FIRST TECHNICAL SESSION

Chairman: F. Valentine

OPEN-POLLINATED PROGENY TESTING IN A BLACK SPRUCE BREEDING PROGRAM

E. K. Morgenstern[1]

ABSTRACT

Selection in black spruce (Picea mariana (Mill.) B.S.P.) will have as its primary objective the improvement of growth rate. Growth rate has a low heritability in wild stands and phenotypic selection of individual trees is inefficient. It is, therefore, proposed that initial selection be carried out rapidly and that seed is collected from individual trees to conduct a form of family selection in progeny tests from open pollination. The tests contribute both selected material and genetic information. In this way they provide another option in new or existing breeding programs.

INTRODUCTION

Many tree improvement programs have been initiated in a similar way: by careful phenotypic selection of individual trees in natural or planted stands followed by establishment of grafted clonal seed orchards. During the last 10 years, more and more breeders have made use of a greater variety of methods, and family selection and seedling seed orchards have been developed more frequently. The objective is to improve the efficiency of selection methods (Ledig 1973) and to adapt methods to the characteristics of individual species. This paper examines the problem of individual-tree and family selection in the breeding of black spruce (Picea mariana (Mill.) B.S.P.).

INDIVIDUAL-TREE VS. FAMILY SELECTION

First some definitions and general explanations. What is individual-tree and what is family selection?

Individual-tree selection is a form of mass selection where suitable phenotypes are picked in natural or planted stands as is done in most plus-tree selection programs. The trees are chosen after ocular comparisons or detailed measurements of height, diameter, stem and branch characters, crown size, and so on. This method appears to be effective when selecting for stem and branch characters because these are strongly inherited. Individual-tree selection for

---

[1] Canadian Forestry Service, Petawawa Forest Experiment Station, Chalk River, Ontario, Canada.

growth rate or yield is more difficult because the heritability of growth rate in natural or planted stands is low as a consequence of differences in site, spacing, and competition - it may be as low as 5% (Namkoong 1970, Ledig 1974). Therefore, individual-tree selection for growth rate must be carried out very carefully on the basis of many measurements, and this makes it very costly. Its efficiency is probably low because the genetic gain per unit of time or $ expended will be small. In a species primarily selected for growth rate, individual-tree selection should not receive much emphasis and be carried out rapidly (Bellmann and Ahrens 1965, Ledig 1973).

Given these conditions, family selection is more promising. It is generally recognized that when heritability is low, the performance of a group of relatives is more easily evaluated than that of individuals. According to Lerner (1958, p. 158), the greater the number of individuals contributing to the family mean, the closer does the average phenotype approach the mean genotype.

Family selection is best practiced in progeny tests and it is then a simple operation. Progenies of open-pollinated mother trees (these progenies may be considered families of half-sibs) are established in replicated tests on uniform sites at a certain spacing. The tests are measured and the families ranked on the basis of their performance. The control exercised over environment raises the heritability beyond that obtainable in wild stands and selection is more efficient (Morgenstern 1974a). This has been recognized by many tree breeders and open-pollinated tests have been initiated or suggested for Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) by Silen (1966), western hemlock (*Tsuga heterophylla* (Raf.) Sarg.) by Piesch (1974), Sitka spruce (*Picea sitchensis* (Bong.) Carr.) by Fletcher and Faulkner (1972), longleaf pine (Pinus *palustris* Mill.) by Snyder (1973), red pine (*Pinus resinosa* Ait) by Wright and Bull (1963), and jack pine (Pinus *banksiana* Lamb.) by Wright (1962), Klein (1968) and Yeatman (1974). Snyder (1969) found that gains for height growth from family selection in longleaf pine were almost three times larger than gains from individual-tree selection.

CHARACTERISTICS OF BLACK SPRUCE AS A GUIDE TO SELECTION METHODS

Black spruce is primarily utilized for the production of pulp and paper. The wood has a high specific gravity and its fibers are long and very tough (Ladell 1970). Tree diameters are small, stems straight and crowns generally narrow with branches of moderate size. There is little need or incentive to improve stem form or branch size. I agree with Carmichael (1960) that at this stage most of the effort in selection should go into the improvement of fiber yield, i.e., wood volume (fig. 1).

Black spruce starts to flower at about 6 years of age and subsequently produces seed at regular intervals every two or three years, with good crops once in about four years (U. S. Forest Service 1948). Seed collections can be made during a good part of the fall

and winter season. Thus propagation by seed is no problem and is much easier than grafting or rooting.

Progeny tests from open pollination are also not difficult. Large clear-cut areas are available in boreal regions on upland sites where black spruce grows in natural stands, often in mixture with jack pine (Rowe 1972). The establishment and maintenance effort for tests on such sites is not great if planting is undertaken soon after cutting and before competitors become established.

All these conditions make it possible to initiate black spruce breeding as follows. Parent trees are chosen by rapid ocular selection in natural stands. Seed from these individual, open-pollinated trees is sown in a greenhouse or nursery and the seedlings transplanted. The transplants are established two or three years later in replicated tests on a number of sites within their region or origin. Because of the early flowering of black spruce, some of the plantations can be designed specifically to serve as seedling seed orchards, which will be thinned on the basis of the results from the progeny tests (Morgenstern 1972, Morgenstern et al. 1974). In this way black spruce breeding would avoid the intensive and costly primary selection in natural stands and its uncertainty of making a substantial genetic gain.

THE TWO FUNCTIONS OF OPEN-POLLINATED TESTS

The open-pollinated tests in mind have two functions: to serve as a basis for family selection and to provide population parameters. Let us look at family selection first.

The progeny of an open-pollinated tree is related through descent from the same mother and may be considered a family of half-sibs. Once the best families have been identified in a test, one could select the best trees within them for seed production and breeding of the next generation. In this way the selection differential is increased and a greater genetic gain made. By taking only one tree from each family, or even only one tree descended from all parent trees in a given stand, inbreeding in future generations will be minimized (Ledig 1974). In such planted stands the rotation period will be shorter than in natural stands; therefore, one could expect to make the final selection at the age of 20-40 years (at one-third to one-half of rotation age).

The second function of open-pollinated tests is to provide estimates of population parameters. These may include: components for various sources of variation, genetic variances and covariances. How will these be used?

If we have the normal situation with a test series in several environments, we could find out through analysis of variance how genetic variation is distributed among the various sources. This will assist planning to achieve an optimum distribution of samples in future tests, taking cost and genetic gain into account:

Sources of variation

- Environment
- Replications in environments
- Families
    - Stands
    - Families in stands
- Families x Environments
    - Stands x Environments
    - Families in stands x Environments
- Plot error
- Within plot

"Optimum distribution" here refers to both collection of seed in the parent stands and establishment of the families in the test environments. Variance components from such an analysis would tell us, for example, whether it would be more important to sample more stands or more trees in stands; and whether the number of test environment chosen was adequate or not (Liang and Walter 1966).

The genetic variances from open-pollinated tests are used to estimate heritability and genetic correlations, There is no doubt that some of these estimates are problematical (Dietrichson 1972): the usual assumption that progenies from open pollination are half-sibs and estimate one-fourth of the additive genetic variance (Falconer 1960) is true only if there is no inbreeding in the population, dominance does not interfere, and many male parents have contributed pollen. If these assumptions are not met, over-estimates of the genetic variances are possible and the heritabilities calculated may be inflated (Namkoong 1966).

Nevertheless, such estimates will be of some value if they are interpreted carefully in the light of additional experiments and observations. To illustrate this point, let us look at the heritability of height growth in four black spruce progeny tests conducted at Petawawa Forest Experiment Station (Table 1). The first test was based on open pollination in five natural stands (Morgenstern 1973). Seed for the remaining three tests had its origin in the same plantation from open pollination, a controlled cross with nested design (Becker 1967) and a diallel cross (see Morgenstern 1974b for more detail.

Table 1 illustrates several points:

1. Although the heritabilities obtained from Test No. 1 and 4 are identical, other values vary with age, test environments and populations sampled;

2. Controlled crosses do not necessarily produce similar results;

3. The sampling of populations and test environments is probably as important as the choice of a good mating design.

Therefore, the results of any test series cannot be accepted without careful consideration of all the factors involved. In the case of black spruce, particularly, we lack heritabilities from a good sample of populations, environments, and more advanced ages. Open-pollinated tests will give us a fast start in this direction. They provide another option to new programs that are being planned, or a complementary approach if used in conjunction with existing programs based on more intensive plus-tree selection and clonal seed orchards.

Table 1.--Narrow-sense heritability estimates (h^2) of height growth in black spruce based on individual trees. Tests No. 2-4 originated from seed obtained in the same plantation.

Test No.	Pollination or Mating Design	Number of families	Measurement age (Years)	Number and type of test environment	Number of replications in each	h^2	Standard Error
1	Open pollination in five natural stands	28	4	2- Nursery	4	0.18	±0.15
2	Open pollination in one plantation	24	1	2- Greenhouse	3	0.42	±0.16
3	Controlled - 7 males mated to 10 females each (nested design)	70	1	2- Greenhouse	3	0.30	±0.19
4	Controlled - 7 × 7 diallel cross	49	1	2- Greenhouse	6	0.18	±0.12

LITERATURE CITED

Becker, Walter A. 1967. Manual of procedures in quantitative genetics. 2nd ed. Washington State Univ. Press. 130 p.

Bellman, K., and H. Ahrens. 1965, Zum gegenwärtigen Stand der Anwendungsmöglichkeiten der biometrischen Genetik in der PflanzenzUchtung. Zlichter 35:156-174.

Carmichael, A. J. 1960. Report to Committee on Forest Tree Breeding, August 1960. Proc. Seventh Meetg. Committee Forest Tree Breedg. in Can., Pt. II, p. B-1 to B-10.

Dietrichson, Jon. 1972. Open pollination sufficiently good or not as a progeny test? IUFRO Genetics - SABRAO Joint Symposia, Tokyo 1972. p. A-11 (V), 1-7.

Falconer, D. S. 1960. Introduction to quantitative genetics, Ronald Press, New York. 365 p.

Fletcher, A. M., and R. Faulkner. 1972. A plan for the improvement of Sitka spruce by selection and breeding. Forestry Comm. Res. and Development Pap. 85. 31 p.

Klein, J. I. 1968. Breeding jack pine for the Manitoba-Saskatchewan region. Proc. Eleventh Meetg, Committee Forest Tree Breedg. in Can., Pt. 2, p. 111-114.

Ladell, J. L. 1970. Quality criteria for black spruce. Proc. Twelfth Meetg. Committee Forest Tree Breedg. in Can., Pt. 2, p. 69-76.

Ledig, F. Thomas. 1973. The application of mass selection in tree improvement. Proc. 20th Northeast. Forest Tree Improv. Conf., p. 69-83.

Ledig, F. Thomas. 1974. An analysis of methods for the selection of trees from wild stands. Forest Sci. 20:2-16.

Lerner, I. Michael. 1958. The genetic basis of selection. Wiley, New York. 298 p.

Liang, George H. L., and T. L. Walter. 1966. Genotype x environment interactions from yield tests and their application to sorghum breeding programs. Can. J. Genet. Cytol. 8:306-311.

Morgenstern, E. K. 1972. Progeny tests of black spruce (Picea mariana (Mill.) B.S.P.) in boreal environments. IUFRO, Proc. Meetg. Working Party on Progeny Testing, Macon, Georgia, October 1972. Publ. by Georgia Forest Res. Council, Macon. p. 48-55.

Morgenstern, E. K. 1973. Heritability and genetic gain for height growth in a nursery experiment with black spruce. Can. Forest. Serv, Inf. Rep. PS-X-44. 10 p.

Morgenstern, E. K. 1974a. Selection of black spruce progenies for the genetic improvement of height growth. Forest. Chron. 50:160-162.

Morgenstern, E. K. 1974b. A diallel cross in black spruce, Picea mariana (Mill.) B.S.P. Silvae Genet. 23:67-70.

Morgenstern, E. K., M. J. Hoist, A. H. Teich and C. W. Yeatman. 1974. Plus-tree selection: review and outlook. Can. Forest. Serv. Publ. (in press).

Namkoong, G. 1966. Inbreeding effects on estimation of genetic additive variance Forest Sci. 12:8-13.

Namkoong, G, 1970. Optimum allocation of selection intensity in two stages of truncation selection. Biometrics 26:465-476.

Piesch, R. F. 1974. Establishment of a western hemlock tree improvement program in coastal British Columbia. Can. Forest. Serv. Inf. Rep. BC-X-89. 87 p.

Rowe, J. S. 1972. Forest regions of Canada. Can. Forest. Serv. Pub. 1300. 172 p.

Silen, Roy, R. 1966. A simple, progressive tree improvement program for Douglas-fir. U. S. Forest Serv. Res. Note PNW-45. 13 p.

Snyder, E. Bayne, 1969. Parental selection versus half-sib family selection of longleaf pine. Proc. Tenth South. Conf. Forest Tree Improvement. p. 84-88.

Snyder, E. Bayne. 1973. 15-year gains from parental and early family selection in longleaf pine. Proc. Twelfth South. Conf. Forest Tree Improvement. p. 46-49.

U. S. Forest Service. 1948. Woody-plant seed manual. U. S. Dept. Agric. Misc, Pub. 654. 416 p.

Wright, J. W. 1962. Genetics of forest tree improvement. FAO, Rome. 399 p.

Wright, J. W., and W. I. Bull. 1963. A one-parent progeny test and seed orchard for the improvement of red pine. J. Forestry 61: 747-750.

Yeatman, C. W. 1974. Seedling seed orchards for jack pine. Proc. 21st Northeast. Forest Tree Improv. Conf. p. 69-71.