Final report

Towards the Sustainable Management of Forest Genetic Resources

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Abstract:

The FORGER project provided science-based recommendations considering: opportunities to improve genetic conservation of four important European tree species; monitoring forest genetic diversity applicable by all EU Member States; implications of past and current transfer of forest reproductive material between different countries; adaptive forest management of genetic resources in the face of climate change; impacts of climate change on the distribution of genetic diversity; effective seed sampling protocols to maintain genetic diversity in future forests.

Keywords :

forest genetic resources, conservation, forest management, forest reproductive material, climate change

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1 Final publishable summary report

1.1 Executive summary

The FORGER project provided the European forest sector with integrated knowledge and information resources for enhanced conservation and use of forest genetic resources (FGR) as part of sustainable forest management. This helps the forest sector in adapting both forests and forest management practices to climate change and to ensure that forests continue to perform all their productive, socio-economic and environmental functions in the future. The project results, especially maps and gap analyses, will help countries to identify areas where they should establish new gene conservation units for forest trees. The integrated databases and the new monitoring protocol to measure genetic diversity will allow a better characterization and monitoring of genetic diversity and genes conserved within these units. Recommendations for seed harvesting, transfer and use of forest reproductive material, management of forest genetic resources in both production forests and the gene conservation units were provided to allow countries harnessing the full potential of forest genetic resources for mitigating the negative effects of climate change and maintain the adaptive potential of forests in the future. FORGER produced deliverables in two main areas crucial for delivering the expected impacts: *conservation* and *use and management of forest genetic resources*.

In the area of *forest genetic resource conservation*, the outputs include improved forest inventories on forest genetic resources and linkages between existing databases, comprehensive assessments of genetic diversity of European beech, pedunculate and sessile oak, Scots pine and Norway spruce, and analyses to determine to what degree the genetic diversity of these species is covered by current gene conservation efforts. In addition, a protocol for monitoring and measuring forest genetic diversity at pan-European level was developed. The use of these outputs by target groups was facilitated through dissemination efforts so that the outputs will be translated into applicable outcomes. These actions are expected to lead to positive changes, i.e. the revision of pan-European and national gene conservation strategies and the genetic characterization and monitoring of gene conservation units.

In the area of *use and management* of forest genetic resources, the outputs include evaluation of historic and current cross-border transfer of forest reproductive material (FRM), identification of eco-geographic patterns in adaptive traits and reaction norms, and analyses of the impacts of climate change projections and forest management on the long-term availability of FGR. The use of these outputs by beneficiaries will translate in the deployment of FGR for mitigating the negative effects of climate change on European forests, in an optimized production and appropriate transfer of FRM, and in better management of FGR in production forests and gene conservation units. At the country level, these outcomes will contribute to a better integration of FGR management into national forest programs and national adaptation strategies, and in the improved management of production forests and gene conservation units.

1.2 Summary description of project context and objectives

Genetic diversity

Genetic diversity, i.e. diversity within-species, allows a species to evolve over time and in space and plays a key role for both the long-term survival of a species and stability of forest ecosystems and sustainable forest management. Genetic diversity is thereby a fundamental and critical part of biodiversity. In Europe, forestry has changed both the genetic composition and diversity of tree populations in many ways and continues to do so. Transfer of forest reproductive material (FRM) is one of the major factors. In addition to forestry, habitat loss, fragmentation, and environmental changes such as air pollution and climate change are important anthropogenic threats to genetic diversity. Genetic diversity in tree species is a public good. It is non-exclusive and non-rival in consumption and this complicates its valuation. Nevertheless the value of genetic diversity, both its non-monetary worth and the utilization of forest genetic resources, are the driving forces in their conservation. Utilization provides an incentive for the conservation of a resource. Thus, genetic conservation is the process that actively preserves genetic diversity of the resource with the view of actual or potential utilization.

Forest genetic resources

Forest trees may have 20,000 up to 30,000 genes. These genes determine growth, form and physiological response of trees. Certain genes make trees grow faster, straighter or enable them to thrive in harsh environments. Admittedly, this is a very simplified view and in reality genes interact with their environment and among each other. Forest genetic resources (FGR) are defined here as any coding and non-coding but functional genetic material (DNA) of forest trees that is of actual or potential value for future generations of humankind. Operationally genetic resources are embedded in FRM such as seeds, seedlings or other propagules. As genetic conservation aims at the utilization of genetic resources, target tree species need to be selected and studies based on social, ecological and economic grounds.

Conservation of forest genetic resources

We define genetic conservation as any *in situ* or *ex situ* maintenance of genetic diversity to secure the future utilization of the genetic resources. *In situ* conservation is a measure taken to conserve tree populations in their natural environment or in the environment where they have developed their distinctive properties. Usually, this refers to designated genetic reserves where the genetic adaptability of forest tree species is maintained by natural processes. Conversely, the *ex situ* conservation of genetic resources entails all measures including the removal of any genetic material (DNA, pollen, seeds, whole plants, populations), their storage in gene banks or in clonal archives or so- called *ex situ* gene reserves as long as the resource is considered valuable. FGR conservation usually does not aim at the static preservation or maximization of genetic diversity as such, but rather tries to preserve the mechanisms that maintain genetic diversity. Utilization is the exploitation of FGR by forest management either directly for economic purposes such as for lumber, veneer or biofuel production or for tree improvement (breeding). The challenge for an effective conservation is to cover a representative sample of appropriate tree populations and to evaluate what amount of the gene pool is conserved.

In general, FGR conservation is a multifaceted issue including risk assessment and valuation of genetic resources, identification of individuals and populations, collecting and evaluating samples, genetic monitoring and *in situ* and *ex situ* maintenance of the FGR. Thus, genetic conservation should be part of any National Forest Program. International activities such as the European Forest Genetic Resources Programme have stimulated genetic conservation through regional collaboration to promote conservation and sustainable utilization of FGR. However, practical conservation actions can only be implemented by national authorities. Therefore, the implementation of FGR conservation is dependent on national forest policy and must be backed by political will. Since every conservation activity involves costs, it is easier to attain political support if the economic value of FGR can be demonstrated in monetary terms. Practising sustainable forest management thus involves handling the technical matters of genetic conservation as well as demonstrating the importance of genetic conservation to politicians, forest managers, conservationists and the general public.

European forests

The area of forests in EU countries is about 150 million ha. These forests are very diverse, not only in ecological conditions and productivity, but also in their history, ownership structure and management practices. European forest ecosystems vary widely, from boreal forests near the tree line in northern Scandinavia, to open woodlands and scrubs in the Mediterranean region (e.g. maquis), from man-made Eucalypt plantations in the Iberian Peninsula to close-to-nature oak forests, from Alpine to lowland riparian forests in central Europe. European forests harbour valuable genetic resources important for current and future production of goods and services. Forests act as essential carbon sinks mitigating climate change, and forests have important economic, ecological, social and cultural roles. The demands for these wood and non-wood forest goods and services are likely to further increase.

However, forests face an unprecedented global change affecting the supply of these goods and services for humankind. The fast growing human population significantly deteriorates the environment by greenhouse gases and pollution at a global scale. Besides atmospheric pollution and overall environmental changes, a number of factors seriously affect the conservation and management of genetic resources. These include past intensive management, artificial regeneration, wide-scale transfers of forest reproductive material, decreased population sizes due to forest fragmentation, and introduction of exotic forest tree species. The long-term consequences of this loss of genetic resources for human welfare are not always recognized.

To make better use of existing potentials and to minimize negative impacts of genetic impoverishment in forests, there is a need for a sound and sustainable management for conservation of genetic resources in European forests. As less than 4% of the European forest area may be considered as undisturbed by humans, we cannot rely on the maintenance of sufficient genetic diversity through spontaneous natural processes. FGR conservation therefore needs to be integrated in sustainable forest management.

Project Objectives

The overall goal of the FORGER project is to enhance the conservation and use of forest genetic resources as part of sustainable forest management in Europe, by making available sound and integrated information on forest genetic resources for forest managers and policymakers. The project has the following objectives to obtain that overall goal:

Objective 1: To improve and analyse inventories on forest genetic resources
Objective 2: To develop a common protocol for measuring and monitoring genetic diversity
Objective 3: To analyse historic, current and future use and management of forest genetic resources
Objective 4: To provide improved tools, guidelines and recommendations for stakeholders
Objective 5: To disseminate and communicate the project's results to stakeholders

Context of the project’s objectives

Inventories of forest genetic resources (Objective 1)

During the past 20 years, European countries have made good progress in conserving forest genetic resources at national and regional levels. The European Forest Genetic Resources Programme, EUFORGEN, was established in October 1994 as an implementation mechanism of Strasbourg Resolution 2 (Conservation of

Forest Genetic Resources) of the first Ministerial Conference on the Protection of Forests in Europe (MCPFE). The aims of the collaborative programme among European countries are: (i) to promote the conservation and sustainable use of forest genetic resources, (ii) to serve as a platform for pan-European collaboration in this area, and (iii) to brings together scientists, managers, policy-makers and other stakeholders for the exchange on knowledge and information. An important result of this collaboration is the European Information System on Forest Genetic Resources, EUFGIS.

Researchers also recognized the importance of studying genetic variation over large geographic scales. These studies focused on: (i) the influence of post-glacial history and migration routes, (ii) range-wide distribution of on genetic variation, (iii) the effects forest fragmentation on forest genetic resources, (iv) forest genetic resources at the margins of the species' area, and (v) the dynamics of diversity in natural and managed forests. The studies, often implemented with EU funding, provided highly valuable information and insight on forest genetic resources. Some of these studies collected large amounts of data on genetic diversity of trees and stored it in the Geo-Referenced Database of Genetic Diversity, GD^2. The EUFGIS and GD2 databases form the foundation for better conservation and use of forest genetic resources in Europe. The two databases were unconnected until now.

Measuring and monitoring genetic diversity (Objective 2)

Monitoring genetic diversity in forest stands

There is currently a strong advance in genomics and statistical tools that make genetic monitoring more efficient and economical. Genetic diversity and driving processes can be measured better than ever before. Neutral genetic markers such as micro-satellites have become an efficient tool to study genetic variation and to infer demographic processes. Recently evidence of association between single nucleotide polymorphism (SNP) and adaptive traits have been found in forest trees. But so far SNPs in adaptive genes have been never applied for monitoring purposes. In short, the rapid developments of new molecular genetic techniques and fast decrease of costs involved, allow genetics to become an important tool for monitoring changes in diversity, both at the neutral and adaptive level.

Assessment of genetic diversity at the European scale

The predicted future global climatic changes and the land use changes will impact forest ecosystems. Impacts of global change on European forests are expected to be acute, resulting in large scale changes in species range, ecosystem functioning and in the interactions among species. The extent to which populations can adapt to local conditions depends on within-population genetic diversity and how this diversity is distributed within and among species trees and appears to rely more on standing genetic variation and recombination than on new mutations. Because trees are long-lived and sessile, their options are: to disappear, to disperse to other places, or to adapt *in situ* to the on-going climatic change over a reduced number of generations. Effective conservation approaches must account for genetic population structures and the overall influence of disturbances acting on habitat templates and species distributions. E.g. sampling strategies to maintain sufficient levels of genetic diversity differ between populations in the centre and at the edge of the species' geographic area. Such insight is important to preserve critical habitats that potentially harbour high genetic diversity, and to predict biological responses to global climate change. A European wide assessment of genetic diversity and knowledge on the processes shaping this is required more than ever before.

Use and management of forest genetic resources (Objective 3)

The unmonitored transfer of forest reproductive material may negatively affect the productivity due to poor adaptation of provenances to target locations, which may be aggravated by climate change. An approach to counteract that is by assisted migration to support natural adaptation processes. Adequate knowledge on the adaptive range of tree populations is indispensable to apply assisted migration. The data collected in provenance trials are excellent to assess the adaptive range of tree. Provenance trials are reciprocal common garden tests where tree populations collected throughout Europe are tested on tree functioning such as growth, vigour and phenology. The gardens themselves are distributed over a wide range of environmental conditions and are widely used to investigate the effects of change of environment on productivity and survival. The response of tree functioning to environmental drivers, such as temperature, has also been used to formulate seed transfer rules and to define seed zones.

A large body of literature exists on the genetic effects both for naturally and artificially regenerated forests. The general pattern is that genetic diversity of artificial regenerated forests is less than naturally regenerated forests. This is probably the result of a lower number of parent trees in artificial regeneration compared to natural regeneration. Such results highlight the need for improved seed collection guidelines, as only stands with large genetic diversity will be able to adapt to future environmental conditions.

Finally, management interventions during the forestry process, such as thinning and tending, influence the genetic composition and diversity in forest stands. Model simulations indicate that the adaptive rate of functional traits such as phenology to climate change is influenced by forest management. A result of this study was that although the highest level of diversity is maintained in unmanaged forests, but that the rate of adaptation to climate change is higher in managed forests. The advantage of the applied individual based approach of genetic modelling is that a future optimal phenotype is not input to the model, but dynamically determined based on the interactions between the individual tree and its environment.

Tools, guidelines and recommendations on the conservation of genetic diversity (Objective 4)

The European Forest Genetic Resources Programme (EUFORGEN) has so far developed technical guidelines for genetic conservation and use of 33 tree species in Europe. These guidelines provide basic conservation recommendations but they do not specify where new gene conservation units should be established or how a network of gene conservation units should be managed at pan-European level, for example. Several years ago, EUFORGEN also initiated the development of so called ‘common action plans’ for selected tree species to facilitate and improve national gene conservation efforts from the pan-European perspective. This initiative also aimed at sharing of responsibilities among European countries and identifying gaps in the existing FGR conservation efforts.

Until recently, the development of such strategies and action plans was hampered by a lack of harmonized and geo-referenced data on tree populations conserved within the gene conservation units. In addition, it was not clear how the units should be managed so that they contribute to gene conservation purposes at pan-European level. The EUFGIS project (April 2007-March 2011) addressed these problems and developed the pan-European minimum requirements and data standards for the gene conservation units before creating the EUFGIS Portal.

Requirements include management recommendations based on the concept of dynamic gene conservation. Dynamic gene conservation emphasizes maintenance of evolutionary processes within tree populations to safeguard their potential for continuous adaptation. This can be done either managing tree populations at their natural sites within the environment to which they are adapted (*in situ*), or artificial but dynamically evolving populations elsewhere (*ex situ*). Therefore, management measures and silvicultural techniques applied should favour genetic processes that maintain the long-term viability of tree populations.

1.3 Main results and foregrounds

WP1 Inventories of forest genetic resources

WP 1 contributed to Objective 1 of FORGER: *To improve and analyse inventories on forest genetic resources.* This objective was achieved by: (i) extending existing databases on inventories of forest genetic resources, and (ii) characterizing of the genetic diversity in gene conservation units.

Task 1.1 Extending existing databases on inventories of forest genetic resources

During the past decades, a vast amount of information on genetic resources of forest trees has been gathered. Ample genetic data exist especially in major tree species in Europe, many of these international projects have been supported by EU. However, to be useful for further investigations, genetic data should be stored in uniform format. The Geo-referenced Database on Genetic Diversity (GD^2) was developed as part of the EVOLTREE project (Evolution of Trees as Drivers of Terrestrial Biodiversity, 2006-2010) and it is maintained by INRA. It contains genetic and geo-referenced passport data on tree populations and single trees that have been sampled for genetic studies. The GD^2 database was developed to make available the genetic data sets (all types of neutral markers) from published studies and it also provides a copy of the publication where a given data set was published. The database makes it possible to display the data in a standardized way and to carry out meta-analyses across species and geographical areas. The GD^2 database contains two types of data: (i) aggregated data per population, such as gene frequencies and gene diversity parameters, and (ii) genotypes of individual trees.

During the FORGER project, inventory of surveys of genetic diversity in tree forest tree genera: *Fagus, Quercus, Pinus* and *Picea* were conducted by literature review of published surveys, preparing templates and spreadsheets to retrieve the data that were sent to authors for completing the spreadsheets, and storing data in the GD^2 data base, which harbors all the data regarding georeferenced surveys of genetic diversity of forest trees (D1.1[1]).

Task 1.2 Characterization of the genetic diversity and network of gene conservation units

Ample genetic data in GD^2 allowed us to infer large scale patterns in amount of genetic diversity in main forest tree species. The data was comprehensive enough to produce pan-European distribution maps for five major forest tree species: beech (*Fagus sylvatica*), sessile oak (*Quercus petraea*), Norway spruce (*Picea abies*), Scots pine (*Pinus sylvestris*) and maritime pine (*Pinus pinaster*). The data on isoenzyme and microsatellite markers has been utilized and related to the chloroplast data, when appropriate.

The results showed trends and patterns in the European distribution of genetic diversity, different markers (enzyme, microsatellite) giving similar results. In beech and sessile oak, genetic diversity increases from east towards west. In Norway spruce, genetic diversity is high in Baltic countries and Finland, lower in Sweden, Norway and Central Europe. In Scots pine genetic diversity is high in the north-eastern part of Europe (part of Czech Republic, Poland, Baltic countries, Scandinavia) and low in south-western part. In *Pinus pinaster*, Italian populations harbored slightly less variation than others and locally differences between adjacent populations were rather large in Spain. Summarizing, western Central Europe is a hot spot of genetic diversity of oaks and beech, whereas northern Europe is the hotspot of genetic diversity for the widely distributed coniferous trees

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[1] See Deliverable list in table 4 at the end of this report

(Scots pine, Norway spruce). In general, the level of genetic variation in present forests is heavily influenced by historical events, i.e., refugia and colonisation routes during and after glaciation.

To assess the environmental coverage of present gene conservation network, environmental, genetic, and geo-referenced data had to be combined. In FORGER, we linked two databases, the GD^2 (geo-referenced data on genetic diversity) and EUFGIS (geo-referenced information on the conservation of forest genetic resources in Europe) databases. The European Information System on Forest Genetic Resources (EUFGIS) contains standardized and geo-referenced information on genetic conservation units of forest trees in Europe. It was developed to improve documentation and management of these conservation units. Before creating the database, the EUFGIS project developed pan-European minimum requirements and data standards for the units in collaboration with the European Forest Genetic Resources Program (EUFORGEN) and a large group of experts and scientists in Europe. The EUFGIS Portal is hosted by Bioversity and maintained as part of EUFORGEN Activities. The data on these units for more than 100 tree species is available through the EUFGIS Portal.

The network of genetic conservation units was assessed in the four main forest tree species (oak, beech, Norway spruce, Scots pine) with respect to various factors: genetic, geographical and environmental coverage, and further information available on habitats and their frequencies with climate change. Information on geographic patterns in adaptive variation, when available, was also used to assess the gene conservation activities. Analyses pinpointed some areas (e.g., westernmost areas in broad-leaved trees, northernmost areas in conifers) and habitats (hot and dry) that seemed to require more attention in the gene conservation network. However, there may be several reasons for the suggested “gaps” in the network. Firstly, some areas may not have conservation units that meet the minimum requirements set for a gene conservation unit that is the case for instance in some gaps in the westernmost distribution areas. Secondly, in some cases in the eastern part of distribution, there might be gene conservation units in some areas, but data are not stored in joint databases (EUFGIS). Furthermore, in some areas in the north, strategies to maintain gene diversity may be different and specific gene conservation units are not nominated for some common species. Thus, reasons for identified gaps are different and thus should be considered case by case, to find the “true” and alarming gaps in the GCU network. Gene conservation should be based on dynamic evolution, and gene conservation network should be dynamic, too. Network is indeed constantly being improved, and some gaps identified in this study have already been filled. However, more genetic research is needed for identification of most crucial gaps in the GCU network. Especially genetic data on adaptive variation would be needed, and adaptive markers developed e.g., in FORGER WP2 (see below) will be highly useful. Marginal areas of distribution should be under serious surveillance. Northern marginal populations will enable migration of species distribution to northwards. Southern marginal populations are even more crucial for gene conservation since there should be enough genetic variation to adapt for even more hot and less humid environment in the future without gene flow from populations that would be adapted to that kind of environment.

Thus, it is recommended that current representativeness of the genetic conservation units should be assessed further, both at country and pan-European level. Full climatic range of species distribution should be covered. Furthermore, GCUs should be evenly distributed across the “climatic range” of a species, rather than evenly distributed across the geographic space. Thus, in cases where environment changes considerably over short distances, GCU network should appropriately cover the deep climatic gradient. GCUs should also be located in hotspots of genetic diversity, across the geographic distribution of the species, particularly in areas with fragmented forests. Finally, research on gene diversity of adaptive traits should be strengthened, and that information should be made available for practical forest management (D1.2, D1.3).

WP2 Measuring and monitoring genetic diversity

WP 2 contributed to Objective 2 of FORGER: *To develop a common protocol for measuring and monitoring genetic diversity.* This objective was achieved by: (i) further develop and apply at the European scale protocols for monitoring of genetic diversity in forest stands to assess the impact of climate change and forest management, and (ii) application of molecular tools to assess adaptive genetic diversity for *Fagus sylvatica, Quercus robur + petraea, Picea abies* and *Pinus pinaster.*

Task 2.1 Further develop and apply at the European scale protocols for monitoring of genetic diversity in forest stands to assess the impact of climate change and forest management

The work on genetic monitoring was subdivided in: (i) selection of sites and determination of monitoring intensity of the pilot study on *Fagus sylvatica*, *Quercus spp*., *Picea abies* and *Pinus pinaster*, (ii) pilot study genetic monitoring on *Quercus robur*, *Fagus sylvatica*, *Picea abies* and *Pinus pinaster* at the European scale, and (iii) formulating improved protocols for the monitoring of genetic diversity of trees in Europe. The protocol was applied in a pilot study for genetic monitoring at a European scale in a total of 16 plots with 4 plots per species (Picea abies, Pinus pinaster, Quercus robur, Fagus sylvatica). The protocol on genetic monitoring was developed in close collaboration with FORGER's stakeholders. Below the main recommendations of these studies are presented, and overall conclusions drawn (D2.1).

Recommendations related to sampling design

Is seed and seedling sampling necessary? Genotyping of seeds allowed estimation of mating system parameters, pollen dispersal and pollen immigration rates. No departure from random mating (insignificant inbreeding) could be observed. Further, genetic diversity was correlated among seeds and other life stages, and the effective population size in seeds was correlated with genetic diversity in adults. We can therefore conclude that data on seeds might not be useful in genetic monitoring protocols. The high costs associated with several visits to monitoring stands, seed harvesting and genotyping of many offspring could thus be spared. Another reason to leave the seed stage out is that a single seed year has only very little impact on the genetic composition of the future adult generation. However, sampling of seedlings should be performed to detect potential changes in genetic structure. There is clear evidence for strong genetic selection in tree populations in the early ontogenetic stages. Here, a dramatic mortality occurs. In particular, our results indicated that a Gregorius genetic distance among adults and seedlings for nSSRs higher than 0.15 might reflect loss of genetic diversity or genetic changes which should be further characterized.

Adult and seedling sampling.

Our results suggested that we should focus on the adult cohort and saplings. A representative sampling over the whole stand (with several transects) should avoid sampling of only a small part of the available genetic diversity in the stand. In order to monitor genetic changes the inventory of the sapling should be repeated every 10 years. At the same time, the adults should be revisited and the mortality should be recorded and new adults (above a threshold diameter) should be sampled and genotyped.

Recommendations related to sample size

Results of the rarefaction study indicated that ranking of genetic diversity (effective number of alleles) among the different populations could not be recovered when a reduction of sample size and number of loci was applied. One result of the genetic monitoring and the assessment of genetic diversity should be to identify those populations with particular high and particular low values of diversity. For this the ranking of genetic diversity should be robustly estimated with our samples. But with our sample sizes, we cannot estimate the real ranking, and it is possible that 96 adult individuals genotyped at 120 nSNPs or at 12 nSSRs do not provide a reliable estimation on ranking of genetic diversity. Simulations on larger datasets are therefore required to answer this question, and also to find the optimum between sample size, number of loci and sampling design. Based on our data so far, we recommend to have a sample size for adults and saplings of 150 individuals in each cohort and to use at least 120 SNPs.

Recommendations related to the type of markers

Our results indicated similar results among nSNP and nSSR markers, therefore only one marker set could be selected. Several parameters should be taken into consideration to find the best marker type. nSNP loci seem to be less affected than nSSR loci by genotyping errors, and the amount of available loci and/or the development of new markers through New Generation Sequencing methods would allow selection of reliable marker sets. By contrast, nSSRs genotyping often result in errors due to stuttering and large-allele dropout. Further, many SSR loci are strongly affected by the presence of null alleles, which further decreases the choice of suitable loci. For this reason, the use of SNP markers might be encouraged. Costs for SNP genotyping are strongly decreasing, which should convince the scientific community to work with SNP. Moreover, the standardisation among labs would be much easier with bi-allelic SNPs, as nSSRs loci are scored according to their DNA fragment size and are very polymorphic (up to 30 different alleles per locus). We also recommend to store the DNA of the monitoring plots in a DNA repository centre for genetic inventories with future methods (new DNA markers, genotyping by sequencing).

Recommendations of parameters to be use in genetic monitoring

Demography

DBH of adults, spatial position of adults and seedlings, and vitality classification allow the estimation of density, spatial structuring and age structure of the stand. This should indicate, together with geographical information, whether high or low genetic diversity is expected. At high latitudes (for beech, oak and spruce), low density, high DBH, and low variation in DBH, high genetic diversity is expected. It might also further suggest that the stand has been planted or that management regimes such as thinning occurred. We recommend to use drills or to apply quick screening methods (e.g. the application of so called resistographs to measure the dynamics of year rings of individual trees. These profiles of year ring growth are very useful aggregated parameters of tree vitality which could be correlated with time series on many environmental parameters (e.g. rainfall, temperatures).

Genetic diversity

Ranking of: effective number of alleles (Ae), unordered number of genotypes (NG), and genetic distance among adults and seedlings (Gregorius), should indicate stands with lower genetic diversity than expected and which might be at risk of genetic loss. High genetic distance among adults and seedlings might further indicate ongoing genetic erosion processes, which could be further clarified with an analysis of gene dispersal.

Reproductive processes

Analysis of reproductive processes expressed as the Effective population size (Ne) did not show strong differences among the study stands and there was no evidence for inbreeding. Further, strong selection among seeds usually occurs in forest tree species, which reduces the probability to observe effects of inbreeding at the adult stage. Therefore, cost-effective protocols of genetic monitoring should not include data on seeds. The estimation of effective population size on adult and seedlings provide further estimation of genetic diversity, but also seed immigration.

Conclusions

Selection of plots

Much more plots per species are needed to estimate the combined impact of different factors such as climate and forest management on genetic composition. The selection of plots should focus on main target factors (environment + forest management). We recommend between 20 to 50 monitoring plots per species. For future studies we suggest to select of near-by pairs of plots varying in only in one factor.

Sample design within plots and genetic analysis

At least 100 (better 150) adult individuals and at least 100 (better 150) saplings sampled should be sampled over the whole plot in parallel transects. The inventory of the saplings should be repeated every 10 years. With the same intervals the mortality and vitality of adults should be checked and new adults with a diameter above threshold should be added. We recommend increasing the number of SNP gene markers including adaptive and non-adaptive ones to more than 150. The genetic differentiation among different ontogenetic stages in the same stand is usually much smaller than genetic differentiation among plots. This should be used to define thresholds which can be applied to detect critical genetic changes. Usually there is only little differentiation in the mating system among plots. Further the impact of a single seed year on next generation of adults is quite small. Seeing the high costs and the low information value we recommend to leave seed studies out of genetic monitoring programs.

Selection of gene markers

There is no need to apply both type of gene markers nSSRs and SNPs because we observed a clear correlation of diversity and differentiation among both marker types. We found similar ranking in estimated parameters of spatial genetic structure, mating system and gene flow. Several points are in favour of the SNPs. So genotyping and scoring errors are supposed to be smaller for bi-allelic nSNPs. A better standardisation among labs can be realized for SNPs compared to nSSRs. Today the genotyping of 120 SNPs have the same costs as 10 nSSRs (10-30 Euros per individual) and the costs are decreasing. The information content of 120 SNPs with 2 alleles per locus is estimated to be higher than the information content of 10 nSSRs with 10 alleles per locus. Finally a combination of adaptive and non-adaptive SNPs could be used to conclude on the impact of different population genetic processes. And a high number of SNPs are more presentative for the whole genome compared to a few SSRs.

Observed correlations with genetic parameters

Over the whole distribution range we observed a positive correlation among genetic diversity and latitude. The genetic diversity in the monitoring plots increases from south to north. Further we found a negative correlation of genetic diversity with tree density, variation of tree diameters within plots and intensity of spatial genetic structures. These correlations indicate tendencies but are based on the limited number of plots not strong enough to recommend demographic or environmental proxies to estimate levels of genetic diversity.

Task 2.2 Application of molecular tools to assess adaptive genetic diversity for Fagus sylvatica, Quercus robur + petraea, Picea abies and Pinus pinaster

Forest trees are examples of adaptive divergence across spatial scales, and local adaptation is the evolutionary process by which populations diverge toward different phenotypic and genetic optima in response to their local ecological conditions. Climate is one of the most important drivers of adaptation in forest tree populations, and understanding the molecular basis of adaptation to climatic conditions is essential to accurately predict trees' responses to global climate change (GCC). New data were collected by sampling natural populations at different geographical scales, micro- and macro-scale (in total 299 populations and about 6450 individuals for the four species), genotyped with at least 100 SNPs (up to 1700 in *Pinus pinaster*) markers and at least 9 nuclear microsatellite (SSR) markers. Both SSR and SNP markers were newly developed for *Pinus pinaster* while for the three other species already existing SSRs and SNP arrays were used. The neutral nuclear SSR markers permitted to identify patterns of variation due to the history of the four species, thus allowing removing the confounding effect of the demography when detecting possible adaptive molecular variation.

Clear geographic patterns related to the presence of glacial refugia and the recolonization process during the post glacial period, were observed for all the four species using Bayesian clustering methods. A strong population structure, but with high admixture, was detected in *Fagus sylvatica*; three main clusters can be identified: western, central-northern and south-Italian-Balkan clusters. In *Pinus pinaster* Bayesian clustering identified 6 groups consistent with the genetic structure pointed out by the PCs: Morocco, Corsica, the Atlantic coast of France and of Iberian Peninsula, Central and South-eastern Spain. Four clusters were distinguished at macro-geographical scale in the other two species. The estimation of species genetic structure is a crucial step in the identification of adaptive loci and its confounding effect in the detection of outlier loci must be taken in consideration. After removing the effect of the demography, SNPs potentially influenced by divergent selection were identified following two main approaches: F_{ST} outlier detection and Genomic-Environment Association (GEA). The two approaches allowed identifying outliers SNPs and several significant associations between allele frequencies and climatic variables, in *Fagus sylvatica, Picea abies* and *Pinus pinaster*. Indications for genomic divergence in relation to the environment were observed. Some potential adaptive loci were found to be associated to climatic variables, in particular with the temperature and the precipitation, at both geographic scales, confirming the importance of this factor in driving adaptation in forest species. Generally, SNPs associated with climate were located in genes involved in growth, cell wall, synthesis of secondary metabolites (as starch biosynthesis), membrane potassium transport, energy supply, protein repair, cell death and abiotic stress response. In *Fagus sylvatica* GEAs analysis pointed a total of 67 GEAs, involving 16 SNPs, sourced from 10 genes, related with 1 to 20 environmental predictors (such as temperature, frost, drought, evapotranspiration, precipitation, etc.) each, thus suggesting that these associations are potential indicators for selection processes. In *Picea abies*, no outliers were detected at micro-geographic scale, unlike it occurred at the macro-geographic scale; moreover, 2 SNPs and 38 SNPs loci showed a significant correlation with climate at micro- and macro-geographic scales, respectively. Finally, 18 SNPs at macro- scale and 4 SNPs at regional scale resulted significantly correlated with climate in *Pinus pinaster*. The two combined approaches of F_{ST}-outliers and environmental associations allowed the detection of potential adaptive genes and support the importance of temperature in affecting genetic diversity and driving adaptation in forest tree species.

Conclusions

Indications for genomic divergence in relation to the environment were found in *Fagus sylvatica* at regional scale. Therefore, maladaptation to climatic changes is expected at the stand level, but the high overall genetic similarity in putatively neutral loci suggests that pre-adapted genes might well spread across the studied geographic range. Sites at the lower marginal end of the environmental clines might serve as source gene pool but might get lost to the species distribution range when climatic conditions become more extreme. At the regional scale, species occurring in a heterogeneous environment might embrace substantial genetic variation mitigating extirpation risk under rapidly changing environmental conditions. These results suggest that population genomic information (e.g. the frequency of beneficial alleles for a particular site identified through environmental association) could be a good proxy for fitness that can be integrated to ameliorate range-shift models. Moreover, breeding predictors could be estimated from adaptive marker genotypes for each particular population/gene pool under different climate change scenarios, and used to guide future reforestation programs. Carefully selected candidate genes can be useful to identify genetic variation underlying adaptation to climate. Adaptive patterns are expected to vary across geographically separated gene pools. Thus, under impending climate change, the success of programs to preserve biological diversity will largely depend on the capacity to identify and understand the distribution and the evolution of adaptive variation in keystone species.

The used experimental design (micro- and macro-geographic scale) and the application of different approaches in the data analysis provided new insights into the underlying genes that may be responsible for local adaptation. First of all, it confirms the importance of taking into consideration the confounding effect of genetic structure in the detection of outlier loci. Therefore, the estimation of species genetic structure is a crucial step in the identification of adaptive loci. The combined analyses of F_{ST}-outliers and environmental associations led to the identification of several potential adaptive genes. For example, some potential adaptive loci were found to be associated to temperature at both geographic scales, corroborating previous suggestions that temperature is an important factor in shaping genetic diversity and driving adaptation in forest tree species (D2.2).

WP3 Use and management of forest genetic resources

WP 3 contributed to Objective 3 of FORGER: *To analyse historic, current and future use and management of forest genetic resources.* This objective was achieved by: (i) analyses of historic and current forest management and FRM transfer based on national records; (ii) formulation of optimized seed harvest strategies for sustainable use of FGR of *Fagus sylvatica, Quercus spp., Pinus sylvestris, P. pinaster* and *Picea abies*; (iii) assessment of reaction norms to environmental changes based on field trials and monitoring, and (iv) prediction of impacts of climate change and forest management on forest genetic resources using a process-based model. These four activities were not strongly linked within WP 3, but each provided input for improved guidelines and recommendations to stakeholders as formulated in WP 4.

Task 3.1 Analysis of historic and current forest management and FRM transfer based on national records

European forest ecosystems have been highly shaped by human impact, and several cycles of forest management have determined the distribution and structure of today’s forests. Each human intervention also causes an impact on the genetic pattern of a forest ecosystem. Large scale clearings, occurring since the early middle ages, have therefore a major impact on the genetic variety of European forests. Besides the elimination of genetic variation, the introduction of alien genotypes can have a major impact on autochthonous populations, and may influence their local adaptation. European forests have experienced both simultaneously.

We analysed both the historic transfer of FRM as well as the current transfer which mostly occurs between European countries. Efforts were concentrated on the most important tree species in Europe. We applied three approaches to analyse the historic and current transfer of forest reproductive material of *Fagus sylvatica*, *Larix decidua*, *Quercus* spp., *Picea abies*, *Pinus sylvestris* and *P. pinaster* over Europe: (1) literature review, (2) consultations of experts in this field by interviews and questionnaires, and (3) compiling the data on forest reproductive material available in national database of EU member states that follow EU directive 1999/105/EC, and similar data available in non-member states.

To integrate the management of forest genetic resources into biodiversity and forest policies and strategies, a better understanding of the past, present and future patterns and dynamics of genetic diversity is certainly needed. Current patterns in the distribution of genetic diversity of forests across Europe can only be understood if there is better information on the past and current exchange of forest reproductive material (e.g. seeds and seedlings) across Europe.

For the first time it was possible to estimate the historic loss of forests of major parts of Central Europe over a 1000 year period starting from 900 AD. Forests lost approximately 1/3 of its area during this period while widely distributed forest tree species were differently affected as indicated by respective remnant areas compared to the 900 AD range: Scots pine 59%, pedunculate oak 60%, sessile oak 61%, beech 64% and sycamore 65%.

Basically along with the European industrialization the use of artificial regeneration increased and changed the natural distribution of tree species. The conversion of primary forest ecosystems into secondary forest types massively enlarged the amount of conifers planted, especially Norway spruce, Scots pine, and European larch. For instance, while beech lost up to 40 % of its German distribution within the period 1800-1885, Scots pine gained up to 1 Mio hectare. The distribution of Norway spruce tripled, while the share of European larch anthropogenically increased even to a higher proportion.

Today it is virtually impossible to trace the exact origin of the seeds used since then until the 20th century, as seeds from distinct provenances were frequently mixed and further details about the used seed stands were not recorded or have been lost. Admixed provenances from several countries certainly were shipped to France, Austria, Denmark, the Netherlands, the United Kingdom, Romania or the Czech Republic. Huge amounts of spruce and pine seeds of Central European origin were spread via Germany to Northern and Eastern Europe. For instance, large amounts of seeds, primarily originating from Germany and Denmark have been imported to Southern Sweden and Norway in the beginning of the 20th century. Since 1950 into the same region large amounts of spruce seeds mainly from Eastern Europe, such as Romania, Czech Republic, Northern Poland, or Belarus have been imported.

Broadleaved species were in general much less traded than conifer species, because their seeds are often larger and heavier, and quickly lose their ability to germinate, thus making transportation less effective; in addition most afforestation efforts in previous decades and centuries were done with conifer species. For example we have found no evidence for historic long distance transfer or European beech or ash, while oak has been transferred to a large extent since the 19th century. Especially during the period 1870-1910 the trade with oaks reached its peak, and seed traders from Germany and Austria spread different provenances harvested in Croatia, Hungary and Prussia throughout Central Europe. Also the trade of conifer seeds climaxed in the 19th century, e.g. and an unknown mixture of provenances of Scots pine was spread all over Europe. Similar holds true for Norway spruce and European larch, while the climatic requirements have prevented a large scale transfer of Maritime pine within Europe.

The analysis of the recent transfer of forest productive material within Europe focused on the period of 2004-2014 and included ash, beech, Norway spruce, pedunculate oak, sessile oak, red oak, Scots pine, and Maritime Pine (see FORGER Policy Briefs No. 2 '*Does the transfer of forest reproductive material significantly affect local tree diversity?*'). The basis for the data used is the national implementation of Council Directive 1999/105/EC and complementing EU-regulations. These and similar legal provisions have been in place for more than five decades, but no evaluation had yet been performed about the trade and the quantity of FRM translocated among Member States. The data were provided by official focal points within the EU countries contacted. The analysis revealed large gaps in documentation. The flows of FRM translocated were difficult to reconstruct systematically for all focal species.

In the period 2004–2014, approximately 302 mio plants (i.e. 30 mio plants/year) of the target species were moved within the EU. This equals a monetary value of approximately 150 mio €. Norway spruce was mostly subjected to such a movement during the period assessed, with on average 24.9 million plants moved each year, accounting for 82% of all translocated plants, while beech and pedunculate oak together amounted to slightly more than 12% of the total volume. The remaining 6 % of translocated plants was distributed among the other forest tree species examined. In order to understand the potential influence of introduced FRM on local tree diversity, an assessment was carried out for Norway spruce, looking at estimated proportions of areas planted with local versus introduced FRM. In Finland, for example, this estimate amounted to 10.1% of non-domestic plant material introduced between 2004 and 2014.

For the first time, EU data on the transfer of FRM was evaluated. Large differences exist among countries. Unfortunately not from all EU Member States data were obtained and also data quality differed significantly. To overcome these shortcomings we suggest the creation of a central database, which offers online-access to national bodies to put in the relevant data and facilitates data evaluation and analysis (D3.1).

Task 3.2 - Optimize seed harvest strategies for sustainable use of FGR of Fagus sylvatica, Quercus spp., Pinus sylvestris, P. pinaster and Picea abies

Forest seed stand are approved according EU Directives and fulfil certain quality requirement, such as superior growth. In order to make sure that these desirable traits are present in forest reproductive material originating from seed stands, the tree population to be harvested must be made up of a large number of spatially well-distributed individual trees to ensure adequate cross-pollination. Theoretical models suggest that no fewer than 15 trees should be sampled, provided that seed samples per tree are large, and the species are characterized by random mating. Small numbers of seeds sampled per tree and departure from random mating require increasing the number of sampled trees. The genetic diversity captured in the seed harvest is dependent on the spatial genetic structure and the reproductive system of forest trees. Forest trees are characterized by intensive gene flow. Although this may increase the genetic diversity per se, it becomes more difficult to minimize genetic differences between the genotype of adults in the seed stand and their seed harvest, when the number of seed trees is increased. The proportion of successful external pollen depends on the relation between the amounts of local pollen production versus the amount of external pollen. Large seed stands with a high number of reproductive trees produce generally a lot of local pollen and minimize genetic pollution. But in any case, promising seed stands must be situated at a sufficient distance from poor stands of the same species to avoid unwanted gene flow. Based on the research findings following recommendation can be made:

- Seed harvesting should preferably be carried out in years of intense flowering and heavy seed crops, thereby maximizing the numbers of individuals participating in mating.
- Trees harvested for seed should be distributed uniformly throughout the seed stand.
- Harvesting seeds from trees growing at the edge of forest stands should be avoided, because a considerable proportion of the seeds they produce result from fertilization with immigrant pollen.
- The number of seeds harvested from every tree should be uniform.
- Whenever possible the selection of large seed stands (more than 10 ha) with many reproductive individuals (N more than 300) is recommended because this ensures a high proportion of the pollen is locally produced and minimizes the risk of pollen contamination from outside.
- Generally any seed harvest of directly neighbouring trees should be avoided. It appears that this is especially important for heavy-fruited tree species, such as oaks and beech. In small seed stands of oak and beech (less than 10 ha) a minimum distance of 20 m is recommended; in large seed stands (more than 10 ha) this distance should be increased to 30 m. If crowns overlap significantly, these distances should be increased.

- The minimum number of seed trees to be harvested in an oak seed stands should be 30 individuals. If seed stands are genetically well isolated (more than 5 km from the next reproductive stand of the same species) this number can probably decrease to 25. Although for beech a much smaller experimental data set than in oak species is available, it seems justified to use the above-mentioned number as guidance. In insect-pollinated tree species, such as wild cherry, a minimum of 25 seed trees are recommended.

The available data from field experiments or simulations in wind-pollinated conifers are very limited and it is very difficult to recommend an ideal seed-harvesting mode. Gene flow from distant sources is generally high in conifers, although directly neighbouring trees disproportionately contribute their pollen to the seed tree. The number of seeds collected from each seed tree is generally high. Therefore a minimum of 20 seed trees for Norway spruce is recommended (D3.2).

Task 3.3 Assess reaction norms to environmental changes based on field trials and monitoring

Phenotypic (quantitative) responses of populations of four model species (*Picea abies, Pinus sylvestris, Fagus sylvatic*a and *Quercus petraea*) originating from different macroclimatic environments (i.e. ‘provenances’). Evolutionary ecology suggests that natural selection, particularly climatic factors, significantly affects the pattern of genetic diversity within the range of distribution of a species. Whether selective differentiation is fast or slow, decisive or negligible, seems to be a rather theoretical issue; however it instantly obtains high priority if the question is raised, to which extent are present tree populations preadapted for projected future changes of climate. Ultimately, the future strategy of forest reproductive material deployment and that of nature conservation depends on the answer whether active human assistance is necessary when a genetic adjustment has to be made. One unique option to investigate the issue is to analyse adaptive response of provenances in common gardens. This task concentrated on the responses observable at low elevations, close to the xeric limits of distribution because this zone will experience rapid and most expressed impacts of expected climatic changes.

Results suggest a remarkable width of adaptability and persistence, and support the substantial conservatism in climatic adaptation in the close-to-optimum range. The inherently high within- and among-population genetic variation present in all tested species confers an unusually high potential of adaptability to changes of weather/climate conditions. However, climate selection may overwrite random, diversity-increasing effects, such as gene flow, especially in the zones of severe selection. With increasing selection pressure under xerothermic (warmer and drier) conditions, growth, genetic diversity and adaptability may decline. Therefore the concept of generally high adaptability of marginal/peripheral populations may be questioned. Marginality close to the distributional limits does not necessarily imply higher adaptability. Contrary to the classical concept of local superiority, the equal or superior production of provenances originally adapted to somewhat different climates is a frequent outcome of provenance tests.

Significant within-species differences and geographic patterns in phenotypic plasticity (stability) could be identified. Although clearly present in all species, plasticity/stability in beech seems to be more expressed than that of spruce and pine. The results support the initial hypothesis that in all four model species quantitative, adaptive responses (growth, phenology, health, survival) can be interpreted as mimicking climatic changes and may support the further development of response models and projections. A significant part of the intraspecific genetic differentiation among populations is linked to macroclimatic adaptation and is the result of climatic selection. The asymmetry of response indicated by response functions implies the simultaneous action of different genetic processes, and maintains an adaptive non-equilibrium. Limits of tolerance are genetically determined. Population fitness declines and may lead to mass mortality when the potential for adaptation is exhausted. Populations at the lower, xeric limits of distribution are the most endangered in all species tested.

The investigations propose the following conclusions:

- At the lower (xeric, trailing) limit of distribution, selection pressure and the increase in frequency of extreme events may narrow genetic variation and lead to further decline of plasticity/stability; adaptation to local environment cannot be considered as an implicitly sufficient basis for future adaption to projected climate shifts.
- In the northern-boreal zone, expected rise of temperature may lead to growth acceleration without significant genetic change. In the temperate-maritime zone, if more moisture becomes available, growth will accelerate too. In the southern continental and Mediterranean zone, relatively minor summer temperature increases may trigger higher susceptibility to diseases and the increase of mortality and may lead to local extinctions and shift of distribution area northward, or upward in altitude.
- As expected rapid changes in the next decades will affect first of all the extant (already existing) forest stands, their adaptation potential will largely depend on the level of phenotypic plasticity/stability. The importance of this trait should be recognized in breeding and improvement.
- Climate selection shapes adaptation primarily through the extremes in individual years which are the really decisive events for survival. The frequency and severity of extremes have to be analysed in detail, both for the recent past and for the projected future.
- When deciding about the use of provenances, juvenile growth has to be considered together with criteria of tolerance and adaptability to expected, often irregularly appearing climate extremes. Prudent provision for adaptability and plasticity increases the probability of success in the next generation.

In summary, analysis of phenotypic behaviour observed in common gardens (provenance tests) is still indispensable; the field tests provide the only realistic possibility to estimate and validate quantitative responses to projected climatic changes. Relevant information, including retrospective data from common gardens should be collected and reanalysed as much as possible (D3.3).

Task 3.4. Prediction of impacts of climate change and forest management on forest genetic resources

This task considered the predictive modelling at the pan-European scale to study the impacts of climate change and forest management on the genetic diversity of *Fagus sylvatica*, *Quercus spp.*, *Pinus sylvestris, Pinus pinaster* and *Picea abies*. This task was performed by testing, improving and applying the process-based model ForGEM. Using this model, the effects of forest management, climate (temperature, precipitation) and transfer of FRM on genetic diversity and rates of adaptive response of functional traits were analysed. The outputs of this activity are pan-European maps with simulated genetic diversity and adaptive responses of key-phenotypic traits related to phenology and water use and impacts on transfer of FRM on genetic diversity and the rate of adaptation of functional traits. These results were essential inputs to WP 4, i.e. Guidelines and Recommendations for forest managers on the consequences of climate change. The activities pursued in this task consisted of: the selection of sites and scenarios, and the parametrization, initialization and validation of the process-model in order to perform the model analyses. The modelling results could partly be compared with the assessment of the reaction norms to environmental changes based on field trials and monitoring (Task 3.3). The results of that comparison are as follows:

- There is a strong reduction in genetic diversity toward the high-temperature, low-precipitation range of the distribution of the tree species analysed, i.e. toward the xeric, trailing limit. This considered adaptive genetic diversity related in particular to water uptake. Reduction of adaptive diversity thus leads to a reduced ability of the tree populations to adapt to further environmental changes and thus limits the stability of the species at the xeric limit.

- In the northern-boreal zone, the loss of genetic diversity due to selection is much less compared to the southern and south-eastern trailing zone of the species distribution. The highest growth acceleration was found in the temperate zone, neither limited by temperature, nor by moisture. Also the effect of elevated ambient CO2 was highest in the relatively moist temperate zone, and reduced both toward the northern limit, where temperature is limiting, and towards the southern limit, where low precipitation is limiting growth.
- The level of adaptive genetic diversity is a key population trait that determines the ability of an adaptive response, as well as the rate of that response, in interaction with the selection pressure exerted by the environment.
- Selection by the climate is exerted in particular by extremes in the temperature series, and especially affects the regeneration phase of the forest.
- Planted forests can grow and survive north of the current species distribution. However, according to the model, no regeneration survives to supply the next generation of trees. Thus, the regeneration phase, in combination with the occurrence of extremes (i.e. both in terms of lack of water in the south of Europe and late frosts in the north of Europe) decisively determine survival and vitality.
- Earlier simulation studies showed a strong interaction between forest management and climate change in the rate of adaptive response of functional traits such as phenology. Now, we analysed the effects of a range of forest management approaches on adaptive genetic diversity during one tree rotation. The results indicated that there are small differences in adaptive genetic diversity in response to management intensities applied.

In summary, the model assessment provides valuable additional information to observed reactions of tree species to climatic factors such as temperature and precipitation. Once a model is parametrised and validated to field observations, many more alternative scenarios can be analysed, much quicker, than can be assessed under field conditions. Thus, model analyses allow scanning for tree traits that particularly react to climate change, their genetic diversity, and for suitable provenances and tree species to use at a particular site. This information can then support forest managers in narrowing their range of options. Though the actual performance of a provenance can only be assessed in a field trial, as growth, vitality and survival depends on many more aspects than can be captured in any simulation model (D3.4).

WP4 Tools, guidelines and recommendations on the conservations of genetic diversity

WP 4 contributed to Objective 4 of FORGER: *To provide improved tools, guidelines and recommendations for stakeholders.* This objective was achieved by: (i) the dynamic linking of the GD^2 and EUFGIS databases, (ii) integration and interpretation of spatial genetic and non-genetic information for EU decision makers, and (iii) formulation of guidelines and recommendations for forest managers based on the results of WP1-3.

Task 4.1 - Dynamic linking of GD^2 and EUFGIS

Bioversity and INRA improved the interoperability between the EUFGIS and GD^2 databases and this task is now fully completed. The joint search engine makes it possible to query the two databases based on country, tree species and the distance between the EUFGIS units and the GD^2 populations (1, 5, 10, 20 and 50km). The EUFGIS and GD^2 databases contain 3925 and 7493 tree populations, respectively, in Europe. Earlier testing of the search engine revealed that the data entered to the fields of countries and species needed harmonization between the two databases. Thus, the names of different countries and tree species have been harmonized in both databases. Furthermore, INRA corrected the coordinates of several GD^2 populations for which the latitude and longitude values had been swapped (D4.1).

Task 4.2 - Integration and interpretation of spatial genetic and non-genetic information for EU decision makers

The research results from WP1-3 into conclusions and recommendations for policymakers on the conservation and use of forest genetic resources in Europe. The conclusions and recommendations, as well as their implication for implementing sustainable forest management in Europe, are presented in three policy briefs. These briefs shall be used in communication and dissemination to policymakers at European and global level. They can be downloaded from http://www.fp7-forger.eu/publications/policy-briefs.

The first policy brief ("*Opportunities to improve genetic conservation of four important European tree species*") gives an outlook on the future utilization of existing Forest Genetic Resources databases. Forest genetic resources (FGR) form the base for adaptation of European forests to future environmental conditions and societal demands. Genetic diversity, i.e. diversity within species, allows a species to evolve over time and in space and plays a key role for both the long-term survival of a species and the stability of forest ecosystems. It is thereby a fundamental and critical part of biodiversity. Much of the data on genetic diversity of economically important forest tree species in Europe is gathered in the GeoReferenced Database of Genetic Diversity (GD^2). This database, constructed and curated by the EVOLTREE network of excellence, compiles all genetic surveys that have been published and documented so far in European forest tree species. Recently, European countries completed an extensive inventory of standardized geo-referenced information on genetic conservation units, and the tree species occurring within these units, as part of the EUFGIS project. One of the main aims of the FORGER project was to link the observations performed on genetic diversity, available in the GD2 database, and the general information on genetic conservation units, available in the EUFGIS database. The linked databases provide stakeholders with a genetic characterization of the FGR currently conserved at pan-European level in the genetic conservation units. Another objective of FORGER was to identify gaps in current FGR conservation efforts. One of those gaps is that gene conservation units are not always covering the ecological envelope of a tree species. In this brief, results and recommendations on these subjects can be found.

The second policy brief ("*Does the transfer of forest reproductive material significantly affect local tree diversity?*") highlights the importance of monitoring the transfer of Forest Reproductive Material (FRM) in Europe. Genetic variation within tree species is an important component of forest biodiversity. It enables forest ecosystems to adapt to environmental changes and it provides genetic material for breeding to sustainably increase production. In the framework of forestry management, tree genetic resources are often transferred in the form of forest reproductive material. Given the crucial role of the quality of FRM (e.g. seeds and seedlings) in successful forestry and the implications for biodiversity conservation, it is of crucial importance to know where it originates from and ideally which reactions norms are specific for the FRM. New data indicate that the movement of FRM is significant, with patterns that may vary considerably across species and among EU Member States. However, data on FRM movements are very scattered. Despite five decades having passed since the first legislation on the trade (quantity and quality) of FRM translocated among member states, no evaluation has yet been performed on it. Both the movement of FRM and its use have been poorly documented by individual countries, despite the importance of this information in supporting the implementation of adaptive forest management practices. We strongly suggest that countries may better document the use of FRM in order to better contribute a better adaptive forest management. In this brief, the results of these evaluations for some of the main tree species in Europe are presented and the effects of the transfer are discussed.

The third policy brief ("*Adaptive management of forests and their genetic resources in the face of climate change*") is about the extent to which four widespread forest tree species in Europe may be affected by climatic change, by making use of field trials and modelling tools. A common practice in forest genetic studies is the planting of trees of different origin in common sites to assess the performance of tree populations across a range of conditions ('provenance trials'). Trees planted at sites with a climate substantially different from their origin are exposed to changes in their environmental conditions that may mimic the effect of climatic changes.

Based on the analysis of the performance of tree populations in these trials, projections of future responses of trees to climatic changes were developed in this WP.

The modelling of tree growth, forest dynamics and forest ecosystem functioning also included genetic processes. The new model developed enables a projection of the adaptive response and evolution of genetic diversity of forest ecosystems exposed to climate change, expressed through growth and survival under changing environmental conditions. Moreover, the model allows an assessment whether the adaptive responses to climate change may be enhanced by particular management practices. In this brief, recommendations are provided to decision makers on measures to improve the adaptive management of forests and their genetic resources, based on insights on expected responses to future climatic changes in four model tree species studied (D4.2).

Task 4.3 - Formulation of guidelines and recommendations for forest managers

Within WP4 two guidelines for forest managers were prepared: (i) Guidelines for seed harvesting in forest seed stands, and (ii) guidelines for the choice of forest reproductive material in the face of climate change.

Guidelines for seed harvesting in forest seed stands

Forest seed stands are certified as basic material if certain requirements (productivity, ecological stability, etc.) are fulfilled. In order to make sure that these desirable traits are present in forest reproductive material originating from seed stands, the tree population to be harvested must be made up of a large number of spatially well-distributed individual trees to ensure adequate cross-pollination. Moreover, promising seed stands must be situated at a sufficient distance from poor stands of the same species to avoid unwanted genetic pollution. These legally binding requirements shall secure that progenies from seed stands are also of a superior quality. A genetically sustainable seed harvest should optimize the genetic diversity in the seeds obtained and minimize genetic differences between seed harvest and the seed stand, respectively. The total number of seed trees used for the seed harvest as well as their spatial arrangement plays a crucial role when a genetically sustainable seed harvest is aimed at. Following general recommendations can be given: (1) seed harvesting should preferably be carried out in years of intense flowering and heavy seed crops, thereby maximizing the numbers of individuals participating in mating; (2) trees harvested for seed should be distributed uniformly throughout the seed stand; (3) harvesting seeds from trees growing at the edge of forest stands should be avoided, because a considerable proportion of the seeds they produce result from fertilization with immigrant pollen; (4) The number of seeds harvested from every tree should be uniform; (5) Whenever possible the selection of large seed stands (more than 10 ha) with many reproductive individuals (N more than 300) is recommended because this ensures a high proportion of the pollen is locally produced and minimizes the risk of pollen contamination from outside. Tree species specific recommendations are that generally any seed harvest of directly neighbouring trees should be avoided. It appears that this is especially important for heavy-fruited tree species, such as oaks and beech. In small seed stands of oak and beech (less than 10 ha) a minimum distance of 20 m is recommended; in large seed stands (more than 10 ha) this distance should be increased to 30 m. If crowns overlap significantly, these distances should be increased. The minimum number of seed trees to be harvested in an oak seed stands should be 30 individuals. If seed stands are genetically well isolated (more than 5 km from the next reproductive stand of the same species) this number can probably decrease to 25. Although for beech a much smaller experimental data set than in oak species is available, it seems justified to use the above-mentioned number as guidance. In insect-pollinated tree species, such as wild cherry, a minimum of 25 seed trees are recommended. The available data from field experiments or simulations in wind-pollinated conifers are very limited and it is very difficult to recommend an ideal seed-harvesting mode. Gene flow from distant sources is generally high in conifers, although directly neighbouring trees disproportionately contribute their pollen to the seed tree. The number of seeds collected from each seed tree is generally high. Therefore a minimum of 20 seed trees for Norway spruce is recommended (D4.3).

Guidelines for the choice of forest reproductive material in the face of climate change

Future performance and resilience of regenerated forest stands depends on the inherited genetic quality of the FRM used. What are the most important facts to consider with regard to forest regeneration? Expected climatic changes will occur within the lifetime of a single tree generation. Future forest stands may survive and remain productive only if there is enough adaptive potential to cope with gradual changes and extreme events. Adaptive potential is based on sufficiently large species diversity and within-species diversity (i.e. genetic diversity). A specific characteristic of forest trees is an extremely effective gene flow that facilitates an exchange of genes among tree populations. Forest trees, mostly wind pollinated, are generally effective in long distance gene flow through pollen. Gene flow is less effective through seed dispersal. Pollen can travel over long distances, so a large proportion of the male genetic contribution may come from large distances, depending on local conditions. This could constitute an advantage, but could also have negative effects if unwanted gene flow is depleting the adaptive potential (migration load). Relying exclusively on the capacity of natural selection is appropriate only if regeneration (natural or artificial) is abundant and has sufficient adaptive potential.

Which arguments for and against human-assisted tree species migration can be put forward? Provenances are defined as populations of a tree species obtained from identified geographic locations of the distribution range. The use of FRM of non-local provenances adapted to conditions which are expected in the future in a particular site, is debated, mainly because foresters tend to rely on the generally recognized high diversity of close-to-nature forests, considered as the basis for adaptability. This is a valid argument, as long as the expected changes in temperature and precipitation remain within the limits of tolerance of the population, maintaining acceptable growth and vitality. In fact, field tests show that the adaptive potential of tree species is considerable, especially in sites located in the central part of the distribution range, as long as precipitation is sufficient. For instance, it has been observed that an increase of 2 C° in annual temperature has been tolerated by beech, oak and even by conifers. On the other hand, field tests confirm that the extent of changes may exceed the adaptive potential of some tree populations; it has to be remembered that the changes will occur within the lifespan of one generation. Therefore, actively supporting natural processes may be advisable in case of extreme changes. Contrary to the commonly held concept ʼlocal is best', it has frequently been observed that the performance of local provenances is not necessarily better than that of certain non-autochthonous tree populations. This can be explained most probably by the action of other genetic effects (gene flow, migration background, and others) operating in parallel to natural selection. The debate about the value of locally adapted populations is somewhat surpassed by the effects of projected climate change, which will alter considerably, and in some cases quite rapidly, local site conditions. The selection of suitable FRM should be based primarily on information about the expected climate changes for a particular region. If the projections indicate that the local conditions will change drastically during the rotation period, causing a significant decline in vitality of the stand, the use of FRM of alternative provenances may be considered. Field tests, and complementary information from silvicultural practice, provide indication on the climate sensitivity of a particular species. The differences in survival and growth of provenances across field trials indicate a need for caution in a selection of foreign provenances, originating far away from the site where they are going to be used, based solely on an assessment of their performance and growth recorded at an early (juvenile) age. Other criteria should be considered in addition, such as the ability to successfully adjust to changing conditions, that is, the potential tolerance of, and adaptability to, extreme climatic events and damages.

These two guidelines can be downloaded under http://www.fp7-forger.eu/publications/guidelines and provide further information.

WP5 Communication, dissemination and knowledge transfer

WP 5 contributed to Objective 5 of FORGER: *To disseminate and communicate the project's results to stakeholders.* This objective was achieved by: (i) development of communication and dissemination materials; (ii) content management of the dissemination section of the project website; (iii) expert consultations with selected target groups (iv)knowledge transfer; and (v) communication and dissemination to policymakers and other target groups at European and global level. The promotion FORGER's efforts and scientific results took place throughout the project, by developing various communication products and organizing consultations and events. The different actions implemented are described in detail in the following sections.

Task 5.1 Development of communication and dissemination materials

A basic dissemination package was developed, including a leaflet, a poster, a factsheet describing the project objectives and a template for PowerPoint presentations. They were made available on the project website. The project logo and user's manual were created to brand all public awareness materials and documents (e.g. leaflet, factsheet, poster, presentation, policy briefs) presenting the project' objectives and expected outputs. The development of the logo was based on both the visualization of scientific concepts and the inclusion of associated graphic elements. The graphic elements used provided an association with the kind of forest trees species investigated by FORGER (broadleaves and conifers) and made reference to the focus of the project on forest genetic resources (D5.1).

Video interviews

Four videos, whose contents are described below, were uploaded and are currently accessible in the multimedia section of the FORGER website (http://www.fp7-forger.eu/publications/multimedia), with direct links to the project channel on YouTube (http://www.youtube.com/user/FORGERproject):

- Video interview with Thomas Geburek (Bundesforschungs-und Ausbildungszentrum fur Wald, Naturgefahren und Landschaft, Austria) who illustrates the research work carried out by his team on forest reproductive material.
- Video interview with Katri Kärkkäinen (Metsantutkimuslaitos, Finland). She explains how the project will analyse and improve the existing inventories on forest genetic resources.
- Interview to FORGER scientists describing how FORGER will contribute to the management of data on forest genetic resources and how the project activities will produce outputs that are relevant for forest management in Europe.
- Video focused on genetic monitoring, shot in the laboratories of vTI (a project partner) in Hamburg and based on an interview with Bernd Degen, director of the Institute of Forest Genetics at vTI. The film, entitled 'Forest in the lab', explains what is forest genetic monitoring and what the FORGER project will do to improve ongoing forest monitoring efforts in Europe. The film available on the project Youtube channel was posted on the project website with an accompanying story 'Forest in the lab – new film explains genetic monitoring of forests'. The video was also launched through Bioversity website together with a short blog post and promoted through Bioversity social media channels (Facebook, twitter).

Audio interviews

The communication section on the FORGER website also features audio interviews carried out during the kick-off meeting of the project, held in Wageningen in March 2012. Audio interviews were carried out with the following contacts:

- Annette Schneegans, European Commission, explains why the FORGER project was selected for funding, the main challenges in its implementation and her recommendations.
- Koen Kramer, coordinator of FORGER from Alterra, The Netherlands, introduces the objectives of the project and the expected outputs.
- Giovanni Giuseppe Vendramin, National Research Council, Plant Genetic Institute, Florence, Italy describes the contribution of his team to the project. The team focused on innovative approaches in the use of molecular markers to monitor genetic diversity and understand adaptation processes in forest trees.
- Bernd Degen, Institute of Forest Genetics, Johann Heinrich von Thünen-Institut (vTI), describes the pilot study implemented to test genetic monitoring protocols at the European scale. He also explains how the research component that he leads will contribute to the development of more rigorous standards for the harvesting of forest reproductive material.

Use of multiple, well targeted, communication channels

Communication about the activities has been shared with various Stakeholders in the course of the projects through targeted communication channels (FORGER and the EUFORGEN websites) and through the participation of Stakeholders to knowledge sharing events organized within the frame of the project. An update on the project activities was included in the October 2014 issue of the EUFORGEN Newsletter and December 2015 Issue. Information on FORGER was also presented in the EVOLTREE portal, where a link to the FORGER website is available: http://www.evoltree.eu/index.php/dissemination/useful-links to increase the project's visibility through this important network of excellence.

News Stories

Four articles based on interviews with scientists and experts on forest genetic resources were published in the 'News and events' section of the website. The first story 'Checking for gaps in the genetic conservation of forest trees' highlights the work on a conservation gap analysis for four selected species, using different information systems. The interviewee is a researcher from the FORGER partner METLA. The second story 'Genetic diversity of forest trees needs more attention' is based on an informal discussion with a group of experts who attended the EUFORGEN/FORGER workshop on FGR inventories in March 2014, and answered questions on topics related to the project. The third story 'Future proofing Europe's forests' summarizes the main project findings and a fourth article 'Helping Europe's forests adapt to climate change' focuses on research on forest reproductive material.

An article to create awareness about FORGER and to promote the FORGER's film on genetic monitoring was developed and published on the CORDIS website of the European Commission: http://cordis.europa.eu/news/rcn/124526_en.html. It was promoted through CORDIS social media channels and EUFORGEN twitter. A link to the article was included on the project website.

Policy briefs and guidelines

A major effort has been invested in developing a series of project briefs (policy briefs and guidelines). The briefs were finalized based on feedback from the Stakeholders, received during the stakeholders' event organized in Dublin, on 18 November 2015. They were developed using an attractive graphic design template, filled with carefully selected visual materials and text edited by a native-English professional science writer. The series is available online at the following link with short and succinct abstracts: http://www.fp7-forger.eu/publications/policy-briefs

A template for the series of policy briefs and guidelines, presenting key outputs of the project, was converted in a format that can be shared with partners for their translation of the policy briefs and guidelines in other languages.

Task 5.2 Content management of the dissemination section of the project website

The project online communication has been based on the latest digital techniques for sharing widely the outputs generated within the framework of the project. A dedicated YouTube channel was set up to host all multimedia products developed within FORGER.

The 'Publications' section of the project website was populated with links to research articles produced by project partners and with accompanying lay summaries for each, to present the contents for the scientific articles in a more general narrative understandable for wide audiences. The list of peer-reviewed articles published in open-access scientific journals with direct links was placed in the publication section of the website, were currently 13 articles can be found (D5.2).

Task 5.3 Expert consultations with selected target groups

The project was promoted in a number of international meetings where work plans and preliminary results were shared and discussed. The first of a series of expert consultations was held in Szombathely (Hungary) on 8-10 May 2012. The workshop was organized in collaboration with the European Forest Genetic Resources Programme (EUFORGEN) and hosted by the Hungarian Forest research Institute (ERTI) at the Kámon Arboretum. The purpose of the workshop was to discuss further development of the EUFGIS Portal, provide an overview of other relevant FGR databases, discuss linking of databases (especially EUFGIS and GD2), and exchange information on progress made in national FGR inventories and other new developments in this area. The workshop was attended by the EUFGIS National Focal Points and other experts on FGR inventories and databases. The relevant database managers of the EVOLTREE Network of Excellence and TREES4FUTURE project were also present at the meeting. The meeting participants contributed to the preparation of the *Pan-European strategy for genetic conservation of forest tree* and the *Development of genetic monitoring methods for genetic conservation units of forest trees.* The workshop offered the opportunity to analyse the EUFGIS portal and database to identify needs and formulate an improvement pathway.

A joint meeting with the EUFORGEN working group on forest reproductive material was organized in Freising, Germany on 4-6 July 2012. The purpose of the meeting was to discuss issues related to the use and transfer of forest reproductive material in Europe and create synergies for further collaboration between EUFORGEN and FORGER on this topic. The event also served as one on of the expert consultations designed to seek inputs from a larger group of experts to the FORGER activities. The meeting was very timely for the preparation of the report on "*Use and transfer of Forest Reproductive Material in the context of climate change*" since it was held just a few days after a meeting of the Standing Forestry Committee, on the development of the new EU Forest Strategy, which will have a great impact on the movement of Forest Reproductive Material in Europe. The results of this consultation were reported to the EUFORGEN Steering Committee.

A workshop on FGR conservation and monitoring was organized in Järvenpää, Finland on 18-20 September 2012 in collaboration with the European Forest Genetic Resources Programme (EUFORGEN). The purpose of the workshop was to discuss the development of a pan-European genetic conservation strategy and a genetic monitoring scheme for forest trees, and how the results of the FORGER project can be used to improve these initiatives. The event also served as one on of the expert consultations designed to seek inputs to the FORGER activities from a larger group of experts (D5.3).

Task 5.4 Knowledge transfer

A training workshop on FGR inventories and databases was organized in Zagreb, Croatia on 25-27 March 2014 in collaboration with the European Forest Genetic Resources Programme (EUFORGEN) and the Faculty of Forestry of the University of Zagreb. The event was targeted to the EUFGIS national focal points and its purpose was to demonstrate the use of the new search engine of the EUFGIS and GD2 databases as well as update the participants on the project activities. Training on other new features in the EUFGIS intranet was also provided to the national focal points. Furthermore, the participants exchanged information on the progress in FGR inventories in different countries since the previous workshop held in 2012. The workshop was an important opportunity for the FORGER project partners to seek feedback on the search engine of the EUFGIS and GD2 databases and to obtain advice for its improvements. A total of 30 participants from 25 countries attended the workshop.

As part of the Knowledge Transfer activities, an online discussion forum was planned to derive recommendations for possible revisions of the pan-European gene conservation strategy of forest trees, based on findings from FORGER. The online discussion was replaced by a Stakeholders' event organized in conjunction with the FORGER final meeting. The discussion involved FORGER partners, representatives of EUFORGEN and other FGR experts. The interactions resulted in a series of key messages that describe the basis for future efforts for the implementation of pan-European gene conservation strategies of forest tree species (D5.4).

Task 5.5 Communication and dissemination to policymakers and other target groups at European and global level

Awareness about the project and its expected results was raised among policymakers and other target groups throughout the project duration. Project leaflets were distributed during the FOREST EUROPE Expert Level meeting (Madrid, Spain, 6-7 March 2013), the 14th Session of the FAO Commission on Genetic Resources for Food and Agriculture (Rome, Italy, 15-19 April 2013), the International Conference on Forests for Food Security and Nutrition (Rome, Italy, 13 – 15 May 2013), the 4th Negotiating Session of the Intergovernmental Negotiating Committee for a Legally Binding Agreement on Forests in Europe (Warsaw, Poland, 10-14 June 2013), the 15th session of the FAO Commission on Genetic Resources for Food and Agriculture, held in Rome, Italy on 19-23 January 2015.

In addition, key communication events were organized and took place successfully: a final scientific meeting and a Stakeholders' event for European policymakers in Brussels. They were largely promoted beforehand with tailored messages delivered through brochures and targeted campaigns.

The final meeting was successfully organized in Dublin (Ireland) on 17 November 2015, back-to-back with the 11th meeting of the EUFORGEN Steering Committee. A Stakeholder's event was also organized on 18 November 2015 to exchange of the project final recommendations with the wider forest genetic resources community of EUFORGEN.

An event for European policymakers was organized at the Forestry House in Brussels on 11 December 2015. This event took advantage of a meeting of the Standing Forestry Committee, scheduled for the day before and attended by key Stakeholders. The event was an opportunity to present recent FORGER findings with policy implications in the area of conservation and management of forest genetic resources. The agenda covered the following topics: a) recent findings from ongoing research initiatives on the conservation and sustainable use of forest genetic resources; b) policy implications from the research work presented and future priorities identified by the European Forest Genetic Resources Programme (EUFORGEN) and the FORGER project, focused on the sustainable management of forest genetic resources in Europe. The presentations were followed by a panel discussion and a general discussion. The themes proposed were highly relevant for the Stakeholders and the meeting was very well attended and characterized by a high level of contributions of participants to the discussions (D5.5).

1.4 Potential impact and main dissemination activities and exploitation of results

Target groups

Distribution ranges of forest tree species in Europe do not respect national or EU borders. For this reason, no single country alone can sustain and manage their forest genetic resources on a meaningful scale. Climate change will also increase European countries' interdependence on forest genetic resources. Depending on their location and predicted impacts of climate change, several countries are expected to increase cross-border transfer and use of forest reproductive material to maintain the production capacity of forests and to facilitate their adaptation to climate change. It is therefore crucial that assessment and monitoring of forest genetic resources as well as development of conservation strategies of forest genetic resources are done at the European level. Similarly, it is necessary that any project aiming to make impacts on sustaining and managing forest genetic resources needs to be carried out at the European scale.

The FORGER measures on communication, dissemination and knowledge transfer focus on selected target groups to facilitate the use of the results in the development of new policies and strategies both at European and national levels, and in practical management of forest genetic resources at national level. The goal of these measures is to ensure that the project results will have an impact. To achieve this, the FORGER consortium identified two target groups:

- policymakers and relevant policy processes at European and global level, in particular:
    - Forest Europe (previously the *Ministerial Conference on the Protection of Forests in Europe, MCPFE*)
    - European Commission (EC)
    - Conference of Parties of the Convention on Biological Diversity (CBD)
    - FAO Commission on Genetic Resources for Food and Agriculture (CGRFA)

- forest managers and experts contributing to the management of forest genetic resources at European and national level, in particular:
    - National Coordinators of the European Forest Genetic Resources Programme (EUFORGEN)
    - National experts contributing to EUFORGEN Working Groups
    - National Focal Points of the European Information System on Forest Genetic Resources (EUFGIS)
    - Relevant database managers of the EVOLTREE Network of Excellence
    - European FGR research community

The activities and agendas of these two target groups that provided the context and direction of the development of the results and dissemination activities for the FORGER project are described below.

European and global level

Forest Europe and the EC provide the basis for influencing development of forest-related policies and strategies in Europe. The Forest Europe process has a key role promoting improvement of national forest policies and implementation of sustainable forest management. It involves a total of 44 Signatories (including the European Community) and a wide range of other stakeholders as observers (forest owners, forest industry, state forest agencies, social NGOs, environmental NGOs and scientific community). Forest Europe has also contributed to the development of the European Forest Strategy (EFS) and forest measures as part of the Common Agricultural Policy (CAP) of the EU. Within the EC, FORGER targets relevant Units and Committees in the area of agriculture, environment and rural development. At the global level, the European region is an active player in policy processes dealing with forest genetic resources, such as the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) and the Convention on Biological Diversity (CBD).

The development of future EU policies dealing with climate change, forests and genetic resources further provided background to FORGER. In June 2009, the Council of Europe concluded that climate change will have an impact on forests and recommended that the EU should take action to ensure that forests continue to perform all their productive, socio-economic and environmental functions in the future. In March 2010, the EC released a Green Paper to debate options for an EU approach to forest protection and information in the framework of the EU Forest Action Plan. The Green Paper focused on how climate change modifies forest management and protection in Europe and how the EU policy should evolve to enhance its contribution to the Member States' forest-related initiatives. The Green Paper also recognized that forest management practices can support the adaptation of forest trees by maintaining high genetic variation and by selecting those elements of the existing gene pool that are best adapted to expected growing conditions in the future. The results of the consultation process (i.e. responses to the Green Paper from the public, Member States, EU institutions and other stakeholders) were released in November 2010. Conservation of forest genetic resources was identified by many stakeholders as one of the key issues in need of further action at the EU level. Other key issues included harmonization of forest information and continuing research on climate change and its effects on forests.

In October 2010, the 10th Conference of Parties of the Convention on Biological Diversity (CBD) adopted a Strategic Plan for Biodiversity 2011-2020 and the Aichi Biodiversity Goals. FORGER results contribute directly or indirectly to the following strategic goals and targets of the CBD:

- the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization
- identification of what EU-level measures are needed to complement the measures to be taken by the Member States to implement the Nagoya Protocol.
- clarification of the of national or EU-level measures on the conservation of genetic resources for food and agriculture, including forest genetic resources

FORGER was set-up to provide relevant information that could be used for the implementation of commitments made by European countries to the CBD:

- In 2002, the sixth COP to the CBD adopted the Expanded Programme of Work on Forest Biological Diversity. Among other objectives, the CBD Programme of Work specifically encourages development of information systems and strategies for *in situ* and *ex situ* conservation to promote sustainable use of forest genetic diversity.
- In 2008, COP 9 Decision IX/5 in 2008 urged Parties to "*promote and implement sustainable forest management and the ecosystem approach to maintain forest biodiversity and ecosystem functions, in all types of forests, promote forest restoration and minimize deforestation and forest degradation so as to achieve the goals and objectives of the programme of work including addressing climate change*".
- COP 9 invited Parties, other governments and international organizations to "*recognize and increase understanding of the potential of forest genetic diversity to address climate change, maintain forest ecosystems resilience and lead to the discovery of new timber and non-timber forest resources.*

Overall, FORGER was designed to provide inputs to discussions on the implementation of the new CBD Strategic Plan for Biodiversity 2011-2020 and the Nagoya Protocol in Europe.

National level

FORGER's results and dissemination activities in particular support the work carried out through the European Forest Genetic Resources Programme (EUFORGEN). EUFORGEN was established in 1994 as an implementation mechanism for Resolution S2 (*Conservation of forest genetic resources*) of the first Ministerial Conference, held in Strasbourg, France in 1990. EUFORGEN also contributes to the implementation of Resolution V4 (*Conserving and enhancing forest biological diversity in Europe*) and Resolution V5 (*Climate change and sustainable forest management in Europe*) which were adopted by the fourth Ministerial Conference in Vienna, Austria in 2003. EUFORGEN is coordinated by Bioversity International and overseen by a Steering Committee, which is composed of National Coordinators from all member countries.

The EUFORGEN National Coordinators contribute to the development of collaborative actions on forest genetic resources at European level and they are also in a key position to lead the use of the project results at national level. At that level, managers, experts and scientists are responsible for implementing various policies and strategies and in managing forest genetic resources in practice. They are thus a crucial target group for FORGER. The EUFORGEN Working Groups provided input to the FORGER activities and they will also benefit from the project results in their work.

FGR documentation and monitoring efforts essential for improving FGR management and in this regard, FORGER is targeting the National Focal Points of the European Information System on Forest Genetic Resources (EUFGIS), relevant database managers of the EVOLTREE Network of Excellence and the European FGR research community.

Potential impact

FORGER provided the European forest sector with integrated knowledge and resources for enhanced conservation and use of forest genetic resources as part of sustainable forest management. This will help the forest sector in adapting both forests and forest management practices to climate change and to ensure that forests continue to perform their productive, socio-economic and environmental functions in the future. Furthermore, FORGER contributes to the implementation of European commitments to various regional and global policy processes on forests, biodiversity and genetic resources. FORGER project formulated concrete science-based recommendations considering:

- opportunities to improve genetic conservation of four important European tree species
- monitoring forest genetic diversity applicable by all EU Member States
- implications of past and current transfer of forest reproductive material between different countries
- adaptive forest management of genetic resources in the face of climate change
- impacts of climate change on the distribution of genetic diversity
- effective seed sampling protocols to maintain genetic diversity in future forests

The potential impacts of these recommendations are here presented. In the area of forest genetic resource conservation and related efforts, the outputs generated include a) improved forest inventories on forest genetic resources and linkages between existing databases, b) comprehensive assessments of genetic diversity of four forest tree species, and c) analyses of the extent to which genetic diversity of the species investigated is covered by current gene conservation efforts.

FORGER contributed with maps and gap analyses that will guide countries in identifying areas where they could establish new gene conservation units for forest trees. The integrated databases (EUFGIS and GD^2) allowed a better characterization of the status of knowledge on genetic diversity across Europe for the studied species. The outputs are expected to contribute to the revision of pan-European and national gene conservation strategies and molecular characterization and genetic monitoring of gene conservation units.

A common protocol for monitoring forest genetic diversity at pan-European level was developed and applied in a pilot study. These outcomes are expected to lead to the revision of pan-European and national gene conservation strategies and molecular characterization and genetic monitoring of gene conservation units.

In the area of FGR use and management, the key outputs generated include: a) an evaluation of historic and current cross-border transfer of forest reproductive material, b) the identification of eco-geographic patterns in adaptive traits and reaction norms, and c) an analyses of the impacts of climate change and forest management on FGR. These research outputs particularly strengthen the work of the European Forest Genetic Resources Programme (EUFORGEN) on the conservation of forest genetic resources. EUFORGEN has been closely involved in various stakeholders interactions promoted by the FORGER project. Furthermore, FORGER helps to make a strong case to better integrate forest genetic resource management into national forest programmes and national adaptation strategies for climate change.

Overall, the recommendations for seed harvesting, transfer and use of forest reproductive material, and conservation and management of forest genetic resources form an important basis for countries to harness the full potential of forest genetic resources to adapt to, and to mitigate the negative effects of, climate change and whilst maintaining the adaptive potential of forests in the future.

Dissemination activities

The FORGER measures on communication and knowledge transfer focused on a series of strategic activities aimed at reaching selected target groups to facilitate the use of the results in the development of new policies and strategies at European and national level, and in practical management of forest genetic resources at national level.

The project partners developed leaflets and posters, project presentations for different target groups, press releases and audio/video interviews, coordinated by Bioversity. These materials are available on the FORGER project website. This dissemination section serves as a repository of the policy briefs and guidelines for forest managers. The Publication section on the project website contains scientific publications and lay summaries of their contents in a simple narrative. Bioversity has also developed an article on FORGER for the EUFORGEN Newsletter.

After the end of the project, the results from FORGER will remain available through the project’s website. Scientific publications will continue to be produced after the end of the project and will be fed into the Publication section on the website for wide dissemination of the results to scientific community.

Actual impacts also have been achieved during the course of the project. The guidelines have been translated into the Hungarian language and disseminated and discussed by Hungarian policy makers and forest managers acknowledging that Hungarian forests are vulnerable for climate change impacts and that the proper use and selection of forest genetic resources are a means to counteract negative consequences.

Similarly, have FORGER’s results been presented and discussed with Dutch owners of nurseries, tree breeders, and forest manager using and selecting that material and recognizing that a climate change should be one component of the selection of forest reproductive material.

Exploitation of results

Forest enterprises were not involved in the FORGER project and the project’s results were not aimed for exploitation. Direct commercial exploitation of the results is therefore not foreseen. However, it can be expected that FORGER’s outcomes strengthen the European forest sector when its concrete guidelines and recommendations on conservation and use of forest genetic resources in the face of climate change are implemented.

2 Use and dissemination of foreground

Section A Public

Table 1. List of publications

No.	Date	Title	Main Author	Title of the periodical or the series	Number, date or frequency	Publisher	Place of publication	Relevant pages	Permanent identifiers	Open Access	Status
1	10.03.13	Within-population genetic structure in beech (Fagus sylvatica L.) stands characterized by different disturbance histories: does forest management simplify population substructure?	Piotti A, Leonardi S, Buiteveld J, Geburek T, Gerber S, Heuertz M, Kramer K, Vettori C, Vendramin GG	PLOS One	2013	PUBLIC LIBRARY SCIENCE	San Francisco, CA	e115499 (1-22)	DOI: 10.1371/journal.pone.0073391	Yes	Published
2	31.12.14	Micro- and Macro-geographic scale effect on the molecular imprint of selection and adaptation in Norway spruce.	Marta Scalfi, Elena Mosca, Erica Adele Di Pierro, Michela Troggio, Giovanni Giuseppe Vendramin, Christoph Sperisen, Nicola La Porta, David B. Neale	PLOS One	2014	Public Library Science	San Francisco, CA (USA)	e115499 (1-22)	DOI: 10.1371/journal.pone.0115499	Yes	Published
3	30.09.14	Clinal variation at phenology related genes in spruce: parallel evolution in FTL2 and Gigantea?	J. Chen, Y. Tsuda, M. Stocks, T. Kallman, N. Xu, K. Karkkainen, T. Huotari, V.L. Semerikovz, G.G. Vendramin, M. Lascoux	Genetics	month	Genetics Society of America	BETHESDA, MD 20814 USA	1025-1038	DOI: 10.1534/genetics.114.163063	Yes	Published

4	16.03.15	Bring in the genes: genetic-ecophysiological modeling of the adaptive response of trees to environmental change. With application to the annual cycle.	Kramer, K., B. van der Werf and M.-J. Schelhaas.	Frontiers in Plant Science. 5	2015			1=10	DOI: 10.3389/fpls.2014.00742	Yes	Published
5	06.10.15	High-density SNP assay development for genetic analysis in maritime pine (Pinus pinaster)	Plomion C, Bartholomé J, Lesur I, Boury C, Rodríguez-Quilón I, Lagraulet H, Ehrenmann F, Bouffier L, Gion JM, Grivet D, de Miguel M, de María N, Cervera M, Bagnoli F, Isik F, Vendramin GG, González-Martínez SC	Molecular Ecology Resources	2015	John Wiley & Sons Ltd		jan-14	DOI: 10.1111/1755-0998.12464	No	Published
6	29.08.13	Decline of genetic diversity of sessile oak at the retracting (xeric) limits	Attila Borovics – Csaba Mátyás	Annals of Forest Science 2013 DOI: 10.1007/s13595-013-0324-6	2013	INRA and Springer-Verlag France 2013		835-844	DOI: 10.1007/s13595-013-0324-6	Yes	Published
7	15.11.13	The incorporation of extreme drought events improves models for beech persistence at its distribution limit	Ervin Rasztovits & Imre Berki & Csaba Mátyás & Kornél Czimber & Elisabeth Pötzelsberger & Norbert Móricz	Annals of Forest Science 2013 DOI 10.1007/s13595-013-0346-0	2013	INRA and Springer-Verlag France 2013		201-210	DOI: 10.1007/s13595-013-0346-0	Yes	Published
8	12.03.14	Forests in a water limited world under climate change	Csaba Matyas, Ge Sun	Environmental Research Letters	2014	IOP PUBLISHING		9:085001	doi:10.1088/1748-9326/9/8/085001	Yes	Published

9	26.08.15	Genomic-environment association study suggests local adaptation to climate at regional scale in Fagus sylvatica	Andrea R. Pluess, Aline Frank, Caroline Heiri, Hadrien Lalagüe, Giovanni G. Vendramin, Sylvie Oddou-Muratorio	New Phytologist		John Wiley & Sons Ltd			10.1111/nph.13809	No	Published
10	27.03.14	Genetic adaptive response: missing issue in climate change assessment studies	Kramer, K., G. Hengeveld, M.J. Schelhaas, B. van der Werf, W. de WInter	Proceedings of the Impact World 2013 conference, May 27-30, 2013, Potsdam, Germany	2013		Potsdam		DOI 12.2312/pik.2013.001	Yes	published
11	12.03.2016	Development and characterization of three highly informative EST-SSR multiplexes for Pinus halepensis Mill. and their transferability to other Mediterranean pines	C. Leonarduzzi, I. Spanu, M. Labriola, SC González-Martínez, A. Piotti, G.G. Vendramin	Plant Molecular Biology Reporter	2016	Springer	New York	1-10	10.1007/s11105-016-0980-4	Yes	Published
12	10.11.14	Climate change increases the drought risk in Central European forests: what are the options for adaptation?	Hlásny T., Mátyás Cs., Seidl R., Kulla L., Merganicová K., Trombik J., Dobor, L., Barcza Z., Konópka B.	Lesnicky Casopis – Forestry Journal	2014	Lesnicky Casopis – Forestry Journal	Praha	5=18	DOI: 10.2478/forj-2014-0001	yes	published
13	10.11.14	[Estimation of increment decline caused by climate change, based on data of a beech provenance trial.] In Hungarian with Engl. summary.	Horváth A., Mátyás Cs.	Erdészettudományi Közlemények	2014	Forest Research Institute Hungary	Sopron	91-99	http://www.erdtudkoz.hu/fileadmin/dokumentumok/emk/erfaved/ErdTudKozl/Szamok/2014-2/9_Horvath.pdf	Yes	published

14	31.12.15	Opportunities to improve genetic conservation of four important European tree species	Kramer, K. and K. Kärkkäinen	Forger Policy Brief	2016				http://www.fp7-forger.eu/publications/policy-briefs	Yes	Published
15	31.12.15	Does the transfer of forest reproductive material significantly affect local tree diversity?	Geburek, T. and S. Jansen	Forger Policy Brief	2016				http://www.fp7-forger.eu/publications/policy-briefs	Yes	Published
16	31.12.15	Adaptive management of forests and their genetic resources in the face of climate change	Mátyas, Cs. and K. Kramer	Forger Policy Brief	2016				http://www.fp7-forger.eu/publications/policy-briefs	Yes	Published
17	31.02.16	Guidelines for forest seed harvesting in forest seed stands	Geburek, T., J. Burczyk and B. Degen	Forger Guidelines and Recommendations	2016				http://www.fp7-forger.eu/publications/guidelines	Yes	Published
18	31.01.16	Guidelines for the choice of forest reproductive material in the face of climate change	Mátyas, Cs.	Forger Guidelines and Recommendations	2016				http://www.fp7-forger.eu/publications/guidelines	Yes	Published

Table 2. List of papers that are submitted or in preparation

No.	Date	Title	Main Author	Title of the periodical or the series	Number, date or frequency	Publisher	Place of publication	Relevant pages	Permanent identifiers	Open Access	Status
	01.03.16	Limited responses of temperate oak populations to climate change across Europe	Sáenz-Romero C, Lamy JB, Ducousso A Musch B, Ehernmann F, Delzon S, Cavers S, Chałupka W, Dağdaş S, Hansen JK, Lee SJ, Liesebach M, Rau HM, Psomas A, Schneck W, Steiner W, Zimmermann NE, Kremer A	Proceedings of the National Academy of Science of the United States of America	-					No	Submitted
	26.01.16	Historic transfer of forest reproductive material in the Nordic region: drivers, scale and implications	Myking T, Rusanen M, Steffenrem A, Kjær ED, Jansson G	Forestry	2016					No	Submitted
	26.01.16	Historic translocations of European larch (Larix decidua Mill.) genetic resources across Europe – a review starting from the 17th century	Jansen S, Geburek T	Forestry	2016					No	Submitted
	26.01.16	Historic deforestation and afforestation in Europe – historic imprint on tree populations?	Geburek T, Kremer A, Myking T	Forestry	2016					No	in preparation
	26.01.16	Historic anthropogenic impacts on forest trees – evolutionary consequences	Geburek T, Myking T	Forestry	2016					No	in preparation

	31.12.15	Monitoring number of seed parents from bulk seed collections in conifers based on chloroplast haplotypes	Burczyk, J., Chybicki, I.J., Sandurska, E.	Methods in Ecology and Evolution	2016					No	in preparation

Table 3. List of all dissemination activities

No.	Type of activities	Main leader (Owner(s))	Title	Date	Place	Type of Audience	Size of audience	Countries addressed
1	oral presentation	NymE	Response of forest trees to rapid climate change, at the retracting (xeric) limits – lessons from common gardens	11.08.15	Baltimore, Maryland, USA	Scientific community, Civil society, Policy makers, Media	120+	US
2	Press release	Bioversity	Checking for gaps in the genetic conservation of forest trees	2013	FORGER website	Civil society, Policy makers, Media	150	EU
3	Press release	Bioversity	Genetic diversity of forest trees needs more attention	2013	FORGER website	Civil society, Policy makers, Media	150	EU
4	Press release	Bioversity	Future proofing Europe’s forests	2015	FORGER website	Civil society, Policy makers, Media	150	EU
5	Press release	Bioversity	Helping Europe’s forests adapt to climate change	2015	FORGER website	Civil society, Policy makers, Media	150	EU
6	Press release	Bioversity	Forest in the lab – new film explains genetic monitoring of forests	31.12.2014	http://www.fp7-forger.eu/events/forest-in-the-lab	Civil society, Policy makers, Media	150	EU
7	Article	Bioversity	Cost effective monitoring to help preserve forest diversity	08.01.2016	http://cordis.europa.eu/news/rcn/124526_en.html	Civil society, Policy makers, Media, research community	100	EU
8	Press release	Bioversity	Forest in the lab – new film explains genetic monitoring of forests	27/08/2015	http://www.bioversityinternational.org/news/detail/forest-in-the-lab-new-film-explains-genetic-monitoring-of-forests/	Scientific community, Civil society, Policy makers, Media	300	EU

9	Youtube channel	Bioversity	YouTube channel FORGER Project	31/12/2013	http://www.youtube.com/user/FORGERproject	Scientific community, Civil society, Policy makers, Media	300	EU
10	video	Bioversity	Documenting movements of forest reproductive material across Europe	2013	https://www.youtube.com/watch?v=K1kFqpBH6og	Scientific community, Civil society, Policy makers, Media	130	EU
11	video	Bioversity	Collating knowledge on forest genetic resources in Europe	2013	https://www.youtube.com/watch?v=E6ojVGGEXTs	Scientific community, Civil society, Policy makers, Media	50	EU
12	video	Bioversity	How will FORGER make a difference?	2013	https://www.youtube.com/watch?v=FO7HgLJAmw8	Scientific community, Civil society, Policy makers, Media	150	EU
13	Film	Bioversity	Forest in the lab	27/08/2015	https://www.youtube.com/watch?v=fdRjOCPLlDw	Scientific community, Civil society, Policy makers, Media	300	EU
14	Audio interview	Bioversity	Interview from the kick-off meeting in Wageningen in March 2012 with Annette Schneegans	2012	http://www.fp7-forger.eu/publications/multimedia	Scientific community, Civil society, Policy makers, Media	100	EU
15	Audio interview	Bioversity	Interview from the kick-off meeting in Wageningen in March 2012 with Giovanni Vendramin	2012	http://www.fp7-forger.eu/publications/multimedia	Scientific community, Civil society, Policy makers, Media	100	EU
16	Audio interview	Bioversity	Interview from the kick-off meeting in Wageningen in March 2012 with Koen Kramer	2012	http://www.fp7-forger.eu/publications/multimedia	Scientific community, Civil society, Policy makers, Media	100	EU
17	Audio interview	Bioversity	Interview from the kick-off meeting in Wageningen in March 2012 with Bernd Degen	2012	http://www.fp7-forger.eu/publications/multimedia	Scientific community, Civil society, Policy makers, Media	100	EU
18	Flyer	Bioversity	Leaflet	2012	http://www.fp7-forger.eu/publications/public-awareness-material	Scientific community, Civil society, Policy makers,	250	EU
19	Flyer	Bioversity	FORGER Factsheet	2012	http://www.fp7-forger.eu/publications/public-awareness-material	Scientific community, Civil society, Policy makers,	250	EU
20	Posters	Bioversity	FORGER Poster	2012	http://www.fp7-forger.eu/publications/public-awareness-material	Scientific community, Civil society, Policy makers,	250	EU
21	Flyer	Bioversity	Flyer for the side event on the Global Plan of Action, organized at the European Forest Week in Rovaniemi, Finland, December 2013.	2013	http://www.fp7-forger.eu/publications/public-awareness-material	Scientific community, Civil society, Policy makers,	100	EU

22	Flyers	Bioversity	Flyer for the science-policy event in Brussels	2015	http://www.euforgen.org/fileadmin/templates/euforgen.org/upload/Documents/AgendaBrux_11Dec2015.pdf	Policy makers	100	EU
23	website	Bioversity	Web page for the science-policy event in Brussels	30/11/2015	http://www.euforgen.org/index.php?id=2032	Policy makers	200	EU
24	website	Alterra	Project website – homepage, dissemination, news and publications sections	31/05/2012	http://www.fp7-forger.eu/	Scientific community, Civil society, Policy makers,	200	EU
25	Media briefings	Bioversity	Mentioning FORGER in EUFORGEN newsletter	30/10/2014	October 2014 issue of the EUFORGEN Newsletter	Scientific community, Civil society, Policy makers,	170	EU
26	Media briefings	Bioversity	Mentioning FORGER in EUFORGEN newsletter	31/12/2015	December 2015 Issue	Scientific community, Civil society, Policy makers,	170	EU
27	Press release	Bioversity	Mentions of the project in @BioversityInt @EUFORGEN twitter account, Bioversity Facebook account, @CORDIS twitter, facebook and Google +	01/01/2016	Internet, Twitter, Google+	Scientific community, Civil society, Policy makers,	170	EU
28	Organisation of workshops	Bioversity	Side event on the Global Plan of Action, organized at the European Forest Week in Rovaniemi, Finland, December 2013.	2013	Rovaniemi, Finland	Scientific community, Civil society, Policy makers	50	EU
29	Organisation of Conference	Bioversity	Science-policy event, Brussels, 11 Dec 2015	12/12/2015	Brussels (Belgium)	Policy makers	35	EU
30	Organisation of workshops	Bioversity	Checking for gaps in the genetic conservation of of forest trees	08/05/2012	Szombathely Hungary	Scientific community, Civil society, Policy makers	30	EU
31	Organisation of workshops	Bioversity	Expert consultation	04/06/2012	Freising Germany	Scientific community, Civil society, Policy makers	15	EU
32	Organisation of workshops	Bioversity	Expert consultation	18/09/2012	Järvenpäa	Scientific community, Civil society, Policy makers	40	EU
33	Oral presentation to a scientific event	Bioversity	EUFORGEN 8th Steering Committee	27.11.2012	Paris	Scientific community, Civil society, Policy makers	30	EU
34	Oral presen-	Bioversity	EUFORGEN 9th Steering Committee	03/12/20	Talinn	Scientific community, Civil socie-	30	EU

	tation to a scientific event			13		ty, Policy makers		
35	Oral presentation to a scientific event	Bioversity	EUFORGEN 10th Steering Committee	16/06/2014	Edinburgh UK	Scientific community, Civil society, Policy makers	30	EU
36	Oral presentation to a scientific event	Bioversity	14th Session of FAO Commission on Genetic Resources for Food and Agriculture	15/04/2013	Rome	Scientific community, Civil society, Policy makers	50	EU
37	Oral presentation to a scientific event	Bioversity	FOREST EUROPE Expert level meeting	06/03/2013	Madrid	Scientific community, Civil society, Policy makers	50	EU
38	Oral presentation to a scientific event	Bioversity	International Conference on Forests foor Food Security and Nutrition	10/06/2013	Warshaw	Scientific community, Civil society, Policy makers	50	EU
39	Website	Bioversity	List of all publications	2012-2016	http://www.fp7-forger.eu/publications-2	Scientific community, Civil society, Policy makers	200	EU
40	Press releases	Bioversity	Lay summaries of scientific articles	31/12/2015	http://www.fp7-forger.eu/publications-2 (pages accessible under each title)	Scientific community, Civil society, Policy makers	200	EU
41	Press releases	Bioversity	Abstracts ofThree policy briefs containing recommendations for informing relevant policies	31/12/2015	http://www.fp7-forger.eu/publications/policy-briefs	Scientific community, Civil society, Policy makers	200	EU
42	Organisation of workshops	Bioversity	Training workshop on FGR inventories and databases	25/03/2014	Zagreb	Scientific community, Civil society, Policy makers	40	EU
43	Posters	Metla	FORGER mukana metsäpuiden geenivarojen in situ suojelutyössä Euroopassa (in Finnish)	29/08/2013	MTT Agrifood Research Finalnd	Scientific community	70	EU
44	Oral presentation to a	BFW	Presentation: " Forstliches Vermehrungsgut im W(H-)andel der Zeit" Overview Project, first results, dis-	29.08.13	Treis-Karden (Germany)	Scientific community, Industry	70	Germany,

	scientific event		cussion (in German)					Austria
45	Oral presentation to a scientific event	NymE	Extreme Drought Events Improves Modelling of Beech Persistence at its Distribution Limit in Hungary	20.09.13	Zürich,	Scientific community, Policy makers, Media	100+	International
46	Oral presentation to a scientific event	Alterra	Microevolution of trees and climate change. A simulation study bridging ecophysiology and quantative genetics	06.02.13	Lunteren, The Netherlands	Scientific community	70	The Netherlands
47	Oral presentation to a scientific event	NymE	Envisioning forest reproductive material for uncertain times	18.11.14	Orleans	Scientific community, Policy makers	50+	France, Germany, Spain, Hungary, Italy, Sweden
48	Oral presentation to a scientific event	NymE	Survival of Quercus petraea provenances under contrasting environments. Insights of its responses under climatic change	19.02.15	Sopron, Hungary	Scientific community, Civil society, Policy makers, Media	50	Hungary, Mexico
49	Interviews	NymE	Climate change project continue	02/03/2015	Budapest	Civil society, Policy makers, Medias	National television	Hungay, Euope
50	Oral presentation to a scientific event	Alterra	Presentation genetic computing for Forger project. Annual meeting of SURFSARA, Dutch National Computing Centre, super D Event “Where science meets e-infrastructure’.	15/12/2015	Amsterdam	Scientific community	30	Netherlands
51	Oral presentation to a scientific event	Alterra	Presentation of FORGER’s results for nursery-owners for: *Green Deal: know which plant material you buy and sell!*	21/01/2016	Wageningen, Netherlands	Scientific society, Industry	50	Netherlands

Table 4. List of Deliverables

Del. No.	Deliverable name	WP no.	Lead partici-pant	Nature	Dissemination level	Delivery date from Annex I	Actual / Forecast delivery date	Comments
D 7.1	Consortium Agreement	WP 7	Alterra	R	PU	M01	04.07.12 (M05)	
D 5.1	Basic communication and dissemination material (leaflet, poster, project presentation)	WP 5	Bioversity	O	PU	M03	22.10.12 (M08)	
D 7.2	Installation and updates external project website	WP 7	Alterra	O	PU	M04	12.12.12 (M10)	
D 5.2	Project website and dissemination section of the project website online	WP 5	Bioversity	O	PU	M08	28.02.13 (M12)	
D 4.1	GD2-EUFGIS search protocol	WP 4	INRA	R	PU	M12	01.04.13 (M14)	
D 5.3	3 experts consultated	WP 5	Bioversity	R	PU	M12	16.03.15 (M37)	16.03.2015 (M37) Accepted: Due to differences between NEF and the final projectplan, the report of the three expert consultation (milestone in the final projectplan but still required as separate deliverable in SESAM), the report was uploaded in M34
D 6.1	Financial section Periodic Report M1-18	WP 6	Alterra	R	PP	M19	31.12.13 (M22)	
D 7.3	Periodic report M1-18	WP 7	Alterra	R	PP	M19	31.12.13 (M22)	
D 1.1	Extended and linked genetic and ecological databases: Extended and linked databases on inventories and environmental data, including GD2, and EUFGIS	WP 1	LUKE	R	PU	M36	06.03.15 (M37)	
D 3.3	Characterization and comparison of reaction norms and	WP 3	NymE	R	PU	M36	16.03.15	

Del. No.	Deliverable name	WP no.	Lead partici-pant	Nature	Dissemination level	Delivery date from Annex I	Actual / Forecast delivery date	Comments
	responses in vitality and survival to environmental change of Fagus sylvatica, Quercus spp., Pinus sylvestris and Picea abies						(M37)	
D 5.4	Documentation on training workshop on 'inter-linked' FGR inventories and databases organized	WP 5	Bioversity	O	PU	M36	12.03.15 (M37)	
D 6.2	Financial section Periodic Report M19-36	WP 6	Alterra	R	PP	M37	28.08.15 (M42)	
D 7.4	Periodic report M19-36	WP 7	Alterra	R	PP	M37	28.04.15 (M38)	
D 5.5	Report/summary of on-line discussion forum on pan-European gene conservation strategies organized	WP 5	Bioversity	O	PU	M40	29.12.15 (M46)	
D 1.2	Maps and pan-European trends (clines) of genetic diversity for Pinus sylvestris, Picea abies, Quercus spp., Fagus sylvatica, Pinus pinaster and Fraxinus spp. (the latter 2 species depending on availability of data)	WP 1	LUKE	R	PU	M42	12.11.15 (M45)	
D 1.3	Evaluation of the present genetic conservation efforts in Pinus sylvestris, Picea abies, Quercus spp., Fagus sylvatica, Pinus pinaster and Fraxinus spp. (the latter 2 species depending on data availability)	WP 1	LUKE	R	PU	M42	10.12.15 (M46)	
D 2.1	Final protocols to monitor genetic diversity of Fagus sylvatica, Quercus spp, Picea abies, Pinus sylvestris and P. pinaster at pan-European scale	WP 2	VTI	R	PU	M42	27.11.15 (M45)	
D 2.2	Comprehensive assessment of genetic diversity of Fagus sylvatica, Quercus spp., Pinus sylvestris, P.pinaster and Picea abies at scale of the species distribution, along geographic and environmental gradients	WP 2	CNR	R	PU	M42	12.11.15 (M45)	

Del. No.	Deliverable name	WP no.	Lead participant	Nature	Dissemination level	Delivery date from Annex I	Actual / Forecast delivery date	Comments
D 3.1	Review of impact of transfer of FRM and forest management in Europe on current distribution of genetic diversity of Fagus sylvatica, Quercus spp, Pinus sylvestris, Picea abies, Pinus pinaster and Fraxinus spp.	WP 3	BFW	R	PU	M42	12.11.15 (M45)	
D 3.2	Model analysis on optimal seed harvest strategies of Fagus sylvatica, Quercus spp., Pinus sylvestris, Picea abies, Pinus pinaster and Fraxinus spp.	WP 3	VTI	R	PU	M42	03.11.15 (M45)	
D 3.4	Assessment of impacts of climate change, forest management and transfer of FRM on genetic diversity of Fagus sylvatica, Quercus spp., Pinus sylvestris, Picea abies, Pinus pinaster and Fraxinus spp. at scale of the species distribution (the latter 2 species as far as data availability allows)	WP 3	Alterra	R	PU	M42	17.12.15 (M46)	
D 4.2	Policy briefs including recommendations for policy makers	WP 4	BFW	R	PU	M42	21.12.15 (M46)	
D 4.3	Guidelines for forest managers	WP 4	BFW	R	PU	M42	12.02.16 (M48)	
D 5.6	Report of final project meeting organized for scientific community	WP 5	Bioversity	R	PU	M47	29.12.15 (M46)	
D 5.7	Report of round-table meeting organized Round-table meeting for European policymakers	WP 5	Bioversity	R	PU	M48	13.01.16 (M47)	
D 6.3	Financial section Periodic Report M37-48	WP 6	Alterra	R	PP	M48	30.03.16 (M49)	
D 6.4	Financial section Final Report	WP 6	Alterra	R	PP	M48	29.04.16 (M50)	
D 7.5	Periodic Report M37-48	WP 7	Alterra	R	PP	M48	28.03.16 (M49)	

Del. No.	Deliverable name	WP no.	Lead partici-pant	Nature	Dissemination level	Delivery date from Annex I	Actual / Forecast delivery date	Comments
D 7.6	Final report	WP 7	Alterra	R	PU	M48	29.04.16 (M50)	

Table 5. List of project partners

Participant Number	Participant name	Participant short name	Country	Date enter project	Date exit project
1 (CO)	Stichting Dienst Landbouwkundig Onderzoek	Alterra	Netherlands	1	48
2	Bundesforschungs-und Ausbildungszentrum fur Wald, Naturgefahren und Landschaft	BFW	Austria	1	48
3	Johann Heinrich von Thünen-Institut Bundesforschungsinstitut für Ländliche Räume, Wald und Fischerei	vTI	Germany	1	48
4	Institut National de la Recherche Agronomique	INRA	France	1	48
5	Luonnonvarakeskus	LUKE	Finland	1	48
6	University of West Hungary	NymE	Hungary	1	48
7	International Plant Genetic Resources Institute	Bioversity	Italy	1	48
8	Consiglio Nazionale delle Richerche	CNR	Italy	1	48
9	Uniwersytet Kazimierza Wielkiego	UKW	Poland	1	48

Section B

There are no patents, trademarks or registered designs resulting from FORGER.
The results do not contain confidential information.