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R.F. Smith and L.D. Yeates**

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**Canadian Forest Service - Maritimes Region
Natural Resources Canada
P.O. Box 4000
Fredericton, N.B., E3B 5P7**

Review of Research Activities in Quebec Under the White Pine Breeding Program

Jean Beaulieu

Canadian Forest Service - Quebec Region

White pine, *Pinus strobus* (L.), is the largest conifer in eastern North America. In the past, this species played an important role in our country's economic and social life. In the 19th century, however, white pine resources were heavily depleted, partly because of massive exports to England after Napoleon blockaded the Baltic Sea, and to the United States during the expansion that followed the American Civil War.

Small-scale reforestation programs, especially for abandoned farmland, were set up in Quebec as in the other provinces and the United States during the first few decades of this century. However, the extensive damage caused by blister rust, *Cronartium ribicola* (JC Fish), and the white pine weevil, *Pissodes strobi* (Peck), led to the termination of these programs.

Delimiting blister rust infection hazard zones (Lavallée 1986), and the use of silvicultural practices such as planting in strip cuts in hardwood stands, have triggered a new interest in reforestation with this species. The success in Ontario in the 1950s in producing blister rust-resistant varieties and the development of promising biotechnology tools convinced researchers and users that it was possible to produce quality wood.

Corriveau and Lamontagne (1977) proposed setting up a white pine breeding program in Quebec. A two-faceted program was developed: one part would concentrate on growth and shape characters, and the other would concentrate on creating hybrids that were resistant to blister rust and the weevil. The breeding program, whose long-term goal is to merge the two types of material generated, is now being led by Dr. Ariane Plourde.

Many activities have been carried out since the start of the white pine breeding program. Today, research into the somatic embryogenesis of this species to develop embryogenic lines is being guided by Dr. Ariane Plourde. Once a sufficient number of ramets (emblings) has been obtained, they will be inoculated with blister rust spores to select resistant material before it is tested in the field. Research is also being carried out by Dr. Richard Hamelin using RAPD markers to estimate the genetic diversity level of blister rust in its whole range. Improved knowledge of the genetic variability in this pathogenic fungus should lead to the development of an inoculum mixture that is representative of the existing classes of virulence, if a link between virulence and variability in the RAPD loci can be demonstrated.

In order to speed up the breeding program, the first breeding orchard made up of plus trees selected from five target populations from southern Quebec was set up in the 1980s in the Cap Tourmente National Wildlife Area, about 40 km east of Quebec City. This breeding orchard was created for the carrying out, as fast as possible, of the intra- and interspecific crossings needed to study the species' genetics. The size of the breeding orchard will be increased later once information on the genetic diversity of white pine throughout its range has been compiled. During the same decade, six clonal seed orchards were also created by the ministère des Ressources naturelles du Québec (Quebec Department of Natural Resources). They are all made up of plus trees mass-selected from natural forests. One of them was field-grafted by Mr. Gaétan Daoust and his team. These seed orchards should provide all the seed needed for the reforestation program until the second-generation material becomes available.

To be effective, breeding strategies must be based on extensive knowledge of the species' genetic diversity, how this diversity is distributed within and among various populations, and the way genes are transmitted from one generation to the next. Such information may be obtained by studying the genes coding the enzymes in megagametophyte cells. In an initial study, ten natural populations were sampled

in Quebec and cones were collected from 30 trees in each of the populations. The data for 18 loci coding 12 enzyme systems were analyzed. The results showed that white pine, like most other conifers, was genetically highly variable (Beaulieu and Simon 1994). The populations in the St. Lawrence valley proved to be less genetically variable than those in the Ottawa River valley, whereas the one on Anticosti Island was amongst the most variable. The gene flow among populations was very high, which explains why the differentiation of populations was a mere 2%.

A complementary study providing an overall picture of the genetic diversity of white pine populations in Quebec is currently being conducted with funding from the Green Plan's National Forest Genetic Resources Centre. The same procedure was used to sample natural populations in the Gaspé, on the North Shore, and in the Mauricie and Témiscamingue regions. The selection program will be reviewed on the basis of the results of these studies to ensure that the first-generation breeding population is at least as genetically variable as a natural population. In addition, these studies will enable the formulation of preliminary proposals regarding conservation measures for the genetic resources of this species.

An extensive gene sampling of white pine populations throughout Quebec was also conducted in the early 1980s. In addition, half-sibling family seed lots were obtained from collaborators elsewhere in Canada and the United States. In 1982 and 1984, genecological studies were initiated in the greenhouse at the Laurentian Forestry Centre (Canadian Forest Service - Quebec Region). The seedlings were planted out the following year at the Valcartier Forest Experiment Station nursery. Two years later, they were transplanted to eight sites with environmental conditions typical of the white pine's natural habitat. Thus, eight genecological tests were established according to a complete randomized block design and following recommended silvicultural practices to minimize the impact of the white pine weevil. Over 450 families are currently being tested.

The nursery results did not show the presence of geographic gradients with regard to growth and hardiness characters. Laboratory tests involving the freezing of needles did not show that southern sources were more sensitive. This last result suggests that southern provenances can be moved slightly northward without any major adaptation problems. Data on growth and stem quality were gathered in tests conducted five years after planting. The preliminary results suggest that selecting the best provenances could initially improve the performance of white pine plantations by 10 to 15% at the age of about ten years (Beaulieu 1994). Research is continuing into refining the statistical analysis methods to obtain estimates of genetic parameters that are as accurate as possible. The aim is to integrate pedologic and light intensity data into the analysis to take into account specific environmental conditions the families have been placed in for comparison purposes. Various spatial analysis models are also being used to measure the impact of microsite heterogeneity on the accuracy of the estimates being sought. These studies will enable us to obtain more precise estimates of the genetic gains due to selecting better parents for the next generation breeding population.

Seedlings of families with the best growth and shape as determined in genecological tests are currently being produced. When they have reached the desired size, they will be subjected to blister rust resistance selection tests through a controlled inoculation of the fungus. These test results will indicate the presence of genes, if there are any, that resist or tolerate blister rust in these families. In addition, they are the first stage in integrating the two facets of the breeding program described above.

The white pine breeding program is well under way in Quebec and is receiving considerable well-earned support. This species is acknowledged for its great economic and social value. Similar species that can be considered a part of the collective imagination are rare.

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