Heritability and Genetic Gains for Height Growth in 20-year-Old Korean White Pine in Korea

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Abstract - The objectives of this study were to examine the genetic variation of 20-year-old tree height and to estimate heritabilities and genetic gains of Korean white pine. Analysis of variance showed that families and family × block interaction had the significant (p=0.01) effects on tree height. However, family variation appears to be much greater than the variation due to family × block interaction. Individual tree heritability was higher ($h_I^2 = 0.73$) than family heritability, ($h_F^2 = 0.83$) therefore, combined selection showed the largest genetic gain (17.76%) in a given equal intensity of selection.

Key words - Variation, Genetic gain, Progeny, Breeding by selection, Korean white pine

Introduction

Intensive studies of genetic testing in growth traits of forest trees have been made to determine the magnitude and probability of improvement for tree breeding (Bongarten and Hanover, 1986; Chon and Kim, 1986 ; Rockwood and Goddard, 1980). The ratio between genetic and phenotypic variances is called heritability which is one of the most important and most frequently used concept in quantitative genetics (Graham et al., 1985).

Information on heritability is necessary not only for the estimation of breeding effects but also for the choice of the schemes of breeding. In this study, we examined genetic variation of tree height for 25 half-sib families of Korean white pine. The objectives of this study were to describe the variance components in total tree height at age 20 and to estimate the narrow sense heritabilities and genetic gains with different selection methods.

Materials and Methods

Materials and measurements

Seed source and establishment procedures have been described in detail in the previous report (Chon and Kim, 1986). A total of 1,166 test tree (20 families × 10 trees per plot × 4 replications) was selected randomly and used in this study. The experimental site located in Kapyoung-gun is a half-sib progeny test site established in 1983 with 2+1 stocks. The site is on a south-estern direction with a slight gra-

dient (20-26°) and has a moderate sandy loam soil. Results obtained in this paper are based on measurements of total height (±0.5cm) taken in December 2003, the time when the trees had completed 20 years of growth from seed.

Statistical analysis

Four blocks were established in a completely randomized block design. ANOVA was performed on tree height, and then the heritability was calculated using the estimated variance components and formulae given in the Table 1.

The variance components used for predicting genetic gains with

Table 1. Analysis of variance for single site, individual tree and family heritability

Source of variance	df	Expected mean squares
Block	b - 1	$\sigma_W^2 + n\sigma_{BF}^2 + nf\sigma_B^2$
Family	f - 1	$\sigma_W^2 + n\sigma_{BF}^2 + nb\sigma_F^2$
Block×Family	(b-1)(f-1)	$\sigma_W^2 + n\sigma_{BF}^2$
Within-plot	fb(n-1)	σ_W^2

$$h_I^2 = \frac{4\sigma_F^2}{\sigma_W^2 + \sigma_{BF}^2 + \sigma_F^2}$$

$$h_F^2 = \frac{\sigma_F^2}{\sigma_W^2/nb + \sigma_{BF}^2/b + \sigma_F^2}$$

* Note : f, b, and n refer to the number of families, blocks, and trees per plot. $\sigma_W^2, \sigma_{BF}^2, \sigma_F^2$ and σ_B^2 are the variances due to within-plot, block×family, family, and block, respectively.

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selection methods; 1) mass selection, 2) family selection, 3) within-family selection, and 4) combined (family + individuals within-family) selection. The calulations of gain were performed based on Cotterill (1986), Krusche *et al.* (1980), and Squillace *et al.* (1967). Top 20% of trees or families were retained for selection, and selection intensity of i=1.40 was determined from the graphs (Namkoong and Snyder, 1969).

Results and Discussion

Growth performance

It was found that there was signifiant family differences in total tree height (Table2). The family height ranged from 7.04m (F 5) to 8.56m (F 20) and averaged 7.65m. In individual tree measurements, significant variations were also found in tree height; from a minimum of

Table 2. Variation of height growth of 20-year-old open-pollinated progenies of Korean white pine in Kapyung site, South Korea

FL	Height (cm)		
	Mean±S.E.	DMRT^A	C.V.(%)
20	856.84±10.06	A	9.17
18	829.60± 8.25	A B	7.57
8	808.28± 8.32	B C	9.20
12	795.75± 9.88	B C D	9.54
1	785.03±12.67	C D E	12.81
9	782.09± 7.65	C D E F	7.94
7	779.55± 9.32	C D E F G	9.93
23	778.81± 9.46	C D E F G H	10.30
21	763.02±10.15	D E F G H I	9.68
17	747.82±12.94	E F G H I J	10.67
22	745.43± 8.65	F G H I J	9.50
2	742.71±10.18	G H I J K	10.44
11	740.82±12.18	H I J K	11.03
10	740.67± 7.84	I J K	8.66
13	739.68± 9.99	I J K	9.55
6	735.52± 9.42	I J K	9.41
15	733.78±10.76	J K	10.27
4	715.66±12.83	J K	14.67
3	710.25±13.06	J K	12.87
5	703.85±12.42	K	11.30
mean	765.04± 2.54		11.35

DMRT^A: Duncan's Multiple Range Test.

Table 3. Estimates of variance components and heritabilities for height growth at age 20.

Source of Variance	df	Mean Square	Variance Components
Block	3	280610.59[***]	1259.22
Family	19	88875.79[***]	716.14
Block×Family	57	15233.22[***]	4951.95
Within-Plot	1086	4951.95	5036.88
	$h_I^2 = 0.73$	$h_F^2 = 0.83$	

[***] : Significant at 1% level.

4.18m in Family 4 to a maximum of 10.47m in Family 20.

Heritabilities and genetic gains

Variance components and heritabilities for tree height are presented in Table 3. Although the sampling error accounts source of variation (σ_F^2=1259.22) in tree height. Variance components of family x block interaction was 56.9% as a percentage of family variance. This relatively small interaction implies moderate changes of family height ranking with different blocks. Individual tree and family heritabilities were 0.73 and 0.83, respectively (Table 3). Its values in this study seem to be higher than those of the relative or similar researches. This result may be caused by intensively controlled extraneous environmental variance that resulted in reduced experimental error.

The method of selection depends to a large degree on the magnitude of heritability. Estimates of genetic gain and relative effectiveness evaluated for tree height are shown in Table 4. Maximum genetic gain of 17.76% (1.36m) and minimum of 7.38% (0.57m) were expected by combined and family selection when best 10% of trees and families were retained for selection, respectively. The expected gain based on within-family selection was 10.38% (0.79m) with equal intensity of selection (i_{wf}=1.40). For a family selection of 0.447, a combined selection intensity of 0.2, that is, i_c=1.40 is derived. Gains expected from individual selection was 13.84% (1.06m). Given equal selection intensity, combined selection showed the best efficiency for selection of tree height. This is the same trend as Kim and Chon's report (1990). According to this result, mass selection seems to be a recommendable selection method.

Heritability for height is well known to be variable with experimental site conditions and experimental design, therefore, it is rather impossible to estimate accurate values of heritability. However, expected genetic gain in a selection program is a function of heritability and selection differential, great care is needed in predicting the gains. Estimates of heritability and gain obtained in this study may be inflated because members of the open-pollinated families are probably more closely related than half-sibs.

Table 4. Expected genetic gains and relative efficiencies for tree height (cm) with different selection method.

Selection method	Mass	Family	Within-family	Combined
Genetic gain	105.91	56.46	79.43	135.89
(%)	13.84	7.38	10.38	17.76

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