Statistical Efficiency of Sampling Plot Size in Half-sib Progeny Test of Korean Pine (*Pinus koraiensis* S. et Z.)[1]

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잣나무 次代檢定에 있어서의 效率的인 Plot Sampling에 關한 硏究[1]

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ABSTRACT

Tree height at age 10 was used to estimate the statistical efficiencies of sampling size in the progeny test of *Pinus koraiensis* S.et Z. Experimental design was RCB design which consists of 25 half-sib families in each of three blocks. The number of families and blocks were fixed, therefore, the number of trees sampled per plot was the only factor that influences the environmental portion of the family mean height. Coefficient of variation, the estimate of the standard error of the family mean height, decreased with increase of sampling plot size, and became stable from 4-tree plot sampling (6.97%). The experimental error was significant from 7-tree sampling plot size. Nonlinear relationship ($\hat{Y}=10.425e^{-0.073x}$; $R^2=0.840$) was found between the sampling plot size and the standard error of family mean height.

Key words ; *Statistical efficiency, half-sib progeny test, RCB design, plot size, coefficient of variation*, Pinus koraiensis.

要 約

난괴법 3反復으로 配置한 잣나무 10年生 半兄妹次代檢定林에서 plot當 任意로 2-10本의 標本木을 選定한 後, 分散分析을 통하여 家系平均 樹高의 誤差를 나타내는 C.V.값을 各 sampling size 別로 推定, 比較하였다. plot當 標本木數를 增加시킴에 따라 C.V.값은 점차 減少되었으며, plot當 4本부터 安定된 C.V.값(6.97%)을 나타내었으나, plot當 7本부터는 實驗誤差가 增加됨을 알 수 있었다. 이들 두 變量間에 $\hat{Y}=10.425e^{-0.073x}$($R^2=0.840$)의 關係式을 推定할 수 있었다.

INTRODUCTION

Genetic test is essential to successful tree improvement program, and is one of the most expensive aspect of that program. Genetic field tests are often installed for multiple purposes including ranking of parents, advanced-generation selection, and variance component estimation. Primary consideration in test design is often placed on the ranking of

parents (McCutchan et al. 1989). If the number of families is not variable, then the number of trees per plot and the number of blocks which represent the environmental portion of the family mean value become important factors affecting the statistical efficiency and the cost of testing in the genetic test. Thus, the environmental portion of the family variance can be manipulated by changing the two environmental factors. The procedure for selecting the trees to be used for estimating the plot value is called the plot sampling technique. An experimental plantation yields the most precise results if laid out so that the amount of site variation among plots within any one block is the smallest(Wright 1976). The general conclusion demonstrated in foreign studies is that statistical efficiency is higher in a test containing small plots and many blocks than in containing larger plots and fewer blocks(Cotterill and James 1984 ; Wright 1973 ; Loo-Dinkins and Tauer 1987). Cotterill and James(1984) recommended single- or two-tree plots for evaluating height and diameter traits from progeny test design. However, 4-to 6-tree row plots are extensively used in many tree improvement program. The significant advantages over the noncontiguous arrangement are ease of layout and tracking in the field, and simplicity in silvicultural thinning by family. The higher the experimental error, the higher the number of replications that should be used ; the higher the sampling variance, the greater the number of samples per plot that should be taken(Gomez and Gomez 1984). This report deals with the statistical efficiency of sample size using different number of trees per plot in half-sib progeny test of Korean pine.

Materials and Methods

Kapyoung experimental site located in northeastern Kapyoung-kun is a half-sib progeny test site established in 1983. This site is on a southeastern

aspect with a moderate gradient(20°-26°), and has a sandy loam soil. The experimental design was randomized complete block design which consists of 25 half-sib families in each of 3 blocks with 25-tree row plots ; the family plots extended up and down the slope. 10-year-old trees were used in this study. Of the 25 trees per plot, sample trees were taken at random two to ten and used to estimate the statistical efficiency of each analysis. Analysis of variance (Zobel and Talbert 1984) was performed on each sampled plot size. Variance components were obtained from the expected mean squares(Table 1).

The variance of family means in a replicated progeny test is

[1] $V(\overline{F}) = \sigma^2_w/NB + \sigma^2_{FB}/B + \sigma^2_F$

where $\overline{F}$ is the family mean, σ^2_w is the within-plot variance components, σ^2_{FB} is the family×block interaction variance component, σ^2_F is the family variance component, N is the number of trees per plot, and B is the number of blocks. From this equation, therefore, the estimates of the variance of environment, denoted as $E_{\overline{F}}$, and of the corresponding C.V.(Coefficient of variation) value can be derived ;

[2] $E_{\overline{F}} = \sigma^2_w/NB + \sigma^2_{FB}/B$

[3] $CV = \sqrt{E_{\overline{F}}}/\overline{X} \times 100(\%)$

where $E_{\overline{F}}$ is the environmental portion of the variance of a family mean, CV is the standard error of the family mean expressed as percent of the mean value, and $\overline{X}$ is the overall mean of the test. The CV provides a convenient method to compare the overall effect of the two plot types on test precision since the $E_{\overline{F}}$ includes all within family variance, both within plot and family×block interaction variances(Lambeth et al. 1983). The family mean CV was used to determine the efficient number of trees per plot in this half-sib progeny test.

Table 1. Analysis of variance for half-sib progeny test.

Source	d.f.	M.S.	F-test	Expected mean square
Blocks	(B-1)	MS_B	$MS_B/MS_{F\times B}$	
Family	(F-1)	MS_F	$MS_F/MS_{F\times B}$	$\sigma^2_w + N\sigma^2_{FB} + NB\sigma^2_F$
Fam.×Bk.	(F-1)(B-1)	$MS_{F\times B}$	$MS_{F\times B}/MS_w$	$\sigma^2_w + N\sigma^2_{FB}$
Within plot	FB(N-1)	MS_w		σ^2_w

RESULTS AND DISCUSSION

The result of ANOVA for tree height from 2 to 10 trees per plot is represented in Table 2. In all cases, family was a significant source of variation of tree height at age 10. Family×block interaction variance increased with number of trees sampled, and showed significant effect from 7-tree row plot design (Table 2). This result indicates that a family plot mean height relative to other families can vary significantly from block to block, therefore, an increase in the number of block is needed to reduce the experimental error from 7 or more sampling trees per plot.

Analysis of variance was also used to estimate the expected mean squares of source of variance from which the variance components were derived. Environmental portion of the variance of a family mean, denoted as $E_{\bar{F}}$, decreased from 470.09 to 120.37 with the number of sample trees per plot (Table 3).

However, statistical theory generally predicts that either increasing plot size or reducing block number increases the variance of a family mean (Cochran and Cox 1957). Because the components of σ^2_w/NB and σ^2_{FB}/B are mainly attributable to environment, the magnitude of $E_{\bar{F}}$ can be altered by changing the number of trees per plot (N) or number of blocks (B) in the test site. Block number (B) was fixed in this study, therefore, the number of trees per plot was a main factor influencing the variance of a family mean. Standard error of the family mean expressed as percent of the mean value (CV) was derived from the estimated $E_{\bar{F}}$ (Table 2). CV values showed that there was a moderate decrease in the magnitude of estimates when the sampling size increased from 2 to 10 trees per plot. The CV value resulting from 2-tree plot sampling (10.62%) was about 2 times greater than those for the 10-tree plot sampling of 5.38%. The results in this study indicate that the experimental error was significant from 7-tree plot sampling (Table 2) and the CV for family mean height became stable from approximately 4-tree sampling size (Fig. 1). Therefore, a considerable stability in precision of family mean height may result from using 4 to 6-tree sampling size in a contiguous plot design of Korean pine. Genetic test

Table 2. Mean squares and F-test for tree height in the same site with different number of trees per plot.

No. of trees	M.S.		
	Family	Family×Block	Within-plot
2	4988.03*	2820.55[ns]	2332.94
3	7103.80**	2815.71[ns]	2070.76
4	9797.43**	2394.24[ns]	2215.59
5	13570.58**	2610.29[ns]	2289.17
6	16643.11**	3031.17[ns]	2322.06
7	18314.28**	3272.54*	2238.86
8	18832.19**	3312.91*	2186.72
9	20569.29**	3705.84**	2165.12
10	22836.96**	3611.05**	2235.52

*,** : significant at 5% and 1% level, respectively
[ns] : non-significant at 5% level

Table 3. Variance components for family mean height in each sampling plot size of the genetic test.

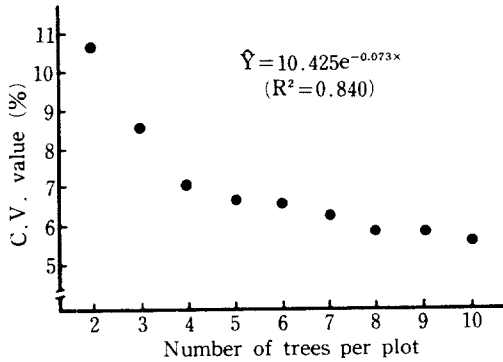| No. of trees	σ^2_F	σ^2_{FB}	σ^2_w	$E_{\bar{F}}$	CV(%)
2	361.25	243.80	2332.94	470.09	10.62
3	476.45	248.31	2070.76	312.86	8.51
4	616.93	44.66	2215.59	199.52	6.97
5	730.69	64.22	2289.17	174.02	6.53
6	756.22	118.19	2322.06	168.40	6.45
7	716.27	147.67	2238.36	155.84	6.18
8	646.64	140.77	2186.72	138.04	5.74
9	624.57	171.19	2165.12	137.25	5.73
10	640.86	137.55	2235.53	120.37	5.38

$\hat{Y} = 10.425e^{-0.073x}$
$(R^2 = 0.840)$

Fig. 1. Relationship between sampling size and standard error of family mean height.

is performed for multiple objectives, e.g., increased growth rate, increased resistance to pests, and advanced-generation selection, etc. A complicating factors in most forestry experiments, and one that makes experimental design difficult, is that some level of unplanned loss occurs in most genetic trials subsequent to their establishment (McCutchan et.al. 1989). Considering the survival ratio of 70% (Kim and Chon 1990) and the tending of stands in mature ages, 15-to 20-tree row plots are recommendable for establishment of genetic test plantations in Korean pine.

LITERATURE CITED

1. Cochran, W.G. and G.M. Cox. 1957. Experimental Designs. John Wiley & Sons, Inc., N. Y.

2. Cotterill, P.P. and J.W. James. 1984. Number of offspring and plot sizes required for progeny testing. Silvae Genet. 33 : 203-209.

3. Gomez, K.A. and A.A. Gomez. 1984. Statistical Procedures for Agricultural Research. John Wiley & Sons, Inc., N.Y.

4. Kim, D.E. and S.K. Chon. 1990. Trends in genetic parameters with age and site for early implications of genetic improvement in Korean white pine. Jour. Korean For. Soc. 79 : 56-70.

5. Lambeth, C.C., W.T. Gladstone, and R.W. Stonecypher. 1983. Statistical efficiencies of row and noncontiguous family plots in genetic tests of loblolly pine. Silvae Genet. 32 : 24-28.

6. Loo-Dinkins, J.A. and C.G. Tauer. 1987. Statistical efficiency of six progeny test field designs on three loblolly pine (P. taeda L.) site types. Can. J. For. Res. 17 : 1066-1070.

7. McCutchan, B.G., G. Namkoong, and F.G Giesbrecht. 1989. Design efficiencies with planned and unplanned unbalance for estimating heritability in forestry. For.Sci. 35 : 801-815.

8. Wright, J.W. 1973. Genotype-environment interaction in north central United States. For. Sci. 19 : 113-123.

9. Wright, J.W. 1976. Introduction to Forest Genetics. Academic Press., Inc. N.Y.

10. Zobel, B.J. and J.T. Talbert. 1984. Applied Forest Tree Improvement. John Wiley & Sons, Inc., N.Y.