



Combining genetic and environmental data to map and model regions of provenance for silver fir (*Abies alba* Mill.) in Italy

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Abstract

Regions of provenance for forest reproductive materials are the basis for wise use of forest resources in a changing climate. In this work a modelling framework is proposed for silver fir (*Abies alba* Mill.) in Italy where genetic clusters described by nuclear microsatellites were combined with high-resolution climatic data. When the genetic clusters were too large or had an uncertain ecological niche expression, an additional subregion division was evaluated according to a climatic assessment. Subsequently each genecological group (Region of Provenance, RoP) was projected in geographic space separately using species distribution modelling (SDM) procedure under current (1991–2020) and a future climate scenario derived from the 6th assessment report for the period 2041–2070. The final division into nine RoPs was able to explain 77.41% of the total climatic variance, a good trade-off between statistical significance and practical usability. The modelling steps then showed a large degree of ecological overlap between RoPs with some of them occurring in similar ecological environments but characterized by a different genetic structure. When projected at the continental scale, the Italian RoPs were found to be suitable for almost all the current European range of silver fir, with potential expansion in Nordic countries in the future, beyond the current distribution range. The study showed that the combination of genetic and ecological data can be a robust way to proceed in areas where a strong genetic differentiation between populations occurs, such as in Italy. New markers such as SNPs can then be used to detect adaptive traits and drive the selection of provenances for common garden experiments in areas where the SDM models currently extrapolate potential sites outside the current natural range.

Keywords Unique lineages · CMIP6 · Climate · Genecology · Forest genetics

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Introduction

The vulnerability of forest systems to climate change and the possible mitigation strategies have attracted the attention of many research groups (Araújo et al. 2005; Peterson St-Laurent et al. 2018). A large body of evidence shows global warming is influencing forest tree species distribution and biology and already visible effects will generate reactions at a population level in the coming decades (Avanzi et al. 2019; Bouchard et al. 2019). Overall, tree species have two options: (i) to adapt to new climate regimes or (ii) to migrate towards new lands. The rate of climate change is predicted to be rapid (Boisvert-Marsh et al. 2014; Peterson St-Laurent et al. 2018) and forest ecosystems may be unable to respond at the speed needed. As a result, a general biodiversity loss is expected (de Koning et al. 2014), in this framework, a wise use of forest reproductive materials, assisted migration and assisted gene flow strategies and sustainable forest management practices are described in the literature (Lindner et al. 2014; Benito-Garzón and Fernández-Manjarrés 2015; Sáenz-Romero et al. 2016; Fuchs et al. 2022; Fady et al. 2022).

One of the most common ways to forecast the most likely effects of climate change on forest systems is by means of statistical models such as species distribution models (SDM), based on the spatial occurrence of tree species at geographic scale (Araújo and New 2007; Pecchi et al. 2019). Various statistical models have also been developed such as reaction norms or response functions (Rehfeldt et al. 1999; Marchi et al. 2022; Zhao and Wang 2023) and trait models (O'Neill et al. 2008; Vizcaíno-Palomar et al. 2020; Benito Garzón 2021; Hallingbäck et al. 2021), mostly when more detailed data are available (i.e. common garden experiments). All these techniques aim at modelling the explained or potential niche of the target species as a function of environmental drivers (mainly climate variables). Large differences exist among the methods, ranging from the less data-demanding but more computationally intense SDMs to the more data dependent response functions (Wang et al. 2010). All the models in their most recent form attempt to include the genetic diversity component into the calculation process, which also represents a very important and emerging trend in literature (Marchi and Coccozza 2021; Fady et al. 2022; Picard et al. 2022; Ray et al. 2022; Vajana et al. 2023). On a very broad extent, the genetic richness represents the degree of available alleles that a population (or a species) has and can use when forced to adapt functional traits under strong environmental pressure (Petit et al. 2003; Erickson et al. 2012; Neale et al. 2017). Phenotypic plasticity is another key component of species and populations being able to acclimate to environmental change (Gratani 2014; Müller et al. 2020). Plastic populations (or species) are able to maintain fitness.

across large environmental gradients (Gratani 2014; Fréjaville et al. 2019) and specialized populations with low plasticity might perform very well in specific environmental conditions but be unable to perform well and survive when translocated or forced to live in new environments (Valladares et al. 2014; Benito Garzón 2021; Marchi et al. 2022; Ding and Brouard 2022). However, it is worth noting that both populations may have unique alleles that can be useful to deal with climate change scenarios. Therefore anyclassification should consider the “Genetic by Environment” (G×E) phenotype concept as well as the general recommendation of conserving all the available genetic diversity to deal with an uncertain future (Müller et al. 2020).

Silver fir (*Abies alba* Mill.) is a good example of climate-sensitive tree species with a long history of glacial refugia and migration (Liepelt et al. 2009; Piotti et al. 2017). The geographic distribution ranges from Spain to Romania and from Italy to Poland. This conifer occurs mainly in mountainous areas, often growing in mixed stands with several species

such as European beech (*Fagus sylvatica* L.), black pine (*Pinus nigra* Arnold spp.), Norway spruce (*Picea abies* L.) and minor trees such as *Acer* spp. and oaks. Another important feature of silver fir is its usage in common garden experiments (Kerr et al. 2015) and inclusion in biogeographical studies, sometimes also involving paleo data about pollen sources, to trace back its autecology (Tinner et al. 2013). Recent genetic analyses using common garden experiments and laboratory tests (Kerr et al. 2015; Vitali et al. 2017) showed significant differences in mortality, growth, eco-physiological and biochemical traits among populations descended from different parts of the distribution area (Kerr et al. 2015). The differentiation observed among populations is also comparatively high and may indicate a long differentiation history. Range-wide studies with molecular markers, revealed several ice-age refugia in the Pyrenees, in France and southern European countries such as Italy and the Balkans (Liepelt et al. 2009; Tinner et al. 2013; Belletti et al. 2017; Piotti et al. 2017; Paluch and Zarek 2020). The species is also very well represented in the EUFGIS system where 268 Genetic Conservation Units (GCU) are available across 14 European countries.

This study is to assess and propose a combination of genetic information and climatic data to map the silver fir 'regions of provenance' (RoPs) in Italy according to the EU Directive 1999/105/CE and to understand its potential use in a changing climate. The current spatial distribution of silver fir in Italy, derived from national forest inventory raw data was studied and associated with the most recent molecular data derived from Piotti et al. (2017) to define genetic groups. Resulting genetic clusters were divided into subgroups (i.e. the RoPs) according to an ecological assessment. Finally, the RoPs were modelled using an SDM approach. Models were also run beyond the national borders to evaluate the possible spread of Italian RoPs at continental scale, using the current climate (1991–2020) and one CMIP6 projection for the period 2041–2070 under ssp370.

Materials and methods

Species occurrence data and genetic clusters definition

According to the most recent National Forest Inventory (INFC2015) silver fir has been recorded across 348 inventory plots, mainly admixed with European beech, black pine and oaks. The species in Italy is distributed mainly across the Apennines chain and lowlands of the Alps, from Calabria to Tuscany also occupying some areas in the western Alps in Piedmont and in the North-east in Trentino-Alto Adige and Veneto regions. The most recent genetic study for silver fir was published by Piotti et al. (2017) for which 21 Italian natural stands were sampled and genotyped using 16 nuclear (nuSSRs) and three chloroplast microsatellite markers (cpSSRs). Four genetic clusters across Italy (STRUCTURE at $K=4$) were then defined as the best aggregation of different phenotypes.

Assuming spatial proximity as a key driver for the genetic structure of silver fir across Italy, in this study the genetic group of the spatially closest natural population studied by Piotti et al. (2017) was assigned to each INF2015 plot, by means of a matrix of spatial distances, created using the spatial coordinates of each INFC2015 point against the 21 natural stands. While this procedure has been recognized as secure for natural stands occurring in INFC2015 of unknown genetic signature, some uncertainties may occur in the case of planted forests. In this framework the genetic assignment procedure assumed that local seed sources were always used for planting, meaning that

seeds were collected from spatially close natural stands which was the most common practice in the past (McKay et al. 2005; Boshier et al. 2015; Whittet et al. 2017).

Climatic data preparation and RoPs definition

Several continental-scale or Global datasets exist and are freely available in the literature. Among these WorldClim surfaces (Hijmans et al. 2005; Fick and Hijmans 2017; Marchi et al. 2019) and CHELSA products (Karger et al. 2017) are the most famous which also includes the new CMIP6 future projections already. Unfortunately, the most recent climatic normal period (i.e. 1991–2020), is still missing in both. In addition, regional models and downscaling techniques have recently proved to be a good source for more reliable climatic data (Wang et al. 2006; Lin et al. 2018; Marchi et al. 2020). In this framework the use of a dynamic lapse-rate calculation for spatial downscaling of climatic surfaces was implemented in downscaling software such as ClimateNA for north America (Wang et al. 2016) and ClimateEU for Europe (Marchi et al. 2020) and in a web portal names ClimateDT and freely available on the web (<https://www.ibbr.cnr.it/climate-dt/>). This last tool was used in this study to downscale the main climatic variables with a monthly resolution (Tmin, Tmax and Precipitation) of CHELSA v2.1 (original spatial resolution is 1 km) up to 500 m and to create the 1991–2020 normal period for the whole Europe. Afterwards, the raw monthly variables were used to calculate a set of nine climatic indices widely used in previous studies (Isaac-Renton et al. 2014; Benito Garzón et al. 2019; Vizcaíno-Palomar et al. 2020; Hallingbäck et al. 2021; Marchi and Coccozza 2021; Ray et al. 2021; Marchi et al. 2022). Climatic indices are generally more adequate to be used as predictor variables in spatial. Nine such climatic indices used in this study were the annual heat moisture index (AHM), the temperature seasonality (bio4), the extreme minimum temperature (EMT), the growing degree days above 5 °C (GDD5), the mean coldest month temperature (MCMT), the mean growing season precipitation (MGSP), the number of frost-free days (NFFD), the summer heat moisture (SHM) and the temperature difference (TD). These climatic indices for the period 1991–2020 were used to evaluate the proportion of climatic variability explained by the four genetic clusters. The proportion of explained variance was calculated as the ratio of between-cluster sum of squares (i.e., the sum of the within-clusters sums of squares) and the total sum of squares of the environment. In case of a low proportion of explained variance (i.e. less than 50%), the larger clusters were divided into subregions according to a new clustering based on climatic variables only and an average linkage of clustering. In order to weight all the climatic indices equally, all were standardized having mean value equal to zero and variance of one. The RoPs were mapped and the four most important climatic variables were used to describe the ecological environmental types and to validate the clustering using the Tukey's multiple comparison post-hoc test.

All climatic indices were generated using the basic functions of ClimateDT and a detailed description of their calculation is available at the website of the downscaling tool (URL?). The same procedure was used for the future scenario period 2041–2070. An intermediate climate forcing trajectory was selected for the IPSL-CM6A-LR model, downloaded from CHELSA website with an original spatial resolution of 30 arc-sec (approx. 1 km) and downscaled to the same resolution of the 1991–2020 baseline.

Spatial models parametrization and projection at national and continental scale

When a trade-off between explained variance and geographic fragmentation was achieved, the climatic layers were used to run a spatial model predicting the climatic suitability of the Italian silver fir RoPs across time and space. In this work, the basic scheme of a Species Distribution Model architecture was considered at an RoP level, afterwards defined as provenance-SDM (pSDM). The main difference between SDM and pSDM relies on the fact that a classic SDM process, calculates the proportion of records falling within a specific ecological range to derive the probability of survival for the target species. This approach limits the ecological niche, transforming abundance data (i.e., the number of records found in a specific ecological class) in probability of success (or performance). The connection between abundance and performance is often weak because plants can perform better in areas where they are less prevalent and vice-versa. Tree species have been intentionally moved and removed by humans across time and space, and sometimes planted where they were not native. While non-native stands can be useful to enlarge the species niche in modelling efforts (Zhao et al. 2023), their abundance in a specific ecological domain can bias a model prediction. According to this, the pSDM method proposed here consists as a separate SDM for each provenance, aimed at maximizing the importance of each spatial group (i.e. RoP) in the model. According to the literature, we used the `biomod2` R package (Thuiller et al. 2023) to compute the pSDMs. Ten pseudo-absence replicates were generated with the SRE method and 30 cross-validation repetitions were run for each presence-pseudo absence combination using a 70–30% training–testing random extraction, averaging the predictions (Barbet-Massin et al. 2012). Four algorithms amongst the nine available in `biomod2` were used in the calculation. Such algorithms were generalised linear model (GLM), artificial neural network (ANN), random forest (RF) and MAXimum ENTropy (MAXENT). An Ensemble model was finally computed for each RoP averaging each algorithm prediction using the true skill statistic (TSS) scores as weight and projected in the current and future climates. A unique map for silver fir was also created, merging the single-RoP prediction and assigning to each pixel the maximum land suitability value predicted by the model to generate a maximum land suitability map for Italian silver fir provenances. To validate the projection, the spatial predictions made by pSDM were overlapped with the current distribution of silver fir in Europe and derived from two sources as a shapefile of native distribution from EUFORGEN website and as mosaic of European national Forest Inventories from Mauri et al. (2017, 2022).

Results

The union between the pure genetic information (four groups) and the raw INFC2015 records showed that this clustering was able to explain only 35.08% of the total environmental variance (i.e., climatological variability) and a further division into sub-groups was necessary. Such low proportion of variance explained was mainly associated to the large number of stands falling into the genetic group number two, including all the INFC2015 records occurring in the North-Eastern part of Italy and some stands in the Central Apennines between Tuscany and Emilia-Romagna regions. However, this was an expected result due to the unclear genetic signature associated to this cluster. In order to improve such classification, four genetic groups were analyzed separately and divided into sub-clusters based

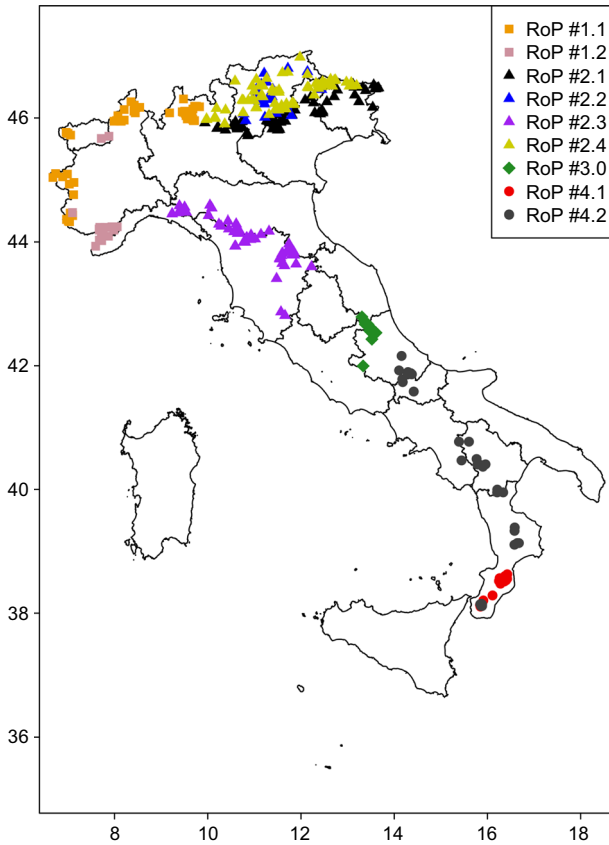


Fig. 1 Spatial distribution of nine RoPs; the shape of the dot (square, triangle, rhombus, circle) represents the genetic cluster while the color within each genetic group represents the environmental subgroup that has been defined according to ecological stratification

on the nine climatic variables. Then nine groups (i.e., RoPs) were delineated (Fig. 1) with two subregions in the cluster 1, four in cluster 2 and two in the last cluster (cluster 4) with a total explained variance of 77.41%.

This final spatial aggregation represents the definitive map of the RoPs for silver fir in Italy. The proportion of occurrence records in each genetic cluster and subregion, i.e., Region of Provenance (RoP) afterwards, is shown in Table 1. The two largest RoPs were the 2.2 occurring in the Central Apennines and 2.3 in the North with around 20% of the total National Forest Inventory records each. The smallest one was RoP 3.0 with just 2.71% of the occurrences and without an internal ecological subdivision.

The evaluation of the climatic variability intercepted with this clustering scheme is graphically shown in Fig. 2 where the four main climatic parameters have been used (MGSP, GDD5, SHM and bio4). While all the RoPs within each genetic cluster were statistically different for temperature-related indices (GDD5 and bio4), the two RoPs of cluster four were not different for MGSP, and were the smallest values observed as expected for the Mediterranean area. The differences on rainfall-related indices became statistically significant when MGSP was used in combination with thermal regimes to

Table 1 Proportion of occurrences (INFC2015 plus Piotti et al. 2017) falling within each genetic group and RoPs (subregion) defined with the climatic clustering

Genetic cluster	Occurrences (%)	Subregion	Occurrences
1	67 (18.16)	1.1	49 (13.28%)
		1.2	18 (4.88%)
		2.1	28 (7.59%)
		2.2	74 (20.05%)
		2.3	77 (20.87%)
2	239 (64.77)	2.4	60 (16.26%)
		3	10 (2.71)
		4	53 (14.36)
		4.1	35 (9.49%)
3	10 (2.71)	4.2	18 (4.88%)
		4.2	18 (4.88%)
Total	369 (100)	—	369 (100%)

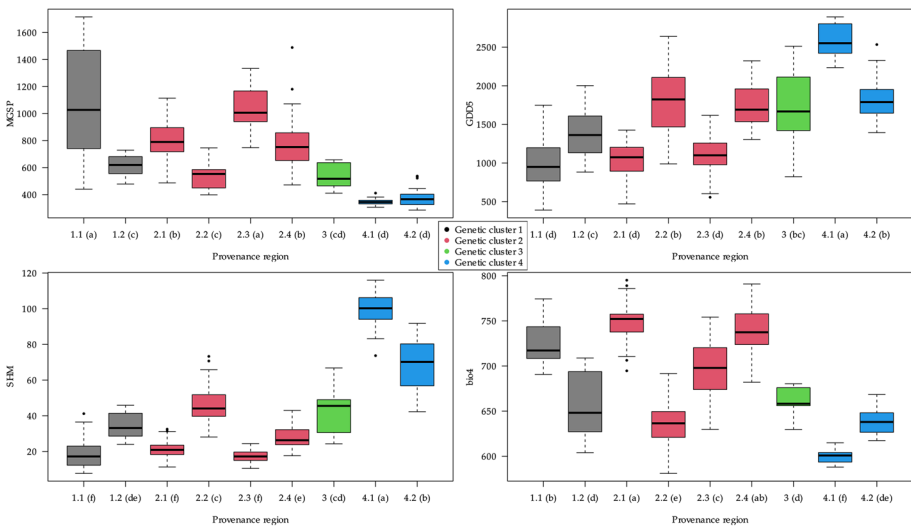


Fig. 2 Environmental differences within and among genetic clusters (different colors) for the four main climatic parameters used in this study. Subregions were marked with a number after the genetic cluster. The grouping statistics according to a Tukey’s multiple comparison post-hoc test was added within brackets to show the differences within each genetic cluster

calculate the SHM indices (which involves MGSP in the calculation) and therefore supporting the creation of two different RoPs also within the genetic cluster 4. The analysis stressed the combination of both genetic information and climatic data were useful to delineate highly differentiated RoPs in terms of genetic signature, climate or both.

According to this result the nine RoPs for silver fir in Italy were modelled using the pSDM approach. The four algorithms performed well, with TSS values ranging between 0.89 and 0.97. The RF algorithm was always the most accurate but the difference between mean values was not statistically significant in an ANOVA and therefore no presence-absence group or algorithm was removed from calculation of the ensemble model. The final output showed the possibility of the Italian RoPs of silver fir to be suited across much of the mountainous areas of Italy (Fig. 3) and even beyond the native

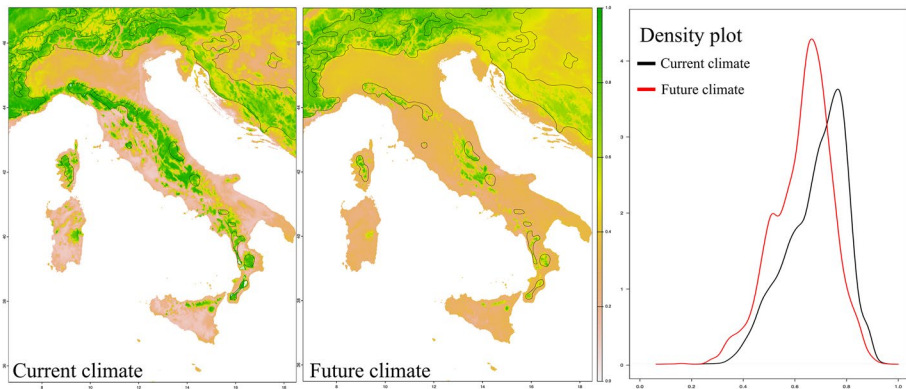


Fig. 3 Spatial projection of the pSDM model using the current climate (left) and the future projection (middle) overlapped with the current species distribution derived from EUFORGEN website in Italy. In this figure also the density plot of the values obtained from the spatial overlay of all the Continental-scale NFI points from Mauri et al. (2017) is shown (right)

range. It was evident for both the current climate and the projected climate a general northward shift and to higher elevations could occur.

The application of the future climate scenario to the pSDM showed the RoPs 2.2 and 4.1 were those more affected by the changing climate. The use of separate models for each RoP allowed an assessment of a lower vulnerability associated with RoPs 3 and 4.2 with which were within the full Mediterranean climate zone and expected to be at high risk of extinction. The model predicted the Mediterranean RoPs able to deal with a warmer and drier climate at the local scale as well as to be able to colonize new areas in the Northern part of Italy, where potential activities of assisted migration and assisted gene flow may be planned. This effect was also detectable at continental scale and in agreement with the Italian scenario. The single-RoP contribution and the spatial overlaps can be graphically observed in the figures delivered as supplementary material (Figures S1 and S2).

Discussion

The definition of RoPs based on both genetic and environmental data can be used in predictive models to show the potential use of forest reproductive materials in the future. This procedure is in agreement with the EU directive 1999/105/CE, where an RoP is defined as “the area or group of areas subject to sufficiently uniform ecological conditions in which stands or seed sources showing similar phenotypic or genetic characters are found, taking into account altitudinal boundaries where appropriate “. The proposed method shows how, for a target species where a genetic structure across a country was detected, RoPs can be mapped and modelled as a function of both genetic diversity and ecological variability. In this framework silver fir (*Abies alba*) in Italy also represents a particular and useful case study due to the several strongly differentiated refugia, the use of genetic data and climatic indices, and the clear genetic structure of populations across the country. However, in central Europe, simple bioclimatic (environmental) zones (e.g., Metzger et al. 2005) may be appropriate geographic areas where uniform ecological conditions occur and that are statistically distant (Metzger et al. 2005, 2013a, b; Tercek et al. 2012). As a consequence, it

is always important to combine different expertise from forest science disciplines provide information on the distribution of the genetic diversity and the environmental variability of sites. Occasionally RoP maps have been created and approved by government with the aim of dividing the country into environmental zones, without any connection between the target species distribution and explained ecological niche. The risk is the unreliable assessment and future use of forest materials. While an environmental zoning of a region, country or continent may have its own statistical robustness, a species-specific analysis may reveal that such differences are not robust. Different thresholds should be then used to define statistically-significant groups and for this reason, RoPs that are only based on low resolution environmental classification (maybe using coarse global datasets in spite of regional higher resolution models, i.e., a resolution of 250 m or more), should be recognized as general, temporary and provisional (Bower et al. 2014) and at least used at a coarse scale until species-specific studies can provide tailored and robust classifications (Hamann et al. 2011; Gray and Hamann 2013; Hamann and Aitken 2013).

Climate change uncertainties and the need of adaptive traits markers to intercept the environmental pressure

Powerful workstations and tuned algorithms are now accessible to research groups. Cloud computing schemes and high-resolution spatial data which feed artificial intelligences (e.g., neural networks) are available in many cases and can be used to predict future scenarios (Maca and Pech 2016; di Biase et al. 2018). The response of forest ecosystems to the changing climate is the application of an expected shift of climate across time and space (Hamann et al. 2011; Chakraborty et al. 2019; Hallingbäck et al. 2021; Marchi et al. 2022). Scientists are aware of the uncertainty in the detail of climate change and therefore several global circulation models (GCM) can allow users to select the most suitable GCM or GCM ensemble for analysis (Gidden et al. 2019; Cook et al. 2020). In this study the IPSL-CM6A-LR model was used, and in contrast of other studies where a GCM ensemble was applied (Noce et al. 2017; Hallingbäck et al. 2021), this model has been acknowledged as an intermediate climate future within the CMIP5 and CMIP6 projections (Knutti et al. 2013; Gidden et al. 2019). The use of an intermediate model trajectory has been recently suggested by some authors as a good choice to avoid unrealistic predictions (Thuiller et al. 2019; Hausfather and Peters 2020). An intermediate model does not mean the uncertainties connected to future climate predictions have been removed, only that the use of an intermediate model has been selected as more reliable than a “synthetic” model calculated from an ensemble.

The genetic clusters described are the result of previous published studies where several silver fir native stands were analyzed (Piotti et al. 2017) by means of nuclear and chloroplast microsatellite markers. The classification work has been based on the assumption of the spatial proximity, i.e., assigning the genetic clusters to all the NFI points according to a geographic distance criteria. The national forest inventory points used in the study have been visited and measured, and are confirmed as plantations. Silver fir has been extensively planted across Italy in the 18th and 19th Centuries (Tinner et al. 2013) although seed sources are mostly unknown. Therefore, a realistic genetic assessment of the stands would need an extensive sampling campaign across all the occurrence records. Given the difficulty and cost of such a field campaign, our assumption was based on a high probability of use of seed from closely occurring natural stands (McKay et al. 2005; Boshier et al. 2015). Indeed, local seed has often been acknowledged as a most suitable source for many decades

in the past (Ivetić et al. 2016; Wilhelmi et al. 2017; Fréjaville et al. 2019; Hayatgheibi et al. 2020), and especially when extensive datasets (genetic data but also climatological data) were unavailable. New data may change the framework. For instance, northern seeds could be used for experimental purposes in the south and vice-versa. For this reason, more data will be necessary to deal with such an approach.

The identification of unique features of some RoPs such as 4.1 and 4.2 which currently held unique lineages and diversified alleles (Piotti et al. 2017) also suggest how forest management and conservation strategies should be tailored to research evidence (Broenimann et al. 2007; Lenoir et al. 2008; Boisvert-Marsh et al. 2014; Monleon and Lintz 2015; Mamet et al. 2019; Rumpf et al. 2019; Picard et al. 2022). For instance, a mixture of active silviculture and conservation strategies might be carried out at a national scale but with different spatial scales of sampling and analysis that could include seed transfer activities, assisted migration, assisted gene flow and *ex-situ* collections (Williams and Dumroese 2013; Benito-Garzón and Fernández-Manjarrés 2015; Sáenz-Romero et al. 2016; Sang et al. 2021). In any case adaptive traits need to be thoroughly investigated, for example by novel molecular techniques such as Single Nucleotide Polymorphism (SNPs) that can work on the DNA regions that are subject to environmental pressure, to identify genetic variation.

FRM usage and knowledge for new common garden experiments

One of the most intriguing features of RoP mapping and the pSDM approach is the possibility to run bi-directional models i.e., looking for the best provenance for a specific site or looking for the best sites to conserve a specific genotype or population in the future (Berlin et al. 2016; Hayatgheibi et al. 2020; Hallingbäck et al. 2021; Marchi and Coccozza 2021). The application of this concept may be fundamental for the future needs where planted forests will require suitable seed sources to deal with the future climate. For the silver fir study, the possibility to collect seed from Southern Italy has been considered a good option for Central European and Northern Countries. Moreover, a geographic extent larger than expected has been found to be suitable for the species. Although modelers warn about the extrapolation issues (Fréjaville et al. 2019; Vizcaíno-Palomar et al. 2020; Hallingbäck et al. 2021; Marchi et al. 2022) and refer to the potential biases when using models to predict values outside the observed range of variation, this study is not affected in such a. The pSDM simply analyzes the expressed ecological niche projected into the geographic space for a selected period (2041–2070 in our case). Therefore, no extrapolation was done. However, it is worth mentioning that the modelled niche is just the realised and not the potential one (Zhao et al. 2023). Even if that is a known issue of SDM-related methods (Vetaas 2002; Booth et al. 2014; Pecchi et al. 2019) the underestimation of the real potential of the target species is actual and likely. For this reason, more complex techniques such as reaction norms and response functions still represent the most powerful methods (O'Neill et al. 2008; Wang et al. 2010; Benito Garzón et al. 2019; Chakraborty et al. 2019; Zhao and Wang 2023), but their requirements concerning common garden data was limiting for this work. In such a framework the need of new common garden experiments is demanding. New environments should be tested even outside the native range with seed sources of known genetic signature and a clear ecological niche expression. Additionally, experiments and research sites should be followed and measured for a long period of time to deal with extreme events and additional disturbances such as for example pests and diseases that may be more common in a warmer and drier climate. The need of additional data

concerning the plasticity of forest tree species in new environments (outside their native range) is demanding (Gray et al. 2016; Booth 2022; Fady and Rihm 2022). The risk when extrapolating models is high and we need to reduce this uncertainty to transform extrapolation into interpolation. According to that scheme, the definition RoPs is the first step for a future trans-national infrastructure with certified forest reproductive materials.

Conclusions

The work here described for *Abies alba* (Mill.) in Italy aims to reflect the definition given by the EU Directive 1999/105/CE and the creation of country-level RoPs for a single species. The fusion between genetic and environmental data generated new input records for the spatial models and the pSDM approach projected each group across space and time under statistical significance. According to that structure the future use of FRM for silver fir will be driven by an adaptive modelling work and not by rigid boundaries of a generalized environmental zoning on its own. This study also showed how Mediterranean sources may hold adaptive traits already able to colonize new environments in central and Northern Europe, confirming the expected scenarios where southern seed sources may be the future stands for the north. However, a key issue is also represented by conservation of endangered gene pools threatened by global change. In this view, both local and continental-scale perspectives are necessary to conserve, to enrich and to boost the forestry sector in a changing climate and society, where ecosystem services are likely to have larger role in the (near) future.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s11056-023-10000-2>.

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Author contributions Conceptualization, methodology, validation, formal analysis, data curation, writing-review and editing, were all curated by MM.

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Data availability All the data used in this study are freely available from the corresponding Author under request.

Declarations

Conflict of interest The author declares no conflict of interest.

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