



GENETIC DIVERSITY  
IN COMMERCIAL TREE SPECIES:

# WHITE SPRUCE

Jean Beaulieu  
and Marie Deslauriers

INFORMATION LEAFLET LFC-30



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## COVER

### PHOTO 1

Ripe white spruce cones  
(Photo: *R. Pâquet*)

### PHOTO 2

White spruce progeny test at Lac Saint-Ignace  
(Photo: *J. Beaulieu*)

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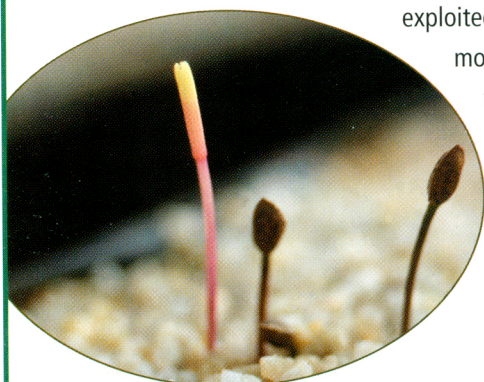
Cette publication est également offerte en français sous le titre «La diversité génétique chez les essences commerciales : l'épinette blanche»  
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## INTRODUCTION

An estimate of genetic diversity and its distribution in tree species is essential for implementing effective genetic resource conservation strategies and supporting the sustainability of forests. The presence of genetic diversity (*Figure 1*) within natural populations and plantations of forest tree species ensures the stability of forest ecosystems by allowing the species to gradually adapt to changing environmental conditions, such as climatic changes and outbreaks of forest insect pests and pathogens.

In Quebec, various aspects of genetic diversity have been studied in forest tree species. For example, genetic diversity research focussing on growth characters revealed that white spruce has a high level of genetic diversity which can be exploited to develop superior varieties. More recently, molecular techniques have been employed in order to generate complementary information about the structure of this diversity within and among natural populations.



*Figure 1*

Illustration of the presence of genetic diversity in a forest species: normal and albino seedlings.

(Photo: C. Moffet)



## MATERIALS and METHODS

### Morphological characters

**M**orphological characters such as tree height or volume are the result of the tree's genetic makeup and its interaction with the environment in which it is growing. The physical appearance of a trait is its phenotype. When we want to evaluate the variability or diversity that results exclusively from the differences in genetic composition that exist between individuals, it is necessary to eliminate the environmental influences shaping the phenotype. To do so, families or provenances of various origins are established in a homogeneous location (plantation or field test) and monitoring is conducted to determine their evolution over time. Studies of this type have been carried out on white spruce in Quebec since the 1950s (*Figure 2*). We now have several dozen provenance and provenance-progeny tests which are providing data that can be used in estimating the genetic diversity of morphological traits of this important species.

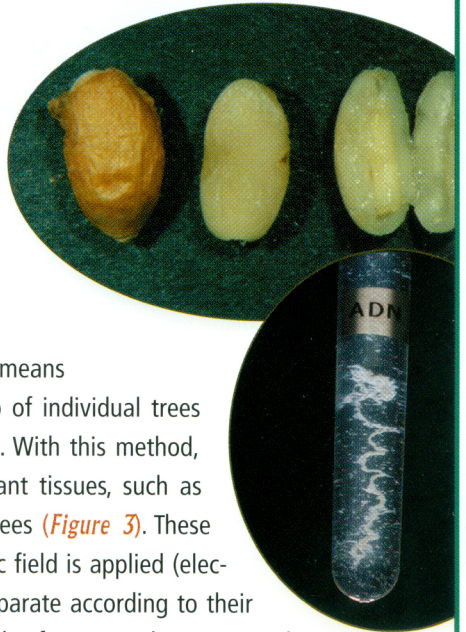


*Figure 2*

White spruce provenance-progeny trial established at the Valcartier Forest Experiment Station (26 years after planting). (Photo: C. Moffet)

### Molecular characters

**M**olecular characters (fragments) provide a means of directly analyzing the genetic makeup of individual trees without having to set up field tests or plantations. With this method, genetic diversity is estimated from extracts of plant tissues, such as seeds and buds, taken from a certain number of trees (*Figure 3*). These extracts are placed in a gel medium and an electric field is applied (electrophoresis), causing the different fragments to separate according to their electrical charge and/or molecular weight. Once the fragments have stopped



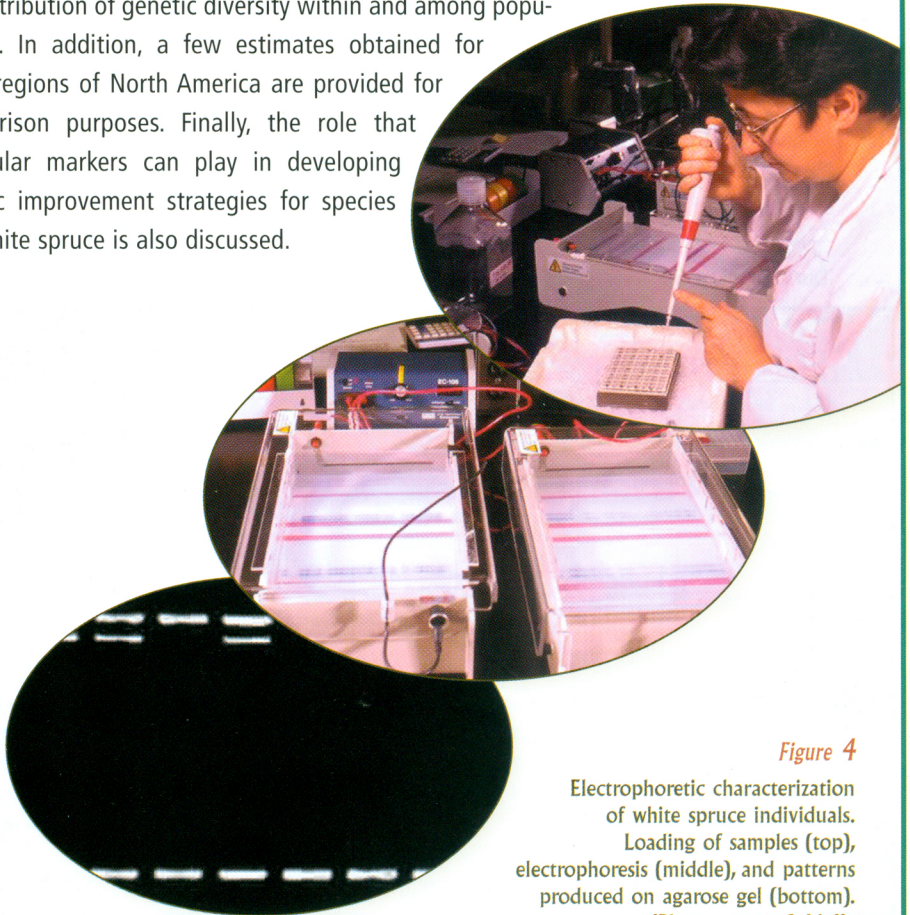
*Figure 3*

Megagametophytes and embryos (top) from which DNA can be extracted (bottom). (Photos: C. Moffet)



moving, they can be identified by adding chemical dye. The relative positions of the detected fragments are used to determine the genotype specific to each individual, when DNA analysis is being performed (Figure 4). Alternatively, their positions can be used to make inferences about the genotypes when proteins (enzymes) are used. By comparing the genotypes of several individuals and several genes, it is possible to characterize populations and species.

At the Laurentian Forestry Centre of the Canadian Forest Service, a variety of analyses have been conducted so far on the genetic diversity of natural populations of white spruce. Some of the results of these studies are presented here, namely estimates of the distribution of genetic diversity within and among populations. In addition, a few estimates obtained for other regions of North America are provided for comparison purposes. Finally, the role that molecular markers can play in developing genetic improvement strategies for species like white spruce is also discussed.



*Figure 4*

Electrophoretic characterization of white spruce individuals.

Loading of samples (top), electrophoresis (middle), and patterns produced on agarose gel (bottom).

(Photos: top - C. Moffet  
middle - C. Moffet

bottom - M. Deslauriers)



## RESULTS and DISCUSSION

Plants, and especially trees, have very high levels of genetic diversity compared with species in the other living kingdoms. This great diversity is especially beneficial for long-lived species, allowing them to survive the major environmental changes likely to occur during their lifetime and to produce progeny that are well adapted to the new conditions. Other characteristics, such as a species' taxonomic status (gymnosperm or angiosperm), the size of its geographic range, its mating system and its mode of dispersal, shed some light on the differences observed among species with regard to their genetic diversity and its distribution within and among populations. For example, forest tree species like white spruce that have a vast geographic range, reproduce through cross-pollination and have wind-dispersed pollen and seeds, generally show a high level of diversity, most of it being within populations (Hamrick and Godt 1989), as confirmed by the results presented in *Table 1*.

*Table 1*

Distribution of estimated genetic diversity in morphological and molecular characters

	% VARIANCE		STUDY AREA	No.	REFERENCES
	WITHIN-POPULATION	AMONG-POPULATION			
<b>MORPHOLOGICAL CHARACTERS</b>					
Height at 8 years	91.8	8.2	Quebec	40	Jaramillo-Correa et al. 2001
Budset at 3 years	75.4	24.6	Quebec	40	Jaramillo-Correa et al. 2001
Wood density at 24 years	89.4	10.6	Quebec, Ontario	28	Beaulieu and Corriveau 1985
Volume at 25 years (Harrington)	94.9	5.1	Quebec, Ontario	25	
<b>MOLECULAR CHARACTERS</b>					
Isoenzymes	98.9	1.1	southern Quebec	10	Deslauriers et al. 1996
	88.7	11.3*	northern Quebec	6	Tremblay and Simon 1989
	99.3	0.7	southeastern Ontario	9	Cheliak et al. 1988
	98.5	1.5	Alaska	4	Alden and Loopstra 1987
	96.2	3.8	Canada, northern United States	22	Furnier et al. 1991
ESTP†	97.6	2.4	southern Quebec	10	Jaramillo-Correa et al. 2001

\* 5.5% when hydrolases are removed

No.: number of populations or provenances studied

† ESTP: expressed sequence tag polymorphism



The genetic diversity analyses conducted on natural populations of white spruce in southern Quebec show a high level of homogeneity among populations (Deslauriers et al. 1996). In fact, only 1.1% of the estimated genetic diversity is attributable to differences among populations. Similar results have been reported for natural populations in Ontario (0.7%) and Alaska (1.5%) and in a provenance test with sources from Canada and the United States (3.8%). The low level of among-population differentiation is due to the species' characteristics. White spruce is an anemophilous species and its pollen is transported over great distances. This factor, combined with the fact that its populations are fairly evenly distributed, promotes the exchange of genes among populations. Hence, it is rare to find alleles that are unique to a given population, and the frequencies of the main alleles are generally similar from one population to another.

As in the case of biochemical markers (isoenzymes), the vast majority of the genetic variability found in the morphological characters of white spruce is located within populations (Table 1). In fact, analyses of provenance tests including sources from southern Ontario and Quebec show that between 5% and 25% of this variability is due to differences among the populations, depending on the trait studied (Figure 5).

Even though there is generally agreement between morphological and molecular characters in this species, some such as budset and wood density seem to respond to adaptive pressure.



*Figure 5*

Illustration of the variability in size of white spruce logs harvested in a provenance test. (Photo: J. Beaulieu)

Isolated white spruce populations located at the northern limit of the species' distribution in northern Quebec (Tremblay and Simon 1989) appear to be more differentiated than populations in the south, with 11.3% of genetic diversity attributable to among-population differences. However, since the studies done in southern and northern Quebec differ in the methodologies used, it is difficult to demonstrate that these differences in genetic differentiation are truly of the order of magnitude observed. Besides, when rarely used enzymes are eliminated, the percentage of population differentiation is considerably reduced. However, greater differentiation in populations could be expected, theoretically at least, at the edge of a species' distribution owing to the more marginal conditions found there and the lower chances of survival after sexual reproduction.

## CONCLUSIONS

Studies on the genetic diversity of white spruce in southern Quebec indicate that conservation efforts need not be directed at any particular population (barring exceptions) because all the populations are fairly similar genetically, despite the huge distances that may separate them (over 800 km). This low level of differentiation among populations can also be seen in the yields obtained in various genetic tests. Although significant differences are observed in the means of the different provenances tested, no signs of poor adaptation have so far been identified in any given provenance of this species.

The forest resource is coming under ever greater pressure from human population growth and the associated increase in demand for wood products. This points up the importance of implementing *in situ* conservation measures, such as parks and reserves, and *ex situ* measures, including seed banks and provenance tests, even if populations show a low level of differentiation, in order to protect the species' potential. In addition, given the uncertainty associated with the possibility of major climate change, it is wise to adopt conservation strategies for using and preserving genetic resources.

Effective genetic improvement strategies can also help us to maintain and even raise the levels of genetic diversity within and among the populations of a given species. For exam-



ple, a study was conducted with isoenzyme markers (Desponts et al. 1993) to assess the impact of selection on the genetic variability of white spruce in Quebec. It was discovered that the few dozen individuals selected for their great adaptability and that made up the breeding population had most of the allele forms present in natural populations. This type of information is particularly important because growing improved varieties of species such as white spruce in areas dedicated to timber production can help in meeting the increasing demand for the resource, while reducing pressure on the natural forest and ensuring the conservation and effective management of genetic resources.

## FOR FURTHER INFORMATION

Anyone with comments or suggestions regarding the information provided in this leaflet is invited to contact the authors by e-mail at [beaulieu@cfl.forestry.ca](mailto:beaulieu@cfl.forestry.ca).

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