COST EFFECTIVE SAMPLING FOR SPECIFIC GRAVITY[1]

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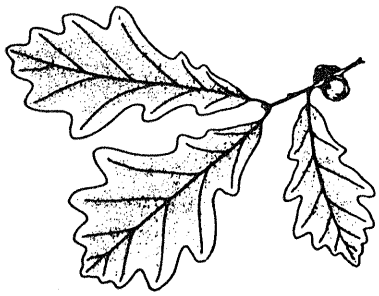

ABSTRACT.--A statistically based method for evaluating increment cores versus stem analysis for sampling for specific gravity in an eastern cottonwood (Populus deltoides Bartr.) clonal study is given. From other studies, specific gravity has been found to be highly variable within and between trees of the same clone. This is because specific gravity is a complex trait that is influenced by many internal and external factors. A model was developed to predict the variability of specific gravity for a specimen taken from a tree within a clone as a function of green volume of the specimen. A cost function also was formulated. With these functions, it was possible to determine the number of trees from a clone and the number of samples from each tree that need to be measured to detect a specified difference in the mean specific gravity between clones.

INTRODUCTION

Specific gravity is an important characteristic that is often analyzed in clonal studies. It is important because it has been found to be directly related to the pulping characteristics and the mechanical strength of wood (Heger, 1974). Although specific gravity is considered to be very important, clonal selection experiments are seldom designed based upon this variable. Because specific gravity is highly variable within trees resulting from hereditary, environmental, physiological and mechanical factors (Farmer and Wilcox, 1966), experimental designs based on other variables might not be very effective in detecting difference in specific gravity between clones.

Presented here are some functions used for calculating both the number of specimens per tree and the number of trees per clone that are needed to detect some specified difference in specific gravity between clones of eastern cottonwood (Populus deltoides var. deltoides Bartr.) in a cost effective manner. These functions were developed to be implicitly and explicitly dependent on the average green volume of specimens taken from the trees used to determine specific gravity. The experimental design when increment cores are used to determine specific gravity can be compared to the design when stem analysis disks are used. The cost of using nondestructive versus destructive sampling methods can be considered in the comparison.

DATA

Data for the models came from a clonal study of eastern cottonwood located in Pottsville Bottoms in southern Illinois. More detailed information about the study can be found in Reddy and Jokela (1982). Briefly, 70 clones were thinned at age 5. The thinned trees used for the study were of the two fastest growing replicates from each of the 15 most promising clones. Cross-sectional disks were obtained from each of the felled trees at heights of .3, 1.5, 2.5, 5.0, 7.5, and 10 meters. On each disk, the girth diameter[3] going through the pith was located and marked. The distance from the center of the pith to each ring on the radius of the girth

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[3]Girth diameter is defined as circumference/π.

diameter was measured. Wood specimens were then taken in each growth ring along both radii. The dimension of each specimen was such that the green volume for each ring was approximately 8 cc. The specimens were then oven dried for 24 to 48 hours at 100°C. After drying, the specimens were weighed and the dried volumes were measured precisely with an Amsler Mercury Meter. Specific gravity was calculated for each ring specimen based on these measures. There were a total of 1872 specimens, approximately 125 specimens per each of the 15 clones.

METHODOLOGY

A mixed nested analysis of variance design (ANOVA) was used to analyze the raw specific gravity data based on the individual ring specimens.[4] The clones were considered to be fixed effects, while specimens within trees were considered to be random effects. Table 1 displays the ANOVA and expected mean square for the nested design. Using Bartlett's test of homogeneity, tests were performed to see if variance of residuals of the model varied with height or ring position. No significant difference in variability was found ($\alpha = .05$) for either height or ring position. To be able to calculate the number of specimens and the number of trees needed to be sampled with increment cores and stem analysis, models were developed to predict both the variance (mean square error) of specimens within trees and of trees within clones as a function of the average green volume of specimens taken from a tree. This was done in a sequential fashion by calculating the specific gravity and green volume based on an increasing number of adjoining rings within each disk and then analyzing the resulting specific gravity measures with the ANOVA.

TABLE 1.--Analysis of variance table for nested design (mixed model).

Source of Variation	Degrees of Freedom	Expected Mean Square Error
Clones	p	$\sigma_1^2 + n \cdot \sigma_2^2 + n \cdot q \Sigma \alpha^2/(p-1)$
Trees within clones	$p(q-1)$	$\sigma_1^2 + n \cdot \sigma_2^2$
Specimens within trees	$p \cdot q(n-1)$	σ_1^2

where p is the number of clones,
q is the number of trees within each clone,
n is the number specimens within each tree,
σ_1^2 is the variance of specimens within trees,
σ_2^2 is the variance among trees,
$n \cdot q \Sigma \alpha^2/(p-1)$ is the variance due to clones.

Figure 1 shows that the variance of the specimens within trees decreases in a negative exponential fashion as the average green volume of the specimens increases. The following model was developed to predict the variance of specimens within trees as a function of the average green volume (gv) of the wood specimens:

$$\hat{s}_1^2 = .0010197 + .002268 \cdot e^{-.07874 \cdot gv} \qquad \text{(Eq. 1)}$$

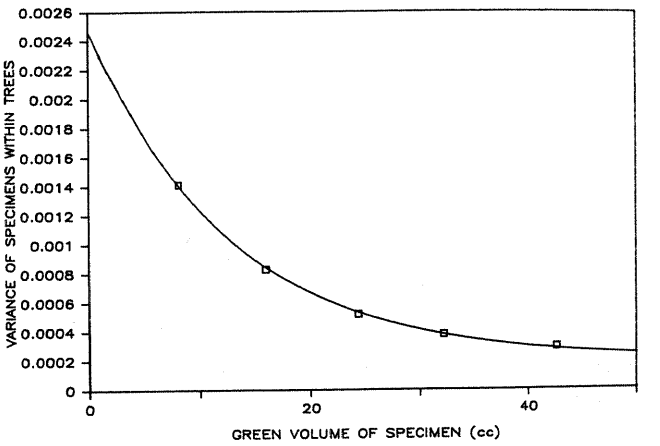

FIGURE 1.--Variance of specimens within trees. [$\hat{s}_1^2$ versus average green volume of specimen (gv)]

As was expected, the estimate of variance among trees, s_2^2, for each of the ANOVA's was found to be nearly constant with a mean of $\bar{s}_2^2 = .001186$. With the mean variance among trees and the predicted variance of the specimens within trees, the variance (mean square) of trees within a clone, s, could then be predicted as a function of gv:

$$s^2 = s_1^2 + n \cdot \bar{s}_2^2 \qquad \text{(Eq. 2)}$$

Sample Size Formulas

Given the objective of designing an experiment to detect some specified difference in the specific gravity of two clones in a cost effective manner, it was possible to formulate equations to give the number of trees within each clone and the number of specimens within each tree to be systematically sampled along the length of the stem. To calculate the minimal number of trees per clone needed to detect a specified difference in the specific gravity between two clones, a two-tailed

[4]Initially, a nested design that included a block factor was entertained, but the factor was found not to be signifcant. In addition, some more elaborate analyses of variance models were considered, however, they were not able to significantly explain any additional variation.

t-test formulated by Shavelson (1981) and then modified for a mixed nested design was used:

$$q = \frac{2(|Z_1| + |Z_2|)^2 \cdot s^2}{d^2 \cdot n} \qquad \text{(Eq. 3)}$$

where Z_1 is a z score (two-tail) for the probability (α) of Type I error (rejection of a true null hypothesis), Z_2 is z score (one-tail) for the probability (β) of Type II error (acceptance of a false null hypothesis), d is the difference in the mean specific gravity of two clones that is desired to be detected and s^2 is tha variance trees within clones. Eq. 2, the predicted variance of trees within clones, was substituted for s^2 in the sample size formula.

Prior to using Eq. 3, the number of specimens per tree, n, is needed. The optimal number of specimens per tree was calculated by defining a simple total cost function for measuring a clone. It was assumed that the total cost to measure a clone could be expressed as

$$C_t = q \cdot C_2 + q \cdot n \cdot C_1$$

where C_t is total cost to measure a clone,
C_2 is the cost of a tree within a clone,
C_1 is the cost to obtain and measure a specimen within a tree.

With the objective of minimizing the cost of the experiment, the optimal number of specimens per tree can be easily shown to be (Sokal and Rohlf, 1969):

$$n = [(C_2 \cdot s_1^2)/(C_1 \cdot s_2^2)]^{1/2}$$

Given that C_2 and C_1 are known[5], n can be calculated for specimens of different green volumes by substituting $\hat{s}_1^2$ (Eq. 1) and $\bar{s}_2^2$ into the equation. Then n can be substituted into Eq. 3 to get the number of trees per clone, q, to meet the precision requirement.

EXAMPLES

These formulas provide a very flexible means of comparing different methods for collecting specimens for specific gravity measurements. For instance, suppose that it is of interest to compare the experimental design when increment cores are taken that have a diameter of 5 mm with an average length of 10 cm, resulting in average green volume of 1.963 cc per increment core, with the design when stem analysis specimens are taken that have an average volume per specimen of 50 cc. With either sampling method, suppose it is also desired to detect a difference in the mean specific gravity of two clones of d = .01, with the probability of falsely rejecting the null hypothesis of α = .05 (Z_1 = 1.96), and with the probability of not rejecting the null hypothesis when it is indeed true of β = .20 (Z_2 = .524).

First consider the case when there is no cost for destroying a tree such that for both increment cores and stem analysis C_2 = 1. This might be reasonable when disks are taken from felled trees from a planned thinning. Figures 2 and 3 respectively show the number of specimens per tree and trees per clone need to be sampled versus the cost of measuring a specimen, C_1. As C_1 increases, the number of increment cores and stem analysis specimens decreases, while the number of trees per clone increases. Because both the number of specimens per tree and the number of trees per clone is smaller for a specified C_1 when stem analysis is used, the total cost (fig. 4) for stem analysis is smaller than increment cores. For the full range of C_1, the total cost for stem analysis will be less expensive even if the cost per specimen is 8 times greater for stem analysis than increment cores.

If there is an additional cost for destroying a tree, stem analysis might not be as cost effective. Figures 2 to 4 also show the plots for the case where stem analysis is used and C_2 = 5. In comparison to the previous example where stem analysis was used, the number of specimens per tree is increased while the number of trees per clone is decreased. The total cost is much higher, and for this case increment cores could be justified for all C_1.

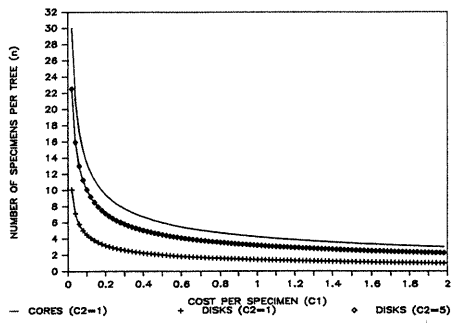

FIGURE 2.--Number of specimens per tree (n) when increment cores (C_2 = 1) and stem analysis (C_2 = 1 and C_2 = 5) are used to determine specific gravity.

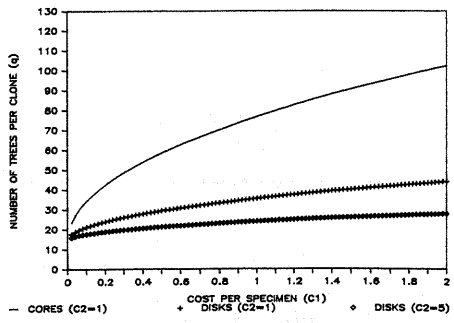

FIGURE 3.--Number of trees per clone (p) versus cost per specimen (C_1) when increment cores (C_2 = 1) and stem analysis (C_2 = 1 and C_2 = 5) are used to determine specific gravity.

[5]Only the relative costs are needed to be known to make the comparisons.

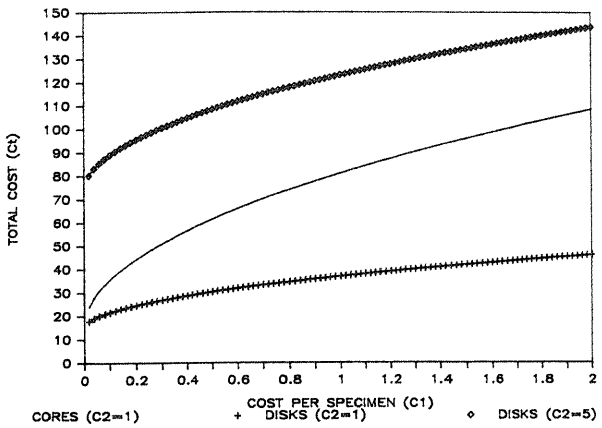

FIGURE 4.--Total cost (C_t) versus cost per specimen (C_1) when increment cores (C_2 = 1 and C_2 = 5) are used to determine specific gravity.

CONCLUSION

From these examples it can be seen that in general, with either sampling method, a large number of trees will have to be sampled to meet the precision requirements. This has to be planned for in the initial designing of the experiment. If increment cores are to be used, a fairly large number of trees will have to be planted in comparison to what is typically planted in most clonal studies. If stem analysis is to be used in order to reduce the number of trees that must be sampled, plans have to be made in advance for a large number of trees to be thinned or removed so as not to affect an on-going experiment. This and other ramifications will be discussed in more detail in a future paper.

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