Broad Sense Heritability Values and Possible Genetic Gains in Clonal Selection of Pinus griffithii McClelland x P. strobus L.

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Introduction

Clones are useful for determining heritability, which indicates the reliability of phenotypic selection and forecasts the effect of breeding.

The use of clones to establish forest plantations is attractive because of the likelihood of large genetic gains from selection. In white pine, in addition to gains in growth rate and improved tree-form, the development of clones could provide a full utilization of trees selected for resistance to blister rust (Cronartium *ribicola* Fisch.) and weevil (Pissodes strobi Peck.).

Review of literature

Broad sense heritability values can be estimated from clonal tests. These realized total heritability values (Wright, 1963), estimates of gross heritability (Einspahr et al., 1963), or repeatability (Falconer, 1960, Becker, 1967), include non-additive genetic variances and are higher than the narrow sense heritability estimates obtained from parent-progeny comparisons.

Heritability values calculated from clonal tests can be used to forecast genetic gain in clonal propagation (Wright, 1962). The reliability of such estimates greatly depends on minimizing the environmental differences between and within clones.

Heritability estimates in white pines are few. Data are available on height growth (Squillace and Bingham, 1960; Hanover and Barnes, 1962; Squillace et al., 1967; Steinhoff and Hoff, 1971 and Kriebel et al., 1972), blister rust resistance (Bingham et al., 1960, and Bingham et al., 1969), and sulfur dioxide and ozone tolerance (Houston and Stairs, 1973). The latter is a repeatability estimate based on clones, with values from 0.468 to 0.597. The rest are narrow sense heritability estimates based on the analyses of sibs and on parent-progeny regressions. These estimates were low to moderate for height growth and for blister rust resistance. Nevertheless, appreciable genetic gains were postulated especially in breeding for blister rust resistance.

Clonal propagation of white pines on a production scale has never been considered. However, recent results in rooting of white pine cuttings (Zsuffa, 1973) indicate the feasibility of this method.

Materials and Methods

Eight clones of P. griffithii McClelland X *strobus* L. are examined in this study. Each clone is represented by five ramets randomly located in the planting.

The clones were members of a half-sib family, raised from the seed of a P. griffithii tree (22932-A) at Arnold Arboretum pollinated by neighbouring P. strobus trees. The number of males which contributed to the cross, and their interrelatedness is not known. The seed was supplied by A. G. Johnson, Institute of Agriculture, University of Minnesota, St. Paul, U.S.A., in 1951. The seedlings were grown at Maple, Ontario experimental nursery and screened for blister rust susceptibility.

The ramets were grafted in the spring of 1960 on P. strobus. They were outplanted at 2.75 X 2.75 m (9 X 9 ft.) spacing on a uniform site located at Maple, Ontario, Canada. The trees were open grown, not pruned, and without any visible damage (Fig. 1). At the time of measurement the grafts were 14 years old.

Total height and the diameter at breast height (DBH at 1.30 m) of each tree was measured in the field. All trees were photographed from the same distance and azimuth. For each photograph, a projection of the tree's stem and branches was drawn on transparent paper (Fig. 1). On the projection, the branch length to the nearest millimeter and the branch angle to the nearest degree were measured of three branches situated in the same two whorls in the middle part of the crown of each tree. The branches chosen were approximately parallel to the plane of the photograph. Branch length is referred to as the length of a straight line connecting the junction at the trunk to the branch tip. Branch angle is referred to as the angle between the centre line of the stem and of the line connecting the base and the middle of the chosen branch (Fig. 1).

The similarity of the three branch lengths and branch angles taken for the same tree was verified with Chi-square tests. Spearman's coefficient of rank correlation (Steel and Torrie, 1960) was calculated for tree height, DBH, branch length and branch angle. An analysis of variance was made for each of these traits. Duncan's multiple range tests (Steel and Torrie, 1960) were calculated for each measured trait.

The derived variance components were used in computation of broad sense heritability values as follows (Wright, 1962):

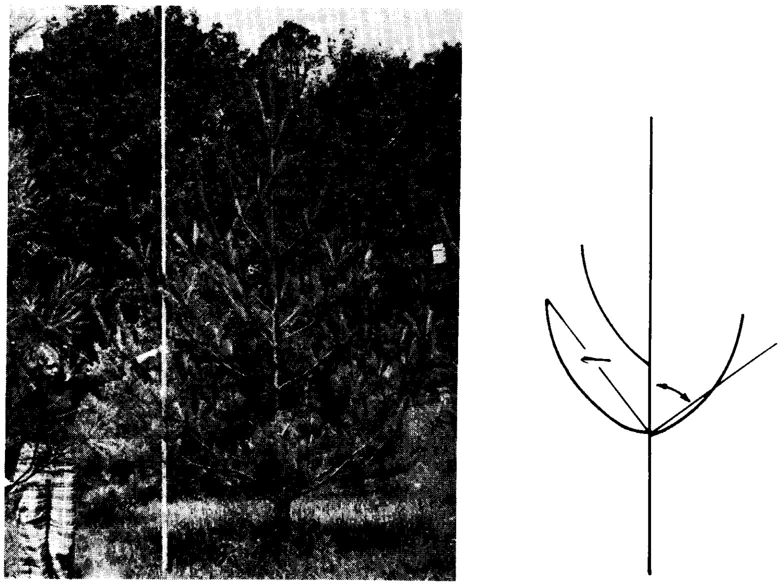
$$h^2 \text{ (broad sense heritability)} = \frac{\sigma^2_c}{\sigma^2_c + \sigma^2_E}$$

σ^2_E = error mean square

$$\sigma^2_c = \frac{\text{clone mean square} - \text{error mean square}}{\text{no. of ramets per clone}}$$

The technique of calculation separated the total observed phenotypic variance into two components, the within clone variance (error variance), which is entirely environmental in origin, and the between clone component, which is genetic.

The genetic gain (AG) for selection within families is calculated as $AG = ih^2\sigma p$ (Falconer, 1960), where "i" (the intensity of selection) is taken as a constant value (i = 1.42,



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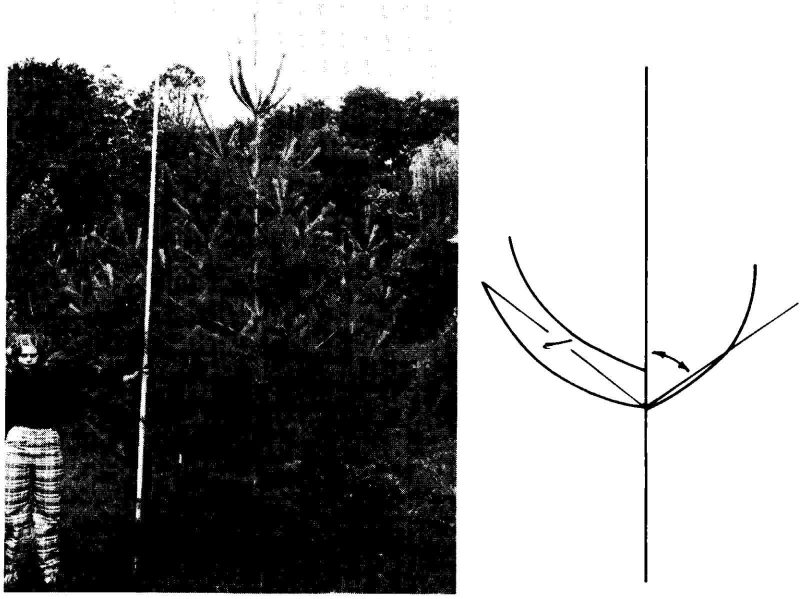

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Figure 1. — Photographs and their projections, with the measure of branch length and branch angle.

from Falconer, 1960, Table 11.1, for selection of 1 out of 8), "h^2" is the estimated broad sense heritability within families and σp equals the square root of the mean of clonal mean square

$$\sigma^2_p = \frac{\text{clonal mean square}}{\text{no. of ramets per clone}}$$

Results

The Chi-square tests showed that the three branch lengths and the three branch angles measured on each tree were similar. Analyses of variance showed that between clone variation was significant and accounted for the greatest proportion of the variability *(Table 1).* Significant differences between the clones were demonstrated in each trait. *(Table 2).* The ranks of tree height and DBH values were identical ($r = 1.00$), while the rank correlation of other traits was not significant ($r = 0.50$ for heights and branch lengths and for diameters and branch lengths; $r = 0.45$ for heights and branch angles and for diameters and branch angles; and $r = 0.05$ for branch lengths and branch angles). The broad sense heritability estimates showed moderate values for tree heights and diameters and higher values for branch lengths and branch angles. The predicted genetic gains varied for the analysed traits, but were in general high *(Table 3).*

Discussion

Large and significant differences were observed between the clones in all analysed traits. The best clones exceeded the clones with lowest values in tree height by 52%, and in DBH by 109%. The differences in tree volumes between the best and worst clones would have amounted to 546%.

Table 1. — Variances and F values.

Source	DF	Tree height		Tree DBH		Branch length		Branch angle	
		SS	F	SS	F	SS	F	SS	F
Total	39	7.37		37.28		1.2604		1,455.16	
Clones	7	4.93	9.24**	19.63	5.08**	0.9886	16.61**	1,076.92	13.02**
Error	32	2.44		17.65		0.2718		378.24	

** significant at 1% level.

Table 2. — Range of mean clonal values in decreasing order and the significance of differences (Duncan's multiple range test, at 5% level).

Clones	Tree height (m)		DBH[1] (cm)		Branch length (m)		Branch angle (degrees)	
841	3.8		4.8	a	1.50		51.6	a b
851	3.4	a	4.1	a b	1.05		56.5	a
842	3.4	a	3.9	b	1.27	a	53.2	a b
850	3.2	a b	3.9	b	1.24	a	45.1	c
848	3.0	b	3.6	b c	1.22	a	45.5	c
849	3.0	b	3.3	b c	1.28	a	51.1	b
845	2.9	b c	2.9	c d	1.19	a	56.1	a
847	2.5	c	2.3	d	0.93		41.2	c

[1] Diameter at breast height (1.30 m).

Table 3. — Averages, phenotypic variances, broad sense heritabilities and predicted genetic gains in individual selection and clonal propagation.

Trait	Mean	σp	h^2	Genetic gain in units	(ΔG) %
Tree height — m	3.1	0.38	0.62	0.33	11
Tree diameter (DBH) — cm	3.6	0.75	0.45	0.48	13
Branch length — m	1.2	0.17	0.76	0.18	15
Branch angle — degrees	50.0	5.55	0.71	5.60	11

The clones fell into three clearly defined groups: high, medium and low (*Table 2*).

The maximum and minimum clonal values for branch length and branch angle varied by 61% and 37% respectively. The general clonal rank for branch lengths was similar to the tree heights and diameters; however, the correlation of the ranks was not significant. The ranking of clones according to branch angle was different (*Table 2*).

Differences among clones include all genetic sources of variation and some non-genetic sources of variation such as effects due to vegetative propagation. Therefore, broad sense heritability estimates from clonal tests set upper limits to the ratio of genotypic variance. These are easy estimates and useful in measuring the genetic determination of a character, especially in clonal propagation. However, caution is needed in application of the values, especially for the impossibility of distinguishing additive from non-additive genetic effects and when working with half-sibs. In this case, the genetic variances are those within a single half-sib family. Since the pollen source was not controlled, the clones may be full-sibs and hence the genetic variance among them may be only that among members of the same full-sib family. According to Namkoong (1966) the scarcity of males contributing to a half-sib, and the relatedness among them increases the genetic covariance within the seed tree family and can lead to an over-estimate of genetic additive variance. In the case of few males pollinating a significant portion of the total genetic variance observed could be due to non-additive genetic effects.

Compared to this study, the narrow sense heritability estimates for height growth of juvenile *P. monticola* Lamb. (Squillace and Bingham, 1960 Hanover and Barnes, 1962, Squillace *et al.*, 1967 and Steinhoff and Hoff, 1971) and *P. strobus* L. (Kriebel *et al.*, 1972) are lower ($h^2 = 0.07$—0.47 compared to $h^2 = 0.592$, *Table 3*) because of the different variance ratios involved. My calculations shows higher heritability for tree height, than for tree diameter. In *Populus deltoides* Marsh clones, Wilcox and Farmer (1967) also estimated higher heritabilities for height ($h^2 = 0.66$ as compared to $h^2 = 0.58$ for diameter). Also, my heritabilities of branch length and branch angle are similar to estimates in several other tree species (Hattemer, 1963, Ehrenberg, 1970).

On the basis of this study, I predicted the genetic gains in clonal selection within the single half-sib family studied. They ranged from 11% to 15% (*Table 3*). The gains in volume, based on the predicted gains in heights and diameters, would have amounted to 36% if simultaneously achieved. It is likely, that the genetic variance observed here is only part of the total genetic variance and that larger genetic gains could be achieved by selection among unrelated clones. There are no published information on the possible genetic gains in clonal development of white pines. In a progeny test of 19 *P. strobus* L. half-sibs differences in height growth of individual trees within a family amounted to 42% from the mean (De Vecchi Pellati, 1967). In these families, by clonal selection, genetic gains similar or higher than calculated here could probably have been obtained.

Abstract

Eight clones of a half-sib were studied. Variation between the largest and smallest clones amounted to 52% in tree height, 109% in diameter (DBH), 61% in branch length and 37% in branch angle. The clonal variance ratios were significant for each trait. The broad sense heritabilities were 0.62 for height, 0.45 for DBH, 0.76 for branch length and 0.71 for branch angle. The genetic gains for these traits in clonal propagation were predicted from 11% to 15%.

Conclusions

The results of this study point to: (i) moderate broad sense heritability values for tree heights and diameters (ii) moderately high broad sense heritability values for branch length and branch angle (iii) significant clonal variation in analysed traits (iv) possibility of between 11% and 15% genetic gain in individual selection within a half-sib family and subsequent clonal development.

Key words: Clonal Selection, Genetic gain, *Pinus griffithii* McClelland × *Pinus strobus* L.

Zusammenfassung

Acht Pfropfklone einer Kreuzungs-Nachkommenschaft (Halbgeschwister-Familie) von *Pinus griffithii* McClelland × *Pinus strobus* L. wurden im Alter 14 auf Gesamthöhe, Brusthöhendurchmesser (∅ in 1,3 m Höhe) und Verzweigung hin untersucht. Zwischen den Klonen wurden in diesen Merkmalen beträchtliche signifikante Unterschiede gefunden. Diese betrugen bis zu 52% bei der Gesamthöhe, 109% beim Brusthöhendurchmesser und rechnerisch 546% beim Volumen. Bei der Zweiglänge und beim Astwinkel gab es Unterschiede bis zu 61% bzw. 37%. Der in dieser Halbgeschwister-Familie durch die Selektion von Einzelbäumen und deren vegetative Vermehrung mögliche genetische Gewinn wird auf 11% bis 15% geschätzt.

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Genetic Variation in Black Spruce (Picea mariana (Mill.) B.S.P) in Newfoundland

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Introduction

Though conifers constitute 87 percent of the merchantable volume on the Island and 99 percent in Labrador (Anon. 1973), there are only two commercially important local species, balsam fir (*Abies balsamea* (L.) Mill.) and black spruce (*Picea mariana* (Mill.) B.S.P.). The high susceptibility of balsam fir to major insect pests reduces the possible benefits from its genetic improvement. Black spruce is relatively free from insect pests and diseases, is adaptable to a wide variety of edaphic and climatic conditions, and is a choice species for pulp on account of its long fibres and high wood density (Besley 1959, Basham and Morawski 1964, Ladell 1971). Consequently, black spruce is the most important species in the recently started program of reforestation in the Province which aims at an annual planting of approximately 2,000 hectares. Genetic improvement of black spruce is, therefore, both important and urgent.

A provenance trial, using Newfoundland and mainland provenances, started in 1968, is one of several studies on the genetic improvement of black spruce currently in progress at the Newfoundland Forest Research Centre of the Canadian Forestry Service. Results of the first phase of this study have been reported elsewhere (Khalil 1973). These results show the performance of the provenances in Newfoundland. The data were further analysed to determine the degree and pattern of variation of important characters in the black spruce populations of insular Newfoundland. This paper presents the results.