



**HAL**  
open science

## Climate change and forest genetic resources – State of knowledge, risks and opportunities

Judy Loo, Bruno Fady, Ian Dawson, Barbara Vinceti, Giulia Baldinelli

### ► To cite this version:

Judy Loo, Bruno Fady, Ian Dawson, Barbara Vinceti, Giulia Baldinelli. Climate change and forest genetic resources – State of knowledge, risks and opportunities. [Technical Report] Background study paper n.56, 2011. hal-02808387

**HAL Id: hal-02808387**

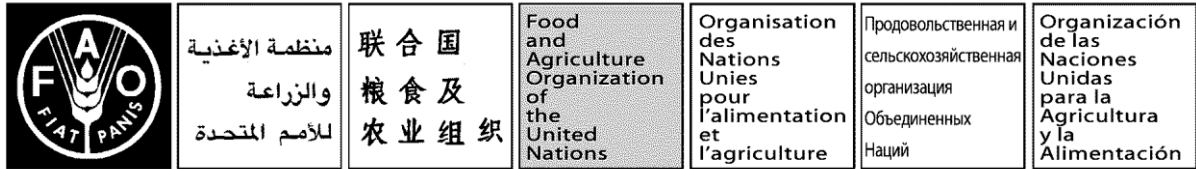
**<https://hal.inrae.fr/hal-02808387v1>**

Submitted on 6 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

July 2011



**COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE**

**CLIMATE CHANGE AND FOREST GENETIC RESOURCES -  
STATE OF KNOWLEDGE, RISKS AND OPPORTUNITIES**

by

Judy Loo<sup>1</sup>, Bruno Fady<sup>2</sup>, Ian Dawson<sup>3</sup>, Barbara Vinceti<sup>1</sup> and Giulia Baldinelli<sup>1</sup>

Prepared for the Thirteenth Regular Session of the Commission on Genetic Resources for Food and Agriculture, 18-22 July 2011, FAO Headquarters, Rome.

This paper is one of several requested by the Commission on Genetic Resources for Food and Agriculture that seek to review and examine the impacts of climate change on genetic resources of organisms that are important for human well-being, and the potential role of these resources in mitigating and adapting to change. This paper, which focuses on forest genetic resources (FGR), does so in the context of trees in natural forests, plantations and agroforestry systems. The paper is structured to match those being prepared by the other sectors and consists of a review of the current state of knowledge, followed by the identification of gaps and priorities for action. A glossary is included to clarify terms.

**The content of this document is entirely the responsibility of the authors, and does not necessarily represent the views of the FAO or its Members.**

<sup>1</sup> Bioversity International, Rome, Italy.

<sup>2</sup> INRA Avignon, France.

<sup>3</sup> World Agroforestry Centre (ICRAF), Nairobi, Kenya.



---

**TABLE OF CONTENTS**


---

	<i>Page</i>
Abstract	1
I. Introduction: forest genetic resources, adaptation and climate change	1
1.1 The impact of climate change on FGR	2
1.2 Adaptation needs at the ecosystem level	3
1.3 The potential role of FGR in responding to climate change	3
1.4 Potential role of FGR to mitigate climate change	7
II. Challenges and opportunities posed by climate change to the use of forest genetic resources	7
2.1 How is climate change expected to affect the FGR?	7
2.2 Specific genetic characteristics/traits needed for adaptation to the challenges identified	8
III. The potential role of forest genetic resources in adapting to and mitigating climate change	9
3.1 Analysis of the present use of FGR: are any of the characteristics needed already in use/available?	9
3.2 Gaps: knowledge, collections, characterization	9
3.3 Efforts needed to identify characteristics relevant to adaptation to climate change	10
IV. Conclusions	11
5.1 Access and use conditions (policies)	11
Literature Cited	14
Annex 1: Example of national guidelines for management of forest genetic resources under climate change from France's Commission on Forest Genetic Resources	22
Box 1. Matching genetic variation with new climate in the Sahel: smallholders' agroforestry and the SAFRUIT project	
Box 2. Plasticity and the use of climate envelope models: the importance of field trials for "ground-truthing"	
Box 3. Changes in seed transfer guidelines in response to climate change: the case of Canada	
Box 4. Glossary	
Table 1. Knowledge gaps and priorities for action for FGR	



## ABSTRACT

In regions where climate change is expected to be extensive and rapid, many tree species are predicted to experience severe stress in their native ranges. Survival will then depend on the capacity to undertake at least one of the following: (1) quickly adapt genetically to new conditions at existing sites; (2) survive changing conditions through a high degree of phenotypic plasticity without genetic change; and/or (3) migrate rapidly to newly evolving environments that match basic physiological requirements. This paper considers forest genetic resources in the different settings where people depend on products and services from trees for a wide variety of purposes, including naturally regenerating forests, commercial plantations, and trees on farms (including planted trees and wild remnants left standing for various functions). The expected impacts of climate change – and hence strategies for responding to it – differ among these environments. Assisted migration and artificial selection for appropriate traits are approaches that can be applied to planted trees, whether in commercial plantations or farms, but are less appropriate for natural forests. However, management actions are confronted with serious challenges, including national and international policies that limit the movement of genetic resources among countries, and long regeneration cycles that make tree breeding time-consuming and costly. Adapting to climate change poses a greater problem for naturally regenerating populations where the potential for natural migration is hindered by forest fragmentation and agricultural expansion, and when confounding factors for adaptation include pests and diseases, reduced population sizes, and simplified forest structures and species compositions. Lack of information on the following hinders our ability to manage climate change impacts better: (1) little is known about the sequences and functions of the genes conferring adaptation; (2) the genetic and epigenetic basis of phenotypic plasticity and its role in producing responses to environmental alterations is unclear; (3) the basic life-history characteristics, ecological determinants and geographic distributions of many trees are not well studied; and (4) meaningful syntheses of such information into predictive models of change and response are poorly developed.

## I. INTRODUCTION: FOREST GENETIC RESOURCES, ADAPTATION AND CLIMATE CHANGE

While in the crop sector genetic improvement programmes use advanced technologies and have proceeded through many breeding cycles, in forestry there is heavy reliance on undomesticated resources. In only a few cases (mostly eucalypts, poplars, and pines and other temperate conifers) have public or private sector breeding programmes advanced beyond the third generation. In the cases where genetic improvement is taking place, a clear “use value” can be ascribed to FGR (often related to traits such as increased yield, increased stem straightness, increased lignin content or resistance to a particular pest or disease), but in other cases resources primarily present an “option value”.

Different ways of estimating the value of genetic resources are available (Sarr *et al.*, 2008), but few have been applied to FGR (although see Bosselmann *et al.*, 2008; Hein and Gatzweiler, 2006). The economic valuation of biodiversity and ecosystem services is particularly challenging to undertake (e.g. Salles, 2010), and this is especially so for often uncharacterized FGR (Elsasser, 2005). Thorsen and Kjaer (2007) suggested that meaningful valuation in the context of climate change should extend beyond traditional measures such as wood production to include indicators related to societal use and ecosystem function.

In this paper, we do not attempt to provide an economic valuation of impacts in terms of the products and services of FGR under climate change, but judging by losses already experienced by the forest industry in British Columbia, Canada, for example, these will be significant. We indicate that the current portfolio of FGR used in breeding programmes, on farms and in conservation units should be increased. In the absence of appropriate mitigation and adaptation measures, there is a significant danger that climate change – together with other inter-related challenges such as high human population growth, fuel scarcity, deforestation, soil degradation and biodiversity loss – may result in catastrophic impacts in many regions of the globe.

## 1.1 The impact of climate change on FGR

Predictions regarding impacts on FGR in natural forests, forest plantations and on farms vary. Although some authors (e.g. Hamrick, 2004) consider that many trees have sufficient phenotypic plasticity<sup>4</sup> and genetic diversity at the population level (bolstered by high gene flow among natural stands) to significantly reduce the negative effects of climate change, others have taken a different viewpoint and predicted severe impacts (e.g. Mátyás 2007; Rehfeldt *et al.*, 2001). Different positions relate partly to the types of species and environments being considered. Authors who make the more pessimistic forecasts often base their views on tropical trees (Dawson *et al.*, 2011) or on marginal populations of temperate species (Mátyás *et al.*, 2009), while more optimistic authors often consider temperate and boreal taxa (Lindner *et al.*, 2010).

Climate change impacts are expected to be severe in dry, high-temperature regions where trees are at their adaptive limit (e.g. Lindner *et al.*, 2010 for Europe) and in confined islands of moist forest that are surrounded by drier land (e.g. moist forests in Australia; Williams *et al.*, 2003). Whereas the ranges of some tree species are expected to expand, others will diminish. In temperate regions, range reduction at the receding edge of distributions (low elevation and low latitude) is expected to be more rapid and of greater magnitude than expansion at the leading edge (high elevation and high latitude) because of a number of factors that limit the ability of tree species to migrate across landscapes. Thuiller *et al.* (2006) have also shown that tree species richness and functional diversity will be impacted more at low than at high latitudes in Europe. In other regions such as the tropics, changes in precipitation rather than temperature may be of key importance (Dawson *et al.*, 2011).

Based on the data available to date, expected impacts of climate change on FGR will be experienced through several demographic, physiological and genetic processes, which may include the following:

- High mortality due to extreme climatic events, in combination with regeneration failure, will result in local population extinction and the loss of FGR. This will be the case particularly at the receding edge of distributions.
- Under changing climatic conditions, pest and disease attack may become more severe in some regions, because of improved environmental conditions for the attackers and because trees experience more stress and are therefore more susceptible.
- The fecundity of trees will change due to sensitivity to spring temperatures (e.g. as observed in the southeastern United States of America; Clark *et al.*, 2011) and other factors (Restoux, 2009). For example, in central Spain, a decline in cone production in *Pinus pinea* over the last 40 years has been correlated with warming, especially with hotter summers (Mutke *et al.*, 2005).
- Changes in climate may result in asynchronous timing between the development of tree flowers and the availability of associated pollinators, leading to low seed production for outbreeding species dependent on animal vectors. Absolute population levels of some pollinators are also likely to be reduced. Many tropical tree species that are pollinated by insects, birds or bats may be affected; in some cases, functional use would be severely affected.
- Increased fire frequency may eliminate fire-sensitive species altogether from woodlands and parklands. In regions that have not regularly experienced wild fires in the past, fire may become the main driver of change, with a rapid transition from fire-sensitive to fire-resistant species.
- Changing climates will result in new species invasions, altered patterns of gene flow and the hybridization of species and populations. Shifting ecological niches will increase the risk of invasion by more competitive tree species that are more precocious or can move more quickly. Invasions of new genes via pollen and seed dispersal may disrupt local evolutionary processes, but could also be a welcome source of new adaptive traits (Hoffmann and Sgro, 2011).

---

<sup>4</sup> A glossary of this and other terms used in this paper are given in Box 4.

## 1.2 Adaptation needs at the ecosystem level

At the ecosystem level, adaptation to climate change requires maintaining options at the species and intra-species levels. Species diversity is a form of insurance that should increase the resilience of natural forests and planted tree stands in the face of environmental variability if the various species present respond differently to disturbances (Kindt *et al.*, 2006). As climate changes, less well-performing species may be replaced through a process of natural selection and competition by other trees that are already present within systems and that are better-suited to new conditions, such that the relative abundance of different species in the landscape alters, although it is not desirable if one taxon alone comes to dominate (see above discussion of species invasions).

At intraspecific level, maintaining genetic diversity within and among tree populations can similarly increase the stability of ecosystems (Whitham *et al.*, 2006; Thorsen and Kjør, 2007), especially when trees are keystone or foundational species. For example, the genetic variation of keystone species has in some cases been correlated with the interspecific diversity of their associated communities (Barbour *et al.*, 2009). In addition, intraspecific diversity promotes the resilience and productivity of individual species. For instance, modelling has shown that optimum production can be attained in plantations by “composite provenancing” and/or by mixing different genotypes from within species (Bosselmann *et al.*, 2008; Hubert and Cottrell, 2007).

Genetic adaptation is a process of shifting fitness trait values over generations to track environmental change and ensure better survival. The speed of adaptive responses at the population level depends on the amount of additive genetic variation in a stand and the heritability of important traits, in combination with the size of the selection pool, the intensity of the selection pressure and generation length. Many tree species are known or believed to have high genetic variability in adaptively important traits and have high fecundity, creating a large selection pool (Petit and Hampe, 2006). Thus, if environmental change is directional and continuous, many tree species have the potential to undergo relatively rapid evolution (Hamrick, 2004). However, the magnitude and speed of climate change are often predicted to surpass the capacity of tree populations to adapt, at least at the receding edge of species distributions where local extirpation may therefore occur (Davis and Shaw, 2001).

Climate change may also be experienced as increased variability in temperature and precipitation, with an associated elevated incidence of extreme events (e.g. drought followed by flooding; IPCC, 2007). The threat posed by increasing storm frequency due to climate change in the Pacific has led to efforts to identify cyclone-resistance species, such as *Endospermum medullosum* (whitewood), for large-scale planting. In Vanuatu, for example, establishment of 20 000 hectares of plantations of the species is planned over the next 20 years, with a resultant high demand for germplasm. Natural selection may, however, not efficiently mediate adaptation in situations of increased weather variability, because at least in the short-term, the selection pressure is not directional and the required traits may be inversely correlated at the gene level (Jump and Penuelas, 2005; although some features for adaptation to, for example, drought, such as deep root systems, should also contribute to tolerance to, for example, flooding).

## 1.3 The potential role of FGR in responding to climate change

*Standing genetic variability.* This comprises the potential of populations to adapt and depends on population size and the amount of diversity expressed in traits that will influence survival and reproduction under new conditions. Many tree species that have been studied have high genetic variability and can grow under a range of conditions (Gutschick and BassiriRad, 2003; Petit and Hampe, 2006). Phenotypic traits of adaptive importance such as drought tolerance, cold-hardiness and flowering and fruiting phenology have been shown to vary within some species across ecological and geographic gradients to an extent that may be as important as the differences often observed among species (Aitken *et al.*, 2008). Similarly, recent molecular-level studies have demonstrated allelic shifts in genes related to drought and heat tolerance among populations; conversely, however, genetic variability within populations can sometimes be low (Jump *et al.*, 2006; Grivet *et al.*, 2011; Hoffmann and Sgro, 2011). Management plans can influence the genetic composition and structure of naturally



regenerating forests, providing opportunities for silvicultural interventions in order to respond to change (Guariguata *et al.*, 2008; Sagnard *et al.*, 2011).

Common garden experiments have been central in demonstrating the extent and distribution of the genetic diversity of fitness-related traits, such as survival, growth, phenology, and adaptation to cold, drought, pests and diseases, in tree species. Most such experiments have been conducted on boreal, temperate or a few commercially important tropical species. Recently there has been a move to include a wider range of indigenous species important to local people (Box 1). Not only is genetic diversity in important adaptive traits expressed across regions and provenances, but it can sometimes be abundant within populations, reinforcing an optimistic view that climate change challenges may be met by standing genetic variation in such species (Hoffmann and Sgro, 2011). An example of the contrast between species is provided by *Pinus halepensis* and *Pinus brutia*, two closely related pines with extensive distributions around the Mediterranean; the amount of among-provenance variation for survival under diverse climatic conditions is greater in the former, encompassing and extending that found in the latter (Bariteau and Pommery, 1992).

**Box 1. Matching genetic variation with new climate in the Sahel: smallholders' agroforestry and the SAFRUIT project**

The current understanding of population-level environmental responses in indigenous tree species planted by small-scale farmers in Africa is limited. New trials have, however, been established to consider climate change effects. Under the Sahelian Fruit Tree project (SAFRUIT, see [www.safruit.org](http://www.safruit.org)), for example, trials on drought stress for important trees for smallholders, such as *Adansonia digitata* (baobab) and *Parkia biglobosa* (African locust bean), are being conducted in the semi-arid West African Sahel, a region that has become drier over the last decades (Jensen *et al.*, 2011). In nursery experiments, populations collected from locations with different rainfall levels have been exposed to a range of watering regimes (Sanou *et al.*, 2007). Characters being measured include photosynthesis, water use efficiency, water potential and chlorophyll fluorescence. The information obtained on the effects of different treatments on root development, seedling vigour and other important adaptive characteristics will inform subsequent germplasm distribution strategies.

In some cases, climate change considerations for seed distribution are already being taken into account in the region. One example is provided by *Prosopis africana*, used for wood production; based on field trials measuring growth, survival and wood density in relation to rainfall patterns across seed collection sites, Weber *et al.* (2008) recommended that germplasm transfers of the species should only be undertaken in a single direction, from drier to (currently) wetter zones. A similar strategy was adopted for a recent International Fund for Agricultural Development agroforestry project in the same region. Different global circulation models used to explain environmental changes in temperature and precipitation profiles vary in future predictions of rainfall in the Sahel, with some indicating drier (e.g. Held *et al.*, 2005) and some wetter (e.g. Shanahan *et al.*, 2009) conditions. Given current uncertainties in projections, an emphasis in the region on matching seed sources to the more limiting scenario of a drier future climate would appear to be the most risk-averse option.

*Phenotypic plasticity.* Plastic tree species and/or provenances are those with flexible morphology and physiology that grow at least reasonably well under a range of different environmental stresses without genetic change (Gienapp *et al.*, 2008). At least in the short term, this characteristic is likely to be more important than genetic adaptation in ensuring persistence in highly variable environments; plastic trees do not need to genetically adapt, but can instead modify their phenotype in response to new conditions. Processes related to phenotypic plasticity may thus oppose those related to genetic adaptation, in that the selection pressure is reduced if plasticity is high, although a heritable basis for plasticity means that there will be selection for genotypes with more flexible responses as the environment becomes more variable. If phenotypic plasticity supports the persistence of trees it may be a particularly desirable trait because of the time taken for trees to mature and reproduce (they need to survive for several years in order to set seed and thereby perpetuate).

A degree of phenotypic plasticity is found in most trees (Piersma and Drent, 2003; Rehfeldt *et al.*, 2001), but varies among and within species (Aitken *et al.*, 2008; Bouvarel, 1960; Skroppa and

Kohmann, 1997). It is likely to be more important in species that contain limited genetic diversity for adaptation (Le Corre and Kremer, 2003). Examples of species with little genetic variation include the rare conifer *Picea omorika* found in Central Europe (Nasri *et al.*, 2008) and *Pinus pinea* found around the Mediterranean (Vendramin *et al.*, 2008); *P. pinea* has in fact been shown to display strong phenotypic plasticity for growth-related traits (Mutke *et al.*, 2010). Selecting “generalist” species and populations using multi-locational field trials and environmental data may be an important strategy with which to respond to climate change, especially for regions where greater variation in weather conditions is anticipated. Sometimes, trials reveal that trees can have more plastic responses than would be expected based on existing geographic distributions (Box 2).

The mechanisms underlying phenotypic plasticity remain poorly understood, but epigenetic effects, where heritable changes in phenotype are the result of the modification of DNA expression but not sequence, for example through methylation to down-regulate gene activity, may be important (Hedhly *et al.*, 2008). Epigenetic effects can be inherited across several generations and be variable across populations and individuals (Bossdorf *et al.*, 2008). According to Aitken *et al.* (2008), it is possible that the epigenome provides a buffer against climatic variability that provides time for the genome to “catch up” with change. Epigenetic effects have been demonstrated in the phenology of bud set in *Picea abies*, where progenies whose embryos develop in warm environments are less cold hardy than those that develop under cold conditions (Johnsen *et al.*, 2005).

**Box 2. Plasticity and the use of climate envelope models: the importance of field trials for “ground-truthing”**

Climate envelope models, which operate on the basis that a species is optimally adapted to the habitat conditions of its current range, are frequently used to predict the impacts of climate change. As demonstrated by van Zonneveld *et al.* (2009), however, they can lead to false assumptions for a number of reasons, including inattention to the degree of phenotypic plasticity exhibited by many species, and the absence of taxa from sites with optimal abiotic conditions due to factors such as competition, barriers to migration and large-scale historical disturbances.

The best way to test the accuracy of climate envelope model predictions is through field trials. Ideally, these should include many seed sources from the entire species range and be planted on a range of sites including some outside the native distribution. Thanks to trials set up by the Central America and Mexico Coniferous Resources Cooperative (CAMCORE) over the past two decades, data from such trials were available to van Zonneveld *et al.* (2009) who found that two Central American pine species, *Pinus tecunumanii* and *P. patula* (both important globally for plantation forestry), performed well outside the ecological space defined by the climate envelopes of current distributions. Both species can thus be expected to perform better under climate change than otherwise anticipated. Unfortunately, such data do not exist for the majority of tree species and many more such field trials are needed to produce accurate predictions.

*Gene flow: migration by pollen and seed.* Gene flow among populations via pollen contributes to genetic variability within populations and hence to adaptive potential (Le Corre and Kremer, 2003). For trees, it is known that pollen travels very long distances, particularly in wind-dispersed social broadleaves and conifers, but also sometimes for animal pollinated species (Jha and Dick, 2010; Kramer *et al.*, 2008; Liepelt *et al.*, 2002; Oddou-Muratorio *et al.*, 2005; Ward *et al.*, 2005). Palaeoecological reconstructions of the recolonization of temperate zones in the Holocene have indicated that seeds were also capable of travelling long distances rapidly (Brewer *et al.*, 2002; Nathan *et al.*, 2002), but these high rates have recently been challenged by new research approaches (e.g. landscape genetics methods), which indicate slower migration (McLachlan *et al.*, 2005).

For natural forests in temperate regions, it has been estimated that migration rates of more than 1 km per year may be needed for trees to overcome physiological mismatching and keep pace with current climate change, a rate around ten-fold greater than that observed in the past after glacial maxima (Pearson, 2006; data from pollen core studies and molecular marker analysis, see e.g. McLachlan *et al.*, 2005; Olago, 2001; Pearson, 2006; Petit *et al.*, 2008). In tropical regions, changes in precipitation may be the key factor to which species have to respond, as evidenced by molecular marker research that indicates dryness as a particular barrier to genetic exchange (e.g. see Muchugi *et al.*, 2006, 2008).

for discussion of the case of the dry East African Rift Valley limiting past migrations). As with temperate regions, natural migration rates in the tropics will not keep up with anthropogenic climate change except in the case of a small range of invasives that can respond very quickly to change because they are highly precocious, seed are dispersed over exceptionally long distances, and/or trees are very quick to reach maturity (Malcolm *et al.*, 2002).

Rates of possible natural migration are reduced by forest degradation and deforestation, increasing vulnerability (Malcolm *et al.*, 2002; Kellomäki *et al.*, 2001). However, in some cases pollen-mediated gene flow can be enhanced by fragmentation (Ward *et al.*, 2005) and trees planted in corridors and as stepping stones in farmland may provide opportunities for “reconnecting” forest patches, allowing forest ecosystems to respond better to environmental change (Bhagwat *et al.*, 2008; Thuiller *et al.*, 2008).

Due to barriers to migration, the response of trees in natural forests to climate change must generally involve adaptation and/or plasticity, at least in the short term. On the other hand, planted trees are amenable to the “facilitated translocation” of germplasm, which involves human movement of tree seed and seedlings, from existing ranges to sites expected to experience analogous environmental conditions in future years (Guariguata *et al.*, 2008; McLachlan *et al.*, 2007). A fundamental presumption is that the global circulation models used to explain the environmental changes in temperature and rainfall profiles that result from anthropogenic climate change can be used to predict change with some certainty at given locations; such predictions are, however, not always reliable or precise (Christensen *et al.*, 2007).

Although the assisted migration of suitably adapted germplasm sources is recognized as an important response to climate change, the approach has not yet been widely implemented through policy recommendations or practice. For example, in France as in most other nations, local germplasm sourcing is often still recommended on the basis that a certain level of local adaptation can be expected (but see Annex 2), even though in a few decades from now the locations of suitable planting zones may have changed significantly. An exception from Canada is given in Box 3.

### **Box 3. Changes in seed transfer guidelines in response to climate change: the case of Canada**

British Columbia, Canada’s most westerly province, has a relatively long history of regulating tree seed movement (Ying and Yanchuk, 2006), but the current concept of “floating” seed zones was not adopted until the mid 1980s. Provenance trials were established for commercially important tree species and concurrently a hierarchical ecological classification of the province’s forest land was completed on the basis of geography, climate and vegetation. The boundary of a seed zone is essentially an overlay of adaptive genetic variation onto the ecological classification of forest lands (Ying and Yanchuk, 2006). A seed zone “floats” in the sense that seedlings may be planted outside of the boundary as long as they are within a zone of adaptation based on a statistical predictive model that establishes geographic patterns of local optimality.

Increasing concern about the effects of climate change has led to a new approach in the province. Potential impacts of change were assessed using an ecosystem-based climate envelope modelling method (Hamann and Wang, 2006) and realized niche space was modelled for tree species under current and predicted future climates. The results of analyses were startling in predicting among other effects that tree species that have their northern range limit in British Columbia could gain new suitable habitat at a rate of at least 100 km per decade.

On the basis of this and similar work (Wang *et al.*, 2006), seed transfer policies in the province were re-examined and British Columbia now claims to be the first jurisdiction to have modified seed transfer standards specifically in response to climate change. The modest modification allows seed of most species in most areas to be moved 100 to 200 m further upwards in elevation (British Columbia Ministry of Forests, Lands and Natural Resource Operations, 2008). This policy change constitutes an implicit recognition and acceptance of the need for assisted migration to ensure that plantations in the province will be adapted to future climates.

If assisted migration is to be widely adopted as a response strategy, it will require moving increased quantities of germplasm across national boundaries for both research and planting purposes. A recent

study, however, indicated that the international transfer of tree germplasm for research purposes has become increasingly difficult and costly in recent years as nations seek to conform to their commitments under the Convention on Biological Diversity; new approaches to facilitate exchange are therefore required (Koskela *et al.*, 2009). At the same time, however, the indiscriminate movement of poorly adapted germplasm, which may be encouraged inadvertently by some regional policies designed to promote free trade in tree seed, is not advisable. In addition, during exchange it is also important to take into account the invasiveness potential of new introductions, which may be enhanced by altering environments (McLachlan *et al.*, 2007; Peterson *et al.*, 2008).

#### **1.4 Potential role of FGR to mitigate climate change**

The role of natural forests and tree planting in mitigating climate change through carbon sequestration is well recognized (see e.g. the UN-REDD program: <http://new.un-redd.org/Home/tabid/565/Default.aspx>). The importance of genetic variation within species for maintaining forests and ensuring productivity in cultivated trees is less often considered. However, as is evident from the discussion above, only adapted and adaptable genetic material will efficiently mitigate, and continue to be able to mitigate, global carbon emissions. For example, mitigation by planted trees will not be successful if poorly adapted seedlings are used; appropriate sourcing of genetic resources is needed with proper site matching. In the case of smallholder plantings in agroforestry systems, trees will only be established if they provide clear livelihood opportunities for local people (Lengkeek and Carsan, 2004). Since the current payment mechanisms to reward farmers for the carbon sequestration functions of agroforestry trees are generally inefficient in reaching growers and modest in value (Jack *et al.*, 2008), the main reason for farmers to plant trees will continue to be for the other products and services that they provide, which depend on quality and yield determined by genetic factors (Roshetko *et al.*, 2007).

There are numerous examples in commercial forestry where poorly-adapted genetic resources have been introduced that have led to massive failures in production. For example, 30 000 ha of *Pinus pinaster* plantations were destroyed by frost in the Landes region of France in the years 1984-5 following the introduction of non frost-resistant material from the Iberian Peninsula (Timbal *et al.*, 2005). The importance of choosing the right genetic resources for climate change mitigation is thus no different from choosing the right genetic material when undertaking assisted migration: germplasm must be appropriately adapted for growing conditions, with some prediction (see above) of how these conditions will change over the productive cycle of the species.

## **II. CHALLENGES AND OPPORTUNITIES POSED BY CLIMATE CHANGE TO THE USE OF FOREST GENETIC RESOURCES**

### **2.1 How is climate change expected to affect the FGR?**

Most tree species will not be able to migrate naturally at a sufficient rate to keep pace with a rapidly changing climate, resulting in elevated mortality rates (Malcolm *et al.*, 2002; Davis *et al.*, 2005; Nathan *et al.*, 2011). High mortality reduces the size of the available gene pool, may increase inbreeding among survivors, and deprives people of the products and services that an intact forest provides. High mortality will be particularly felt in marginal populations at the receding edges of distributions or in localized populations in specific, threatened environments. Tree species that have a mixed mating system (self-fertilization is possible as well as outcrossing) may be somewhat better equipped against environmental changes because inbreeding depression caused by reduced census numbers may not be as severe. The species composition of natural forest will shift with changing climate. In some cases, high-value, less common species will be replaced by “invasive” trees (Malcolm *et al.*, 2002). In these cases, the erosion of genetic resources in high-value species will likely be accelerated by competition for habitat by the invasive taxa. The modification of species composition in mixed stand forests will require changes in silvicultural practice for productive forests (Guariguata *et al.*, 2008).

In plantation forestry, the impact of climate-change mediated insect epidemics can already be observed in western Canada where the mountain pine beetle (*Dendroctonus ponderosae*) has devastated the forest industry throughout much of the interior of the province of British Columbia (Konkin and Hopkins, 2009). The beetle is now attacking more than 13 million hectares of forest in the province. The sustained outbreak is blamed on a long series of unusually warm winters. In addition to the loss of hundreds of thousands of hectares of plantation (and natural) forest, many genetic trials that constituted important sources of genetic information and, in some cases, live genebanks, have been destroyed by the insect. Much of the natural forest will regenerate without the substantial loss of genetic resources, but the destruction of the genetic tests represents an irretrievable loss (although any trees alive in trials after beetle attack may provide a “genetic screen” that points to resistant genotypes).

The interdependence among countries in their needs for tree germplasm is likely to increase because of demands for restoration planting, plantation and agroforestry use; new species and better-adapted varieties will be required. Countries with large-scale plantations of species such as *Pinus radiata* and *Pseudotsuga menziesii* that have been widely planted across (warming) temperate zones of the world, may be particularly affected if such species have low resilience to environmental change because of the material chosen for planting. Breeding programmes will need to consider plasticity and adaptation to increased drought, a substantial change from current practice. In theory, pest and disease attacks caused by climate change could also be addressed through breeding for resistance or tolerance, but Yanchuk and Allard (2009) have suggested that the time required to do so may be too long in relation to the rapid rate of change. Instead, the use of tolerant genotypes already found in nature, or of entirely new species, may be required.

## 2.2 Specific genetic characteristics/traits needed for adaptation to the challenges identified

A number of climate-related traits in some conifers, such as the timing of bud break in spring, leader shoot growth cessation in summer, bud set in autumn and annual ring lignification, are regulated by temperature during female reproduction; temperature-induced regulation of the level of gene expression (through methylation) in the developing embryos is apparently maintained in the developing trees as an “epigenetic memory”. Many such epigenetic responses have been documented in plants exposed to environmental stresses (Madlung and Comai, 2004), but the mechanisms involved are not fully understood.

Under changing environmental conditions, trees must first survive and then reproduce. To be useful to humans, they must also continue to produce the products and services for which they are valued. Some important traits needed for adaptation to different climatic conditions, but which are not often considered in breeding programmes include the following:

- *Drought resistance*: This is a complex trait that may include deep rooting systems, water use efficiency and deciduous habit. For many tree species, altered moisture regimes will be of greater concern than temperature changes.
- *Pest resistance*: Pest and disease resistance has received little attention in tree breeding. Climate-change mediated increases in pest and disease attacks are becoming a crucial issue in plantation forestry (see above). Conventional breeding approaches are inadequate as a response (Yanchuk and Allard, 2009).
- *Fire resistance/tolerance*: Increased fire frequency results from decreased precipitation and elevated temperatures combined with human activities such as forest clearance (Malhi *et al.*, 2009). Many tree species growing in semi-arid regions have developed mechanisms to confer a degree of resistance to periodic fires, but this may not be the case in more humid forest. Increased fire frequency will require adaptations such as thicker bark.
- *Cyclone resistance/salt tolerance*: The combined effects of a rising sea level and increased storm frequency have the potential to wreak heavy damage on coastal forests. Low-elevation islands are at particular risk. A differential ability to withstand storms and salt may be found more commonly among species than within, but the possibility of selection for suitable types within species needs to be explored.

- *Phenotypic plasticity*: As already discussed, this is an important but little understood characteristic that is vital for an adaptive response to changing climate and can vary at intraspecific level.

### III. THE POTENTIAL ROLE OF FOREST GENETIC RESOURCES IN ADAPTING TO AND MITIGATING CLIMATE CHANGE

#### 3.1 Analysis of the present use of FGR: are any of the characteristics needed already in use/available?

The very fact that tree species contain high genetic diversity in many of the traits and genes analysed provides an insurance policy or “option value” against future environmental change (Jump *et al.*, 2008). This option value provides “high evolvability” that supports the persistence of natural forest stands that provide useful products (fuel, food, timber, medicine, etc.) and environmental services (biodiversity conservation, watershed protection, carbon sequestration, etc.) to humans. The same variation supports breeding programmes and allows the selection of appropriate genotypes for planting to adapt to and mitigate climate change.

Provenance trials that have been established at multiple locations using germplasm sourced from a variety of ecological conditions demonstrate that variation in adaptive traits is often present within tree species. However, many provenance trials were established before the need to respond to anthropogenic environmental change was considered to be an important research issue, and so the traits measured in trials have often not been the most important ones from a climate change perspective. Nevertheless, the performance of provenances in old multilocational trials provide an insight into behaviour under climate change scenarios and allow sources of (likely) adapted material to be identified while new trials specifically established to assess climate change responses are being established (see Box 1).

There has, however, been a general decline in the establishment of provenance trials in recent years for a variety of reasons, including increased difficulty in international germplasm transfer (see above; Koskela *et al.*, 2009), their cost to maintain and measure, greater emphasis on social issues in the forestry sector and more attention to new technologies such as molecular marker analysis of genetic variation. While the latter can provide particular insights, for example in the new discipline of “climate change genomics” (Neale and Ingvarsson, 2008; Reusch and Wood, 2007), molecular analysis should be seen as complementary to field trial analysis and not as an alternative to it. Genomic studies are beginning to focus on the search for candidate genes that may be important in drought tolerance (Hoffmann and Willi, 2008). Association genetic studies in natural stands, where allelic patterns at candidate genes are correlated to phenotypic traits and ecological conditions, are also becoming more common in trees, making it possible to identify genes and variation linked to adaptation (Grivet *et al.*, 2011).

#### 3.2 Gaps: knowledge, collections, characterization

As noted above, there is little documented knowledge about adaptive traits or life history characteristics of the majority of tree species globally, particularly in the tropics where species diversity is very high. Although many boreal and temperate tree species are relatively well represented in genebanks, the majority of tropical species are absent. Partly, this reflects the recalcitrant or intermediate properties of the seed of many tropical species, which means that they cannot be stored for any length of time in seed genebanks. Even with boreal and temperate trees, however, capturing the range of genetic variability in species in seed collections has generally received only a low priority.

For all categories of FGR, therefore, there is a general lack of representative seed collections that could form the basis for designing climate change responses. It follows that trials to study adaptive traits important under climate change have also only received limited attention, with significant work done on only a few tree species, mostly those of importance for plantation forestry but not necessarily priority species for other growers (but see Box 1). Even in commercially important species where

extensive provenance tests have been undertaken, range margins and atypical populations that may be crucial for climate change responses are rarely well represented. There is, therefore, a general lack of information on which to base proper tree–site matching during translocation. Understanding of the molecular architecture of adaptation is also in its infancy, even for so-called model trees; the application of molecular breeding to combat climate change is, therefore, also not well advanced.

Fundamental to predicting the future geographic “domains” in which particular tree species will (if given the opportunity) grow well depends on understanding current species distributions, information on which is also often lacking (e.g. [www.lifemapper.org](http://www.lifemapper.org)), and the ecological niche model that is adopted (Peterson *et al.*, 2008). Projections of future growth domains are in any case more difficult for perennials than for annual crops, as the long lifespans of trees mean that they can realize products and services (such as carbon storage) over considerable periods of time, possibly centuries from now when climatic conditions will depend on the effectiveness of current mitigation measures (IPCC 2007). This makes tree–site matching for the future very difficult.

### 3.3 Efforts needed to identify characteristics relevant to adaptation to climate change

Although field and nursery trials have fallen out of favour in recent years, such tests are vital for understanding climate change responses and need to receive new attention. More such trials are needed on a wider range of species important to commercial foresters and small-scale planters, in which emphasis is placed on sampling from all parts of the ecological range of the species under study, not just those populations where survival, growth and biomass yield are best (Aitken *et al.*, 2008). It is in “marginal” populations that the most interesting adaptations may be found. During evaluation, more attention needs to be given to the traits that are involved in responses to environmental change.

In addition, genomic studies, in which the quantitative trait loci believed to control responses are studied at the gene level (Namroud *et al.*, 2008; Neale and Ingvarsson, 2008; Reusch and Wood, 2007), could be applied. In the case of drought tolerance, which may be a particularly important feature in responding to new climatic conditions, candidate genes include those involved in the synthesis of abscisic acid, transcriptional regulators of drought-inducible pathways, and late embryogenesis abundant proteins; shifts at such loci have been linked to responses to global warming (Hoffmann and Willi, 2008). DNA-based techniques for genomic research are developing very rapidly and need to be extended from temperate model species to a wider range of boreal, temperate and tropical trees, using modern approaches to study relationships between phenotype and genotype, though methodological problems remain to be overcome (Bessega *et al.*, 2009; Pauwels *et al.*, 2008; Pemberton, 2008).

Neutral molecular markers have been employed to describe patterns of genetic diversity within many tree species and contribute to an understanding of responses to past climate change events through describing genetic disjunctions and refugia (Petit *et al.*, 2003, 2008). This information is very helpful for understanding past and current gene flow and population structure and is highly relevant for designing *in situ* conservation networks and prioritizing populations to archive *ex situ*. Generally, however, neutral genetic markers do not improve our understanding of adaptive traits, except perhaps in species with low population sizes (such as rare or endemic species) where demographic bottlenecks are likely to have affected neutral and adaptive genetic diversity similarly (Le Corre and Kremer, 2003).

As well as studies on trees, more research is needed on the impact of climate change on pollinators in forest and agroforestry systems, especially when tree species have specialized relationships with particular animal vectors (Bazzaz, 1998). Declining tree–pollinator interactions that may occur as a result of climate change (NRC, 2007; FAO, 2008) would limit gene flow in tree stands, reducing the effective size of populations and therefore adaptive capacity. The extent of climate change impacts on tree pollinators is, however, not well understood.

Finally, foresters and scientists need to learn from the success and failure of current planting initiatives in responding to climate change. By monitoring die back, mortality and other features in existing stands, much can be learnt when related to the origin of planting material and the silvicultural

management that has been applied. Some plantation forests should be left to “suffer” altered environmental conditions in order to observe responses, even when these forests can no longer be considered productive and so would otherwise be replaced.

#### IV. CONCLUSIONS

Unlike major agricultural crops, the genetic resources of many important tree species have been little studied. Genetic evaluation of a few commercially important species that have been widely planted has mainly aimed to understand the inheritance of productivity-related traits rather than adaptive traits that could be important under climate change, although a few model species are the subjects of genomic research to understand the gene expression of important characteristics. For most trees, understanding the genetic basis of adaptation is still in its infancy and as a result predictions of responses to changing climates are largely based on theory. Furthermore, breeding programmes are generally based on maximizing productivity rather than increasing resilience, for example, through using more genetically diverse varieties and mixtures. Table 1 presents significant knowledge gaps and the action priorities that are needed to address these.

Seed zones and regions of provenance as they exist today, mainly in OECD countries, to define adaptation zones, will likely be of limited value under climate change and will need to be redesigned for climates of the future. The assisted migration of germplasm from existing ranges to sites expected to experience analogous environmental conditions in future years is a possibility for high value species, particularly in the case of managed, plantation and agroforestry ecosystems. Crucial, however, is a greater understanding of trends in climate that will allow proper tree–site matching during translocation (Sáenz-Romero *et al.*, 2010). Assisted migration may not only involve the movement of tree germplasm, but also of associated micro-organisms (such as nitrogen-fixing bacteria essential for the growth of leguminous trees) and important animal pollinators. In the case of natural forests, seed or pollen could be broadcast in areas where current populations are expected to become maladapted under future conditions, and other management actions such as reducing harvesting intensity may be appropriate to respond to change (Guariguata *et al.*, 2008). Genetic resource conservation must be dynamic, as it is the evolutionary potential rather than the genes themselves that require conservation, if climate change responses are to be adequate.

##### 5.1 Access and use conditions (policies)

New approaches and flexible solutions are needed in order to allow more effective transfer of germplasm across national borders and in some cases within countries, possibly through greater inclusion of tree genetic resources within multilateral agreements such as the International Treaty on Plant Genetic Resources for Food and Agriculture and by harmonization of phytosanitary requirements (Koskela *et al.*, 2009).

Policies and regulations will also need to be developed or modified in the following three areas if future generations are to benefit from the potential of today’s forest genetic resources:

- Regulations will need to be developed in coming years to meet the requirements of the Nagoya Protocol. It will be important to ensure that these regulations have the intended effect of actively promoting increased research on, access to and exchange of forest genetic resources, while at the same time guaranteeing the fair and equitable sharing of benefits arising from their utilization, bearing in mind that increased access will in the end foster benefits for all.
- National policies defining seed zones will need to be modified to allow the assisted migration of genetic material within countries and across country boundaries in order to respond to the speed of climate change.
- Market mechanisms are needed to reward the use of appropriate germplasm and conservation activities by growers, especially smallholder farmers, who are increasingly important as harbourers of tree biodiversity in the tropics.



**Table 1. Knowledge gaps and priorities for action for FGR**

<b>Knowledge gaps</b>	<b>Action priorities</b>
<b><i>Scientific information</i></b>	
1. Adaptive potential of traits of importance under climate change and the underlying genetic mechanisms	Field and nursery experiments to understand patterns of variation; harness genomic tools to improve understanding of genes that are important in drought tolerance and resistance, flood tolerance, phenology, response to elevated CO <sub>2</sub> levels, etc. Transfer knowledge obtained from model species in temperate regions to less known “local” species that are of high importance to people in the developing world.
2. The degree of phenotypic plasticity and its underlying genetic and epigenetic basis	Phenotypic characterization through more field trials designed to understand impacts and responses to environmental changes.
3. Effect of changes in interspecific competition and reproductive potential in relation to changing growth rhythms as temperature changes but photoperiod stays constant	Small-scale assisted migration operations should be carried out and monitored to determine whether the expected disconnect between temperature regimes and photoperiod can be mitigated by mixing genetic sources and allowing natural selection.
4. Population dynamics and environmental limits for pollinator species	In all areas where trees depend on pollinator species, action is needed to understand and respond to threats.
5. Species distributions and effects of fragmentation on gene flow	Map species distributions, accounting for rapidly expanding agricultural land and other developments, and considering historical data; develop predictive models that take into account life-history characteristics, the effects of fragmentation and levels of gene flow, in different parts of a species range.
6. Requirements for maximizing productivity of trees in agricultural landscapes under changing climate	Develop a portfolio of varieties that have phenotypic plasticity and that perform well across a range of environments (national/regional level)
<b><i>Availability and use</i></b>	
7. Past and current flows of germplasm, including quantities, origin of material and survival at the destination	Improve documentation of germplasm flows, molecular typing of origin.
8. Design of effective germplasm delivery systems for large-scale plantation establishers and smallholders	Improve international transfer of germplasm to make available high-quality site-matched planting material of high-value trees to planters, with a broad genetic base to ensure adaptive potential. Improve linkages between international exchange and smallholders through revitalizing the role of national tree seed centres in developing countries
9. Cultivation requirements of currently or potentially useful species	Improve access to information through education and training.

<i>Conservation</i>	
10. Regions where high genetic diversity and significant threats coincide	Implement risk assessments and threat analyses to identify coincidence. Prioritize conservation of populations on the basis of importance to people, high diversity and significant threat.
11. Most effective mix of <i>in situ</i> , <i>circa situ</i> and <i>ex situ</i> approaches to ensure conservation and maintain evolutionary processes	Increase population representation and genetic diversity of important and threatened species in conservation areas, in farmland and in seed collections.
12. Seed storage behaviour and germination requirements for many important species	New approaches for “genebanking” are needed for many tropical species through seed physiology research, cryopreservation, pollen storage, etc. Active conservation measures are needed for species that are important for human well-being and are seriously threatened.
13. Costs and benefits of FGR conservation	Application of economic valuation approaches developed for other sectors to FGR, with an emphasis on high-value species for foresters and small-scale farmers.

#### Box 4. Glossary

**Adaptation:** The process of genetic change in structure and/or function that makes an organism or a population better suited to survive in an environment (FAO 2003; Koski *et al.*, 1997).

**Assisted migration:** Otherwise known as facilitated translocation, a response under climate change in which populations are moved to compensate for environmental alterations to new sites expected to experience analogous conditions to the ones they originated in (Aitken *et al.*, 2008).

**Common garden experiments:** field experiments in which seed sources from different locations are brought together for assessment under common environmental conditions.

**Epigenetics:** The study of heritable changes in gene expression and function that cannot be explained by changes in DNA sequence. These changes are based on a set of molecular processes that can activate, reduce or completely disable the activity of particular genes. The different classes of processes are not independent from each other but often regulate gene activity in a complex, interactive fashion (Berger, 2007; Bird, 2007; Bossdorf *et al.*, 2008; Grant-Downton and Dickinson, 2005; Richards, 2006).

**Leading edge:** In a model of colonization under changing climate, the leading edge is the front of the distribution expanding into new, suitable territory. Expansion may be controlled by rare long-distance dispersal events followed by exponential population growth (Hampe and Petit, 2005).

**Phenotypic plasticity:** the ability of an organism to change its phenotype in response to changes in the environment without genetic change (Gienapp *et al.*, 2008; Price *et al.*, 2003).

**Provenance:** The geographical and/or genetic origin of an individual (FAO, FLD, IPGRI, 2004).

**Receding edge:** In a model of colonization under changing climate, the receding edge is the range margin which is eroding and where populations are likely to experience demographic bottlenecks. Populations located at eroding range margins may migrate with climate change or remain trapped in suitable environments while the general range of the species is moving (Hampe and Petit, 2005).

**Resilience:** resilience is one possible ecosystem response to a perturbation or disturbance. A resilient ecosystem resists damage and recovers quickly from disturbances such as fires, flooding, windstorms, insect population explosions, and human activities such as deforestation and the introduction of exotic plants or animals. However, disturbances of sufficient magnitude or duration may force an ecosystem to reach a threshold beyond which a different regime of processes and structures predominates. The “demographic” and “microclimatic” inertia (caused by longevity and the control of own climate, respectively) of trees may promote a level of resilience.

**LITERATURE CITED**

- Aitken, S. N., Yeaman, S., Holliday, J., Wang, T., Curtis-McLane, S. (2008). Adaptation, migration or extirpation: climate change outcomes for tree populations. *Evolutionary Applications*, 1(1), 95-111.
- Barbour, R. C., O' Reilly-Wapstra, J. M., De Little, D. W., Jordan, G. J., Steane, D. A., Humphreys, J. R., Bailey, J.K., Whitham, T.G., Potts, B.M.(2009). A geographic mosaic of genetic variation within a foundation tree species and its community-level consequences. *Ecology*, 90(7), 1762-1772.
- Bariteau, M., & Pommery, J. (1992). Variabilité géographique et adaptation aux contraintes du milieu méditerranéen des pins de la section halepensis: résultats (provisoires) d'un essai en plantations comparatives en France. *Annals of Forest Sciences*, 49(3), 261-276.
- Bazzaz, F.A. (1998). Tropical forests in a future climate: changes in biological diversity and impact on the global carbon cycle. *Climate Change*, 39: 317-336.
- Berger, S. L. (2007). The complex language of chromatin regulation during transcription. *Nature*, 447, 407-412.
- Besega, C., Saidman, B. O., Darquier, M. R., Ewens, M., Sánchez, L., Rozenberg, P., Vilardi, J.C. (2009). Consistency between marker- and genealogy-based heritability estimates in an experimental stand of *Prosopis alba* (Leguminosae). *American Journal of Botany*, 96, 458-465.
- Bhagwat, S. A., Willis, K. J., Birks, H. J. B., Whittaker, R. J. (2008). Agroforestry: a refuge for tropical biodiversity? *Trends in Ecology and Evolution*, 23, 261-267.
- Bird, A. (2007). Perceptions of epigenetics. *Nature*, 447, 396-398.
- Bossdorf, O., Richards, C. L., Pigliucci, M. (2008). Epigenetics for ecologists. *Ecology Letters*, 11(2), 106-15.
- Bosselmann, A. S., Jacobsen, J. B., Kjær, E. D., Thorsen, B. J. (2008). Climate change, uncertainty and the economic value of genetic diversity : A pilot study on methodologies. *Landscape*. Hørsholm, Denmark.
- Bouvarel, P. (1960). Note sur la résistance au froid de quelques provenances de pin maritime. *Revue Forestière Française*, (7), 495.
- Brewer, S., Cheddadi, R., Beaulieu, J. L. de, Reille, M. (2002). The spread of deciduous *Quercus* throughout Europe since the last glacial period. *Forest Ecology and Management*, 156(1-3), 27-48.
- British Columbia Ministry of Forests, Lands and Natural Resource Operations. (2008) Amendments to the Standards: Climate Based Upward Elevation Changes. Retrieved May 29, 2011, from <http://www.for.gov.bc.ca/code/cfstandards/amendmentNov08.htm>.
- Christensen, J. H., Hewitson, B., Busuioc, A., Chen, A., Gao, X., Held, I., Jones, R., Kolli, R.K., Kwon, W.T., Laprise, R., Magandez, C.G., Ranen, J., Magana Rueda, V., Mearns, L., Menendez, C.G., Raisanen, J., Rinke, A., Sarr, A., Whetton, P. (2007). Regional climate projections. In H. L. Solomon, S., Qin, D., Manning, M., Chen, Z., Marquis, M., Averyt, K.B., Tignor, M., Miller (Eds.), *Climate change 2007: the physical science basis. Contribution of working group I to the fourth assessment report of the intergovernmental panel on climate change*. (p. 847-940). Cambridge: Cambridge University Press.
- Clark, J. S., Bell, D. M., Hersh, M. H., Nichols, L. (2011). Climate change vulnerability of forest biodiversity: climate and competition tracking of demographic rates. *Global Change Biology*, 17, 1834-1849.

Davis, M. B., & Shaw, R. G. (2001). Range Shifts and Adaptive Responses to Quaternary Climate Change. *Science*, 292, 673-679.

Davis, M. B., Shaw, R. G., Etterson, J. R. (2005). Evolutionary responses to changing climate. *Ecology*, 86, 1704-14.

Dawson, I. K., Vinceti, B., Weber, J. C., Neufeldt, H., Russell, J., Lengkeek, A. G., Kalinganire, A., Kindt, R., Lillesø, J.-P. B., Roshetko, J., Jamnadass, R. (2011). Climate change and tree genetic resource management: maintaining and enhancing the productivity and value of smallholder tropical agroforestry landscapes. A review. *Agroforestry Systems*, 81, 67-78.

Elsasser, P. (2005). Economic methodologies for valuing forest genetic resources. In T. Gebure & J. Turok (Eds.), *Conservation and management of forest genetic resources in Europe* (pp. 89-109). Zvolen, Slovakia: Arbora publishers.

Folke, C., Carpenter, S., Walker, B., Scheffer, M., Elmqvist, T., Gunderson, L., Holling, C.S. (2004). Regime Shifts, Resilience, and Biodiversity in Ecosystem Management. *Annual Review of Ecology, Evolution, and Systematics*, 35(1), 557-581.

FAO (2003). Glossary on forest genetic resources (English version). *Development*. Rome, Italy.

FAO (2008). Rapid assessment of pollinators' status: a contribution to the International Initiative for the Conservation and Sustainable Use of Pollinators. Global Action on Pollination Services for Sustainable Agriculture. Food and Agriculture Organization of the United Nations, Rome, Italy.

FAO, FLD, IPGRI (2004). Forest genetic resources conservation and management. Vol. 3: In plantations and genebanks (*in situ*). Rome, Italy: International Plant Genetic Resources Institute.

Gienapp, P., Teplitsky, C., Alho, J.S., Mills, J.A., Merila, J. (2008) Climate change and evolution: disentangling environmental and genetic responses. *Molecular Ecology*, 17: 167-178.

Grant-Downton, R. T., & Dickinson, H. G. (2005). Epigenetics and its Implications for Plant Biology. 1. The Epigenetic Network in Plants. *Annals of Botany*, 96(7), 1143-1164.

Grivet, D., Sebastiani, F., Alia, R., Bataillon, T., Torre, S. (2011). Molecular Footprints of Local Adaptation in Two Mediterranean Conifers. *Molecular Biology and Evolution*, 28(1), 101-116.

Guariguata, M. R., Cornelius, J. P., Locatelli, B., Forner, C., Sanchez-Azofeifa, G. A. (2008). Mitigation needs adaptation: tropical forestry and climate change. *Mitigation and Adaptation Strategies for Global Change*, 13, 793-808.

Gutschick, V. P., & BassiriRad, H. (2003). Extreme events as shaping physiology, ecology, and evolution of plants: toward a unified definition and evaluation of their consequences. *New Phytologist*, 160(1), 21-42.

Hamann, A., & Wang, T. (2006). Potential effects of climate change on ecosystem and tree species distribution in British Columbia. *Ecology*, 87(11), 2773-2786.

Hampe, A., & Petit, R.J. (2005). Conserving biodiversity under climate change: the rear edge matters. *Ecology Letters*, 8(5), 461-467.

Hamrick, J. L. (2004). Response of forest trees to global environmental changes. *Forest Ecology Management*, 197(1-3), 323-335.

Hedhly, A., Hormaza, J.I., Herrero, M. (2008) Global warming and sexual plant reproduction. *Trends in Plant Science*, 14: 30-36.

- Hein, L. & Gatzweiler, F. (2006). The economic value of coffee (*Coffea arabica*) genetic resources. *Ecological Economics*, 60: 176-185.
- Held, I. M., Delworth, T. L., Lu, J., Findell, K. L., Knutson, T. R. (2005). Simulation of Sahel drought in the 20th and 21st centuries. *Proceedings of the National Academy of Sciences of the USA*, 102, 17891-17896.
- Hoffmann, A.A., & Sgro, C.M. (2011). Climate change and evolutionary adaptation. *Nature*, 470(7335), 479-485.
- Hoffmann, A.A., & Willi, Y. (2008). Detecting genetic responses to environmental change. *Nature reviews. Genetics*, 9(6), 421-32.
- Hubert, J. & Cottrell, J. (2007) The role of forest genetic resources in helping British forests respond to climate change. Information Note. Forestry Commission, Edinburgh, UK.
- IPCC (2007) Climate change 2007. The Fourth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press, Cambridge, UK.
- Jack, B.K., Kousky, C., Sims, K.R.E. (2008). Designing payments for ecosystem services: lessons from previous experience with incentive-based mechanisms. *Proceedings of the National Academy of Sciences of the USA*, 105: 9465-9470.
- Jensen, J.S., Bayala, J., Sanou, H., Korbo, A., Ræbild, A., Kambou, S., Tougiani, A., Bouda, H.-N., Larsen, A.S., Parkouda, C. (2011) A research approach supporting domestication of Baobab (*Adansonia digitata* L.) in West Africa. *New Forests*, 41: 317-335.
- Jha, S., & Dick, C. W. (2010). Native bees mediate long-distance pollen dispersal in a shade coffee landscape mosaic. *Proceedings of the National Academy of Sciences of the USA*, 107, 3760-13764.
- Johnsen, O., Fossdal, C. G., Nagy, N., Molmann, J., Daehlen, O. G., Skrøppa, T. (2005). Climatic adaptation in *Picea abies* progenies is affected by the temperature during zygotic embryogenesis and seed maturation. *Plant, Cell and Environment*, 28, 1090-1102.
- Jump, A. S., & Penueles, J. (2005). Running to stand still: adaptation and the response of plants to rapid climate change. *Ecology Letters*, 8, 1010-1020.
- Jump, A. S., Hunt, J. M., Martinez-Izquierdo, J. A., Peñuelas, J. (2006). Natural selection and climate change: temperature-linked spatial and temporal trends in gene frequency in *Fagus sylvatica*. *Molecular Ecology*, 15(11), 3469-3480.
- Jump, A. S., Marchant, R., Penueles, J. (2008). Environmental change and the option value of genetic diversity. *Trends in Plant Science*, 14(1), 51-58.
- Kellomäki, S., Rouvinen, I., Peltola, H., Strandman, H., Steinbrecher, R. (2001). Impact of global warming on the tree species composition of boreal forests in Finland and effects on emission of isoprenoids. *Global Change Biology*, 7, 531-44.
- Kindt, R., Damme, P., Simons, J., Beeckman, H. (2006). Planning tree species diversification in Kenya based on differences in tree species composition between farms. I. Analysis of tree uses. *Agroforestry Systems*, 67(3), 215-228.
- Konkin, D., & Hopkins, K. (2009). Learning to deal with climate change and catastrophic forest disturbances. *Unasylva*, 60, 17-23.
- Koskela, J., Vinceti, B., Dvorak, W., Bush, D., Dawson, I., Loo, J., Kjaer, E.D., Navarro, C., Padolina, C., Jamnadass, R., Graudal, L., Ramamonjisoa, L. (2010). The use and exchange of forest genetic resources for food and agriculture. Background Study Paper No. 44. The Commission on

Genetic Resources for Food and Agriculture, Food and Agriculture Organization of the United Nations, Rome, Italy.

Koski, V., Skroppa, T., Paule, L., Turok, J. (1997). *Technical guidelines for genetic conservation of Norway spruce (Picea abies (L.) Karst.)*. EUFORGEN. IPGRI.

Kramer, A. T., Ison, J. L., Ashley, M. V., Howe, H. F. (2008). The paradox of forest fragmentation genetics. *Conservation Biology*, 22, 878-885.

Le Corre, V., & Kremer, A. (2003). Genetic variability at neutral markers, quantitative trait loci and trait in a subdivided population under selection. *Genetics*, 164, 1205-1219.

Lengkeek, A.G., & Carsan, S. (2004). The process of a participatory tree domestication project in Meru, Kenya. *Development in Practice*, 14: 445-451.

Liepert, S., Bialozyt, R., Ziegenhagen, B. (2002). Wind-dispersed pollen mediates postglacial gene flow among refugia. *PNAS*, 99(22), 14590-14594.

Lindner, M., Maroschek, M., Netherer, S., Kremer, Antoine, Barbati, A., Garcia-Gonzalo, J., Seidl, R., Delzon, S., Corona, P., Kolström, M. (2010). Climate change impacts, adaptive capacity, and vulnerability of European forest ecosystems. *Forest Ecology and Management*, 259(4), 698-709.

Madlung, A., & Comai, L. (2004). The effect of stress on genome regulation and structure. *Annals of botany*, 94(4), 481-95.

Malcolm, J.R., Markham, A., Neilson, R.P., Garaci, M. (2002). Estimated migration rates under scenarios of global climate change. *Journal of Biogeography*, 29, 835-849.

Malhi, Y., Aragao, L.E.O.C., Galbraith, D., Huntingford, C., Fisher, R., Zelazowski, P., Sitch, S., McSweeney, C., Meir, P. (2009). Exploring the likelihood and mechanism of a climate-change-induced dieback of the Amazon rainforest. *Proceedings of the National Academy of Sciences of the USA*, 106: 20610-20615.

McLachlan, J.S., Clark, J.S., Manos, P.S. (2005). Molecular indicators of tree migration capacity under rapid climate change. *Ecology*, 86, 2088-2098.

McLachlan, J.S., Hellmann, J.J., Schwartz, M.W. (2007). A framework for debate of assisted migration in an era of climate change. *Conservation biology: the journal of the Society for Conservation Biology*, 21(2), 297-302.

Muchugi, A., Lengkeek, A., Kadu, C., Muluvi, G., Njagi, E., Dawson, I. (2006). Genetic variation in the threatened medicinal tree *Prunus africana* in Cameroon and Kenya: Implications for current management and evolutionary history. *South African Journal of Botany*, 72(4), 498-506.

Muchugi, A., Muluvi, G. M., Kindt, R., Kadu, C. a C., Simons, a J., Jamnadass, R. H. (2008). Genetic structuring of important medicinal species of genus *Warburgia* as revealed by AFLP analysis. *Tree Genetics & Genomes*, 4(4), 787-795.

Mutke, S., Gordo, J., Chambel, M. R., Aránzazu Prada, M., Álvarez, D., Iglesias, S., Gil, L. (2010). Phenotypic plasticity is stronger than adaptive differentiation among Mediterranean stone pine provenances. *Forest Systems*, 19(3), 354-366.

Mutke, S., Gordo, J., Gil, L. (2005). Variability of Mediterranean Stone pine cone production: Yield loss as response to climate change. *Agricultural and Forest Meteorology*, 132, 263-272.

Mátyás, C. (2007). What do field trials tell about the future use of forest reproductive material? In J. Koskela, A. Buck, E. Teissier du Cros (Eds.), *Climate change and forest genetic diversity*:

- Implications for sustainable forest management in Europe* (p. 53-69). Rome, Italy: Bioversity International.
- Mátyás, C., Vendramin, G. G., Fady, B. (2009). Forests at the limit: evolutionary - genetic consequences of environmental changes at the receding (xeric) edge of distribution. Report from a research workshop. *Annals of Forest Science*, 66(8), Article number: 800.
- Namroud, M.-C., Beaulieu, J., Juge, N., Laroche, J., Bousquet, J. (2008). Scanning the genome for gene single nucleotide polymorphisms involved in adaptive population differentiation in white spruce. *Mol Ecol*, 17, 3599-3613.
- Nasri, N., Bojovic, S., Vendramin, G. G., Fady, B. (2008). Population genetic structure of the relict Serbian spruce, *Picea omorika* [Panč.] Purk, inferred from plastid DNA. *Plant Systematics and Evolution*, 271, 1-7.
- Nathan, R., Katul, G. G., Horn, H. S., Suvi, M. T., Oren, R., Avissar, O., Pacala, S.W., Levin, S.A. (2002). Mechanisms of long-distance dispersal of seeds by wind. *Nature*, 418, 409-413.
- Nathan, R., Horvitz, N., He, Y., Kuparinen, A., Schurr, F.M., Katul, G.G. (2011). Spread of North American wind-dispersed trees in future environments. *Ecology Letters*, 14(3), 211-219.
- Neale, D. B., & Ingvarsson, P. K. (2008). Population, quantitative and comparative genomics of adaptation in forest trees. *Current Opinions in Plant Biology*, 11, 149-155.
- NRC (2007). Status of pollinators in North America. Committee on the Status of Pollinators in North America, the National Research Council. Washington DC, USA: The National Academies Press.
- Oddou-Muratorio, S., Klein, E. K., Austerlitz, F. (2005). Pollen flow in the wildservice tree, *Sorbus torminalis* (L.) Crantz. II. Pollen dispersal and heterogeneity in mating success inferred from parent-offspring analysis. *Molecular Ecology*, 14(14), 4441-4452.
- Olago, D.O. (2001). Vegetation changes over palaeo-time scales in Africa. *Clim Res*, 17, 105-121.
- Pauwels, M., Roosens, N., Frerot, H., Saumitou-Laprade, P. (2008). When population genetics serves genomics: putting adaptation back in a spatial and historical context. *Curr Opin Plant Biol*, 11, 129-134.
- Pearson, R. G. (2006). Climate change and the migration capacity of species. *Trends in Ecology and Evolution*, 21, 111-113.
- Pemberton, J. M. (2008). Wild pedigrees: the way forward. *Proceedings of the Royal Society B: Biological Sciences*, 275(1635), 613-621.
- Peterson, A. T., Stewart, A., Mohamed, K. I., Araujo, M. B. (2008). Shifting global invasive potential of European plants with climate change. *PLoS ONE* 3:e2441. Retrieved from www.plosone.org.
- Petit, R.J., Aguinalalde, I., de Beaulieu, J.-L., Bittkau, C., Brewer, S., Cheddadi, R., Ennos, R., Fineschi, S., Grivet, D., Lascoux, M., Mohanty, A., Müller-Starck, G., Demesure-Musch, B., Palmé, A., Martín, J.P., Rendell, S., Vendramin, G.G. (2003). Glacial refugia: hotspots but not melting pots of genetic diversity. *Science*, 300: 1563-5.
- Petit, R. J., & Hampe, A. (2006). Some evolutionary consequences of being a tree. *Annual Review of Ecology, Evolution and Systematics*, 37(1), 187-214.
- Petit, R.J., Hu, S. S., Dick, C. W. (2008). Forests of the past: A window to future changes. *Science*, 320(5882), 1450-1452.

- Piersma, T., & Drent, J. (2003). Phenotypic flexibility and the evolution of organismal design. *Trends in Ecology & Evolution*, 18(5), 228-233.
- Price, T. D., Qvarnström, A., Irwin, D. E. (2003). The role of phenotypic plasticity in driving genetic evolution. *Proceedings of the Royal Society B: Biological Sciences*, 270(1523), 1433-40.
- Pujol, B., Shu-Rong, Z., Vilas Sanchez, J., Pannell, J. R. (2009). Reduced inbreeding depression after species range expansion. *Proceedings of the National Academy of Sciences USA*, 106(36), 15379-15383.
- Rehfeldt, G.E., Tchebakova, N. M., Parfenova, Y. I., Wykoff, W.R., Kuzmina, N. A., Milyutin, L. I. (2002). Intraspecific responses to climate in *Pinus sylvestris*. *Global Change Biology*, 8(9), 912-929.
- Rehfeldt, G. E., Wykoff, William R., Cheng, C. Y. (2001). Physiologic plasticity, evolution, and impacts of a changing climate on *Pinus Contorta*. *Climatic Change*, 50, 355-76.
- Restoux, G., E Silva, D., Sagnard, F., Torre, F., Klein, E., Fady, B. (2008). Life at the margin: the mating system of Mediterranean conifers. *Web Ecology*, 8, 94-102.
- Reusch, T.B.H., & Wood, T.E. (2007). Molecular ecology of global change. *Molecular Ecology*, 16, 3973-3992.
- Richards, E.J. (2006). Inherited epigenetic variation - revisiting soft inheritance. *Nature Reviews Genetics*, 7, 395-401.
- Roshetko, J.M., Lasco, R.D., Delos Angeles, M.S. (2007). Smallholder agroforestry systems for carbon storage. *Mitigation and Adaptation Strategies for Global Change*, 12: 219-242.
- Sáenz-Romero, C., Rehfeldt, G.E., Crookston, N.L., Duval, P., St-Amant, R., Beaulieu, J., Richardson, B.A. (2010). Spline models of contemporary, 2030, 2060 and 2090 climates for Mexico and their use in understanding climate change impacts on the vegetation. *Climatic Change*, 102: 595-623.
- Sagnard, F., Oddou-Muratorio, S., Pichot, C., Vendramin, G. G., Fady, B. (2011). Effect of seed dispersal, adult tree and seedling density on the spatial genetic structure of regeneration at fine temporal and spatial scales. *Tree Genetics and Genomes*, 7, 37-48.
- Salles, J. M. (2010). Evaluer la biodiversité et les services écosystémiques: pourquoi, comment et avec quels résultats? *Natures Sciences Sociétés*, 18, 414-423.
- Sanou, H., Korbo, A., Tougani, A., Rabiou, A., Kambou, S., Ouedraogo, M., Diallo, B.O., Parkouda, C., Jensen, J.S. (2007). Protocol for establishment of trials with Baobab and Tamarind within the SAFRUIT project. *Landscape*. Hørsholm, Denmark.
- Sarr, M., Goeschl, T., Swanson, T. (2008). The value of conserving genetic resources for R&D: A survey. *Ecological Economics*, 67(2), 184-193.
- Savolainen, O., Bokma, F., Knürr, T., Kärkkäinen, K., Pyhäjärvi, T., Wachowiak, W. (2007). Adaptation of forest trees to climate change. In J. Koskela, A. Buck, E. Teissier du Cros (Eds.), *Climate change and forest genetic diversity: Implications for sustainable forest management in Europe* (p. 19-30). Rome, Italy: Bioersivity International.
- Shanahan, T. M., Overpeck, J. T., Anchukaitis, K. J., Beck, J. W., Cole, J. E., Dettman, D. L., Peck, J.A., Scholz, C.A., King, J.W. (2009). Atlantic forcing of persistent drought in West Africa. *Science*, 324, 377-380.
- Skroppa, T., & Kohmann, K. (1997). Adaptation to local conditions after one generation in Norway spruce. *Forest Research*, 4(3), 171-177.



Steffan-Dewenter, I., Kessler, M., Barkmann, J., Bos, M. M., Buchori, D., Erasmi, S., Faust, H., Gerold, G., Glenk, K., Gradstein, S.R., Guhardja, E., Harteveld, M., Hertel, D., Höhn, P., Kappas, M., Köhler, S., Leuschner, C., Maertens, M., Marggraf, R., Migge-Kleian, S., Mogeia, J., Pitopang, R., Schaefer, M., Schwarze, S., Sporn, S.G., Steingrebe, A., Tjitrosoedirdjo, S.S., Tjitrosoemito, S., Twele, A., Weber, R., Woltmann, L., Zeller, M., Tscharrntke, T. (2007). Tradeoffs between income, biodiversity, and ecosystem functioning during tropical rainforest conversion and agroforestry intensification. *Proceedings of the National Academy of Sciences of the USA*, 104(12), 4973-8.

Thorsen, B.J., & Kjær, E.D. (2007). Forest genetic diversity and climate change: economic considerations. In J. Koskela, A. Buck, E. Teissier du Cros (Eds.), *Climate change and forest genetic diversity: Implications for sustainable forest management in Europe* (p. 69-84). Rome, Italy: Bioversity International.

Thuiller, W., Albert, C., Araujo, M. B., Berry, P. M., Cabeza, M., Guisan, A., Hickler, T., Midgley, G.F., Paterson, J., Schurr, F.M., Sykes, M.T., Zimmermann, N.E. (2008). Predicting global change impacts on plant species' distributions: future challenges. *Perspectives in Plant Ecology, Evolution and Systematics*, 9, 137-152.

Thuiller, W., Lavorel, S., Sykes, M. T., Araújo, M. B. (2006). Using niche-based modelling to assess the impact of climate change on tree functional diversity in Europe. *Diversity and Distributions*, 12, 49-60.

Timbal, J., Bonneau, M., Landmann, G., Trouvilliez, J., Bouhot-Delduc, L. (2005). European non boreal conifer forests. In F.A. Andersson (Eds.), *Ecosystems of the world (6): Coniferous forests* (pp. 131-162). Amsterdam, The Netherlands: Elsevier.

Valladares, F., Arrieta, S., Aranda, I., Lorenzo, D., Sánchez-Gómez, D., Tena, D., Suárez, F., Alberto Pardos, J. (2005). Shade tolerance, photoinhibition sensitivity and phenotypic plasticity of *Ilex aquifolium* in continental Mediterranean sites. *Tree physiology*, 25(8), 1041-52.

Vendramin, G. G., Fady, B., González-Martínez, S. C., Hu, F. S., Scotti, I., Sebastiani, F., Soto, A., Petit, R.J. (2008). Genetically depauperate but widespread: the case of an emblematic Mediterranean pine. *Evolution*, 62(3), 680-688.

Wang, T., Hamann, A., Yanchuk, A., O'Neill, G. A., Aitken, S.N. (2006). Use of response functions in selecting lodgepole pine populations for future climates. *Global Change Biology*, 12(12), 2404-2416.

Ward, M., Dick, C. W., Lowe, A. J. (2005). To self, or not to self... A review of outcrossing and pollen-mediated gene flow in neotropical trees. *Heredity*, 95, 246-254.

Weber, J. C., Larwanou, M., Abasse, T. A., Kalinganire, A. (2008). Growth and survival of *Prosopis africana* provenances related to rainfall gradients in the West African Sahel. *Forest Ecology and Management*, 256, 585-592.

Whitham, T.G., Bailey, J.K., Schweitzer, J.A., Shuster, S.M., Bangert, R.K., LeRoy, C.J., Lonsdorf, E.V., Allan, G.J., DiFazio S.P., Potts, B.M., Fischer, D.G., Gehring, C.A., Lindroth, R.L., Marks, J.C., Hart, S.C., Wimp, G.M., Wooley, S.C. (2006). A framework for community and ecosystem genetics: from genes to ecosystems. *Nature Reviews: Genetics*, 7, 510-523.

Williams, S. E., Bolitho, E. E., Fox, S. (2003). Climate change in Australian tropical rainforests: an impending environmental catastrophe. *Proceedings of the Royal Society of London*, 270, 1887-1892.

Yanchuk, A., & Allard, G. (2009). Tree improvement programmes for forest health - can they keep pace with climate changes? *Unsylva*, 60, 50-56.

Ying, C. C., & Yanchuk, A. D. (2006). The development of British Columbia's tree seed transfer guidelines: Purpose, concept, methodology, and implementation. *Forest Ecology and Management*, 227, 1-13.

Zonneveld, M. J. van, Jarvis, A., Dvorak, W., Lema, G., Leibing, C. (2009). Climate change impact predictions on *Pinus patula* and *Pinus tecunumanii* populations in Mexico and Central America. *Forest Ecology and Management*, 257(7), 1566-76.

## ANNEX 1

## EXAMPLE OF NATIONAL GUIDELINES FOR MANAGEMENT OF FOREST GENETIC RESOURCES UNDER CLIMATE CHANGE FROM FRANCE'S COMMISSION ON FOREST GENETIC RESOURCES



LEMINISTRE  
DE L'AGRICULTURE  
ET DE LA PÊCHE

DDPAAAT/SOUS-DIRECTION DE LA FORÊT ET DU BOIS

Commission on  
Forest  
Genetic  
Resources

**Preservation and use  
of the diversity of forest genetic resources  
to strengthen the adaptability  
of forests to climate change**

**G**enetic resources cover an area of biodiversity of actual or potential value. In forests, genetic diversity of trees is also a key factor which fosters general biodiversity of the ecosystem and interacts with its function. The diversity within species is not always easy to observe but it exists between and within populations of trees. Driven by the laws of genetics, it is dynamic, through seed and pollen flows between stands and by selection, be it natural or artificial. In the context of climate change, sustainable long term preservation of this legacy is both supportive and dependent upon the local management of forest.



We deal here with the management of genetic diversity within each species, while acknowledging that mixed species silvicultural treatments are, of course, fully justified for sustainable management in the context of climate change.

We make some important general recommendations, without systematically detailing each type of forest management. In many cases, several options are open and there is no unique solution.

In parallel to these recommendations devoted to standard forest management, specific programmes for conservation and experimental transfer of genetic resources will be led by researchers, in particular on CRGF's initiative

---

### Commission Ressources Génétiques Forestières/Commission on Forest Genetic Resources (\*)

(\*) This commission, whose membership is made up of scientists, public and private forest managers, and a representative of the "forest" network of France Nature Environnement, advises the Ministry of Agriculture, Food & Fisheries, implements a strategy for the evaluation and the conservation of genetic diversity in forest tree species in France.

President: François Lefèvre (Email: francois.lefevre@avignon.inra.fr), Secretary: Eric Collin (Email: eric.collin@comagref.fr)

## 1 – The climatic context: a continuous change with sharp annual and regional variations

The experts of the Intergovernmental Panel on Climate Change (IPCC) predict a significant change in the climate over the next century, with a sharp rise in average temperature, changes in rainfall and more frequent extreme events (heat waves, droughts, floods, storms, etc.). These changes, while certain, will vary from one region to another. Many uncertainties remain as to the amplitude of annual variations (e.g. will the increase in average temperature be accompanied by the disappearance of frost risk?) as well as global ecological changes induced by climate change (parasites, mycorrhizae, pollinators, seed dispersers, new invasive species etc.).

Climate change is a long-term process. During the course of the next century, forests will need to cope with a series of environmental conditions which are difficult to foresee and will no doubt be completely novel as regards their physical (temperature, drought) and biological dimensions. It is over the same timescale that today's decisions will produce effects.



## 2 – Genetic context: an adaptive potential to be fully used...

If current forest ecosystems are to remain in good health, much will depend on the capacity of existing trees to survive and reproduce and on adaptive changes in the forthcoming regeneration phases. The adaptive potential of a

forest is its capacity to evolve genetically from one generation to the next. The drivers of genetic evolution can be natural, artificial, or both.

It is generally difficult to predict existing trees' capacity to respond to the changes they will experience in coming years (notwithstanding the uncertainty as to future climatic and ecological scenarios). On the other hand, what we do know is that forest trees are usually characterised by wide genetic diversity within individual stands: such diversity is the essential "fuel" for the proper functioning of natural selection, the mechanism which leads to adaptation. Diversity within stands varies between species (generally more limited for species whose areas are fragmented), and also for the same species from the centre to the margin of its distribution area. However, historical examples of forest material transfer have shown that genetic diversity is sufficient to encompass major adaptive changes in no more than one or two generations.

Convinced that major ecological changes will occur, but unable to describe accurately the environment of the future, we need to take maximum advantage of the adaptive potential. Consequently, we must follow two objectives:

- ▣> the maintenance of genetic diversity over the long term by using appropriate forestry practices, and
- ▣> the fostering of evolutionary processes to keep stands adapted to their changing environment as closely as possible in what is a "race for change".

### QUALITY NOTIONS IN GENETIC RESOURCES

The "best quality" = a subjective criterion based on multiple parameters (economic, ecological, etc.) in relation to the goals assigned to the forest at a given time.

Adaptation = quality of population survival, growth and reproduction in the prevailing environment.

Adaptability = capacity of a population to change in a changing environment, including the plasticity (variation in morphology or physiology as a response to environmental change) of existing trees and genetic evolutions from generation to generation.

Local regions of provenance offer guarantees of good adaptation to local conditions. Their adaptability will not necessarily be sufficient: this will depend on their genetic diversity and on the intensity of environmental change.

**3 – Recommendations:  
graduated responses matching  
dieback intensity in forest ranges  
or regions**



There is today a need for gradual response to raising issues, and for avoiding ill-founded measures of adaptation. While remaining active and vigilant, two pitfalls must be avoided:

- ▣ the substitution of provenances or species may be necessary in some cases, but hasty moves towards com-

plete replacement and reckless elimination of genotypes which might survive in new conditions would not meet the objective of fostering the evolution of our genetic resources in the long term.

- ▣ the immoderate use of a single Forest Reproductive Material (FRM) supposed to be the panacea, which might endanger the preservation of genetic diversity in our resources.

Forestry practices may influence genetic diversity and evolution processes in the context of climate change. Natural selection between seedling or sapling is an important evolutionary process. Choosing natural re-generation allows the most effective advantage to be taken from the genetic diversity available within the stand. Planting can be beneficial using FRM from recommended sources and varieties selected for their adaptive characteristics or plasticity. In this case, a higher initial density of the species will enhance the opportunity for further natural selection.

Renewal by:	Natural regeneration	Planting of material from the local region of provenance	Planting of introduced material (In an area where the species is already present)
Advantages	<ul style="list-style-type: none"> <li>- good adaptation</li> <li>- good sampling of locally available genetic diversity</li> <li>- allows natural selection to operate</li> <li>- good integration into the ecosystem, reinforcing its general resistance (co-adaptation)</li> </ul>	<ul style="list-style-type: none"> <li>- good adaptation</li> <li>- material usually from selected stands chosen for their quality</li> <li>- fairly good integration into the ecosystem, ensuring satisfactory general resistance</li> </ul>	<ul style="list-style-type: none"> <li>- remedies a lack of local genetic diversity</li> <li>- contributes to new adaptations</li> </ul>
Disadvantages	<ul style="list-style-type: none"> <li>- risk of a limited number of effectively reproducing trees</li> <li>- risk of a small number of seedlings</li> <li>- risk that local genetic diversity is too limited and ultimately unable to adapt to the scale of changes</li> </ul>	<ul style="list-style-type: none"> <li>- risk of poor sampling of the genetic diversity during seed harvest</li> <li>- leaves less room for natural selection</li> <li>- risk that regional genetic diversity is too limited and ultimately unable to adapt to the scale of changes</li> </ul>	<ul style="list-style-type: none"> <li>- risk of maladaptation</li> <li>- risk that overall genetic diversity will decline in case of massive introduction of material with a narrow genetic basis</li> <li>- risk of inducing "genetic suffocation" of a local resource under threat</li> <li>- risk of further disturbance to an already weakened ecosystem</li> </ul>
Recommended management practices	<ul style="list-style-type: none"> <li>- maximise the effective number of reproductive trees</li> <li>- ensure sufficient seedling density at least in the very early stage, or consider additional planting</li> </ul>	<ul style="list-style-type: none"> <li>- mix selected stands within the region of provenance where technically feasible</li> <li>- increase the initial planting density</li> </ul>	<ul style="list-style-type: none"> <li>- introduce material originating from a neighbouring region, in principle one with a drier climate</li> <li>- introduce material with a broad genetic base</li> </ul>



There is a distinction between different situations, depending on the observed impact of climate change.

**The diagnosis of dieback attributed to climate change must be verified and refined, specifically in the light of past management practices :**

a) Where there is no significant dieback in local stands, encourage natural selection through high levels of genetic diversity in the earliest stages of growth in the stand :

❑ In the case of natural or artificial regeneration, ensure sufficiently dense regeneration relative to the size of the final target population (distinction between social and scattered species) ;

❑ In the case of natural regeneration, maximise the genetic diversity in the seedlings by increasing the contribution from a maximum number of reproductive trees (also considering the duration of the regeneration phase).



b) If the areas of dieback significantly reduce the potential number of reproductive trees in the stand but spare at least half the healthy individuals, we recommend that regeneration be supplemented or the stand replanted, using FRM fully representative of the selected stands in the local region of provenance. In order to enhance adaptability, the use of "genetic enrichment" can be considered by using FRM representing neighbouring regions of provenance (in principle, with a hotter, dry climate).

c) If the dieback is generalised, affecting all age classes, and if local extinction of the species appears inevitable across the entire forest, there will be no alternative except the introduction of exotic provenances of the same species,

considered to be better adapted to future conditions, or, if unavailable, to the changing of the target species. Then, the emphasis should be put on the genetic diversity of the introduced material and on its provenance, including that used for infilling and reinforcement planting (all documentation relating to this material should be retained). Meanwhile, particular attention should be paid to surviving trees possibly carrying specific genetic characteristics advantageous to adaptation. After unusual events, adjustments to the conservation strategy will need to be considered.

Before planting (genetic enrichment, transfer, substitution), it will be necessary to obtain guarantees of high genetic quality for the FRM from the seed and plant industry (broad genetic base, adaptation, phenotypic plasticity). The current recommendations given for the use of FRM, which are based on concepts of local adaptation and performance in a constant environment, will need to be adjusted to reflect the changing conditions. The definitions of regions of provenance and the use of

FRM must over time take into account changes in the climatic zones. This is not to cast doubt in any way on the advantages of regulating trade in FRM, which guarantees quality of information provided to users. Indeed, it is the only efficient tool to ensure the diversity of the FGR actually used. The use of forest varieties with a narrow genetic base must be thoroughly evaluated and controlled in order to avoid excessive homogeneity, with a view to maintaining genetic diversity in the countryside. Additionally, regulatory control of FRM makes it possible to monitor all movements of genetic resources, this being of fundamental importance in the context of the climatic instability now being encountered.

### IN BRIEF

- ❑ If the rotation period is shorter than 20 years (poplars, short-rotation coppice and plantation), choose the best adapted FRM while avoiding excessive uniformity across the region.
- ❑ If the rotation period exceeds 20 years, it will be necessary to take into account adaptation and adaptability. The higher the harvest age, the greater the environmental changes experienced between juvenile and harvest time, and thus the more urgent need for genetic diversity.
- ❑ For mature stands, adaptation of forestry practices must also take into account the preparation of regeneration phases to ensure adequate seedling quantities and genetic diversity.
- ❑ During the renewal phase, whether based on natural regeneration or planting, seek to ensure sufficient genetic diversity to allow for subsequent natural selection.

Websites to visit: <http://agriculture.gouv.fr/sections/thematiques/foret-bois/conservation-ressources>  
<http://agriculture.gouv.fr/sections/thematiques/foret-bois/graines-et-plants-forestiers>  
[http://www.brg.prd.fr/brg/pages/les\\_rg\\_en\\_france/rgv\\_arbresForestiers.php](http://www.brg.prd.fr/brg/pages/les_rg_en_france/rgv_arbresForestiers.php)

June 2008