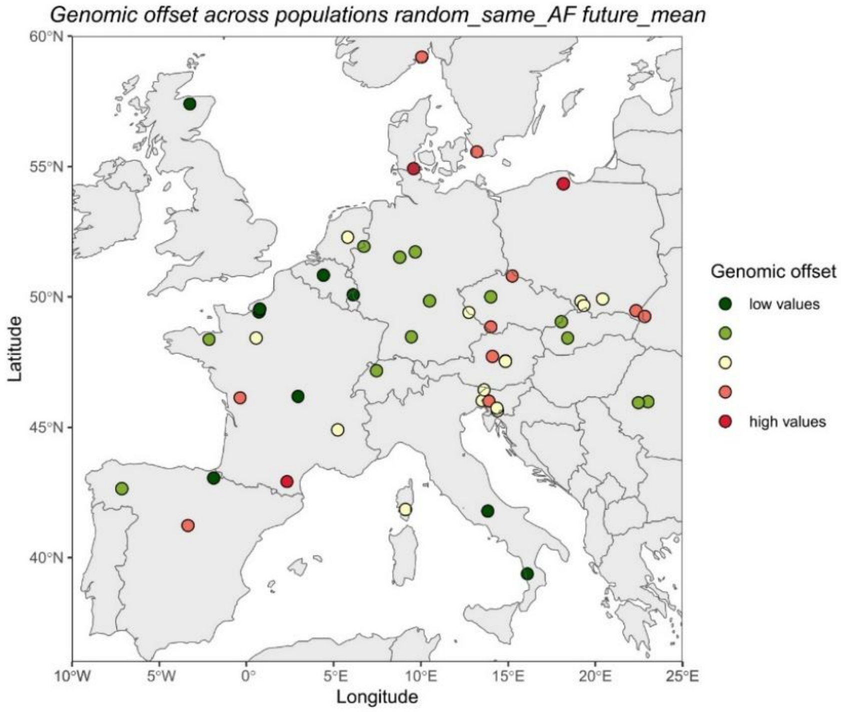

Figure 3: Genomic offset predictions for the pRDA model using the set of 292 SNPs randomly selected from the full set of SNPs. Genomic offset predictions were standardised to range from zero (low - green) to one (high - red) and categorised into five classes.

Of all the genomic offset predictions, those shown in Figures 2 and 3 expressed the highest correlation (Pearson's coefficient = 0.68). The observed trend towards higher values of the genomic offset statistic in the north-eastern populations is consistent with the species' ecology, as the continental climate may not meet its requirements for humid atmosphere (typically 600–1000 mm; Leuschner et al., 2006) and might threaten the trees in springtime, considering that beech is sensitive to late spring frosts despite its general tolerance to cold winters (Paule, 1995; Houston Durrant et al., 2016). Summer drought is one of the main factors limiting the species' distribution (Ellenberg, 1988; Leuschner et al., 2001; Granier et al., 2007), which coincides with the high genomic offset values observed in some of the easternmost sampled populations from the northern foothills of the Bohemian Massif and northwestern Carpathians, as well as in some populations from southern and southwestern edges of the species' distribution range (central Iberian peninsula, parts of southern France).

This pattern differs considerably from the results obtained with the GF model (Figure 4), in which a trend of increasing genomic offset values was observed from northern-central European populations towards the western ones, which coincides, although not entirely, with results of Lazić et al. (2024). Using the GF model, the highest genetic offset values were observed in populations from northern Spain and parts of France, northwestern Scotland, southern Poland, and Slovenia.

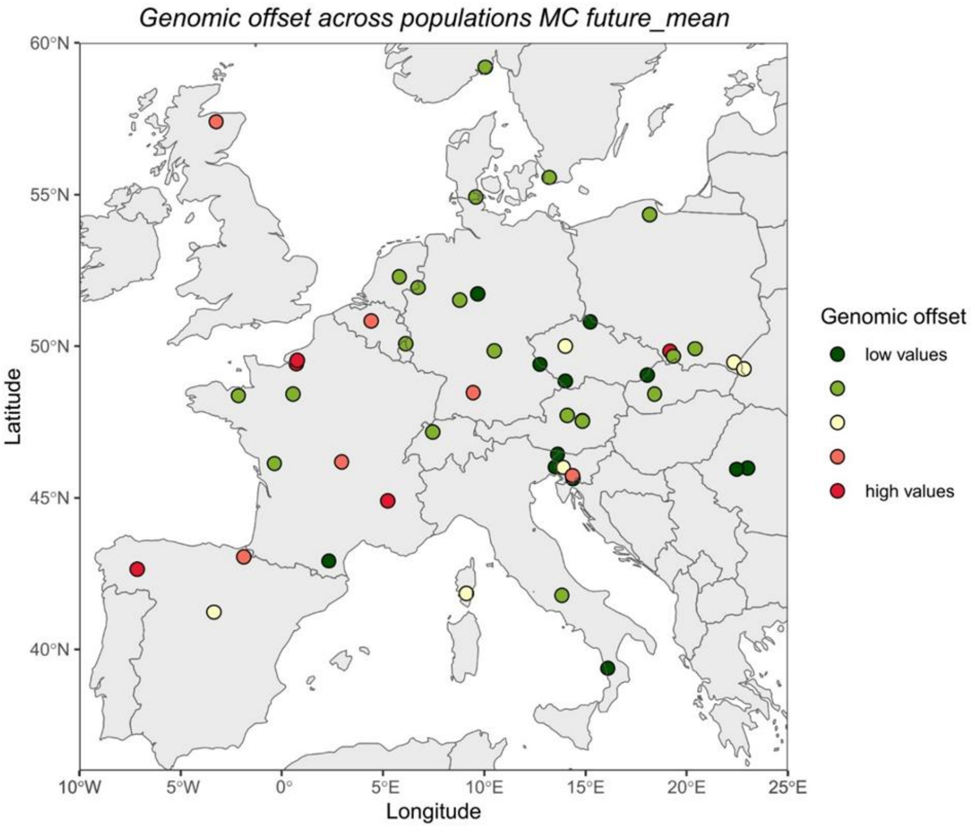

Figure 4: Genomic offset predictions for the GF model the set of 292 SNPs candidate SNPs identified by at least two GEA methods. Genomic offset predictions were standardised to range from zero (low - green) to one (high - red) and categorised into five classes.

2.2 Scots pine

2.2.1 Methods

Twenty-one populations of Scots pine, sampled across a steep gradient in environment across the species' natural distribution in Scotland, UK were used for genomic offset testing. All populations were represented in a common garden trial series established in the UK (Beaton et al 2022), offering the opportunity to test offset predictions based on straight genome-environment associations but also to incorporate estimates of phenotypic plasticity, obtained by assessing provenances across multiple common garden sites in contrasting environments.

All trees (N = 21 populations x 8 families x 10 [average] individuals = 1680) were genotyped using the Scots pine-specific PiSy50K Axiom array (ThermoFisher). SNP data were filtered to exclude sites with more than 10 % missing data and with a minimum allele frequency <0.05. Taxa with call rates <90 % were excluded. The final dataset comprised a total of 32302 SNPs.

Climatic data was obtained from the CHESS-SCAPE dataset, a 1-km resolution dataset over the United Kingdom (Robinson et al., 2023), freely available from the NERC EDS Centre for Environmental Data Analysis: https://doi.org/10.5285/8194b416cbee482b89e0dfbe17c5786c After initial assessment, the selected climatic variables were: Summer near-surface relative humidity (%), Summer precipitation flux (kg m-2 s-1), Summer surface downwelling shortwave radiation (W m-2), Winter wind speed (m s-1), Annual near-surface air temperature (K).

Six methods for estimating offset were evaluated: Generalized Dissimilarity Modeling (GDM), Gradient Forest (GF), Latent Factor Mixed Model (LFMM_K1) with K = 1 latent factor (i.e., minimal correction for neutral population genetic structure), Latent Factor Mixed Model (LFMM_K4) with K = 4 latent factors, Redundancy Analysis (RDA) and Partial Redundancy Analysis (pRDA)

Two RCP scenarios (RCP2.6, RCP8.5) and two time periods for future predictions (2030-2050, 2060-2080) were evaluated; four ensemble climate models were tested. Climatic distances were calculated as the absolute difference between future and reference values for each climatic variable or the Euclidean climatic distance integrating all selected climatic variables.

2.2.2 Results

The genomic offset approaches were broadly in agreement, apart from the GDM approach. Subsequent results are reported for outcomes only for the other five approaches.

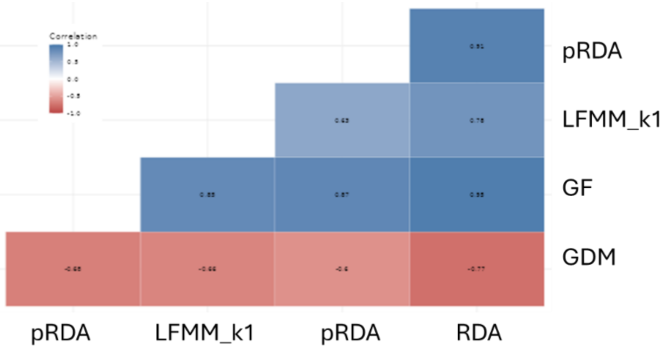

Figure 5: Pairwise correlation among genomic offset estimates depending on method used. Example shows offset estimated for RCP2.6 scenario for 2030-2050.

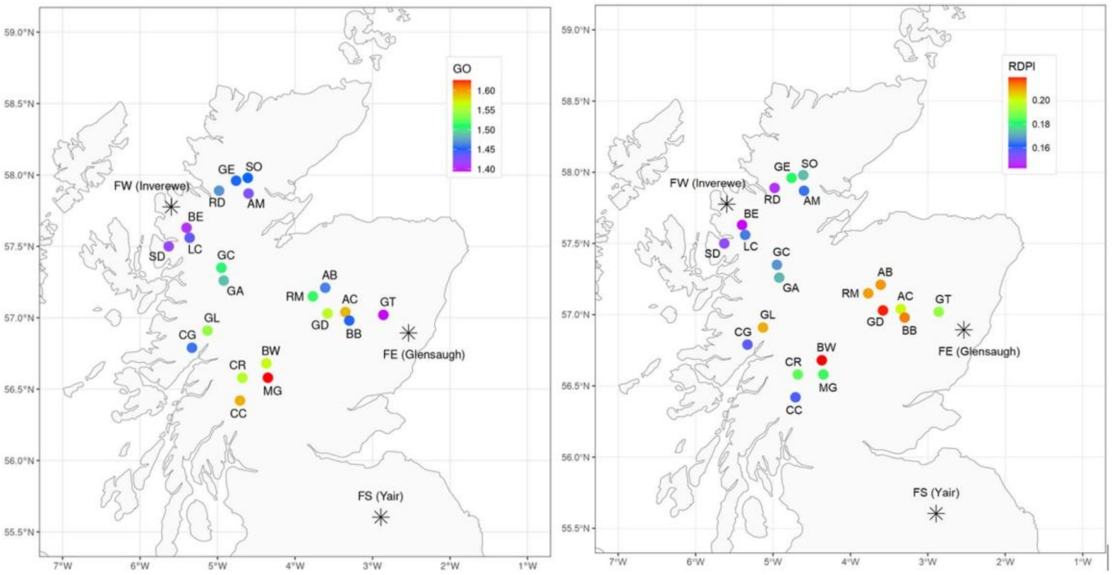

Figure 6. Left: Genomic offset predictions (RCP2.6, 2060-2080) using the GF approach. Right: Phenotypic plasticity (RDPI index; right panel) estimated for each of the 21 Scots pine populations, based on multisite common garden data.

Genomic offset predictions (Figure 6, left) suggest that populations to the north and west of the range evaluated had generally lower offset than those to the south and east. Some previous work has suggested that population in the eastern part of the range experience generally harsher (drier, colder) and more variable conditions (Salmela et al 2013); if populations at these sites were under stronger selection than those in other parts of the range, this could be consistent with offset predictions. Equally, climate change at these sites also expected to be greater than elsewhere.

The analysis showed that populations in this part of the range also had generally higher levels of plasticity (Figure 6, right). Salmela et al (2013) documented the fact that these sites experience higher temporal variability in climate, through a combination of altitude and generally more continental conditions, which was expressed at higher levels of variability in the trait assessed in common gardens. Higher levels of plasticity could 'buy time' for population adaptation to climate change, and thus reduce the risk of maladaptation in these populations (in particular in cases where evolvability is also high).

3 Conclusions

3.1 *European beech*

Maps of genomic offset in European beech showed variation across populations, including some in close proximity, and across the statistical approaches used. However, some consistent patterns are evident, indicating that populations from the Iberian Peninsula, parts of France, Poland, and Slovenia are potentially more vulnerable to climate change than those from other studied parts of the species’ distribution range. This may be due to the lower frequency of polymorphisms pre-adapted to future climates (i.e., higher genomic offset).

3.2 Scots pine

Variability in performance among genomic offset models suggest significant care is needed in interpretation of outcomes (Archambeau et al, 2025). Our results illustrate this issue, with strong negative correlations among some models. However, the majority of approaches were in clear agreement and indicate significant offsets for populations in specific parts of the range in Scotland (predominantly those in the east). The reasons underlying the differences are not yet clear but could be due to storing spatial variation in environment, different modes of local adaptation or variation in the forecasted extent of climate change. Variation in the extent of phenotypic plasticity among populations may also play a role in determining the ultimate response of populations to the coming changes.

4 Partners involved in the work

GIS, INIA-CSIC, INRAE, CNR, UKCEH, FR, Luke

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