

(Fagus sylvatica L.)







# Guidelines for Sustainable Forest Management of Beech (Fagus sylvatica L.)

Deliverable: Section of the guidelines on management activities in forest conservation areas in climate change for each of the 4 species/genera complexes targeted



## 1. Introduction

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European beech (*Fagus sylvatica* L.) is a wind pollinated monoecious species with a life span of up to 300 years, reaching the height of 40 to 60 m. It is a stand-forming species growing in pure or mixed stands throughout Europe. In the south-east it may interbreed with *Fagus orientalis* Lipsky (Figure 1.1). It grows on a wide range of soils, except compacted and waterlogged ones, and prefers humid climates. Since it is susceptible to high temperatures, summer droughts and late frosts, its distribution is limited in the Mediterranean and in continental parts of the western and northern Europe (Westergren *et al.*, 2020).

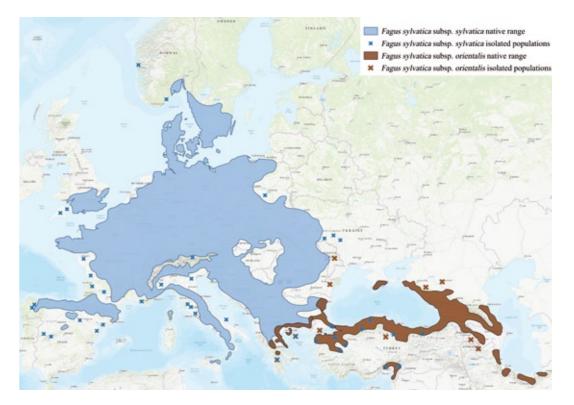


Figure 1.1. European beech distribution range (www.euforgen.org) by Caudullo G., CC BY 4.0 <a href="https://creativecommons.org/licenses/by/4.0">https://creativecommons.org/licenses/by/4.0</a>, via Wikimedia Commons.

The European beech is characterised by a low genetic structure across the European continent. The populations of the Iberian Peninsula and south-west France, the Italian Peninsula and the south-eastern Balkans (there may be other gene pools in the region) each belong to different gene pools, while the central European gene pool mixes with the Balkan gene pool and expands towards the northern range of the species (Demesure *et al.*, 1996; Magri *et al.*, 2006; GenTree, 2021; Höhn *et al.*, 2021), with isolation by distance playing an important role in differentiation (Höhn *et al.*, 2021). The genetic diversity of beech appears to be highest in glacial refugia (GenTree, 2021). Overall, populations in the centre of the range are more similar in terms of diversity and structure (GenTree, 2021).

# LIFE SySTEMIC PROJECT DESCRIPTION

The LIFE Programme is the European Union's instrument to finance projects for the conservation of the environment, biodiversity and the fight against climate change.

The aim of LIFE SySTEMiC Project (Close-to-nature Forest Sustainable Management under Climate Changes) is to use the "modeling tool" based on genetic diversity to determine best silviculture practices in order to protect our forests in times of climate change. The basic idea is simple: the greater the genetic diversity of trees in a forest, the more likely it is that some trees have genetic characteristics that make them more adaptable to climate change, increasing the resistance and resilience of the forest system.

Based on these premises, the main project objectives are to:

- Investigate the relationships between forest management and genetic diversity for eight forest tree species in three European countries (Croatia, Italy, Slovenia) in order to identify the silvicultural systems that maintain high levels of genetic diversity.
- Develop an innovative Genetic Biodiversity and Silvicultural model (GenBioSilvi) based on the combination of advanced landscape genomics, applied genetics and silvicultural models to support Sustainable Forest Management.
- Spread the knowledge of the method across Europe and transfer its use in forestry practice by involving different types of stakeholders.

The Web page of LIFE SySTEMiC project, including project deliverables: https://www.lifesystemic.eu/



# 2. Guidelines on Sustainable Forest Management and Adaptation of beech forests to climate change

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Sustainable and close-to-nature forestry uses forest management methods that promote the conservation of nature and forests to preserve it as a natural ecosystem of all its diverse life forms and relations formed therein. It is based on detailed forest management planning, adapted to individual site and stand conditions and forest functions, and considering natural processes and structures specific to natural forest ecosystems (Veselič, 2008).



Figure 2.1. Irregular shelterwood system is a common way for management of beech stands.

Silvicultural systems for beech stands should be carefully selected to promote close-to-nature approaches and mimic natural processes in forest stands. Within LIFE SySTEMiC four silvicultural approaches in beech stands have been analysed (Table 2.1). In LIFE SySTEMiC project 12 beech stands, which correspond to 4 European Forest Types (EFT) have been studied: 6.6 Illyrian sub mountainous beech forest; 7.2 Central European mountainous beech forest; 7.3 Apennine-Corsican mountainous beech forest and 7.4 Illyrian mountainous beech forest. Results, described in previous chapters, show that silvicultural systems with reduced impact are more favourable in light of genetic variability preservation, such as individual tree selection and low-scale irregular shelterwood systems.

ld	Site name	Country	Species	EFT *	Structure	Silvicultural system
01	Pian degli Ontani	Italy	F. sylvatica	7.3	Even-aged	Uniform shelterwood
02	Baldo's forest	Italy	F. sylvatica	7.3	Uneven- aged	Individual tree selection
03	Pian dei Ciliegi	Italy	F. sylvatica	7.3	Even-aged	Uniform shelterwood
04	Caselle 1	Italy	F. sylvatica	7.3	Even-aged	Uniform shelterwood
05	Caselle 2	Italy	F. sylvatica	7.3	Even-aged	Uniform shelterwood
11	Fonte Novello	Italy	F. sylvatica	7.3	Uneven- aged/Old- growth	Unmanaged
12	Venacquaro	Italy	F. sylvatica	7.3	Even-aged	Uniform shelterwood
14	Ogulin	Croatia	F. sylvatica	7.2	Even-aged	Uniform shelterwood
23	Osankarica	Slovenia	F. sylvatica	7.2	Even-aged	Irregular shelterwood
24	Pri Studencu	Slovenia	F. sylvatica	6.6	Even-aged	Irregular shelterwood
25	Rajhenavski Rog	Slovenia	F. sylvatica	7.4	Uneven- aged/Old- growth	Unmanaged
29	Gorski kotar, Vrbovsko	Croatia	F. sylvatica	7.2	Uneven- aged	Individual tree selection

Table 2.1. List of the sites for Fagus sylvatica L. of the LIFE SySTEMiC project.

\* EFT = European Forest Type: 6.6 Illyrian submountainous beech forest; 7.2 Central European mountainous beech forest; 7.3 Apennine-Corsican mountainous beech forest; 7.4 Illyrian mountainous beech forest.

Beech is a shade-tolerant tree species that is present in many forest plant communities in Europe and different forest types, mostly as dominant or in some cases as affiliated tree species. It is characterized by slow growth in youth, which culminates only after 45 years when light conditions allow that. Beech volume increment reaches its maximum very late, on some sites only after 75 years. In general, the average total volume increment does not show signs of decline up to the age of 150 years. Beech also responds to silvicultural measures or thinning until old age and surpasses all the other tree species (Diaci, 2006).

Beech is relatively resistant to most diseases. It does not suffer from massive predations by pests that lead to a total dieback of stands. Late spring frosts often damage young trees or flowers, which emerge simultaneously with leaf flush. Intense sunlight may damage the stem surface (Wuelisch 2010). The main threats to beech forests due to climate change are natural disasters such as sleet and snow break (Figure 2.2) at higher altitudes, as well as wind can cause major damage to these forests.



Figure 2.2. Sleet can be very harmful for beech stands on higher altitudes.

Beech forests on warmer sites can be at risk due to stronger summer droughts. Forests on northern slopes are less threatened (ZGS, 2021). The stability of beech stands with a higher proportion of other species is strongly threatened by the health status of those species (for example spruce and gradations of bark beetle). There is also an increased risk of the introduction and spread of invasive non-native species in forests near settlements and infrastructure facilities (roads, railways).

Through the natural regeneration of beech forest stands, trees' adaptability to conditions of specific growing sites and natural dynamics is preserved. Beech forest stands should be renewed naturally and should imitate a mixture of tree species and forest stands of natural forests (ZGS, 2021). Natural regeneration of beech stands is generally not problematic. Young beech stands are characterized by high density with vigorous stratification. In gaps and uneven young stands dominant trees quickly develop overgrown crowns (Diaci, 2006).

The most common way for the regeneration of beech stands is under canopy cover. Regeneration is set in the sequence of felling, mostly as a uniform shelterwood silvicultural system (Nocentini, 2009) or as a part of an irregular shelterwood system (Westergren *et al.* 2015). This is planned in small rejuvenation gaps which are then gradually connected over time. A very suitable system is also a individual tree selection system, especially in mixed stands with silver fir and on areas, where the pressure of a climatically unstable environment is very high (ZGS, 2021). Regeneration can also be introduced on slightly larger areas, which should be spatially separated by mature stands.

Regeneration in gaps should start after the seed year with a felling intensity of around 1/3 of the wood growing stock (Matić *et al.* 2003). It is necessary to prepare the stand for natural regeneration by cutting the understory trees and the shrub layer. Where possible, natural regeneration is used, as this preserves the genetic diversity of forest tree populations. After the appearance of high-quality saplings, restoration is continued with a higher intensity of felling to increase the competitiveness

of other important species, that are part of beech forest communities. With the final feelings, the restoration is completed at the latest when the young trees are 1 to 2 meters high. All regeneration feelings on areas with already established young stands have to be carried out outside the vegetation period (ZGS 2021). When natural regeneration fails, it is recommended to restore the forest by planting and enrichment planting of beech seedlings with an admixture of other site-suitable tree species (such as oaks, sycamore maple, and other noble hardwood species). Enrichment planting should be carried out only in small groups of trees. The size of the areas for restoration should be as small as possible - the mosaic structure of future stands is increasing their resilience to threats of climate change.

The disadvantage of natural regeneration is that forest resources can be endangered since longlived tree species cannot adapt to new diseases and pests quickly enough simply by transferring genetic information through natural evolutionary processes. Particularly problematic are damaged areas where trees have damaged regenerative parts of their crowns, which are supposed to ensure natural rejuvenation.

From a silvicultural point of view, beech, at a suitable density, quickly clears its branches so thinning measures at young stages mostly include the removal of poorly formed, damaged, and pre-grown trees (Figure 2.3). Trees in the understory shouldn't be removed since they are an important part of future stand stability (ZGS 2021). By regulating the tree composition, tree species biodiversity should be maintained and the proportion of unwanted tree species reduced. Special attention should be paid to the stability of the beech stands, especially on slopes. So-called situational thinning, which considers the classic silvicultural principles, but focuses on a small number of selected target trees is a more suitable solution. When choosing target trees, vitality and stability take priority over quality, which in turn takes precedence over the distance between target trees. The intensity of the removal of competing trees for individual target trees is adjusted to the conditions in the forest stand and tree species (Sever *et al.* 2022; Diaci, 2021).

A gradual natural transformation (restoration) of adult beech stands is necessary only where tree species composition is changed to the extent that endangers its stability. The change should go in the direction of natural renewal with deciduous trees, especially beech and all noble deciduous trees including cherry and linden (ZGS 2021).



Figure 2.3. Thinning is still a part of beech stands management in their adult age.

The main measures to adapt forest management of beech stands to climate change are focusing on the adaptation of tree composition in beech forest stands, an increase of forest resilience by diverse structures of forest stands on all levels, especially genetic, through advanced forest regeneration and reforestation measures, and increase of their stability by early enough tending measures (e.g. thinning), formation of multilayered and selective forest structures in suitable stands, and (last but not least) monitoring and conservation of forest biodiversity, starting at genetic diversity (Bajc *et al.*, 2020).



Figure 2.4. Successful regeneration of beech stands with planting depends on quality and genetically diverse seed sources.

To ensure the adaptability of future stands to changes in the environment, it is necessary to use genetically diverse forest reproductive material (FRM), by obtaining seeds from a large number of trees during the period of strong flowering and fruiting, professionally appropriate mixing of the FRM, and, based on provenance tests, scientifically grounded transfer of different local provenances between different ecological environments. In addition, appropriate medium-term planning of the storage of seed stocks in the seed bank and the constant availability of appropriate seedlings are important (Kraigher *et al.*, 2019).

## 3. Landscape genomics

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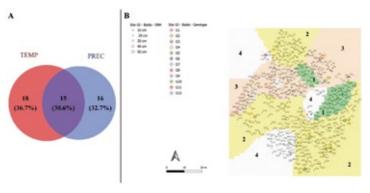
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Landscape Genomics approache was carried on to analyze the neutral and adaptive components of genetic diversity to highlight possible signatures of local adaptation in the beech populations. We used neutral and adaptive molecular markers in combination with spatial data and bioclimatic indicators. As a result of *Fagus sylvatica* L. target re-sequencing, about 1400 SNPs were observed in 18 genomic regions relevant for response to one or more abiotic stresses (results reported in deliverable Action B1: SNP road-map of each study site). Through the spatial distribution of SNPs (results reported in deliverable Action B1: SNP road map of each study site), it was possible to observe a higher number of site-specific and region-specific SNPs for Italian sites. This could be interpreted as a sign of adaptation to a Mediterranean bio-climatic regime that characterizes the Italian peninsula and sets it apart from the more continental climate found in Slovenia and Croatia.

To identify local adaptation signatures, we conducted Genome Environment Associations (GEA) analyses. The results showed the presence of an association between 98 allelic variants and the mean values of the 12 bioclimatic indicators considered for these analyses (as reported in Deliverable Action B1: Production of maps of the spatial distribution of genetic diversity and correlation between allele distribution and environmental variation). The presence of site-specific allelic variants could be correlated with the local rather than regional pattern of adaptation. In the environmental association analysis (EAA) it is important to account for neutral genetic structure (Rellstab *et al.* 2015), as the neutral genetic structure can produce patterns similar to those expected under non-neutral processes (Excoffier & Ray 2008; Excoffier *et al.* 2009; Sillanpää 2011). Furthermore, the genetic structure of populations was analyzed using STRUCTURE (Pritchard *et al.*, 2000) and GENELAND software (Guillot *et al.*, 2008).

In general, we found a high number of specific allelic variants in unmanaged sites and old-growth forests. The presence of a high number of SNPs associated with adaptation to bioclimatic indicators at these sites could be correlated with the neutral genetic structure observed for these sites

Figure 3.1. LFMM analysis results and genotype distribution map of Site 02 - Baldo's forest. (A) Venn diagram showed the overlapping between SNP associated with temperature-related and precipitation-related bioclimatic indicators, as a result of LFMM analysis. (B) Spatial distribution of Genotype and organization into 4 clusters (GENELAND results). The map displays the individuals present



within the study site (circle with black border) and the sequenced individuals. The latter are characterized by coloured circles according to the genotype observed. Identical colours mean identical genotypes. (Aravanopoulos, 2018; Paffetti *et al.*, 2012; Stiers *et al.*, 2018). Indeed, some studies have observed that these sites are characterized by a complex neutral genetic structure, characterized by a high number of family clusters. This great variability may allow a higher probability for the appearance of new allelic variants that could enrich the adaptive potential of this species for current and future climate change. A similar situation was observed in stands managed with reduced-impact management regimes: single tree selection system. The number of allelic variants specific to each site is high. Baldo's forest site has the highest number of SNPs associated with bioclimatic indicators (Figure 3.1). The creation of gaps in forest cover and the complexity of structure characterizing these stands could be linked to a higher probability of gene recombination between genotypes belonging to different family clusters. These patterns are like those found in old-growth forests and unmanaged populations. Thus, the potential for reduced-impact silvicultural management to conserve adaptive genetic diversity appears promising. These data are further supported by the analysis of the other beech sites in the study.

Less impactful management types, such as individual tree selection, appear to report a population with a high number of allelic variants associated with response to bioclimatic indicators. Similar results have been observed in unmanaged stands and old-growth forests. The results reported in this study could be important in silvicultural management planning, where knowledge of genetic variability from an adaptive perspective could help decision-making processes. In addition, this knowledge could also be used in anticipation of assisted migration works. This is important to preserve the current Forest Genetics Resources (FGR) but also to enrich the existing stand with potentially favorable genotypes.

# 4. Soil biodiversity

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Vital soil resulting from interaction of physical, chemical and biological soil properties is critical for sustaining forest growth and ecosystem services. High soil biodiversity supports functional flexibility for adaptation to unknown changes that may occur in the future.

Ectomycorrhizal root tips (Figure 4.1) support specific and diverse populations of bacteria and microfungi, including bacteria that help to establish mycorrhizal symbioses. Tree roots also harbor dark septate endophytes and wood-decomposing fungi (Baldrian, 2017). Besides mycorrhizal mycelia and associated organisms, bulk soil hosts saprotrophic fungi and bacteria (Baldrian, 2017). A considerable part of soil biota, including many soil invertebrates, relies on the flow of photosynthetic carbon from the trees belowground (Prescott and Grayston, 2023).



Figure 4.1. Ectomycorrhizal fungi are tree symbionts that support tree growth with their access to nutrients and water in exchange for tree photosynthetic carbon.

In managed forests, the quantity of photosynthetic carbon allocated belowground to fine roots and root-associated microorganisms decreases (Noormets *et al.*, 2015). Therefore, changes in alpha and beta diversity of root and soil microbiota are expected with increasing management intensity. We aim to achieve the intensity of forest management that still supports high soil biodiversity. In the LIFE SySTEMiC project, the short-term effects of individual tree cutting and long-term effects of four silvicultural systems were evaluated for soil biodiversity.

Short-term effects of individual tree removal were evident as decreased taxa richness (number of different taxa, i.e. species) and a lower Shannon diversity index (an index which considers the number of species and their relative abundance) of ectomycorrhizal fungi developed on the roots of the remaining trees. However, the removal of individual trees did not affect the richness and diversity of the total fungal community. On the other hand, the fungal communities did change in composition, seen as an increase in saprotrophic fungi, likely a result of increased necromass (dead organic matter, e.g. dead roots, mycorrhizal mycelia and all organisms that depend on them) and a decrease in the relative abundance of ectomycorrhizal fungi. The decline in ectomycorrhizal fungi was most probably due to the removal of their photosynthetic partners and the resulting decrease of carbon flow belowground.

The study of long-term effects included unmanaged forests, individual tree selection, irregular shelterwood and uniform shelterwood silvicultural systems. Generally, unmanaged forests, known for their high amounts of deadwood, and forests with individual tree selection but considerable amount of deadwood (around  $25 \text{ m}^3/\text{ha}$ ), hosted the highest richness of fungi. Ectomycorrhizal fungi appeared more enhanced in individual tree selection systems, most likely due to the higher complexity of forest structure combined with the removal of individual canopy trees, which prevents the transition into the climax state of succession. According to Twieg *et al.* (2007) the highest species richness of ectomycorrhizal fungi occurs at canopy closure. This phase is characterized by the highest tree growth rates and maximal leaf area, corresponding to higher carbon allocation belowground, to roots and

root symbionts. The other two silvicultural systems were comparable to unmanaged forests in terms of ectomycorrhizal fungal richness. Several studies emphasize the importance of preserving trees in patches or as single trees for so-called continuous root forestry. In such systems, single trees should not be more than 15 meters apart from each other to ensure that belowground biodiversity is sustained (Prescott and Grayston, 2023).

While silvicultural systems do have an impact on fungal communities (See example in Figure 4.2), their effect is often overshadowed by stronger influences of location and bedrock when these factors are accounted for. The significant effects of these variables suggest that local environmental conditions and regional differences are crucial determinants of fungal diversity and community structure. Consequently, while management practices are important, they should be considered alongside these other influential factors for effective conservation and management of fungal biodiversity.

Even though non-significant, the graph shows a declining trend in fungal community richness in managed forests, compared to the unmanaged control.

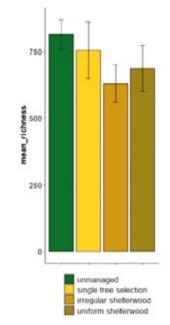


Figure 4.2. Mean fungal OTU (operational taxonomic unit) richness under different silvicultural systems.

# 5. GenBioSilvi model

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To investigate biodiversity in forest ecosystems, we analyzed indicators including genetic diversity, forest structure, deadwood, soil diversity, and microhabitat conditions using collected data from other project tasks. In Fagus sylvatica L. stands, we observed that unmanaged and old-growth forests conserved and increased biodiversity. Managed sites with individual tree selection system showed similar biodiversity levels. Genetic diversity analysis using nuclear microsatellite (nSSR) revealed that old-growth forests and individual tree selection sites had complex spatial genetic structures, unlike regular and irregular shelterwood-managed stands. Numerous SNPs correlated with bioclimatic indicators were identified, particularly in Site 02 - Baldo's Forest, which had a complex genetic structure. Dendrometric data suggested that the best structure was a multi-layered uneven-aged forest, seen in Site 02 - Baldo's Forest, Site 11- Fonte Novello, and Site 25 - Rajhenavski Rog. Unmanaged sites had the highest deadwood volume and many saproxylic microhabitats, especially in old trees. Most sites were pure beech stands with some sporadic species that should be preserved. Soil diversity was highest in old-growth and minimally impacted managed sites. We hypothesized that the best management practice for high biodiversity is individual tree selection system, mimicking old-growth conditions, and promoting natural regeneration. This promotes pollen dispersal, genetic diversity, and new allelic variants crucial for climate change adaptation. We developed a model focusing on key indicators such as deadwood, microhabitat, and species diversity to represent biodiversity and guide sustainable management practices. Genetic and soil diversity data were excluded from the user form due to observational difficulties (Table 5.1).

Table 5.1. Description of selected indicator useful for users to describe the status of the stand.

Categories	Indicators	Description
Forest structure	DBH standard deviation	Variability in tree DBH within the stand
	Percentage of trees in regeneration layer	Presence of the target species natural regeneration
	DBH class distribution curve	Complexity of horizontal and vertical forest structure
	No. of population strata	
Deadwood	Standing deadwood presence	Description the presence of deadwood functioning as microhabitat
	Coarse woody debris	
Species diversity	Species richness	Number of all species present in the stand regarding both the presence of adults' individuals and regeneration
	Percentage of non-target individuals regeneration	
Microhabitat	Percentage of individuals with cavities	Presence of key microhabitat form for biodiversity
	Percentage of individuals with Injuries and wounds	
	Percentage of individuals with Deformation	

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Figure 5.1. Forest population assessment form structure with Site 02-Baldo's data.

Below is an example of the form that showed the compiled form based on the actual data obtained from Site 02 - Baldo's forest (Figure 5.1).

# 6. Recommendations for Sustainable Forest Management of Beech (*Fagus sylvatica* L.)

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<sup>1</sup> Slovenian Forestry Institute (SFI), Slovenia

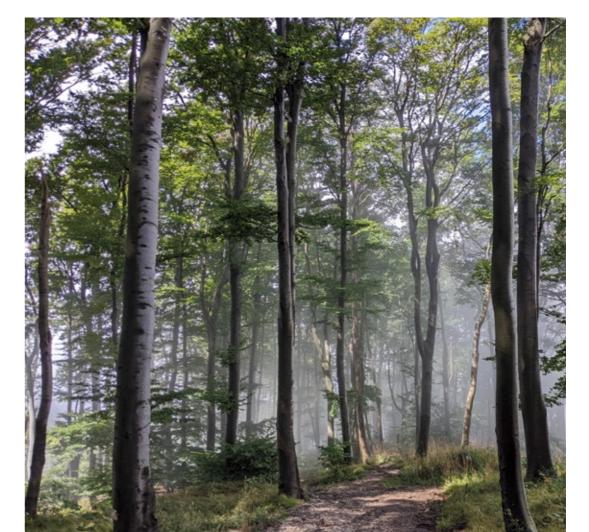
- <sup>2</sup> Slovenia Forest Service (SFS), Slovenia
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### Recommendations for Sustainable Forest Management of Beech (Fagus sylvatica L.)

- Silvicultural systems for beech stands should be carefully selected to promote close-to-nature approaches and mimic natural processes in beech forest stands.
- Silvicultural systems with reduced impact are more favourable in light of beech forests genetic variability preservation, such as individual tree selection and low-scale irregular shelterwood systems.
- Beech is a shade-tolerant tree species, characterized by slow growth in youth and late culmination of volume increment, which does not show signs of decline up to the late age.
- Beech is relatively ressilient to most diseases, but suscepctible to late spring frosts, stem surface damages by intense sunlight and natural disasters such as sleet, snow break and windstorms.
- Through the natural regeneration of beech forest stands, trees' adaptability to conditions of specific growing sites and natural dynamics is preserved so beech forest stands should be renewed naturally.
- The most common way for the regeneration of beech stands is under canopy cover where regeneration is set in the sequence of felling mostly as a part of an irregular shelterwood system.
- Regeneration in gaps should start after the mast seed year, accompanied with preparation of the stand for natural regeneration by cutting the understory trees and the shrub layer.
- When natural regeneration fails, it is recommended to restore the forest by planting and enrichment planting of beech seedlings in small groups of trees with an admixture of other sitesuitable tree species.
- Special attention should be paid to the stability of the beech stands, especially on slopes.
- Very suitable solution for beech stands is situational thinning, which focuses on a small number of selected target trees in a stand.
- The main measures to adapt forest management of beech stands to climate change are the adaptation of tree composition in beech forest stands, an increase of forest resilience by diverse structures of forest stands on all levels, especially genetic, through advanced forest regeneration and reforestation measures, and increase of their stability by early enough and adapted tending measures.
- Landscape Genomics is essential to assess neutral and adaptive genetic diversity for understanding the signature of local adaptation in the populations to drive silvicultural management. The results have indicated that sites managed according to individual tree selection reported the most complex spatial genetic structure among the managed sites and the highest number of SNPs associated to bioclimatic indicators which are important for the resilience to climatic changes.
- Knowledge of genetic variability from an adaptive perspective can improve forest management decisions and anticipate assisted migration efforts. This is crucial for preserving Forest Genetic Resources (FGR) and enriching stands with favorable genotypes, ensuring forest resilience and genetic diversity.
- For *Fagus sylvatica* L. stands, we recommend less impactful management practices, such as individual tree selective thinning, which are associated with populations having a high number

of allelic variants in response to environmental variables. Similar results have been observed in unmanaged stands and old-growth forests.

- The monitoring and study of biodiversity in all its components is crucial for understanding forest ecosystem resilience. For this reason, it is important to collect information regarding genetic diversity, forest structure, deadwood, soil diversity, and microhabitat conditions.
- For Fagus sylvatica L. stands that showed similar characteristics to those included in our study, we suggest using a type of management that increases forest stand complexity with a multi-layered vertical structure that facilitates pollen dispersal, promotes genetic diversity, and increases new allelic variants crucial for climate change adaptation. In our study these characteristics are found in stands managed according to individual tree selective thinning.
- The use of the GenBioSilvi model could support forest users in checking the current status of stand biodiversity and providing guidelines for sustainable management. In fact, we identified key indicators that indirectly describe genetic diversity and represent biodiversity, focusing on deadwood, microhabitat, and species diversity. We concentrated on observable key indicators to describe the current status of the analyzed stand.
- To ensure the adaptability of future stands to changes in the environment, it is necessary to use genetically diverse forest reproductive material (FRM), by obtaining seeds from a large number of trees during the period of strong flowering and fruiting, professionally appropriate mixing of the FRM, and, based on provenance tests, scientifically grounded transfer of provenances from different ecological environments, mainly form more south-eastern regions towards northwestern locations.



<sup>6</sup> Guidelines for Sustainable Forest Management of Beech (Fagus sylvatica L.)

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