

A roadmap for future transatlantic research cooperation on adaptation of forest trees to environmental change

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FORESTTRAC

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EXECUTIVE SUMMARY

The issues

Climate change and habitat fragmentation are imposing profound pressures on the forest ecosystems of Europe and North America to adapt faster than they ever have before. Trees and forests are central to environmental health. Forests cover nearly 40% of Europe and North America, providing important ecosystem services, biomass and wood. Moreover, trees are the foundation species of numerous terrestrial ecosystems and as such are key drivers of ecosystem processes and stability. Ensuring the continued health of our forests is a vital step in sustaining overall ecosystem stability.

Most forest tree species retain appreciable genetic variation in their natural and domesticated populations, but there is only anecdotal evidence that tree populations can adapt or migrate rapidly enough to survive the current rate of environmental change. This raises two key questions: To what extent do trees have the evolutionary potential to adapt? And if they cannot adapt rapidly enough, what role can humans play in mitigating negative impacts of climate change on forests? The answers to these and many other key questions are simply not known at present, nor will they be known without a concerted, long-term research effort.

Scientists from a wide range of disciplines and institutions across Europe and North America joined forces within the framework of the European-Union-funded FoResTTraC initiative (Forest ecosystem genomics Research: supporTing Transatlantic Cooperation; www.foresttrac.eu) to draft a research roadmap that outlines key issues to be addressed in the coming decade.

Addressing the issues

Given the scope and global nature of the issues raised, addressing them requires an internationally integrated research effort linking disciplines such as genetics, ecology, plant physiology, genomics and evolution. At a minimum, this effort should:

- Quantify how environmental change will trigger adaptive responses at different hierarchical levels (from molecular processes to ecosystems).
- Develop generic and global approaches to assess key adaptive responses throughout the northern hemisphere.
- Combine historical, ecological, and genetic research to enable predictions of long-term adaptive responses.
- Determine how human activities can mitigate impacts of climate change on tree populations.

• Develop and integrate the resources and experimental infrastructures needed to implement transatlantic research collaboration.

Implementation of the roadmap

The FoResTTraC roadmap provides the groundwork for future coordinated research plans between Europe and North America by linking the work already being carried out in Europe, the United States and Canada, and proposing future integrated approaches.

Europe and North America share ecologically diverse, temperate, boreal and Mediterranean types of forest ecosystem, and the predicted impacts of and selection pressures imposed by climate change are very similar on the two continents. Many of the tree genera (or families) found in Europe are common to North America, easing the choice of model genera in tree genomics and ecology. It would therefore be of mutual benefit to partners on both sides of the Atlantic to collaborate on research into the impacts of climate change on forest species and efforts to mitigate these effects.

The research framework presented in this roadmap also provides avenues for practical application of the findings in forestry operations, informing silvicultural practices.

Experimental infrastructure is already in place in both Europe and North America to support the research areas identified in this roadmap, but additional research infrastructure and resources will be needed in order to accomplish the research tasks described and achieve the expected impact. Resources and infrastructure needed belong to four main categories: (1) genetic resources and common garden experiments; (2) monitoring and observation sites; (3) integrated databases; and (4) biological resources, such as tissue samples, genomic DNA extracts, cDNA clones and BAC libraries.

Funding the research outlined by this roadmap will require concerted effort with funding bodies to align their selection criteria and timetables; a review of existing funding sources in Europe and North America for research on forest genomics found a wide range of selection criteria and timetables. Mobilizing the funder community from both sides of the Atlantic to support the integrated collaborative programme described will be a considerable challenge.

This roadmap also addresses the need to provide training opportunities to train the next generation of researchers working in the field of forest genetics, genomics and ecosystems, and outlines actions needed to reach out to stakeholders to ensure buy-in to the objectives and implementation of the programme's findings.

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The document is based on the results from a series of workshops organized by the ForesTTraC partners and attended by invited experts from Europe and North America. The workshops produced reviews of current understanding and future research priorities on the following topics:

- Epigenetic response to climatic change
- Evolutionary genetic change in response to climatic change
- Genomics of forest and ecosystem health in the Fagaceae
- Genomics of conifers
- Interoperability and integration of databases in Europe and North America
- Landscape genomics
- Long distance gene flow and adaptation
- Role of foundation species in ecological processes

Several other scientists from Europe and North America also provided useful information and feedback to the preparation of this roadmap. Furthermore, the development of the roadmap benefitted from the contributions of representatives of various funding bodies. Finally, this roadmap was presented to representatives of the European Commission and other stakeholders in Brussels on 26 October 2011. It was also shared with the National Coordinators of the European Forest Genetic Resources Programme (EUFORGEN).

The graphic design was developed by Patrizia Tazza, and the language editing was done by Paul Neate.



INTRODUCTION

Forests cover nearly 40% of Europe and North America, providing important ecosystem services, biomass and wood resources. Trees are the foundation species of numerous terrestrial ecosystems. But their role as key drivers of ecosystem processes and stability is threatened today by climate change, which is occurring much faster than during past natural climatic oscillations. Though common garden and genetic trials have demonstrated most forest tree species retain much genetic variation, there is only anecdotal evidence that tree populations can adapt and/or migrate rapidly enough to cope with predicted climatic and environmental changes.

This raises two key questions: Given the anticipated scale of environmental change, to what extent do trees have the evolutionary potential to adapt? And if they cannot adapt fast enough, what role can humans play in mitigating the negative impacts of climate change on trees and forests?

Given the scope and global nature of these questions, answering them requires the development and implementation of an internationally integrated research effort linking disciplines such as genetics, ecology, genomics and evolution.

1.1 Horizon scanning

Evidence of climate change has been increasing in recent years, as documented in reports from the Intergovernmental Panel on Climate Change (www. ipcc.ch). The likely impacts of climate change on forest ecosystems are now raising considerable concern. A recent review commissioned by the European Commission¹ showed that the expected impacts will be driven by both gradual changes, such as those in temperature and rainfall, and increasing frequency and severity of episodic events such as droughts, floods, wind, fire and pest and disease outbreaks. While the effects of gradual changes are hard to detect over short time spans in long-lived species, the impact of events such as wind storms (1999 in Europe), harsh droughts (2003 in Central Europe) and insect outbreaks (USA and Canada) are already readily apparent.

1 Lindner M., Garcia-Gonzalo J., Kolström M., Green T., Reguera R., Maroschek M., Seidl R., Lexer M.J., Netherer S., Schopf A., Kremer A., Delzon S., Barbati A., Marchetti M. and Corona P. 2008. Impacts of climate change on european forests and options for adaptation. AGRI-2007-G4-06, Report to the European Commission Directorate-General for Agriculture and Rural Development. 223 pages. Available at: http://ec.europa.eu/agriculture/analysis/external/euro_forests/full_report_en.pdf The predicted consequences of climate change for forest ecosystems vary significantly across regions. Major changes are foreseen in forest species composition, tree distribution ranges, incidence and severity of drought, nutritional conditions, tree growth and community interactions. Though there will be differences between regions, it is anticipated that the current strong similarities between Europe and North America will persist. In the boreal regions of both continents, increases in temperature and longer growing seasons will likely enhance tree growth and production, but increase insect and disease outbreaks due to milder winters. Broadleaved species are expected to migrate northwards, perhaps reaching boreal regions, in both Europe and North America. Prolonged droughts in southern Europe and the southern USA will increase the frequency and extent of forest fires and hasten the retreat of the more drought-sensitive species at the trailing edge of ecological zones.

In addition to sharing similarities of risks and impacts due to climate changes, the two continents share strong similarities in the species that will be exposed to these changes, including pines, firs, spruces, oaks and beech.

1.2 Adaptive challenges

Adaptive challenges that trees will be facing can be best illustrated by the predicted rate of climate change (temperature, rainfall and CO_2 concentration) and the anticipated shifts of bioclimatic envelopes for tree species.

It is predicted that bioclimatic envelopes in Europe and North America will move northwards by 300 to 800 km within one century, depending on which climate or greenhouse gas emission model or scenario is used. This implies that current tree populations at the trailing and leading edges of the range will face new adaptive challenges. Populations at the southern margins will face climatic conditions that are already limiting species growth and causing forest decline. Will these populations have the evolutionary potential to adapt to these conditions before going extinct? Their persistence will depend on whether the evolutionary or demographic constraints currently preventing their establishment in warmer or drier climates will be low enough to enable expansion of species' fundamental niches. Conversely, at the northern margins, new areas will become suitable for growth. Will the genetic make-up of pioneer trees allow them to colonize these new areas, or will it limit their ability to adapt at the northern margin in the future? Finally the populations at the core of the species' distribution will be subjected to an evolutionary race to keep pace with the moving adaptive optima imposed by environmental change.

The large bioclimatic envelope of many forest trees hides a collection of highly differentiated populations and genotypes with a wide range of adaptive potential to local climate and soils. Shifts in climatic envelopes therefore are likely to generate not only potential local extinction and recolonization, but also large reorganization of genetic diversity within the species range. Evolutionary challenges faced by populations at the margins of the range may be very different to those faced by populations at the core of the range, due in particular to very different demographic constraints (i.e., population reduction due to drift and selection). These different evolutionary challenges across the species distribution are expected in both Europe and North America, where climatic conditions vary across similar extremes.

The two continents are thus similar in terms of (1) new selection pressures due to climate change and occurrences of extreme climatic events, (2) target adaptive traits to be dissected, and (3) model species to be investigated. This should facilitate the development of research projects addressing the response of tree populations to climate change in both continents.



STRATEGIC OBJECTIVES

To date, scientific communities in North America and Europe have pursued somewhat disparate research efforts focussing on the responses of forest ecosystems to climate change. These efforts have generally consisted of:

- prediction of the impacts of climate change under various scenarios of climate and greenhouse gas emissions
- modelling of bioclimatic envelopes
- elucidation of the genetic basis of traits of adaptive significance and
- monitoring of species range limits.

Moreover, research efforts in these areas are often duplicated by scientists on either side of the Atlantic. Integrating research efforts across disciplines and between countries would significantly enhance efficiency of research addressing the evolutionary responses of tree populations. Such an integrated research effort would address, as a minimum, the following strategic objectives:

- Quantify how environmental change will trigger adaptive responses at different hierarchical levels (from molecular processes to ecosystems).
- Develop generic and global approaches to assess key adaptive responses throughout the northern hemisphere.
- Combine historical, ecological and genetic research to enable predictions of long-term adaptive responses.
- Determine how human activities can mitigate impacts of climate change on tree populations.
- Develop and integrate the resources and experimental infrastructures needed to implement transatlantic research collaboration.



RESEARCH AREAS

A two-dimensional matrix has been created to capture the overall scope of research topics required to adequately address the strategic objectives noted above (Table 1). The elements of the matrix define the research topics to be addressed.

Headings on the horizontal axis identify the research objectives, from basic research goals to societal implications. Objective 1 addresses the elucidation of evolutionary processes, their effects and rates that will trigger adaptive change. Objective 2 identifies relevant indicators that can be assessed separately. Objective 3 identifies modelling efforts needed to provide insights on likely outcomes under different scenarios. Objective 4 focuses on human actions needed to address the predicted outcomes identified under objective 3.

Labels on the vertical axis identify the hierarchical elements of forest ecosystems that are likely to undergo evolutionary changes as a result of climate change. Climate change is expected to have impacts and impose selection pressures at all hierarchical levels, from single trees to communities and landscapes, with different research approaches noted for each.

This matrix provides a general framework for defining future areas of research emphasis. It is flexible and can be enhanced or altered as new research areas emerge as a result of ongoing conceptual or technological developments, without hindering the central strategic and research objectives.

3.1 Objective 1: Estimate effects and rates of adaptive processes in forest ecosystems

Adaptation is the result of evolutionary processes acting separately or in combination. Knowledge of the effects of these processes and their rates under different ecological settings is essential if we are to predict future responses of tree populations and their associated species. This section focuses on the various processes that can be deciphered through retrospective or contemporary analysis of evolutionary trajectories.

3.1.1 Plasticity

Phenotypic plasticity is the capacity of a single genotype to produce different phenotypes in response to varying environmental conditions. Understanding plastic responses is crucial for predicting and managing the effects of climate change on forest tree species.

Forest trees are long-lived organisms with complex life cycles. Their long generation intervals make them less able to respond to rapid changes using the longer-term evolutionary processes involving their genetic diversity. However, trees display a wide range of phenotypic plasticity; they are able to tolerate a very wide range of growing conditions and extreme seasonal changes, which makes them true masters in acclimation to changes in the environment. Consequently, phenotypic plasticity is likely to be of great importance in the ability of both individual trees and forest populations to adapt to climate change. However, we have only a relatively rudimentary knowledge of the extent and mechanisms of phenotypic plasticity in a variety of stress responses and developmental traits in forest trees. There is also a shortage of knowledge of the true adaptive value of the modification of physiological traits in the face of a change in the availability of resources. A better understanding of the mechanisms underlying plasticity of traits related to the fitness and success of individuals in a given environment (adaptive plasticity) will contribute to prediction of the global fitness of a genotype as well as of changes in species distribution. This information is required for the design of efficient programmes of forest management and breeding under a changing climate.

3.1.2 Epigenetic responses

Epigenetic modifications can alter gene expression and phenotypic responses without changing the actual

TABLE 1. Two-dimensional matrix to define the research topics needed to address the overall scope of the strategic objectives of the transatlantic research collaboration on the impact of climate change on forest species.

	Objective 1 Effects & Rates	Objective 2 Indicators	Objective 3 Predictions	Objective 4 Human measures
Trees	3.1.1 [†] Plasticity 3.1.2 Epigenetic responses	3.2.1. Genes, traits, fitness	3.3.1 Individual- or population-based models coupling genetic and ecological processes	
Populations	3.1.3 Local adaptation	3.2.2. Adaptive diversity and divergence	3.3.1 Individual- or population-based models coupling genetic, physiological and ecological processes	3.4.1 Reaction norms and transfer functions
	3.1.4 Rescue from maladaptation			3.4.2 Regeneration regimes
Communities	3.1.5 Hybridization 3.1.6 Community trajectories	3.2.3. Cascading effects on the evolution of community members	3.3.2 Models incorporating biotic interactions	3.4.3 Community reaction norms
Landscapes	3.1.7 Long distance gene flow3.1.8 Migration and colonization	3.2.4 Associations between ecological and genomic variations	3.3.2 Models incorporating biotic interactions	3.4.4. Management of diversity at the landscape level
	3.1.9 Altered species interactions			
	3.1.10 Divergent selection			

[†] Numbers refer to section numbers in the text.

sequence of the genome. Thus, epigenetic modifications may be thought of as relatively "plastic" changes that allow for rapid adaptation and, at the same time, might act as a buffer to deleterious allelic variation occurring naturally.

It has been suggested that epigenetic variation contributes to the phenotypic plasticity and adaptive potential of plant species, especially in long-lived organisms with complex life cycles, such as forest trees. Insights into epigenetic variation, and its relationship to phenotypic plasticity, will contribute to the understanding of adaptive responses of trees and might help to evaluate the risk to long-lived species of both short-term and long-term fluctuations in the environment. Moreover, understanding the interplay between epigenetic mechanisms and genetic variability should enhance our understanding of evolutionary trajectories, as natural selection also directly targets the proportion of phenotypic variation that is shaped by epigenetic phenomena. Diverse environmental stresses, as well as hybridization and polyploidization events, can create heritable epigenetic marks that can be transmitted to subsequent generations as a form of molecular "memory" of past experiences. Crucially, such modifications can be reversible. Epigenetic changes may also contribute to the ability of plants to colonize or persist in variable environments. Despite the profound impact that epigenetics might have in determining environmental compatibility, relatively few studies have investigated the extent of natural epigenetic variation and its relationship to phenotypic variation and adaptation potential.

3.1.3 Local adaptation

Under climate change, local adaptation can be pictured as a race between the shifting of local phenotypic optima and the evolutionary changes in the population. It is of utmost importance to estimate the rates of evolutionary change in comparison to the velocities of climate change.

Comparisons of differentiation for neutral markers and adaptive traits in trees repeatedly suggest that extensive gene flow has not prevented local adaptation. Where direct evidence of local adaptation is not available, phenotypic variation following environmental clines provides indirect evidence of such adaptation. Thus, most tree species show local adaptation, which has contributed to healthier and more productive forests. To be able to maintain forest services, it is likely that new patterns of genetic structure and local adaptation corresponding to changed climatic patterns will need to evolve. Evaluating the effects of various factors that influence this potential will be a critical research area, both in modelling and for empirical research.

3.1.4 Rescue from maladaptation

Increased drought at the southern limits of the distribution of tree species will expose populations to severe stress that may ultimately lead to population extinction. However, it may be possible to rescue such populations from maladaptation before they become extinct.

Populations at the extreme southern margins of the distribution of tree species are likely to be exposed to high levels of genetic drift, as severe stress may reduce population sizes substantially. Under such circumstances populations are more vulnerable to extinction due to demographic stochasticity. Maladaptation may be tolerated as long as the population size is above a critical threshold. It is therefore of utmost importance to determine genetic and demographic tipping points likely to lead to population and species extinction or to rescue from maladaptation. It will also be important to develop mitigation measures to counteract negative consequences of maladaptation.

3.1.5 Hybridization

The species composition of forests is changing as a consequence of climate-change-induced migration and artificial plantations giving rise to non-analogue genetic combinations through hybridization.

Forest composition has been profoundly modified by the extensive use of plantations. These human-induced changes have been further enhanced by the natural colonization of abandoned farmland by forest trees and by the migration of species induced by climate change. All these changes in species composition increase the occurrence of natural hybridization and new genetic combinations. Hybridization events between species (native or exotic) are responsible for a large number of speciation and introgression events. The consequences of dynamic genomic recombination following hybridization for tree adaptation and evolution is a major research issue to be explored in the context of climate change. While the adaptive consequences of hybridization may be long term, the occurrence of hybridization (and introgression) events can be assessed at shorter time scales. Future changes in species composition are expected to be greater and consequent hybrids more common in transition zones between Mediterranean and temperate regions than was the case in the past.

3.1.6 Community trajectories

The changes in the species composition of forests in response to global climate change will affect the thousands of species that are supported by these foundation tree species.

Recent studies have demonstrated that diverse organisms, from microbes to vertebrates, are affected by the genetics of foundation species (i.e., species that structure a community by creating locally stable conditions for other species and by modulating and stabilizing fundamental ecosystem processes). As trees are the epitome of the foundation species concept, it is especially important to understand their genetic-based impacts on the ecology and evolution of whole communities and ecosystem processes. Thus, as climate change, fragmentation and forest management affect trees, both ecologically and evolutionarily, it is essential to understand how changes to foundation tree species will affect their dependent communities, which involve thousands of species. For example, drought-tolerant genotypes selected to cope with climate-change-induced drought will favour different community members compared to the current genotypes and alter ecosystem processes such as nutrient cycling. These impacts on the community and ecosystem can be thought of as altered community and ecosystem trajectories, in which a given level of change in a foundation species will have some predictable and some unpredictable impacts on biodiversity, the genetic-based interactions among associated community members, patterns of extinction and invasions by exotic species. These issues can be studied through observational studies in the wild and experimental studies in common gardens, and require a multidisciplinary approach from genes to ecosystems.

3.1.7 Long-distance gene flow

Climate change presents forest tree species with new adaptive challenges in the core and at the edges of their distribution. Long-distance gene flow could compensate for the long generation time of trees and enhance evolutionary change in a changing climate.

Abundant evidence of long-distance effective gene flow in trees indicates that genes may move within one generation over larger scales than predicted habitat shifts resulting from climate change. The adaptive responses can be very differently mediated by gene flow, depending on the direction of pollen and seed flow relative to the direction of habitat shifts. Long-distance gene flow may trigger rapid local adaptation at the centre or leading edge of tree distributions. These processes can best be studied at sites in Europe and North America with different meteorological and ecological conditions that offer contrasting directionalities of climate change and gene flow.

3.1.8 Migration and colonization

Migration and adaptation are alternative responses to environmental change: trees can either adapt to novel conditions without migrating, or can migrate to sites with favourable conditions without evolving. Trees are expected to adjust to climate change by moving their distribution to higher latitudes or elevation.

Occupation of new habitats made available by climate change is the outcome of successive demographic and ecological processes: seed dispersal, colonization, intraand interspecific competition and establishment. While retrospective compilations of forest tree inventories have already indicated that species range limits have shifted to higher latitudes and elevations, the dynamics of these shifts relative to the velocity of climate change is not yet well understood. Such retrospective analyses need to be complemented by experimental approaches and simulations to enable us to predict the rate of successful migration at the range limits.

3.1.9 Altered species interactions

Foundation tree species and their diverse dependent communities have co-evolved over evolutionary time, hence changes in foundation tree species will affect their dependent communities and vice versa.

Global climate change alters the genetic structure of many forest species, and these changes will affect the ecology and evolution of dependent community members. For example, climate change and forest managers may favour specific tree genotypes and source populations over others, resulting in changes in the genetic base of the forest tree population and consequent changes in the genetic-based interactions with diverse community members. These altered interactions with mycorrhizal mutualists, insect herbivores, pathogens and diverse community members occupying different trophic levels in turn feed back to affect the survival and performance of the foundation tree species. Such feedbacks are important, but very poorly understood. To understand these interactions and their basic and applied implications, it is important to study the genetic covariances among community members and foundation tree species in simplified plantation settings, in their more complex natural settings and in multispecies provenance trials.

3.1.10 Divergent selection

Common garden experiments (or provenance tests) of trees indicate that population differentiation is large and follows clinal patterns with regard to environmental gradients. These patterns suggest that past divergent selection across contrasting environments generated adaptive divergence and that such selection will most likely trigger future divergence as well. Populations of widespread species of trees, such as Scots pine in Europe and Asia or lodgepole pine in Canada, inhabit a wide range of environments. Extensive studies have shown extensive phenotypic differentiation in many important traits related adaptation to climate change, e.g. timing of growth or drought tolerance, despite extensive gene flow. This provides direct evidence of strong differential selection between environments. The strength of selection has rarely been quantified, despite being a critical parameter in all quantitative genetic models related to predicting evolutionary responses. Research is thus needed to quantify the strength of selection, and to determine which are the most relevant traits being selected for by different ecological drivers in a wide range of environmental conditions.

3.2 Objective 2: Provide indicators that have predictive value for adaptive processes

Evolutionary theory allows predictions to be made of future responses according to genetic or demographic parameters that can be measured in contemporary populations. Some of these indicators can be indirectly assessed via ecological and genetic approaches and surveys that are summarized here.

3.2.1 Identify genes and traits that have adaptive significance, and assess fitness of trees

Certain genes and traits will likely take on new or more prominent adaptive significance under changing climates. Direct access to genes is paramount in order to develop time-saving diagnostic tools to survey populations, in addition to shedding light on molecular and physiological processes.

Bud phenology and dormancy are well-studied traits that vary extensively among and within species, and represent useful indicators of adaptation to the local climate. On the other hand, resilience to stresses such as drought or temperature extremes and general phenotypic plasticity are only partly described in many forest tree species. Functional tests under controlled environments can be used to evaluate such traits under different scenarios of anticipated change. Together with recently developed gene catalogues and genome-wide analysis tools, such as microarrays, these functional tests will enable the identification of genes that condition adaptive traits. Most traits of adaptive significance are expected to have quantitative patterns of variation; therefore, they are likely to be controlled by many genes, each with a small effect. Innovative research is needed to identify groups of genes that contribute to trait expression through their combined action. Genes that matter will likely be involved in sensing both normal and exceptional climatic

variation and regulating the requisite responses. While individual genes have been identified in recent years, more comprehensive categorizations are needed in order to describe the regulatory cascades and biochemical pathways, as well as groups of co-expressed genes. In addition to tracking genes based on their expression and the predicted function of their product, determining the evolutionary trajectory of gene families may provide important clues for revealing functional diversification. For example, recently duplicated genes and genes that vary in copy number may be recruited in processes supporting evolutionary adaptation.

3.2.2 Characterize adaptive diversity and divergence in extant populations

The extent of population response to new selection pressures induced by climate change is dependent on the amount of adaptive diversity existing within populations. Adaptive diversity and divergence are very important indicators of population evolution.

Genetic differentiation and local adaptation are major features in many widespread tree species. There are, however, also examples of small, fragmented populations (or narrowly-distributed species) in which genetic differentiation may be due to drift and whose response to environmental variation is largely due to phenotypic plasticity. It will be important to identify these different kinds of species and populations. This is possible through comparisons of neutral marker diversity and adaptive variation over populations, both with respect to diversity and relative to divergence of populations. Study of environmental correlations with traits will also help identify adaptive patterns. The description of these present patterns of genetic diversity, along with the evaluation of strength for future selection, will provide much of the basic information needed for predicting population responses to climate change.

3.2.3 Assess cascading effects on the evolution of community members

Because foundation tree species "drive" whole communities and ecosystems, it is important to understand how the evolution of dependent community members will be affected by changes in genotypic frequencies of foundation tree species and the genetic structure of planted forests.

Recent studies have shown that intraspecific genetic differences among trees can affect the ecology and evolution of associated pests, pathogens and other community members occupying different trophic levels. For example, genetically engineered trees incorporating Bt genes select for Bt-resistant insect herbivores, and

naturally occurring hybridization in trees has resulted in cryptic speciation in arthropods that have evolved to live only on hybrids. Global climate change and forest management practices act as agents of selection on foundation tree species, and are thus likely to have basic and applied evolutionary impacts on the diverse communities that rely upon these trees for their survival. Because these community members interact with one another in a complex network of interactions, it is important to study how anthropogenic selection on foundation tree species affects the evolution of diverse community members occupying multiple trophic levels.

3.2.4 Identify associations between ecological and genomic variations

Genomic technologies now provide the opportunity to discover the genes that underlie complex adaptive traits and the allelic variation in them. The current challenge is to discover these genes and alleles and to associate this variation with fine-scale environmental variation using spatially explicit samples.

Common garden studies have repeatedly show finescale patterns of adaptation in complex adaptive traits. Knowledge derived from such studies could guide forest management activities aimed at mitigating the effects of climate change, but this would require studies of many species and environments across spatial scales. There is neither sufficient time nor resources to develop common garden studies at the scale that would be needed. The alternative is to use a landscape genomics approach, where genetic variation in suites of genes underlying complex adaptive traits can be associated with environmental variation.

3.3 Objective 3: Integrate processes to build predictive models

Evolutionary mechanisms do not act individually but concurrently across the different levels, from trees to landscapes. Knowledge of the integration of these mechanisms is needed to build predictions of adaptive responses to climate change. Integration can be seen in various steps by coupling different mechanisms (ecological and genetic) and/or different hierarchical levels (trees to communities). This is a rather innovative research field that feeds from new theoretical and experimental approaches.

3.3.1 Develop individual- or population-based models coupling genetic, physiological and ecological processes *Predictive models of tree adaptation can be built by coupling knowledge of various evolutionary and ecological processes that has been acquired from diverse research disciplines (e.g., evolution, ecology and climatology).*

Approaches to modelling of complex systems are very field-specific and very little effort has been made to integrate physiological and ecological modelling with models of evolutionary processes and genetics. Such integration is however needed to accurately predict the impact of environmental changes on species persistence over the next century and at the continental scale. The modelling approach should overlay predictions from a variety of sources, including: (1) construction of adaptive traits based on ecophysiolgical processes; (2) modelling of future bioclimatic envelopes; (3) modelling of colonization and pollen flow over geographical ranges; and (4) modelling of evolutionary adaptation of local populations. The models can be validated using retrospective analysis of evolution of tree populations in North America and Europe growing along environmental gradients that mimic climate change.

3.3.2 Adapt existing models incorporating biotic interactions for predicting community responses or develop new theoretical models

Analytical and simulation approaches need to be extended from the intraspecific level to communities by incorporating species interactions. This is a new field of research that needs to be explored to predict responses at the community level.

The expected rate of evolutionary change is likely to differ between species, thus generating additional interspecific interactions, either mutualistic or antagonistic. Interspecific processes will in return interfere with intraspecific processes and lead to differing responses by individual trees depending on the spatial, geographic or community context of forest ecosystems. Both categories of process should be incorporated in theoretical analytical models, and should also be included in simulations models of individual trees. Acquiring a knowledge of the combination of positive and negative species interactions together with intraspecific evolutionary mechanisms would greatly improve our ability to predict the scale and distribution of the effects of climate change on forest ecosystems.

3.4 Objective 4: Anticipate adaptive responses and propose human-assisted measures

The ultimate objective is to provide societies with management measures that allow them to anticipate and counteract negative effects of climate change. This will follow the logical output of the predictive models. Such measures – either facilitating adaptation or mitigating negative effects – should be science-based and ultimately combine natural science with social science approaches.

3.4.1 Estimate reaction norms and transfer functions from multisite provenance tests

Multisite provenance tests offer the unique possibility to assess the response of a given population under different environmental conditions, i.e., the reaction norm. This information is needed to make recommendations for seed transfer if assisted migration were to be implemented.

Provenancetestshavebeen established in Europeand North America, sometimes through reciprocal translocations (North American species planted in European provenance tests and vice versa). They provide crucial information on the level of genetic variation for fitness related traits within and between populations that has resulted from divergent selection across populations, gene flow and random genetic drift. The results of such tests can be used to construct reaction norms of populations (provenances) that describe the responses of a population across a wide range of environmental conditions. Standardization of heterogeneous data coming from tests managed by different research institutes in different countries is a necessary initial collaborative step before norms of reactions and transfer functions can be computed and potentially applied to assisted-migration issues.

3.4.2 Adapt and design appropriate regeneration regimes

New forests are established through natural or artificial seeding, and planting by humans. The ultimate choice of regeneration regimes should enhance the adaptive potential of the new forests.

The adaptive potential of new forests can be enhanced by increasing their fitness through natural or artificial means, that is, by increasing the level of genetic diversity or importing better adapted seeds or seedlings. Research is needed to secure the adaptive potential of reproductive material and develop practical measures to be adopted in operational forestry, including seed collection procedures in seed stands, seed transfer rules, traceability of reproductive material, monitoring of seed crop, and creating conditions for natural regeneration or introduction of new genotypes.

3.4.3 Estimate community reaction norms from multispecies provenance tests

Robust use of provenance trials is a key experimental approach to studying the genetic-based impacts of foundation tree species on their dependent communities and the feedbacks of these communities on foundation tree species. Because species interact, it is recommended that an approach that involves planting multiple foundation tree species over large geographical region

so that studies can be conducted within a community context.

The time-honoured practice of using provenance trials to study local adaptation and identify superior genotypes for economically important traits should now be expanded to study whole communities and ecosystem processes. Establishing trials over elevational and latitudinal gradients in both Europe and North American will greatly facilitate the study of the impacts of climate change on foundation tree species and their dependent communities. In addition to identifying superior genotypes and source populations for traits such as drought tolerance and resistance to pests, the same trials can identify genotypes and source populations that promote the greatest biodiversity and community stability, as well as those that are best suited to forest restoration and that are most likely to survive climate change. The results from these trials would also facilitate development of genetic-based climate change models; these, in turn, can utilize the trial sites in Europe and North American to calibrate and validate models to enhance their predictive capabilities. Such trials also serve as an integrative focal point for researchers with diverse skills and approaches to merge their findings on individual tree genotypes of known pedigree. Through such facilities, a new level of integration and international collaboration can be achieved.

3.4.4 Management of diversity at the landscape level In the context of ecological uncertainty generated by climate change, managing diversity at intraspecific and interspecific levels may secure adaptive evolutionary trajectories.

Very little is known about the use of the different components of biodiversity as tools to combat climate change. Research should be implemented in two different directions: (1) design landscape configurations favouring the maintenance of genetic connectivity among forested areas; and (2) establish mixed stands with controlled, a priori-defined levels of intra- and interspecific diversity as "fuel" for natural selection induced by climate change.

IMPLEMENTATION

4.1 Need for joint science plans

Europe and North America share ecologically diverse, temperate, boreal and Mediterranean types of forest ecosystem, and the predicted impacts of and selection pressures imposed by climate change are very similar on the two continents. Many of the tree genera (or families) found in Europe are common to North America, easing the choice for model genera in tree genomics and ecology. It is therefore of mutual benefit to partners on both sides of the Atlantic to collaborate on research into the impacts of climate change on forest species and efforts to mitigate these effects. Added values and expected benefits of joint science plans can be foreseen in various areas:

- Transatlantic cooperative projects will facilitate the exploration of existing large-scale transplantation experiments that have been conducted over many years as provenance tests. Environmental changes associated to these transfers mimic in some cases predicted climate changes and provenance tests would therefore constitute unique experimental settings to monitor evolutionary change at contemporary time scales.
- On both continents, climatic changes occurred recurrently at longer time scales in the past, most notably during the succession of glacial and interglacial periods, and the historical evolutionary trajectories of tree species have been recently reconstructed by combining historical and genetic approaches allowing estimating the pace at which adaptation occurred. The comparison of past trajectories on both continents will facilitate the identification of the most important processes enhancing adaptation.
- Collaborative studies across a wide range of ecological settings in Europe and North America will increase our ability to determine the adaptability of forest ecosystems, providing a larger spectrum of responses that can be studied and reinforcing conclusions that can be drawn.

Joint science plans can be implemented at various levels along a gradient of loose to tight integration and collaboration. Examples of collaboration might include:

- Access to experiments and biological and electronic resources. Separate research projects may be implemented independently by making independent use of resources on both continents.
- Sharing and testing of common research hypotheses in a reciprocal way on both continents.

Implementation of joint research projects should follow the sequence of objectives presented in Section 3 of this document. It is essential that the mechanisms and processes governing adaptation are well understood before any predictions and human measures be explored. High priority should be given to those processes acting at contemporary time scales, such as plasticity or epigenetic responses, rather than to those operating at longer time scales. A substantial body of knowledge can also be derived at a limited cost from existing experimental trials on both sides of the Atlantic. Their value should be thoroughly considered for future cooperative project.

4.2 Experimental infrastructures and resources

Research projects targeting the various areas described above need to be based on solid experimental infrastructures. Many such resources are already in place as a legacy of long international cooperation between forest geneticists. Others need to be constructed in a coordinated way. We briefly review the existing resources and highlight future needs. Infrastructure and resources needed consist of four components: (1) genetic resources and common garden experiments; (2) monitoring and observation sites; (3) integrated databases; and (4) biological resources, such as tissue samples, genomic DNA extracts, cDNA clones and BAC libraries.

4.2.1 Genetic resources and common garden experiments

Genetic resources needed include: natural populations; elite germplasm (with distinct genetic attributes not normally found in wild populations); artificial populations (controlled crosses involving parents that differ for traits of interest, mapping populations, associations populations); and even mutant stocks. Such resources are available for all economically important species in Europe and North America, mostly in the form of long-established plantations (provenance/progeny/clonal test). Some of these resources have been exchanged and reciprocally installed in Europe and North America, offering unique opportunities to observe responses to new environmental conditions. They may need to be completed for ecologically important species. Provenance trials are a very valuable category of resources for climate change research; in these, a set of populations from one species is planted at several sites across the species' natural range and also outside its natural distribution. However, all the existing provenance trials were established in plantations, and hence do not capture the important impact of natural selection operating during seedling establishment. While experimental plantations are needed to evaluate the adaptive potential of populations and to identify genes and traits of adaptive significance, they need to

be complemented by observation sites under natural conditions to track the various sources of evolutionary change. It would be very valuable to establish observation sites along similar ecological gradients (altitude and or latitude) in Europe and North America. Comparative monitoring under natural conditions and in common garden experiments would enable responses due to genetic adaptation and plasticity to be elucidated.

4.2.2 Monitoring and observation sites

Assessing evolutionary changes under natural conditions requires long-term observation sites. In Europe, Intensive Study Sites (ISSs) have been installed by the EVOLTREE network. ISSs are large-scale ecosystem plots covering a few thousand hectares where trees and selected associated species are mapped, genotyped and phenotyped. The sites comprise entire portions of landscapes (agricultural land and forests) where trees are present in various configurations ranging from forest to single tree. ISSs are used to assess evolutionary processes in trees and their associated species through demographic and genetic approaches over different spatial scales, and to monitor interactions between species (trees, other plants, vertebrates, insects and microorganisms). ISSs are also used for experimental purposes and host reciprocal transplantations. In Canada, a new generation of provenance tests was established as experiments for testing assisted migration. The translocation of species into habitable locations outside their current range (assisted migration) is implemented as a means of saving vulnerable species from extinction from climate change. These are the best examples of replicated elevational/latitudinal field trials, with clear hypotheses being addressed, including expectations from meteorological climate-change models. Similar facilities need to be installed in larger numbers in Europe and North America at the northern and southern margins and in the core of forest distributions to allow the rate and extent of evolutionary change to be measured under natural conditions.

4.2.3 Integrated databases

Integration of genetic and genomic data has been pursued independently in Europe and North America. EVOLTREE, funded by the European Union (EU), has generated a very large number of databases containing information on genetic, genomic and ecological characteristics of genes, genome sequences, and natural and experimental plantations, including genetic maps, expressed sequence tags and gene sequences, genetic diversity, genetic markers, provenances, etc. All these distributed electronic resources are integrated into a single information system, eLab (http://www.evoltree.eu/index.php/elab). A centralized search engine allows queries to be made against the whole set of databases. In Canada, attempts are being made to integrate the resources from the two genome projects funded since 2001, while in the USA, Dendrome (dendrome. ucdavis.edu) provides access to a collection of forest tree genome databases and other information. The status of genomics resources was evaluated in 2011 at a FoResTTraC workshop, "Interoperability and Integration of Databases in Europe and North America," but the greatest challenge was identified as integrating phenotypic resources. There is need to compile data from field trials. Data currently exist as spreadsheets built by geneticists with no common format. There is also a strong need to link the genetic data with the ecological, climate and niche-modelling data in order to construct models that integrate ecological and evolutionary processes.

4.2.4 Biological resources

Repository centres with easily accessible biological resources are needed to ensure that samples of valuable genetic resources are made available in a standardized way to the scientific community. Samples may consist of tissue (leaf, pollen, seed) or genomic resources (genomic DNA extracts, cDNA clones and bacterial artificial chromosome [BAC] libraries) of trees that have been scanned for their phenotypes and genomes and that are part of the experimental plantations described above. Concentrating research on reference samples will facilitate the elucidation of the molecular basis of adaptation. Such a centralized facility was installed at the Austrian Institute of Technology, in Vienna, as part of EVOLTREE and serves today as a source of material for genomic and physiological research on traits that have adaptive significance. Additional repository centres may be needed, especially in North America, to facilitate the implementation of a cooperative transatlantic research project.

4.3 Funding schemes 4.3.1 Opportunities in the EU

The European Commission funds research through the Framework Programmes (FPs). The current FP, FP7, will end in 2013, so there is one call remaining that will be opened in July 2012. The Cooperation programme supports all types of research activities carried out by different research bodies in transnational cooperation and aims to gain or consolidate leadership in key scientific and technology areas. The Cooperation programme is divided into 10 themes, of which two concern forestry: Environment, and Food, Agriculture and Fisheries, and Biotechnology. The latter aims at building a European Knowledge Based Bio-economy (KBBE). An annual work programme for each theme is published in July. Projects generally receive between €3 million and €9 million. The

Environment theme has five sub-themes, of which two, "Coping with climate change" and "Sustainable use and management of land and seas," could concern forestry.

Another instrument of the Cooperation programme, the ERA-NET scheme, aims at developing and strengthening the coordination of national and regional research programmes by:

- providing a framework for actors implementing public research programmes to improve coordination through new ERA-NETs or by broadening and deepening existing ERA-NETs and
- providing, in a limited number of cases, additional EU financial support to participants who create a common fund for the purpose of joint calls for proposals among national and regional programmes (ERA-NET PLUS).

Under this scheme, the partners are often science ministries or funding agencies and the majority of the research funding comes from national programmes. ERA-NETs generally organise one or more calls for transnational proposals. One ERA-NET under the KBBE theme (FORESTERRA) addresses forest research in the Mediterranean. In recent years, there have been very few ERA-NETs under the Environment theme.

Also under FP7, the Ideas programme offers a new type of bottom-up funding through the European Research Council (ERC). ERC Synergy Grants under the Ideas programme are intended to enable a small group of principal investigators and their teams to bring together complementary skills, knowledge and resources in new ways, in order to jointly address research problems. The aim is to promote substantial advances in the frontiers of knowledge. These grants provide up to €15 million for up to six years.

The Capacities programme also funds infrastructurebased projects with the key objective of integrating and federating key national research infrastructures at EU level and facilitating access to them from the wider community. Calls are both targeted and bottom up. There would therefore be an opportunity for an infrastructure project based on forest genetic tools, resources and databases.

Beyond 2013, work is now underway to finalize the next Common Strategic Framework, also known as Horizon 2020. This will have a strong emphasis on societal challenges. However, it is too early to know the exact contents of this programme, which will have its first call in 2014.

Each EU member state also has national funding agencies that fund national research projects in a wide variety of scientific domains, including forestry.

4.3.2 Opportunities in Canada *Genome Canada*

Genome Canada (GC) funds research projects in five key areas, of which forestry is one. Funding for large research projects (C\$5million–C\$30 million) is provided by the Government of Canada, conditional on provincial sources providing matching funds. GC requests funding from the government on an annual basis, which limits medium- or long-term strategic planning. Forestry was GC's priority topic in 2010, while human health was the priority in 2011. It is not clear at the moment when forestry will again be the priority theme. For the purpose of this roadmap we can assume that a likely date may be 2015 (on the basis of one key area funded per year). As future research priorities are proposed via white papers, this roadmap should feed into the white-paper process.

However, GC can in the meantime fund the Canadian part of an international collaboration up to a total of C\$5 million (to be confirmed). Therefore an EU or US project with dedicated Canadian work packages or subprojects could be funded by GC.

Natural Resources Canada

The Genomics R&D Initiative (GRDI) was established by the Canadian Government to build and maintain genomics research capacity in government and to deliver valueadded applications for responding to national priorities and government mandates as well as for building wealth for Canadians. It is managed by the National Research Council (NRC). Natural Resources Canada (NRCan) is one of the federal government departments receiving funds from GRDI to support research in forest genomics in Canada. NRCan has supported research in forest genetics for the last 60 years, including provenance/progeny testing, population genetics and phylogeography studies, development of transfer functions and adaptation to climate change. NRCan scientists have also collaborated over the years with scientists of other Canadian and non-Canadian research organizations and such collaboration in important issues related to national priorities will continue to be strongly supported.

4.3.3 Opportunities in the USA *National Science Foundation*

The main source of research funding from the National Science Foundation (NSF) is its Core Programmes, which currently offer funding of US\$1.5 million–US\$2.0 million per project; this amount is expected to increase in coming years. Main opportunities for funding part of the FoResTTRaC roadmap would be under the Research Coordination Networks (RCN) program and the Dimensions of Biodiversity campaign.

The RCN program is a potential source of funds but NSF does not fund non-US collaborators or work so other funding sources would need to be found. The goal of the RCN programme is to advance a field or create new directions in research or education. RCN supports groups of investigators to communicate and coordinate their research, training and educational activities across disciplinary, organizational, geographic and international boundaries. It provides opportunities to foster new collaborations, including international partnerships, and address interdisciplinary topics. Innovative ideas for implementing novel networking strategies, collaborative technologies and development of community standards for data and metadata are especially encouraged. RCN proposals in biological sciences can be submitted at any time unless there is a targeted call for proposals. Funding is in the order of US\$750 000 for a maximum of five years.

The Dimensions of Biodiversity campaign promotes novel, integrated approaches to identifying and understanding the evolutionary and ecological significance of biodiversity amidst the changing environment of the present day and in the geologic past. Research awards are made for up to five years duration and up to a total of US\$2 million for individual or collaborative projects.

National Institute of Food and Agriculture

The National Institute of Food and Agriculture (NIFA) is an agency within the United States Department of Agriculture. NIFA's Agriculture and Food Research Initiative awards grants to address priorities in United States agriculture in six areas, two of which are relevant here: Priority D – Renewable energy, natural resources, and environment; and Priority E – Agriculture systems and technology. Grants have a ceiling of US\$10 million over a term of up to 10 years. NIFA also has a forest programme that aims to expand the knowledge of forest ecosystems, train future forestry professionals and put research-based management practices into action through extension activities.

4.3.4 Foundations

The Gordon and Betty Moore Foundation (USA) funds breakthrough, high-impact science that makes a difference, has enduring impact, has measurable outcomes and contributes to a portfolio effect (i.e., combined funding sources). The Foundation proposes stand-alone grants with the objective "to increase open access to scientific research and data, as well as improve scientific information exchange capabilities. In some cases, projects indirectly support the Foundation's work in environmental conservation through the development of new tools and techniques etc." Grants are in the order of US\$1.5 million – US\$2.5 million. The Foundation usually seeks out interesting research work and then formulates a call for proposal based on their search results.

The Packard Foundation (USA) funds targeted research projects that increase the impact of relevant research on decision-makers. Projects should have specific, measurable outcomes that are achievable over one to three years. They must have an impact in terms of policy-making and decision-making. A letter of interest can be submitted before June for projects to be funded the following year.

4.3.5 Funding schemes: summary

It is clear from the above that no single funding mechanism, body or programme could fund all of the components of a large transatlantic research collaboration in the field of forest ecosystem genomics. Instead, funding should be sought from a variety of sources. It is therefore important that any proposed project is structured in such as way that the various components (work packages, subprojects, etc.) can be funded by the different EU, US and Canadian programmes. However, in order to make this workable it is important that each funding body ensures that:

- the priorities defined within the FoResTTraC roadmap are integrated into the relevant thematic programmes of the different funding agencies;
- these priorities have a clear and, when possible, coordinated time-scale across the various programmes of the funding bodies, in order to make it feasible to roll out collaborative research projects, considering that different parts may be funded by different funding bodies; and
- the evaluation teams of transatlantic projects have representatives (evaluators) from the various funding agencies (e.g., an EU-funded project with a work package led by a US and/or Canadian partner and supported by a US/Canadian funder should include an NSF/Genome Canada representative in the evaluation team).

4.4 Training

Traditional research proposals commonly incorporate training opportunities for graduate students, postdoctoral fellows and, occasionally, undergraduate students. We propose that individual elements of future proposals consider some or all of the following training opportunities when identifying resource requirements and personnel.

Undergraduate training: Work study

Principle investigators are encouraged to consider options for employing students in work-study jobs that provide exposure to fundamental scientific concepts and experimental design. Such positions may last one semester or more, and may contain elements that would be eligible for course credits.

Undergraduate training: Internships

Internships would entail more responsibilities than workstudy assignments, and would ideally last an entire year or more, exposing the student to multiple facets of the study, from project design and implementation to data gathering and analysis.

Graduate students

Each research proposal should strive to provide training opportunities for graduate students, leading to an advanced degree. Graduate students should participate in the design and implementation of experiments and direct other project staff, such as undergraduate trainees.

Postdoctoral fellows

Projects are encouraged to host and train postdoctoral students to spread expertise and best practice, especially where particular laboratories possess expertise not available everywhere.

4.5 Awareness building and outreach

Outside scientific circles, it is not generally known that genetic diversity has a crucial role in ensuring that forest trees can survive, adapt and evolve under changing environmental conditions, or that genetic diversity is also needed to maintain the vitality of forests, allowing them to cope with pests and diseases. It is therefore a priority to enhance public understanding of these issues.

The general public also have concerns about genomics research, particularly in Europe, and this must be addressed. Some concerns derive from a misunderstanding of what genomic research entails, and reflect a disconnection between science, technology, regulatory frameworks and public acceptance. Societal perception is quite different between Europe and North America, and the actions to be implemented within this roadmap must thus be adapted to the different contexts.

Targeted actions should be implemented to reach out to various stakeholders, including scientists from disciplines such as forestry and ecology, experts on plant genetics and genomics, policy-makers, representatives of funding agencies and technology platforms. This will be achieved through public awareness materials adapted to the different target audiences and events such as science fairs, workshops and conferences.

CONCLUSIONS

The FoResTTaC roadmap provides national research agencies and funding bodies with a 10-year research framework that will enable to address the impact of global change on forest ecosystems through investigation of the effects of environmental changes and the adaptive processes in place. The research agenda proposed has the potential to lead to important breakthroughs in predictive ecology and biology by integrating outcomes from experimental and theoretical approaches.

During the last decade, evolutionary trajectories of tree species as a response to natural warming have been elucidated by linking genetic and historical approaches. This was a major achievement, and has placed tree species at the centre as model organisms, ideal for investigating evolutionary biology during the Holocene period.

This roadmap builds on these past achievements and provides a framework for exploring the range of evolutionary mechanisms that will be acting under future climate change, including those that will become progressively easier to investigate by means of the most recent technologies offered by genomics. This roadmap offers also a stepping stone for bridging research in genetics and genomics with ecology and ecophysiology, providing data for innovative predictive models of tree responses to climate change.

The global challenges raised by climate change demand that cooperative research efforts be strengthened during the next decade to secure the maintenance of ecosystem services provided by forests to human societies. Thus, the FoResTTaC roadmap prepares for future coordinated research plans between Europe and North America by linking the work already carried out in Europe, the United States and Canada, and proposing future integrating approaches. The added value of international cooperation lies in comparative analysis across similar ecological conditions. This will allow us to determine whether similar adaptive responses are to be expected under similar ecologies, or if variable outcomes are foreseen.

Together with scientific achievements, the research framework promoted by this roadmap will provide avenues for important practical applications in operational forestry, setting important objectives addressing management and regeneration of forest stands to cope with climate change. This roadmap indeed suggests exploring how adaptive mechanisms can be enhanced by silvicultural practices if inherent adaptive capacities are insufficient.

The roadmap encourages the establishment of additional experimental infrastructure and genomic resources, along the lines of what the community of forest geneticists has achieved through long-standing international cooperation, as illustrated by the common garden experiments installed through shared efforts in the past. However, the synergies in the existing diverse funding mechanisms operating in Europe and North America, necessary to support transatlantic research efforts, are difficult to achieve due to the particular structure, selection criteria and timetable followed by each funding body.

This roadmap also emphasises the need of bettertailored training activities to match the international, multidisciplinary structure of research collaborations. Finally, the importance of outreach and awareness-raising is highlighted.

The preparation of the FoResTTraC roadmap was sponsored by the European Commission, within the 7th Framework Programme for Research and Innovation, through the Coordination and Support Action, titled "Forest ecosystem genomics Research: supporTing Transatlantic Cooperation". This roadmap was prepared by experts from Europe and North America and presents a strategic framework for future coordinated transatlantic research plans, aimed at enhancing understanding of adaptation of forest trees to climate change, a priority for research in both contents. Trees are the foundation species of numerous terrestrial ecosystems and as such are key drivers of ecosystem processes and stability.

FORESTTRAC

The FORESTTRAC project is financially supported by the European Commission under the 7th Framework Programme

www.foresttrac.eu

