



Breeding program and strategy for white spruce in Quebec

Jean Beaulieu

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ABSTRACT

This information report presents the strategy for the genetic improvement of white spruce (*Picea glauca* [Moench] Voss) set up in Quebec by the Canadian Forest Service. A brief overview of the land ownership in Quebec and of the context in which the breeding program was initiated and developed is set out. Furthermore, from the report, one can see that the breeding strategy is based on material developed and genetic information acquired over many decades. As the Canadian Forest Service moves away from the management of the white spruce breeding program, this report will be essential for technology transfer.

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RÉSUMÉ

Ce rapport d'information présente la stratégie d'amélioration génétique de l'épinette blanche (*Picea glauca* [Moench] Voss) mise en place au Québec par le Service canadien des forêts. On y fait un bref survol du régime de propriété existant au Québec et du contexte dans lequel le programme d'amélioration a été initié et poursuivi. De plus, on pourra constater au cours de la lecture de ce rapport que la stratégie d'amélioration s'appuie sur du matériel génétique divers et sur des connaissances de la génétique de l'espèce acquises au cours de plusieurs décennies. Le Service canadien des forêts délaissant la direction du programme d'amélioration, ce document se veut aussi un moyen privilégié de transfert de technologie.

INTRODUCTION

Since plants first began to be domesticated 10,000 years ago in the Near East (Simmonds 1988), spectacular increases have been seen in the productivity of certain species, especially agricultural crops. However, these remarkable results have sometimes been attained at the expense of a reduction in the genetic diversity of the target species. The strategy of conserving only the best performing varieties has made species more vulnerable to adverse biotic and abiotic agents. The loss of diversity has been caused to a large extent by reliance on the practice of recurrent selections without any concern for preserving the so-called wild varieties of species. A number of anthropologists even believe that the disappearance of the Mayan civilization can be linked to the destruction, by a virus, of the handful of corn varieties the Mayans used for food (Rhoades 1991). Fortunately, humankind has learned some lessons from such errors. In fact, conservation of biodiversity and genetic diversity have become important watchwords in today's world.

The domestication of forest species began much later and has, with a few exceptions, tended to be fairly passive (Libby 1987). Hence, the domestication work done so far is unlikely to have caused a deterioration of forest gene pools. However, this does not mean that all human intervention has had no adverse effects. For example, inappropriate harvesting methods may have had negative, albeit unintentional, impacts in some cases. Harvesting methods like those used a few decades ago whereby all the quality stems were removed without ensuring adequate protection for natural regeneration may have created dysgenic effects in forest populations (Ledig 1992). On the other hand, since foresters, unlike agronomists, do not seek to adapt the environment to suit the cultivated species (Palmberg-Lerche 1993), the risks are not as great as in agriculture.

Nonetheless, the forest resource is under ever-greater pressure from population growth (annual world demand for wood is expected to reach 5 billion m³ in the year 2010 (Hägglund 1994), and the resulting habitat destruction. Effective breeding strategies may aid in controlling and even raising levels of genetic diversity within and among populations, increasing yield on reforested land, thereby reducing pressure on the natural forest and maximizing the use of available genetic resources with a view to sustainable development.

To be able to avert errors that could lead to genetic impoverishment and to implement the most

effective strategies possible, tree breeders must have an in-depth knowledge of the extent of genetic variation present in the species. They must also know the mating system and the genetic differences related to viability, fertility and reproductive success (Brown *et al.* 1984). In short, they need to understand the mechanisms involved in creating the new generation while also preserving the heritage of previous generations. This information is particularly important for ensuring effective management of future seed orchards and formulating an enlightened policy on deploying improved material in a given territory.

LAND OWNERSHIP AND ADMINISTRATIVE RESPONSIBILITIES

More than 90% of the land in Quebec is publicly owned (Parent 1994). Furthermore, less than 14% of private land is made up of large single holdings of over 800 ha. The federal and provincial governments both conduct research in forestry; however, management of publicly owned forest land comes under exclusive provincial jurisdiction, although the federal government provides funding through sectoral agreements. The Quebec government, through its Forest Act, has undertaken to provide the seed required to reforest public and private land. Research on genetic improvement of forest species is carried out by researchers with the Ministère des Ressources naturelles du Québec and the Canadian Forest Service. In Quebec, unlike elsewhere in Canada and in the United States, there are no co-operatives that represent the interests of all organizations involved in tree improvement activities. Some private companies have in the past expressed interest in setting up a structure of this type and even initiated breeding programs; however, under the current land ownership and forestry regime, their eagerness to get involved has diminished considerably. It is in this context that provincial and federal researchers have reached an agreement on how to split the responsibilities related to the different tree breeding programs in Quebec. The object of this agreement is to avoid duplication of effort and respect existing jurisdictions. In addition, the federal government has stated that it intends to withdraw from tree breeding programs as of 1996 and thereafter focus on advanced genetics and biotechnology research. This document is therefore intended as a summary of the strategy that we have been pursuing

with respect to white spruce in Quebec. It should make it possible to better publicize the results obtained in this area and ease the transfer of white spruce breeding programs to the future managers of this activity.

WHITE SPRUCE

White spruce (*Picea glauca* (Moench) Voss) is a coniferous species whose range encompasses nearly all of Canada and extends into the United States, particularly Alaska and the Great Lakes States. Although white spruce rarely forms pure stands, it is very abundant and is one of the most important species for the lumber and pulp and paper industries (Hosie 1972). White spruce is an allogamous plant that reproduces mainly through intraspecific crosses (Cheliak *et al.* 1985, Schoen and Stewart 1986), although interspecific crosses can occur (Gordon 1976, 1990) and the species forms natural hybrids with Sitka (*Picea sitchensis* (Bong.) Carr.) and Engelmann spruce (*Picea engelmannii* Parry ex Engelm.) in the western part of its range. It is also capable of self-pollination (Coles and Fowler 1976, Fowler and Park 1983, Park *et al.* 1984). White spruce grows in a variety of soils and climates, which shows its considerable adaptability, but performs best on well-drained or rocky, silty soils (Marie-Victorin 1964). The trees can attain heights of 35 m and diameters of up to 1.2 m. Reforestation efforts directed at this species in Quebec began in the 1960s and peaked in 1988, when nearly 70 million white spruce seedlings were planted. Since then, this activity has declined, and projections to the year 2000 indicate that 33 million seedlings will be planted annually (Masse and April 1993).

ESTABLISHMENT OF THE QUEBEC BREEDING PROGRAM FOR WHITE SPRUCE

The earliest research in Quebec directed at understanding the genecology of white spruce dates back to the late 1950s and early 1960s. About a dozen provenance tests were set up in Quebec during that period (Beaulieu 1994). In addition, half-sib progeny tests including open-pollinated families from Quebec and Ontario were established during the 1970s and 1980s for the same purpose. Numerous studies have been conducted since then using this material, in order to quantify the level of genetic variability present in white spruce. Among the traits

studied are survival after outplanting, height and diameter growth, and phenology (Corriveau and Boudoux 1971, Li *et al.* 1993b); wood density (Beaulieu and Corriveau 1985, Corriveau *et al.* 1987; Corriveau *et al.* 1990, Corriveau *et al.* 1991); and enzyme molecular forms (Despouts *et al.* 1993, Tremblay and Simon 1989). Results reported in these studies and in others have indicated that like most conifers, white spruce is genetically highly variable and that it would be advantageous to pursue research and development work to use this variability to obtain better products (Nienstaedt 1969, Nienstaedt and Teich 1971). Furthermore, the technological advances of recent decades in fields such as plant propagation and biotechnology are opening up new horizons and promising avenues for implementing increasingly effective strategies.

BREEDING ZONES

Where little or no change occurs in the demand for wood products manufactured from a given tree species and there are, in a given territory, varieties that are fairly well adapted to local environmental conditions, a single breeding population can generally be used to develop so-called plastic varieties, that is, ones which will generally perform well throughout the territory. This strategy may nonetheless prove unproductive in certain specific situations. Obviously, it is difficult to have precise knowledge of all the different environmental conditions in which the varieties derived from the single breeding population will be used. Furthermore, economic and environmental changes may jeopardize the work accomplished (Namkoong *et al.* 1988).

The presence of limited adaptive ability, as suspected or detected by a genotype-environment interaction in genetic testing, has led tree breeders to delineate seed transfer and breeding zones. The maximum number of breeding zones is generally constrained by economic factors, since for each zone, a separate breeding population and crossing, testing and selection programs must be maintained.

Genotype-environment interactions have been noted in many species in Quebec (Beaulieu *et al.* 1989; Corriveau *et al.* 1989), although the occurrence in white spruce appears to be low. In a study conducted at three test sites on the height of 8-year-old trees from 285 white spruce families representing 57 seed sources, no genotype-environment interaction was detected (Li *et al.* 1993b). Further phenotypic surveys were carried out on these trees at age 13. Principal component analyses were then conducted

using data on total seedling heights (at ages 1, 2 and 3), on budburst and budset at age 3, as well as height at 8 and 13 years of age, at genecological test sites. A linear regression model was built relating family scores on the two main axes to the geographic locations of the seed sources (Li *et al.* 1993a). The results of this study showed that it would be better to divide the portion of Quebec covered by the white spruce reforestation program into two parts based mainly on latitude. Based on these results, we proposed that two breeding zones be created for the white spruce in Quebec on an interim basis. The first is essentially the maple forest zone and the second is the balsam fir/yellow birch vegetation zone.

BREEDING STRATEGY

The ultimate goal of any tree breeding program is to change, within a breeding population, the frequency of genes responsible for the expression of desired traits, while conserving genetic variability among the genes involved in the species' adaptation. To do this, trees with desirable traits are selected, and using genetic recombination, new individuals are generated from which the next generation of parent trees is selected. This process is called recurrent selection. Mating systems of varying degrees of sophistication, depending on the purposes at hand and the life-history characteristics of the species concerned, can be used to cross the selected individuals and create successive generations.

The size of the breeding population is of great importance in a breeding program. In fact, use of the recurrent selection method in a small population promotes high levels of inbreeding after a few generations. The rate at which co-ancestry is introduced depends to a great extent on the size of the original population (number of parents in generation 0). The size of the breeding population also has a marked influence on the probability of loss of favorable alleles owing to the phenomenon of random genetic drift (Weir and Todd 1993). Theoretical studies have shown that, for a breeding population of an allogamous species, 50 is the smallest number of individuals for which inbreeding and the risk of loss of favorable alleles can be controlled over the long term (Namkoong *et al.* 1980). In the first breeding generations, however, it is advantageous to maintain much larger populations (Namkoong *et al.* 1988).

Multiple populations and breeding groups

A wide range of strategies can be proposed, from simple recurrent selections within a single breeding population to methods designed to capitalize on heterosis among hybrids in multiple populations. The approach that is adopted should, in addition to allowing the tree breeder to attain certain goals, provide the flexibility needed to cope with future environmental and economic changes. From this perspective, a strategy drawing on several populations or subdivided populations would appear to be better than one based on a single population. With such an approach, it should conceivably be possible to develop synthetic varieties that have improved traits or are better adapted to sites of given quality, and to readily integrate new genotypes into the existing breeding process by forming a new population.

The tree breeder must also develop a breeding strategy that can be used to establish seed orchards where the degree of relatedness among the different members can be controlled. Hence, not only is it essential to favor a maximum level of intercrossing between trees, but the trees must also be as genetically diverse as possible.

Van Buijtenen (1976) proposed a breeding strategy that can completely eliminate related matings in seed orchards. This strategy was tested, among others, on the loblolly pine (*Pinus taeda*) (Van Buijtenen and Lowe 1979), and a variation of the strategy was adopted for spruce in the Maritimes (Fowler 1986).

Under this strategy, the original breeding population is divided into separate groups, and controlled crosses are carried out exclusively within these groups. The amount of time it takes for inbreeding to occur depends on the mating and selection methods used and the size of the group. Co-ancestry effects occur in the long term particularly in relation to the quantity of seed produced by controlled crosses, and this is another factor with which tree breeders eventually have to grapple. However, Woods and Heaman (1989) showed that, in Douglas-fir, an inbreeding level of 0.25 or lower, namely that resulting from full-sib matings, is acceptable in this regard.

By subdividing a breeding population, it is feasible when establishing seed orchards to restrict crossings to the intergroup type. In such a case, only one tree per breeding group would be selected to be part of the seed orchard. In this way, the breeder would ensure long-term quality of the seed produced and co-ancestry control. However, when this strategy is used, selection intensity tends to be lower than when a larger single population is employed.

The breeding strategy that we advocate and are applying to white spruce is based on the model Van Buijtenen proposed in 1976. Breeding populations will be made up of 240 superior individuals once completed and will be subdivided into breeding groups within which double-pair matings will be made. To produce improved propagules, we recommend various methods, such as establishing seed orchards made up of unrelated individuals. The progress achieved so far and the remaining stages in this work are described below.

First generation

Selection criteria

Owing to the integration of the lumber and pulp and paper industries, for many years now most of the material harvested in forests has been directed to sawmills, with wood residues and chips then going to pulp and paper mills. White spruce, as one of the main species exploited by these two industries, is valued primarily for its dimensions and its straight trunk. Hence, these are two of the characteristics used in selecting trees for the first-generation breeding population. Other criteria have also been employed, for example, branch size and angle, adaptation as reflected in a low mortality rate, and tolerance or resistance to insects and disease and adverse abiotic factors, such as drought and freezing.

Selection of parents

As noted above, research on the genetics of white spruce in Quebec has spanned several decades and has produced information that is of variable value as far as genetics is concerned. However, the fact that this work has been done over such a lengthy period has fostered the development of a breeding strategy that makes use of multiple populations that are subdivided into breeding groups.

First set of trees selected

A first set of about 100 trees included in the first-generation breeding population was formed by making plus-tree selections in the best-performing

seed sources as identified in provenance trials initiated in the 1950s and 1960s (Appendix 1). A dozen or so provenances are represented (Appendix 2). The overall 20-year height average of recommended provenances was approximately 15% greater than that of seed sources sampled in Quebec and included in these trials.

Breeding groups

The first set of trees selected included in the breeding population was subdivided into six breeding groups, each with some 20 individuals. Trees with potential parental links, that is, selected from the same seed source, were placed in the same group. Similarly, provenances that came from basically the same forest region were placed in the same breeding group (Appendix 2). In following this procedure, our aim was to ensure that any co-ancestry that existed at the outset would be confined within the breeding groups.

Other sets of trees selected

Three other sets of trees, including an elite population, were formed on the basis of selections made in half-sib progeny tests established during the 1970s and 1980s. Breeding values for mother trees and selection indices for each progeny were calculated for height growth using the Best Linear Prediction method (White and Hodge 1989). To perform the necessary calculations, the genetic tests were grouped according to their composition. For example, the Rivière-Bleue and Amqui tests were analyzed jointly. They are part of Phase 1 of Experiment E410 carried out by the Canadian Forest Service in Quebec. For the Mirabel, Portage-du-Fort and Robidoux tests, forming Phase 2 of the E410 series, another joint analysis was conducted. The last group consisted of the La Patrie, Mastigouche and Dablon tests, all of which were part of the E560 series. Statistical analyses were performed to estimate family variance, both between experimental plots and within plots, along with heritabilities and Type B genetic correlations, i.e. between sites, so as to be able to estimate the breeding values and selection indices.

A forward selection was then made based on the results obtained. The families with the highest predicted breeding values were selected first, and then a mass selection was made from within these families by incorporating the other customary selection criteria. Whenever possible, trees were selected on every site. A maximum of four trees was selected from each family. The genetic values calculated for each progeny

from the computed selection indices are considered approximations of the expected genetic gains. The gains expected from the family selection alone, shown in Appendix 3, include a height increase of about 16% for so-called support breeding populations, that is, those which are not part of the elite, and 26% for the elite population. The latter was formed by selecting trees from each of the 10 families with the highest breeding values.

In all, some 360 trees were selected (Appendix 4) to complete the breeding populations. More than 5,000 grafts were produced during the winter of 1994. A number of the resulting clones will be part of the breeding populations in both breeding zones, whereas others will be used exclusively for one or the other.

The number of trees selected to date is greater than the final size of the breeding populations. It will be reduced within about 5 years based on wood density and each tree's propensity for early flowering. After this final selection phase, 240 trees, including 40 from the elite population and the plus-trees selected from superior seed sources, will serve as the basis for future generations in each breeding zone. All these trees will be placed in breeding orchards and submitted to flower induction treatments to speed up the breeding cycle.

Breeding groups

The superior genotypes selected within half-sib families will also be assembled in breeding groups, each containing 20 trees. The proposed strategy that was implemented for the first generation and will be repeated over subsequent generations is presented in Figure 1.

Mating designs

Polycross

General combining ability of selected trees will be estimated, using progeny, at multiple test sites. The progeny are obtained through controlled crossing using a mixture of pollen from a certain number of trees. The polymix, or pollen mixture, is composed of an equal amount of pollen from some 20 different trees in keeping with the recommendations of Fowler (1987). Two conditions had to be met in selecting the pollen donor trees: they all had to be from the same region as the individuals to be used for seed orchards so as to ensure pollen compatibility, and they had to be able to produce enough pollen for the current generation. The

controlled crosses required to evaluate the general combining ability of the first set of selected trees were conducted over the past few years.

Partial diallel

We are using a different mating design to generate the material that will be used to make up the breeding groups for subsequent generations. This design is a partial diallel, meaning that each individual is crossed with two others to produce full-sib families. Pairing of parents is random as regards their breeding value. The full-sibs will be planted on two sites so as to create large square plots at each location (~100 trees); however, the second plantation will be established merely as a safeguard. The use of large plots will help to increase the efficiency of the within-family mass selection.

Thus, under this mating design, 40 full-sib families are generated for each breeding group of 20 trees. The families will be ranked using a best mate index (Cotterill and Dean 1990). This index is based on the assumption that the performance of full-sib progeny can be estimated as the sum of the general combining abilities of their two parents:

$$I_{BM}^m = GCA^f_j + GCA^m_j,$$

where, I_{BM}^m = best mate index,

GCA^f_j = general combining ability of the mother for trait j,

GCA^m_j = general combining ability of the father for trait j.

More than 90% of the crosses planned for the first six breeding groups created from the 100 or so first parents selected in provenance tests have already been carried out. A first group of seed lots was sown in winter 1995 in the Laurentian Forestry Centre greenhouses. Production of seedlings to create the two selection plantations will be completed during 1996.

With regard to the trees recently selected within half-sib families to complete the breeding populations, crosses within breeding groups will be permitted only between unrelated individuals. Hence, no tree can be crossed with another tree from its own family, and each family can be represented by a maximum of four trees.

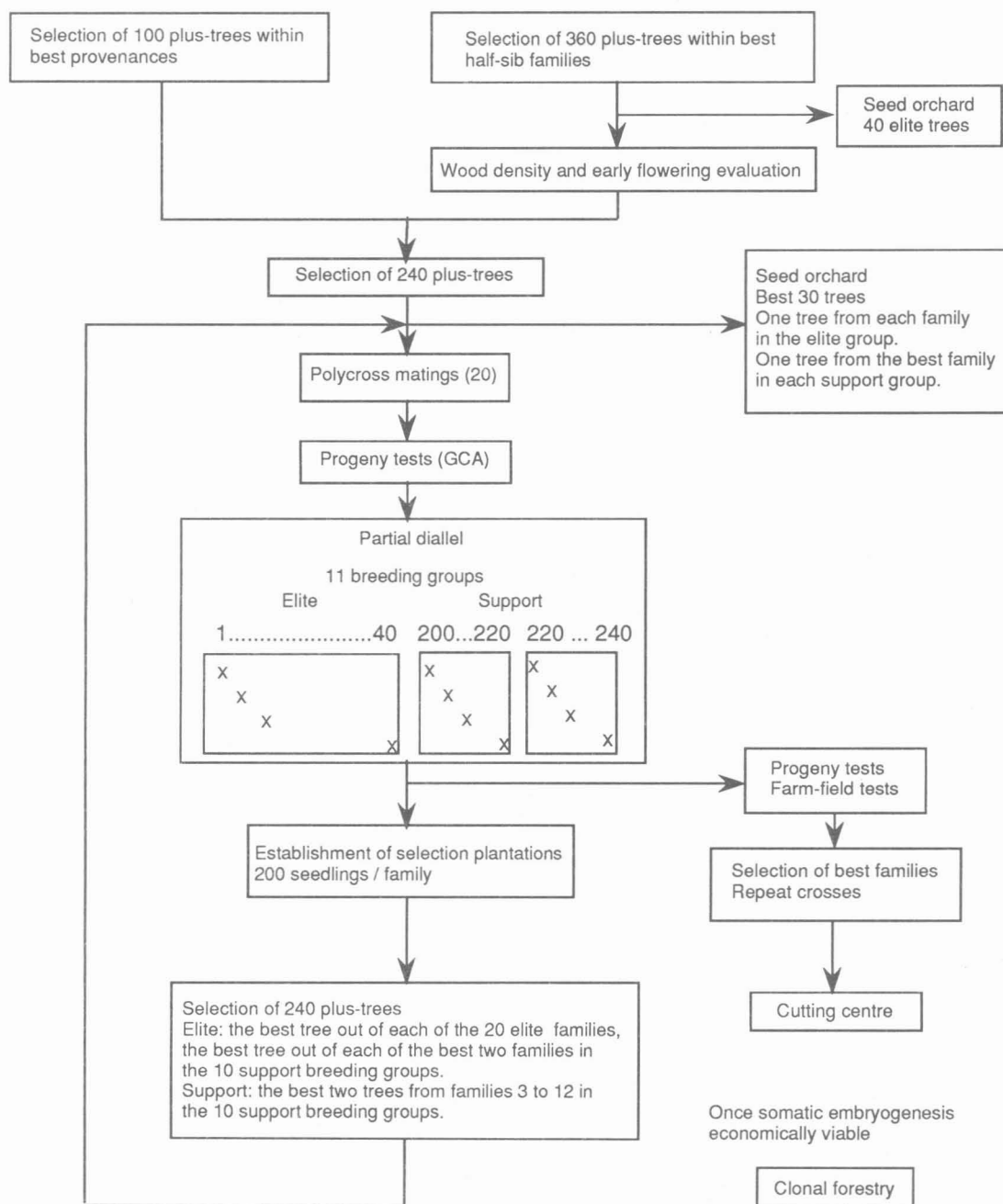


Figure 1. Strategy for breeding white spruce and producing improved material in Quebec.

Unrelated progeny

Once the individuals in the elite group reach reproductive age, they will be ranked on the basis of their breeding value. Crosses will then be performed among the trees based on rank, using an approach called positive assortative mating. Through this method, we aim to achieve higher genetic gains compared with an approach using randomly ranked parents (Mahalovich and Bridgwater 1989). Each parent will be crossed with only one other parent, thereby generating 20 families of unrelated full-sibs. They will be planted in selection plantations with the other families derived from the partial diallel mating design.

Testing

Seven field tests are planned for southern Quebec in 1997 and 1998 in order to evaluate the general combining abilities of the first 100 or so parents for which polycross matings were made. Phenotype measurements taken at about age 10 will be used to calculate the desired estimates. Seeding was carried out in February 1995 in the Laurentian Forestry Centre greenhouses. The test sites will be spread out across Quebec so as to cover the widest possible range of ecological conditions. An experimental design with eight interlocking blocks will be used (Libby and Cockerham 1980). Two-tree plots will be employed to minimize the number of plots left empty owing to mortality and to facilitate analysis. The interlocking layout is especially useful because it permits systematic thinning while also maintaining a balanced experimental design.

Once the new selections made within half-sib family tests have produced the desired progeny through polycross matings, other tests will be set up to assess the general combining ability of this new series of parent trees. The same experimental design will be used again.

In order to be able to compare the estimates of general combining ability obtained for parents in two separate series of tests, some control lots are included in each test. These control lots include progeny from Lac Iroquois and Saint-Roch-de-Mékinac, which were selected because they had shown an average yield in previous genecological tests. In addition, we are using progeny representing a recommended provenance, i.e. the Cushing seed source, and bulked seeds harvested in the breeding orchard to obtain a preliminary estimate of the progress achieved through selection and breeding.

Deployment of improved material

Further to the agreement reached in the 1970s on the division of responsibility, researchers with the Ministère des Ressources naturelles du Québec were mandated to produce improved seed. Since then, the Ministère has established a network of 17 first-generation clonal seed orchards, in order to provide an ongoing supply of quality seed over the short term. Each orchard contains approximately 200 clones. During the period when parents were being selected, only sketchy information was available to ensure safe seed transfer throughout the territory. As a result, these orchards were composed primarily of phenotypically superior trees selected in natural forests in each of the regions served by the orchards. Copies of these plus-trees are being conserved in clone banks as well. This material is due to be evaluated over the next few years, after which part of the material might be integrated into the breeding program that is already under way. It could also constitute a reservoir of genetic diversity containing well-characterized material and eventually be used to support existing breeding populations. Evaluation of the parent trees used to set up seed orchards will also make it possible to direct cone collection efforts to a subset of trees in such a way as to enhance the genetic gains realized.

Part of the improved material is deployed also in the form of vegetatively reproduced propagules. The forest seed division of the Ministère des Ressources naturelles du Québec performs controlled crosses on a regular basis among individuals from the breeding populations in order to supply the vegetative propagation centre located in Saint-Modeste. The seeds produced are propagated through cutting cycles and the rooted cuttings are then used directly in reforestation. By this method, multifamily varieties are created, which are composed of clone mixtures representing a large number of families.

To capitalize on the recent data obtained from the E410 and E560 series genecological tests and increase the expected genetic gains, we recommend also that new clonal seed orchards be established right away using members of families whose parent trees have higher breeding values (Fig. 1). These seed orchards could reach full production around the year 2010 and serve as an intermediate stage between the existing first-generation orchards and second-generation ones.

Advanced generations

Selection of parents

Breeding populations of subsequent generations will be of a fixed size, that is 240 trees from the selection plantations. They will be gathered together in breeding groups of 20 trees, with the exception of the elite group, which will include 40 individuals. Each breeding group will thus be formed again by selecting the two best phenotypes from each 100-tree plot representing unrelated full-sib families ranked from 3 to 12 among the 40 generated by the partial diallel. The families will be ranked by means of a best mate index.

With regard to the elite group, half of its members will be progeny of its constituent trees during the previous generation. Each of the unrelated full-sib families obtained through controlled crosses will contribute its single best progeny. The other 20 members of the elite group will be selected from among the full-sibs in the 10 breeding groups, by taking one tree from each of the two families in each group with the highest best mate indices. The objective of this approach is to control the relatedness of the individuals comprising the elite group and, with each new generation, to integrate new members into this group that may potentially contribute greater genetic variability.

Mating designs

The three mating designs used for the first generation will be repeated across successive generations. However, beginning with the second generation, the pollen mixture used for the crosses required to evaluate the general combining abilities of the parent trees will be changed. Twenty trees that are not related to the parents in the breeding populations, but which come from the same regions, will have to be identified and propagated vegetatively to secure a continuous supply of pollen. These trees should have breeding values of zero or close to zero so that the differences observed among the progeny merely reflect differences among the mother trees only, i.e. those in the breeding populations.

Testing

Starting with the second generation, in addition to implementing genetic tests similar to those used with the first generation, we recommend that farm-field tests be established in nurseries to identify the most promising specific crosses. Parental pairs with the best specific combining abilities can be determined based on the results of their progeny at 5 years of age.

Crosses between the identified pairs can then be repeated in order to supply the Saint-Modeste cutting centre with improved seed.

Farm-field tests should be set up in nurseries or on intensively prepared sites. In this type of test, it is necessary to control for any effects due to competition. Spacings of seedlings should be narrower than those normally used for standard genetic tests in the forest, because these field tests are of quite short duration. However, an interlocking block design should be used so that thinnings can be carried out without destroying the layout structure in the event the test is to be maintained for a longer period.

Deployment of improved material

Clonal seed orchards should also be used to produce improved material in advanced generations. We recommend, however, that these orchards be indoors so as to control sources of contamination. In addition, mass-pollination could be used to ensure good panmixia within the orchards. The orchards should be made up of the best phenotype of each full-sib family derived from the elite population and the best phenotype from the family with the highest best mate index in each breeding group. Thus, each seed orchard would be composed of 30 superior genotypes. The goal of establishing indoor clonal orchards is to develop varieties with good plasticity, vigor, form and wood quality characteristics.

Part of the improved material should still be produced in the form of multifamily varieties in the advanced generation stage. If the additional cost associated with this type of propagation declines in the future, a higher percentage of reforestation could be carried out using this type of propagule, given the additional genetic gains that could be expected.

MONITORING LONG-TERM PROGRESS

The progress achieved through genetic improvement should be monitored over the long term. Tests should be set up to compare the yield of improved material of a given generation with that of varieties created in preceding generations. Furthermore, to permit comparison, these tests should also include control progeny representing unimproved provenances. This would make it possible to assess as accurately as possible the genetic gains realized in each generation.

With regard to the multifamily varieties produced by using cuttings from seedlings derived through controlled crosses, it would also be advisable, here again for comparison purposes, to establish tests

which, in addition to including improved multifamily varieties from the current generation, would incorporate multifamily varieties representing unimproved provenances and others from the previous breeding generation.

FUTURE PROSPECTS

Improvements should be made to many of the operations that are integral to the breeding program so that the expected genetic gains can be achieved. Van Buijtenen (1993) has identified four areas to which we need to devote attention. They are: 1) using non-additive genetic variance; 2) increasing selection intensity; 3) eliminating pollen contamination in seed orchards; and 4) using the best genotypes on the best sites.

In the near future, vegetative propagation techniques, such as somatic embryogenesis, either used alone or in combination with cutting methods, should be effective enough to be operational and to compete in terms of cost with classical methods of propagule production. Therefore, the breeding strategy presented here could be modified to make broader use of clonal forestry techniques and varieties adapted to specific environmental conditions. This would allow us to capitalize more on the specific combining ability of certain genotypes and increase the number of breeding populations. In the meantime, however, these vegetative propagation techniques will allow us to generate enough copies of a large number of genotypes to be able to establish true clonal tests. These will enable us to estimate the extent of non-additive genetic variance and hence determine the relevance of pursuing research work to establish a true clonal forestry approach.

In advanced genetics, ever greater use is being made of molecular biology and genetic engineering. Research is currently under way to develop genetic markers linked to characteristics such as wood density. These markers will assist tree breeders in selecting parent trees. A few needles will be the only material needed to extract the required DNA and characterize each tree. Hence, it is conceivable that in selecting the best single progeny of each family in selection plantations, this type of marker could be used to identify the genotype with the best potential among a few candidates chosen on the basis of other characteristics. It is likely that genetic markers will also be available for other traits, giving breeders a better basis for decision making. Genetic markers will make it possible to increase selection intensity

considerably without going through all the normal testing stages.

Genetic transformation is another tool that tree breeders will be able to use in the future. Research is continuing at present to introduce *Bt* toxin genes into the white spruce genome. Such a transformation would open up the possibility of developing varieties that are resistant to the spruce budworm. A prudent strategy should be formulated for deploying this transformed material in order to avoid undue selection pressure on the insect, which could result in strains resistant to *Bt*.

Research dealing with seed production in indoor orchards is currently being carried out at the Ministère des Ressources naturelles du Québec. The results of this work, coupled with the knowledge acquired through flower induction and mass-pollination, will undoubtedly help to meet expectations with respect to achieving genetic gains in advanced generations.

CONCLUSIONS

The white spruce breeding program in Quebec is one of the most important and certainly the most advanced of its kind. In view of the fact that the Canadian Forest Service is withdrawing from the tree breeding sector, even greater concerted efforts will be required on the part of the individuals and organizations concerned with this species and related improvement work. In this document, we have described the breeding strategy that we initiated and have been carrying out in recent years, together with the most significant progress achieved. We hope that this summary will enable those who are taking over this responsibility to do so with as few problems as possible.

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progress achieved so far, he served as a source of intellectual motivation for all the members of his team.

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The success of a breeding program can also be measured by the interest that users show in the material produced. Our colleagues in the forest seed division have always been very supportive, and we thank them accordingly, especially Luc Masse.

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REFERENCES

- Beaulieu, J. 1994. L'amélioration génétique et le reboisement. Pages 107-133 in A.L. D'Aoust et R. Doucet, org. La régénération de la zone de la forêt mixte. Compte rendu du Colloque no 112 de l'ACFAS. Le 19 mai 1994, Université du Québec à Montréal, Montréal, Qc.
- Beaulieu, J.; Corriveau, A. 1985. Variabilité de la densité du bois et de la production des provenances d'épinette blanche, 20 ans après plantation. Can. J. For. Res. 15:833-838.
- Beaulieu, J.; Corriveau, A.; Daoust, G. 1989. Phenotypic stability and delineation of black spruce breeding zones in Quebec. For. Can. - Quebec Region, Inf. Rep. LAU-X-85E.
- Brown, A.H.D.; Barret, S.C.H.; Morgan, G.F. 1984. Mating system estimation in forest trees: models, methods and meanings. Pages 32-49 in H.-R. Gregorius, ed. Population genetics in forestry. Proc. IUFRO working party Ecological and population genetics. Gottingen, August 21-24, 1984. Springer-Verlag.
- Cheliak, W.M.; Pitel, J.A.; Murray, G. 1985. Population structure and the mating system of white spruce. Can. J. For. Res. 15:301-308.
- Coles, J.F.; Fowler, D.P. 1976. Inbreeding in neighboring trees in two white spruce populations. Silvae Genet. 25:29-34.
- Corriveau, A.; Boudoux, M. 1971. Le développement des provenances d'épinette blanche de la région forestière des Grands-Lacs et du Saint-Laurent au Québec. Serv. can. pêches, Serv. can. for., Lab. rech. for., Sainte-Foy, Qc. Rapp. inf. Q-F-X-15.
- Corriveau, A.; Beaulieu, J.; Daoust, G. 1989. Phenotypic stability and productivity of Central European Norway spruce provenances in Québec, Canada. In L.-G. Stener and M. Werner, eds. Proc. IUFRO Working Party S 2.02-11 meeting. Rep. No. 11: 28-51.
- Corriveau, A.; Beaulieu, J.; Daoust, G. 1991. Heritability and genetic correlations of wood characters of Upper Ottawa Valley white spruce populations grown in Quebec. For. Chron. 67:698-705.
- Corriveau, A.; Beaulieu, J.; Mothe, F. 1987. Wood density of natural white spruce populations in Quebec. Can. J. For. Res. 17:675-682.
- Corriveau, A.; Beaulieu, J.; Mothe, F.; Poliquin, J.; Doucet, J. 1990. Densité et largeur des cernes des populations d'épinettes blanches de la région forestière des Grands-Lacs et du Saint-Laurent. Can. J. For. Res. 20:121-129.
- Cotterill, P.P.; Dean, C.A. 1990. Successful tree breeding with index selection. CSIRO, Australia.
- Despots, M.; Plourde, A.; Beaulieu, J.; Daoust, G. 1993. Impact de la sélection sur la variabilité génétique de l'épinette blanche au Québec. Can. J. For. Res. 23:1196-1202.
- Fowler, D.P. 1986. Strategies for the genetic improvement of important tree species in the Maritimes. Can. For. Serv., Maritimes, Fredericton, N.B. Inf. Rep. M-X-156.
- Fowler, D.P. 1987. In defense of the polycross. Can. J. For. Res. 17:1624-1627.
- Fowler, D.P.; Park, Y.S. 1983. Population studies of white spruce. I. Effects of self-pollination. Can. J. For. Res. 13:1133-1138.
- Gordon, A.G. 1976. The taxonomy and genetics of *Picea rubens* and its relationship to *Picea mariana*. Can. J. Bot. 54:781-813.
- Gordon, A.G. 1990. Crossability in the Genus *Picea* with Special Emphasis on the Mexican Species. Joint Meeting of Western Forest Genetics Association and IUFRO Working Parties S2.02-05, 06, 12 and 14. Olympia, Wash. August 20-24, 1990.
- Hägglund, B. 1994. Biodiversity conservation and modern forestry practices. Pages 47-55 in Tree breeding, population genetics and conservation of genes. The Marcus Wallenberg Foundation. Symp. Proc. 9.
- Hosie, R.C. 1972. Native Trees of Canada. Environ. Can., Can. For. Serv., Ottawa, Ont.
- Ledig, F.T. 1992. Human impacts on genetic diversity in forest ecosystems. Oikos 63:87-108.
- Li, P.; Beaulieu, J.; Bousquet, J. 1993a. Developing provisional seed transfer guidelines for white spruce in Quebec: a research outline. Pages 27-29 in G. Daoust and J. Beaulieu, org. Proceedings of the one-day symposium on research and development work on the genetics of white spruce in Quebec. Nat. Resour. Can., Can. For. Serv., Sainte-Foy, Qc. Inf. Rep. LAU-X-105B.
- Li, P.; Beaulieu, J.; Corriveau, A.; Bousquet, J. 1993b. Genetic variation in juvenile growth and phenology in a white spruce provenance-progeny test. Silvae Genet. 42:52-60.
- Libby, W.J. 1987. Genetic resources and variation in forest trees. Pages 199-209 in A.J. Abbott and R.K. Atkin, eds. Improving vegetatively propagated crops. Academic Press Ltd., New York. Chap. 11.
- Libby, W.J.; Cockerham, C.C. 1980. Random non-contiguous plots in interlocking field layouts. Silvae Genet. 29:183-190.
- Mahalovich, M.F.; Bridgwater, F.E. 1989. Modelling elite populations and positive assortative mating in recurrent selection programs for general combining ability. Pages 43-49 in Proc. 20th Southern Forest Tree Improvement Conf. Charleston, S.C. Nat. Tech. Inf. Serv., Springfield, Va.

- Marie-Victorin, frère, F.E.C. 1964. Flore laurentienne. Les Presses de l'Université de Montréal, Montréal, Qc.
- Masse, L.; April, R. 1993. Supply of white spruce seeds. Page 30 in G. Daoust and J. Beaulieu, org. Proceedings of the one-day symposium on research and development work on the genetics of white spruce in Quebec. Nat. Resour. Can., Can. For. Serv., Sainte-Foy, Qc. Inf. Rep. LAU-X-105B.
- Namkoong, G.; Barnes, R.D.; Burley, J. 1980. A philosophy of breeding strategy for tropical forest trees. Commonwealth For. Inst., Oxford. Tropical For. Pap. No. 16.
- Namkoong, G.; Kang, H.C.; Brouard, J.S. 1988. Tree Breeding: Principles and Strategies. Monographs on Theoretical and Applied Genetics. Springer-Verlag, New York.
- Nienstaedt, H. 1969. White spruce seed source variation and adaptation to 14 planting sites in northeastern United States and Canada. Pages 183-194 in Proc. 11th Meeting Comm. For. Tree Breed. in Canada, Macdonald College, Ste-Anne-de-Bellevue, Qc.
- Nienstaedt, H.; Teich, A. 1971. The genetics of white spruce. U.S. Dept. Agric., For. Serv. Res. Pap. WO-15.
- Palmberg-Lerche, C. 1993. The conservation of forest genetic resources. Diversity 9(3):26-29.
- Parent, B. 1994. Ressource et industrie forestières. Portrait statistique. Édition 1994. Gouv. du Québec, Minist. For. Québec, Dir. polit. for. Publ. RN94-3099.
- Park, Y.S.; Fowler, D.P.; Coles, J.F. 1984. Population studies of white spruce. II. Natural inbreeding and relatedness among neighboring trees. Can. J. For. Res. 14:909-913.
- Rhoades, R.E. 1991. The World's Food Supply at Risk. Natl. Geogr. 179(4):74-105.
- Schoen, D.J.; Stewart, S.C. 1986. Variation in male reproductive investment and male reproductive success in white spruce. Evolution 40:1109-1120.
- Simmonds, N.W. 1988. Principes d'amélioration génétique des végétaux. C.A. St-Pierre, trad. Les Presses de l'Université Laval, Sainte-Foy, Qc.
- Tremblay, M.; Simon, J.-P. 1989. Genetic structure of marginal populations of white spruce (*Picea glauca*) at its northern limit of distribution in Nouveau-Québec. Can. J. For. Res. 19:1371-1379.
- Van Buijtenen, J.P. 1976. Mating Designs. Pages 11-20 in Proc. IUFRO Joint meeting genetic working parties on advanced-generation breeding. Bordeaux, France.
- Van Buijtenen, J.P. 1993. Overview of advanced generation breeding and production. Pages 2-9 in J. Lavereau, ed. Proc. 24th meeting CTIA, Part 2. Fredericton, N.B., Aug. 15-19, 1993.
- Van Buijtenen, J.P.; Lowe, W.J. 1979. The use of breeding groups in advanced generation breeding. Pages 59-65 in Proc. 15th South. For. Tree Improv. Conf., Starkville, Miss. June 9-21, 1979.
- Weir, R.J.; Todd, D. 1993. Third-cycle breeding strategy: a description and economic appraisal for the North Carolina State University-Industry Cooperative Tree Improvement Program. Pages 41-51 in J. Lavereau, ed. The future forests: options and economics. Proc. 24th meeting CTIA, Part 2. Fredericton, N.B., Aug. 15-19 1993.
- White, T.L.; Hodge, G.R. 1989. Predicting breeding values with applications in forest tree improvement. Kluwer Academic Publishers, Dordrecht. Forestry Sciences Vol. 33.
- Woods, J.H.; Heaman, J.C. 1989. Effect of different inbreeding levels on filled seed production in Douglas-fir. Can. J. For. Res. 19:54-59.

APPENDIX 1

Superiority of white spruce provenances from which parent trees were selected, compared with the median values for Quebec seed sources tested in Drummondville and Harrington^a

ORIGIN OF PROVENANCES	Drummondville		Harrington		
	Height ^b at age 20 (m)	Volume ^c at age 25 (m ³ /ha)	Height at age 20 (m)	Volume thinned (m ³ /ha)	Volume at age 25 (m ³ /ha)
Provenances selected					
Algonquin Park 1			6.28	138	162
Algonquin Park 2			6.53	161	125
Carnarvon	6.48	158	4.26	98	83
Sundridge	6.53	149	5.93	127	112
Monaghan			6.24	180	168
Rama Tp	6.27	142	5.64	135	120
Petawawa Natl. For. Inst.	7.00	165	6.35	172	159
Median	6.57	154	5.89	145	133
Provenances from Quebec					
Maniwaki	5.23	109	5.30	81	77
L'Annonciation	5.73	108	4.80	68	97
St-Donat	5.90	118	5.19	76	89
Harrington	5.37	128	4.02	60	49
St-Zénon	5.17	98	5.04	72	76
St-Charles-de-Mandeville	5.75	124	4.98	89	71
St-Maurice	5.75	121	4.93	89	78
Rivière-aux-Rats			5.16	100	118
Median	5.58	116	4.93	85	87
Superiority of provenances selected (%)	17.8	33.18	19.53	70.00	52.80

^a These provenance tests were established in 1958. They were made up of three complete random blocks. Each square plot initially included 144 and 81 trees spaced 1.2 m apart respectively at Drummondville and Harrington. Systematic thinning to remove every second row was carried out on each site in 1979. The volumes were estimated using Popovitch's tables (1972).

^b Superior phenotypes for use in forming the breeding population were selected on the basis of tree height observed in 1974.

^c The volumes shown are the total volumes reported per hectare, taking into account the survival rate of each provenance, following systematic thinning of every second row.

Superiority of white spruce provenances from which parent trees were selected, compared with the median values for Quebec seed sources tested at Harrington, St-Jacques-des-Piles, Grandes-Piles and Casey^a

ORIGIN OF PROVENANCES	Harrington		St-Jacques-des-Piles		Grandes-Piles		Casey	
	Height ^b at age 14 (m)	Volume at age 24 (m ³ /ha)	Height at age 14 (m)	Volume at age 24 (m ³ /ha)	Height at age 14 (m)	Volume at age 24 (m ³ /ha)	Height at age 14 (m)	Volume at age 24 (m ³ /ha)
Provenances selected								
Peterborough	3.33	132	3.09	90	3.81	217	2.21	20
Beachburg	-	-	-	-	3.57	205	2.28	14
Cushing	3.32	144	2.75	67	3.68	208	2.30	18
Beloil	3.43	150	2.85	62	3.83	225	2.03	17
Median	3.36	142	2.90	73	3.72	214	2.21	17
Provenances from Quebec								
Grandes-Piles	3.03	134	2.63	54	3.28	157	1.75	11
St-Raymond	2.92	107	2.91	76	3.42	190	1.91	12
Casey	2.91	103	2.77	63	3.46	179	1.97	12
Lac Mattawin	3.06	108	2.58	63	3.41	188	1.83	12
Franchère	3.16	116	2.75	68	3.13	169	1.99	11
Lac Baskatong	3.05	119	2.54	51	3.20	149	1.85	10
Lac Dumoine	2.91	103	3.02	74	2.95	128	2.00	9
Lac McNally	-	-	-	-	2.93	141	1.67	11
N.-D.-du-Laus	3.03	115	2.59	52	3.10	153	1.99	13
St-Sylvestre	-	-	2.67	58	2.55	90	1.96	12
Monk	3.12	124	2.71	58	3.33	129	2.17	19
Price	2.80	100	2.63	57	3.24	144	2.08	15
Lac Mitchinamicus	3.18	115	2.49	45	3.13	116	1.99	13
Lac Simard	3.10	92	2.86	65	3.23	134	1.83	9
Valcartier	2.77	108	2.59	60	3.45	153	1.88	13
Riv. Shipshaw	-	-	2.77	60	2.73	109	2.07	14
Median*	3.05	116	2.71	57	3.05	153	1.96	13
Superiority of provenances selected (%)	10.2	20.6	6.9	18.9	22.1	32.0	12.5	25.1

^a These provenance tests were established in 1964 and 1965. They consisted of 6 to 9 random blocks. Each plot contained 7 to 36 trees spaced 1.82 m apart. The volumes were estimated using Popovich's tables (1972).

^b Superior phenotypes for use in forming the breeding population were selected on the basis of tree height observed in 1974 and 1975.

* Including the Cushing and Beloil seed sources.

APPENDIX 2

List of provenances from which the parent trees of the first white spruce breeding population were selected and breeding groups.

Provenance			Number of trees	Group No.
Name	Latitude N.	Longitude W.		
Monaghan Township, Ont.	44° 10'	78° 19'	7	1
Peterborough, Ont.	44° 33'	78° 15'	13	1
Carnarvon, Ont.	45° 04'	78° 42'	10	2
Hungerford, Ont.	44° 28'	77° 15'	9	2
Rama Township, Ont.	44° 43'	79° 15'	1	2
Algonquin Park, Ont.	45° 50'	78° 30'	10	3
Sand Lake, Ont.	44° 56'	77° 02'	2	3
Sundridge, Ont.	45° 46'	79° 20'	8	3
Bromley Township, Ont.	45° 35'	76° 58'	4	4
Cormac, Ont.	45° 28'	77° 18'	2	4
Petawawa Natl. For. Inst., Ont.	45° 54'	77° 20'	14	4
At. Energy Can. Ltd., Ont.	46° 46'	77° 32'	2	5
Beachburg, Ont.	45° 44'	76° 51'	6	5
Beloeil, Qc	45° 34'	73° 12'	3	5
Cushing, Qc	45° 36'	74° 28'	4	5
Westmeath Township, Ont.	45° 45'	76° 55'	2	5
St-Maurice River, Qc	46° 55'	72° 56'	4	6
St-Zenon, Qc	46° 35'	73° 49'	6	6

APPENDIX 3

Breeding values and genetic gains expected from the selection of white spruce families

Identification	Lot	LFC	LFC	Breeding zone	Number of trees selected	Genetic gains (%)							
	number	number	number			Rivière-Bleue	Amqui	Mirabel	Portage-du-Fort	Robidoux	La Patrie	Dablon	Mastigouche
		410	560										
Cap des Rosiers	3-1	28		C	4	8.52	6.95	9.22	7.86	6.35			
Canton Garin	14-13	40		C	4	10.55	9.60	13.78	13.39	10.13			
Canton Laterrière	21-8	53		C	3	19.33	16.50	16.86	16.03	11.45			
Canton Laterrière	21-?	54		C	4	7.91	8.33	19.90	15.68	11.34			
Canton Laterrière	21-?	57		N	4	10.52	10.25	3.85	2.63	2.48			
Canton Blais	30-14	83		C	4	6.30	6.41	6.90	8.25	6.68			
Canton Quimet	31-5	86		C	4	7.08	6.46	6.39	4.77	5.02			
Canton Lesage	34-3	94		S	4			17.93	16.12	11.77			
Canton Chaumonot	36-10	108		C	4	11.36	9.13	8.47	7.31	5.84			
Canton Desaulniers	37-9	112		C	4	7.62	7.90	16.31	11.80	8.58			
St-Roch-de-Mékinac	471-1	130	126	N	4	5.24	4.89				23.60	18.30	21.49
St-Roch-de-Mékinac	471-2	131	127	C	4			22.18	18.66	15.30	22.47	18.31	18.11
St-Roch-de-Mékinac	471-4	133	129	S	4			16.45	13.63	9.88	13.63	13.19	17.15
St-Roch-de-Mékinac	471-5	134	130	C	4			14.39	13.04	9.23	38.24	29.81	28.75
Kamouraska	472-5	139	135	N	4	7.83	6.13				31.47	28.53	25.65
Carleton	477-3	160	148	C	4	13.86	11.10	24.66	19.99	14.63			
Carleton	477-4	161	149	C	4	7.36	6.48	25.56	20.99	16.41			
Lac à l'Ours	480-2	174	162	S	4						21.88	16.78	15.37
Lac à l'Ours	480-4	176	164	C	4	6.44	6.28				10.46	7.27	9.40
Parc Chibougamau	481-2	179	167	N	4	4.20					20.93	14.31	16.28
Parc Chibougamau 1	481-5	182	170	C *	6			16.98	11.73	11.03	38.14	26.38	29.72
Valcartier	482-2	184	172	N	4	8.33	7.00				14.89	10.02	9.62
Valcartier	482-4	186	174	S	4			30.12	24.37	18.03			
Valcartier	482-5	187	175	C	4	14.72	12.66	19.51	15.55	10.78			
Parc des Laurentides 2	484-4	196	179	C	4			30.48	24.03	17.08	18.02	12.69	12.74
Beauceville	491-1	206	186	C	3	12.38	11.14				5.48	2.48	7.33
Beauceville	491-4	209	189	S	4						24.79	19.24	20.56
Beauceville	491-5	210	190	S	3						25.38	17.86	16.82
Lambton	492-1	211	191	C	4	11.18	11.15	22.08	22.39	16.39	19.82	16.05	20.05
Lambton	492-6	214	194	S	3			9.19	8.66	6.34			
Bois Franc Pierriche	497-5	225	250	N	4	12.09	11.56				10.16	8.34	
St-Damien-de-Brandon	498-1	226	201	S	4			17.06	13.90	11.42			
St-Damien-de-Brandon	498-4	229	204	S	4			10.86	7.76	5.14	14.51	12.71	12.87
St-Damien-de-Brandon	498-8	230	205	S	4			8.70	10.35	7.69	30.39	22.81	22.72
Ste-Émilie-de-l'Énergie	499-10	235		C	4	15.59	13.98	21.26	19.82	13.81			
Racine	502-2	237	211	S	4			19.02	15.30	11.16			
Racine	502-6	241	215	N	4	9.78	8.23				25.61	20.92	21.22
Havelock, Ont.		251		S	4			17.93	13.98	11.20			
Havelock, Ont.		252		S	4			22.37	16.37	13.56			
Havelock, Ont.		253		S	4			16.76	13.13	9.45			
Havelock, Ont.		254		S	4			26.86	18.36	13.49			
Derby Township, Ont.		256		C	4	16.94	14.89	12.46	12.88	10.45			
Derby Township, Ont.		258		C	4	12.23	8.81	22.89	19.89	15.10			
Derby Township, Ont.		259		C	4	10.44	10.77	19.22	15.43	14.20			
Whitney, Ont.		260		C	4	9.36	7.90	15.90	13.21	9.97			
Whitney, Ont.		263		S	4			25.03	20.39	14.89			
Whitney, Ont.		264		C	4	8.38	6.64	11.60	11.70	8.89			
French Township, Ont.		265		C	4			15.88	14.70	11.27			

APPENDIX 3 (cont'd)

Identification	Lot number	LFC number	LFC number	Breeding zone	Number of trees selected	Genetic gains (%)							
						Rivière-Bleue	Amqui	Mirabel	Portage-du-Fort	Robidoux	La Patrie	Dablon	Mastigouche
		410	560										
Rutherglen, Ont.		270		C	4	9.51	8.57	19.28	18.71	15.29			
Estaire, Ont.		277		C	4	11.00	9.47	15.42	12.92	10.58			
Estaire, Ont.		278		S	4			17.85	14.31	10.11			
Foresters Falls, Ont.		290		S	4			21.75	16.14	11.83			
Foresters Falls, Ont.		291		S	4			15.19	9.78	7.03			
Irvine Creek, Ont.		292		C	4			18.17	15.34	11.03			
Irvine Creek, Ont.		295		C	4	12.53	10.38						
Renfrew, Ont.		297		C	2			20.95	16.59	12.28			
Renfrew, Ont.		299		C	4	8.07	7.61	10.73	11.94	9.37			
Renfrew, Ont.		301		C	4	5.37	5.36	19.01	13.66	10.09			
Antrim, Ont.		307		S	4			21.28	20.11	15.07			
Cobalt, Ont.		313		S	4			15.66	13.63	9.56			
Rainy River, Ont.		389		S	4			15.68	12.36	10.77			
Davis Mills, Ont.		403		S	4			32.92	26.25	20.71			
Shannonville, Ont.		405		S	4			16.04	15.60	11.44			
Shannonville, Ont.		406		S	4			26.08	23.11	17.67			
Amour Township, Ont.		409		S	4			15.53	12.73	9.81			
Timmins Township, Ont.		410		S	4			19.11	13.36	8.98			
Davis Mills, Ont.		431		C *	6	21.89	19.84	29.89	21.18	15.56			
Davis Mills, Ont.		432		S	4			22.67	19.07	14.20			
Davis Mills, Ont.		433		S	4			15.21	13.52	10.43			
Davis Mills, Ont.		434		C	4	6.43	6.15	15.26	12.73	9.72			
Beachburg, Ont.		437		S	4			18.73	14.43	11.03			
Canton Boyer	18-1		41	C *	6						34.39	24.80	21.50
Canton Boyer	18-4		42	C *	6						38.70	27.71	31.43
Canton Boyer	18-8	11	43	C	4						27.83	21.49	20.73
Canton Boyer	18-11		44	C	2						19.41	16.67	16.59
Canton Boyer	18-15	14	45	S	4						43.36	31.27	33.97
Canton Booth	19-10		48	C	4						20.86	13.31	16.79
Canton Dasserat	20-15		55	C *	5						17.30	18.28	22.03
Canton Cimon	22-15		60	C *	6						21.76	18.26	17.45
Canton Hébecourt	28-4		77	C *	6						40.10	29.16	32.72
Canton McGill	32-4		97	C *	6						33.33	23.08	32.95
Canton Chaumonot	36-1		101	S	4						31.43	23.82	18.23
Canton Chaumonot	36-4		102	C	4						13.39	11.40	11.33
Canton Desaulniers	37-1		106	C	4						15.24	14.12	15.66
Canton Desaulniers	37-4		107	C *	6						25.32	24.49	18.92
Canton Desaulniers	37-8		109	C *	6						32.23	24.21	23.08
Canton Desaulniers	37-15		110	C	4						15.21	14.91	13.98
Canton Lesage	34-8		118	C	4						19.89	13.64	18.51
Total					363								

N: northern zone (fir), S: southern zone (maple), C: utilization in both zones, *: elite.

APPENDIX 4

List of trees selected

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
1	E410D2	28	7	4	2.76	0.25	AS	941029
1	E410D3	28	7	4	3.28	0.09	AS	941054
1	E410D4	28	3	2	4.10	0.7858	AS	941196
1	E410D6	28	6	1	3.9	0.32	AS	941140
2	E410D2	40	3	3	3	0.24	AS	941014
2	E410D3	40	1	2	3.66	0.2	AS	941035
2	E410D4	40	3	4	4.30	0.2029	AS	941199
2	E410D6	40	1	1	3.55	0.2	AS	941072
3	E560 A2	41	6	3	4.90	0.8152	E	941234
3	E560 A2	41	6	1	4.95	0.8332	E	941233
3	E560 A2	41	3	2	4.25	0.9061	E	941268
3	E560 A3	41	2	5	4.70	0.7297	E	941344
3	E560 A3	41	6	3	4.20	0.3220	E	941318
3	E560 A3	41	5	4	4.40	0.8991	E	941289
4	E560 A2	42	5	3	4.28	0.7165	E	941250
4	E560 A2	42	6	5	4.88	1.1649	E	941232
4	E560 A2	42	5	1	5.15	1.0298	E	941249
4	E560 A3	42	4	5	4.50	0.5693	E	941316
4	E560 A3	42	4	3	4.60	0.6117	E	941315
4	E560 A3	42	2	5	4.80	0.8298	E	941295
5	E560 A2	43	6	5	4.85	0.7164	AS	941238
5	E560 A2	43	5	5	4.30	1.1050	AS	941252
5	E560 A3	43	3	1	4.00	0.8186	AS	941284
5	E560 A3	43	4	4	4.10	0.5730	AS	941348
6	E560 A2	44	4	5	5.30	0.7265	AS	941256
6	E560 A2	44	4	4	4.60	0.4745	AS	941255
7	E560 A3	45	2	4	4.20	0.7028	AS	941292
7	E560 A3	45	6	4	4.00	0.5368	AS	941322
7	E560 A3	45	6	1	4.75	0.8545	AS	941287
7	E560 A3	45	6	3	4.00	0.5368	AS	941321
8	E560 A2	48	5	5	4.00	0.8533	AS	941247
8	E560 A2	48	4	3	3.90	0.4192	AS	941239
8	E560 A3	48	1	3	4.40	0.6459	AS	941307
8	E560 A3	48	1	2	4.60	0.7306	AS	941306
9	E410D2	53	3	3	3.07	0.37	AS	941015
9	E410D3	53	7	3	3.46	0.25	AS	941055
9	E410D6	53	3	4	3.9	0.34	AS	941106
10	E410D2	54	7	3	4.05	0.4480	AS	941354
10	E410D2	54	6	3	3.07	0.18	AS	941023
10	E410D3	54	2	3	3.35	0.2	AS	941041
10	E410D6	54	2	2	3.36	0.14	AS	941095
11	E560 A2	55	5	2	4.95	0.5418	E	941253
11	E560 A2	55	1	1	4.60	0.4235	E	941276
11	E560 A2	55	5	3	4.60	0.4473	E	941254

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
11	E560 A2	55	1	5	4.50	0.3875	E	941277
11	E560 A2	55	4	4	6.10	1.0150	E	941243
12	E410D2	57	5	3	3.38	0.22	AS	941018
12	E410D2	57	7	1	3.54	0.25	AS	941032
12	E410D3	57	8	3	2.28	0.11	AS	941071
12	E410D3	57	7	1	3.07	0.2	AS	941056
13	E560 A2	60	6	5	4.75	0.5540	E	941226
13	E560 A2	60	5	2	4.80	0.2443	E	941263
13	E560 A2	60	5	4	5.60	0.5323	E	941259
13	E560 A3	77	2	2	4.55	0.7856	E	941345
13	E560 A3	60	2	3	3.85	0.4090	E	941340
13	E560 A3	60	1	2	4.00	0.6310	E	941305
13	E560 A3	60	2	5	4.05	0.4937	E	941341
14	E560 A2	77	5	3	4.10	1.0410	E	941260
14	E560 A2	77	1	2	3.98	0.9035	E	941283
14	E560 A2	77	3	1	4.45	0.8703	E	941269
14	E560 A3	77	4	5	3.75	0.4944	E	941311
14	E560 A3	77	4	3	4.05	0.6215	E	941310
15	E410D2	83	2	4	3.7	0.19	AS	941004
15	E410D3	83	5	2	2.56	0.13	AS	941066
15	E410D4	83	2	4	4.50	0.5855	AS	941184
15	E410D6	83	4	4	3.24	0.24	AS	941115
16	E410D2	86	3	4	3.1	0.2	AS	941016
16	E410D3	86*1	8	4	2.75	0.09	AS	941062
16	E410D4	86	7	4	3.85	0.5767	AS	941360
16	E410D6	86	2	4	3.76	0.26	AS	941096
17	E410D4	94	1	4	4.50	0.6385	AS	941172
17	E410D4	94	2	3	4.00	0.6175	AS	941185
17	E410D6	94	6	1	3.29	0.35	AS	941141
17	E410D6	94	3	3	3.4	0.27	AS	941107
18	E560 A2	97	1	1	5.45	0.9681	E	941274
18	E560 A2	97	6	1	4.45	0.9221	E	941227
18	E560 A2	97	1	5	4.75	0.7161	E	941275
18	E560 A3	97	1	5	4.43	1.0486	E	941296
18	E560 A3	97	2	2	4.10	0.7310	E	941343
18	E560 A3	97	2	1	3.70	0.5615	E	941342
19	E560 A3	101	4	5	4.05	0.5094	AS	941312
19	E560 A3	101	5	4	4.95	0.7201	AS	941336
19	E560 A3	101	5	5	5.05	0.7625	AS	941337
19	E560 A3	101	5	3	4.50	0.5295	AS	941335
20	E560 A2	102	5	4	4.80	0.8270	AS	941251
20	E560 A2	102	4	1	4.00	0.2239	AS	941244
20	E560 A3	102	3	2	4.10	0.5795	AS	941329
20	E560 A3	102	3	1	3.80	0.4524	AS	941328
21	E560 A2	106	5	5	4.40	0.3816	AS	941262
21	E560 A2	106	5	1	5.20	0.6697	AS	941261
21	E560 A3	106	6	4	3.70	0.6962	AS	941326
21	E560 A3	106	4	2	4.15	0.8922	AS	941314

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
22	E560 A2	107	6	2	5.73	0.9980	E	941235
22	E560 A2	107	2	2	4.20	0.8835	E	941271
22	E560 A2	107	6	4	5.25	0.8252	E	941236
22	E560 A3	107	1	2	4.10	0.6565	E	941309
22	E560 A3	107	4	3	3.90	0.5805	E	941313
22	E560 A3	107	6	5	4.00	0.5348	E	941320
23	E410D2	108	5	1	3	0.17	AS	941019
23	E410D3	108	2	1	3.93	0.19	AS	941042
23	E410D4	108	6	3	3.40	0.6562	AS	941220
23	E410D6	108	1	1	3.5	0.14	AS	941073
24	E560 A2	109	5	1	5.00	1.5692	E	941246
24	E560 A2	109	4	3	4.90	0.5711	E	941240
24	E560 A2	109	3	2	4.90	0.7439	E	941266
24	E560 A3	109	5	5	4.40	0.6261	E	941338
24	E560 A3	109	1	1	3.70	0.8114	E	941304
24	E560 A3	109	2	4	5.10	1.0232	E	941291
25	E560 A2	110	2	3	4.25	0.4994	AS	941270
25	E560 A2	110	3	5	4.75	0.6017	AS	941264
25	E560 A3	110	6	1	4.00	0.6277	AS	941325
25	E560 A3	110	1	1	4.70	0.7686	AS	941297
26	E410D2	112	6	4	3.95	0.21	AS	941024
26	E410D3	112	5	2	3.1	0.22	AS	941051
26	E410D4	112	7	2	4.20	0.5813	AS	941355
26	E410D6	112	1	4	3.55	0.1	AS	941074
27	E560 A2	118	4	1	4.00	0.5039	AS	941257
27	E560 A2	118	1	3	4.05	0.3817	AS	941278
27	E560 A3	118	1	4	3.10	0.2952	AS	941303
27	E560 A3	118	1	2	4.00	0.6364	AS	941302
28	E410D2	130	2	1	3.45	0.1	AS	941005
28	E410D3	130	3	1	3.4	0.15	AS	941045
28	E560 A2	126	1	4	4.90	0.9763	AS	941279
28	E560 A2	126	1	5	5.08	1.0411	AS	941280
29	E410D4	131	2	4	4.10	0.7388	AS	941190
29	E410D6	131	1	2	4.2	0.27	AS	941075
29	E560 A2	127	4	2	5.95	0.9929	AS	941242
29	E560 A3	127	3	5	4.10	0.5080	AS	941330
30	E410D4	133	3	4	4.50	0.5576	AS	941215
30	E410D6	133	4	4	3.42	0.37	AS	941116
30	E560 A3	129	2	2	3.75	0.5505	AS	941293
30	E560 A3	129	6	4	3.60	0.4418	AS	941319
31	E410D6	134	2	2	3.7	0.28	AS	941097
31	E560 A2	130	4	5	5.25	0.8934	AS	941245
31	E560 A2	130	1	2	5.50	1.0387	AS	941272
31	E560 A3	130	1	3	4.65	0.6857	AS	941301
32	E410D2	139	7	3	2.85	0.2	AS	941030
32	E410D3	139	1	2	3.8	0.13	AS	941036
32	E560 A2	135	1	2	4.25	0.5904	AS	941273
32	E560 A2	135	6	2	4.75	0.6203	AS	941228

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
33	E410D2	160	6	2	3.31	0.3	AS	941025
33	E410D3	160	7	2	3.8	0.21	AS	941057
33	E410D4	160	1	1	5.30	0.5414	AS	941182
33	E410D6	160	1	4	3.85	0.34	AS	941076
34	E410D3	161	2	3	2.95	0.12	AS	941043
34	E410D4	161	7	3	4.00	0.4625	AS	941357
34	E410D6	161	5	3	3.3	0.21	AS	941127
34	E410D6	161	1	4	3.7	0.27	AS	941077
35	E560 A3	162	6	1	4.75	0.7653	AS	941286
35	E560 A3	162	1	3	4.10	0.5429	AS	941299
35	E560 A3	162	5	2	4.10	0.5588	AS	941339
35	E560 A3	162	1	4	4.15	0.5641	AS	941300
36	E410D2	176	1	1	3.1	0.07	AS	941001
36	E410D3	176	1	4	3.11	0.19	AS	941037
36	E560 A2	164	3	1	4.25	0.3950	AS	941265
36	E560 A3	164	6	1	4.55	0.6273	AS	941285
37	E410D2	179	1	4	3.3	0.19	AS	941002
37	E410D3	179	1	2	3.06	0.16	AS	941038
37	E560 A2	167	4	5	4.70	0.7803	AS	941241
37	E560 A2	167	5	2	5.10	1.0945	AS	941258
38	E410D4	182	1	1	3.95	0.4991	E	941163
38	E410D6	182	2	2	3.52	0.05	E	941098
38	E410D6	182	6	4	3.8	0.28	E	941142
38	E560 A2	170	6	1	4.50	1.0633	E	941231
38	E560 A2	170	1	1	5.50	0.8126	E	941281
38	E560 A3	170	6	2	4.00	0.5983	E	941327
39	E410D2	184	6	2	3.19	0.22	AS	941026
39	E410D3	184	7	4	2.98	0.12	AS	941067
39	E560 A2	172	6	5	4.55	0.3031	AS	941230
39	E560 A2	172	6	2	5.60	0.6812	AS	941229
40	E410D4	186	3	3	4.30	0.7494	AS	941201
40	E410D4	186	3	1	4.70	0.9739	AS	941200
40	E410D6	186	2	1	3.18	0.27	AS	941099
40	E410D6	186	4	3	4.05	0.51	AS	941117
41	E410D2	187	2	4	3.15	0.36	AS	941006
41	E410D3	187*2	7	4	3.42	0.25	AS	941058
41	E410D4	187	2	3	4.50	0.8145	AS	941188
41	E410D6	187	4	1	3.45	0.34	AS	941118
42	E410D4	196	7	2	3.80	0.5859	AS	941351
42	E410D6	196	1	2	3.45	0.27	AS	941078
42	E560 A2	179	6	5	5.05	0.9052	AS	941237
42	E560 A3	179	4	2	4.85	0.7842	AS	941290
43	E410D2	206	4	3	3.72	0.26	AS	941017
43	E410D3	206	6	3	2.95	0.18	AS	941053
43	E560 A3	186	5	4	3.65	0.3695	AS	941332
44	E560 A3	189	5	5	4.00	0.5884	AS	941331
44	E560 A3	189	2	1	4.45	0.7308	AS	941294
44	E560 A3	189	6	3	3.85	0.5298	AS	941323

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
44	E560 A3	189	1	4	3.50	0.4130	AS	941308
45	E560 A3	190	5	2	3.90	0.1768	AS	941333
45	E560 A3	190	1	5	4.10	0.5796	AS	941298
45	E560 A3	190	5	3	4.40	0.3885	AS	941334
46	E410D3	211	4	4	3.15	0.13	AS	941048
46	E410D4	211	1	3	3.95	0.3796	AS	941168
46	E410D6	211	2	3	4.04	0.47	AS	941100
46	E560 A3	191	6	1	4.50	0.6067	AS	941317
47	E410D4	214	3	2	3.75	0.5118	AS	941211
47	E410D6	214	5	3	3.7	0.24	AS	941144
47	E410D6	214	6	2	3	0.23	AS	941143
48	E410D2	225	5	1	3.05	0.22	AS	941020
48	E410D3	225	8	3	2.55	0.1	AS	941069
48	E410D3	225	1	1	2.66	0.14	AS	941068
48	E560 A2	250	3	1	4.3	0.32	AS	941267
49	E410D4	226	3	1	3.90	0.6757	AS	941206
49	E410D4	226	3	3	3.65	0.5354	AS	941207
49	E410D6	226	5	4	3.5	0.37	AS	941128
49	E410D6	226	4	3	3.26	0.27	AS	941119
50	E410D4	229	1	4	3.65	0.3242	AS	941164
50	E410D4	229	4	2	3.65	0.2260	AS	941194
50	E560 A3	204	1	4	4.10	0.4732	AS	941347
50	E560 A3	204	1	1	4.55	0.6161	AS	941346
51	E410D4	230	2	4	4.00	0.5053	AS	941191
51	E410D6	230	6	2	3.9	0.29	AS	941145
51	E560 A3	205	6	5	4.30	0.7282	AS	941324
51	E560 A3	205	5	5	5.15	0.8519	AS	941288
52	E410D2	235	2	1	3.45	0.44	AS	941007
52	E410D3	235	3	4	2.96	0.22	AS	941046
52	E410D4	235	2	3	4.55	0.5649	AS	941192
52	E410D6	235	1	2	4.5	0.45	AS	941079
53	E410D4	237	7	4	4.20	0.6534	AS	941353
53	E410D4	237	1	2	3.90	0.3167	AS	941162
53	E410D6	237	6	3	3.81	0.43	AS	941146
53	E410D6	237	1	4	4	0.37	AS	941080
54	E410D2	241	2	1	4.1	0.3	AS	941008
54	E410D3	241	8	1	3.4	0.13	AS	941063
54	E560 A2	215	5	3	5.40	0.6177	AS	941248
54	E560 A2	215	1	2	4.80	0.8472	AS	941282
55	E410D4	251	1	3	3.80	0.6665	AS	941180
55	E410D4	251	3	2	3.80	0.5543	AS	941210
55	E410D6	251	6	2	3.56	0.27	AS	941147
55	E410D6	251	4	3	3.6	0.31	AS	941120
56	E410D4	252	1	4	5.50	1.0220	AS	941173
56	E410D4	252	7	2	4.00	0.6011	AS	941352
56	E410D6	252	4	2	3.36	0.26	AS	941121
56	E410D6	252	1	2	3.3	0.2	AS	941081
57	E410D4	253	1	1	4.85	0.5593	AS	941177

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
57	E410D4	253	4	4	4.85	1.0574	AS	941212
57	E410D6	253	1	1	3.15	0.23	AS	941082
57	E410D6	253	2	3	3.45	0.34	AS	941101
58	E410D4	254	2	4	4.80	0.5363	AS	941187
58	E410D4	254	4	2	3.95	0.4782	AS	941197
58	E410D6	254	1	1	3.6	0.41	AS	941083
58	E410D6	254	6	3	2.79	0.22	AS	941148
59	E410D2	256	2	2	4	0.37	AS	941009
59	E410D3	256	8	2	3.35	0.21	AS	941064
59	E410D4	256	1	1	4.10	0.3461	AS	941178
59	E410D6	256	1	4	3.75	0.21	AS	941084
60	E410D2	258	7	1	3.38	0.26	AS	941031
60	E410D3	258	8	4	3.1	0.16	AS	941065
60	E410D4	258	1	2	4.00	0.4049	AS	941167
60	E410D6	258	2	1	4.05	0.3	AS	941102
61	E410D2	259	2	2	5.35	0.42	AS	941010
61	E410D3	259	4	3	2.9	0.18	AS	941049
61	E410D4	259	7	2	4.00	0.5369	AS	941361
61	E410D6	259	3	4	3.8	0.23	AS	941108
62	E410D2	260	6	2	3.49	0.22	AS	941027
62	E410D3	260	3	2	2.66	0.15	AS	941047
62	E410D4	260	3	1	4.80	0.8983	AS	941195
62	E410D6	260	5	4	3.65	0.4	AS	941129
63	E410D4	263	6	3	4.50	0.4130	AS	941223
63	E410D4	263	2	4	4.60	0.9461	AS	941183
63	E410D6	263	5	3	3.08	0.25	AS	941130
63	E410D6	263	2	1	3.3	0.33	AS	941103
64	E410D2	264	2	2	3.25	0.24	AS	941011
64	E410D3	264	7	1	2.81	0.13	AS	941059
64	E410D4	264	1	1	3.90	0.2993	AS	941181
64	E410D6	264	6	3	3.42	0.24	AS	941149
65	E410D4	265	6	2	4.20	0.7156	AS	941222
65	E410D4	265	1	3	4.60	0.4701	AS	941170
65	E410D6	265	6	3	3.96	0.37	AS	941150
65	E410D6	265	5	2	3.75	0.35	AS	941131
66	E410D2	270	2	2	3.4	0.17	AS	941012
66	E410D3	270	1	3	3.2	0.15	AS	941039
66	E410D4	270	7	2	4.20	0.4255	AS	941224
66	E410D6	270	5	1	4	0.32	AS	941132
67	E410D2	277	2	3	3	0.24	AS	941013
67	E410D3	277	7	2	2.87	0.17	AS	941060
67	E410D4	277	2	4	4.95	0.7234	AS	941204
67	E410D6	277	5	4	3.5	0.26	AS	941133
68	E410D4	278	6	4	3.50	0.2866	AS	941219
68	E410D4	278	2	4	3.70	0.6023	AS	941203
68	E410D6	278	5	3	3.15	0.28	AS	941134
68	E410D6	278	3	2	3.55	0.35	AS	941109
69	E410D4	290	6	3	4.00	0.7469	AS	941221

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
69	E410D4	290	7	4	4.50	0.5365	AS	941350
69	E410D6	290	5	3	3.1	0.25	AS	941135
69	E410D6	290	1	3	3.4	0.25	AS	941085
71	E410D4	291	6	2	3.70	0.3063	AS	941218
71	E410D4	291	1	2	4.65	0.4537	AS	941161
71	E410D6	291	2	4	3.52	0.22	AS	941104
71	E410D6	291	6	4	3.46	0.27	AS	941151
72	E410D4	292	1	4	3.80	0.1999	AS	941179
72	E410D4	292	1	2	3.90	0.2560	AS	941169
72	E410D6	292	3	3	3.7	0.34	AS	941110
72	E410D6	292	1	1	3.75	0.33	AS	941086
73	E410D2	295	7	1	2.8	0.26	AS	941033
73	E410D2	295	1	3	3.1	0.25	AS	941003
73	E410D3	295	5	3	2.75	0.14	AS	941052
73	E410D3	295	1	2	2.46	0.12	AS	941070
74	E410D6	297	6	3	3.35	0.28	AS	941152
74	E410D6	297	1	2	3.3	0.14	AS	941087
75	E410D2	299	7	4	2.75	0.19	AS	941034
75	E410D3	299	7	1	2.75	0.12	AS	941061
75	E410D4	299	1	4	3.60	0.3504	AS	941166
75	E410D6	299	1	1	3.8	0.13	AS	941088
76	E410D2	301	5	3	3.19	0.17	AS	941021
76	E410D3	301	4	2	3.2	0.13	AS	941050
76	E410D4	301	7	4	4.55	0.6532	AS	941362
76	E410D6	301	4	4	2.92	0.19	AS	941122
77	E410D4	307	3	2	4.10	0.3127	AS	941208
77	E410D4	307	4	1	3.60	0.7967	AS	941213
77	E410D6	307	6	3	3.15	0.27	AS	941153
77	E410D6	307	3	1	3.15	0.31	AS	941111
78	E410D4	313	7	2	3.90	0.5372	AS	941356
78	E410D4	313	3	3	4.20	0.3688	AS	941209
78	E410D6	313	5	2	3.1	0.21	AS	941136
78	E410D6	313	6	2	3.07	0.2	AS	941154
79	E410D4	389	1	4	4.65	0.3901	AS	941175
79	E410D4	389	1	3	4.50	0.3059	AS	941174
79	E410D6	389	1	4	4.05	0.27	AS	941089
79	E410D6	389	6	1	3.27	0.22	AS	941155
80	E410D4	403	6	2	4.10	0.8229	AS	941217
80	E410D4	403	4	2	4.00	0.8299	AS	941193
80	E410D6	403	1	4	3.6	0.33	AS	941090
80	E410D6	403	1	3	3.75	0.38	AS	941091
81	E410D4	405	3	3	4.50	0.6111	AS	941214
81	E410D4	405	7	4	3.65	0.4794	AS	941359
81	E410D6	405	2	4	3.69	0.37	AS	941105
81	E410D6	405	4	1	3.25	0.27	AS	941123
82	E410D4	406	7	3	4.20	0.6800	AS	941363
82	E410D4	406	1	2	4.80	0.7879	AS	941171
82	E410D6	406	1	1	4.2	0.32	AS	941092

APPENDIX 4 (cont'd)

No.	Test	Fam. No.	Block No.	Tree No.	Height (m)	G1	No.	Clone
82	E410D6	406	5	4	3.15	0.3	AS	941137
83	E410D4	409	7	3	3.70	0.5985	AS	941358
83	E410D4	409	2	2	4.10	0.2408	AS	941189
83	E410D6	409	4	3	3.89	0.3	AS	941124
83	E410D6	409	6	1	3.62	0.27	AS	941156
84	E410D4	410	1	3	4.75	0.5845	AS	941176
84	E410D4	410	2	3	3.75	0.4792	AS	941205
84	E410D6	410	3	4	3.4	0.17	AS	941112
84	E410D6	410	5	3	3.15	0.2	AS	941138
85	E410D2	431	6	3	3.39	0.32	E	941028
85	E410D3	431	2	1	3.75	0.32	E	941044
85	E410D4	431	1	1	4.80	0.4025	E	941159
85	E410D4	431	1	3	4.70	0.3464	E	941160
85	E410D4	431	3	2	4.30	0.4797	E	941216
85	E410D6	431	6	3	3	0.1	E	941157
86	E410D4	432	1	2	3.95	1.0051	AS	941165
86	E410D4	432	3	1	4.30	0.6261	AS	941202
86	E410D6	432	1	4	3.65	0.39	AS	941093
86	E410D6	432	3	3	3.7	0.31	AS	941113
87	E410D4	433	7	3	3.75	0.3868	AS	941349
87	E410D4	433	7	1	4.00	0.4921	AS	941225
87	E410D6	433	4	3	3.65	0.31	AS	941125
87	E410D6	433	5	1	3.5	0.24	AS	941139
88	E410D2	434	5	4	3.41	0.23	AS	941022
88	E410D3	434	1	1	3.24	0.12	AS	941040
88	E410D4	434	3	3	3.80	0.4643	AS	941198
88	E410D6	434	4	3	3.11	0.29	AS	941126
89	E410D4	437	2	2	4.70	0.6775	AS	941186
89	E410D4	437	1	1	5.30	0.9791	AS	941158
89	E410D6	437	3	1	2.9	0.27	AS	941114
89	E410D6	437	1	1	4.75	0.34	AS	941094

