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Variation and Heritability of some Quantitative Characters in Cryptomeria

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Introduction

The selection of elite trees is the only basis for practical forest tree breeding at the present time. It is safe and can be applied without any special preparatory work. Moreover it appears to be a reliable method, because the natural populations of forest trees have accumulated an enormous variation. But at the present time we have no information to tell us how great an improvement can be expected through selection of this kind.

The effect of selection can be calculated from the heritability and the selection ratio. Heritability (LUSH, 1949) is defined as "the fraction of the observed or phenotypic variance which was caused by differences between the genes or the genotypes of the individuals". In other words. it can be expressed as the relative amount of variance which can be passed on to the next generation by each individual.

Phenotypic variance can be divided in accordance with the cause of variation. This may be stated with the aid of symbols as follows:

$$\sigma^2_P = \sigma^2_g + \sigma^2_d + \sigma^2_i + \sigma^2_e + \sigma^2_j = \sigma^2_h + \sigma^2_E$$

where, σ^2_P is the total phenotypic variance in the population, σ^2_g is the genic or additive genetic variance, σ^2_d and σ^2_i represent non-additive genetic variance caused by dominance and epistasis respectively. These three fractions are sometimes put into one single unit as genetic variance, σ^2_h, because they are all caused by the differences between individual genotypes. σ^2_e is the variance due to linear effects of the environment and σ^2_j due to non-linear interactions between heredity and environment. These two fractions can be combined into one as environmental variance, σ^2_E.

When the material is propagated by sexual means, the non-additive effects of individual genotypes cannot be passed on to their progenies, so the term heritability (h^2) must be employed in its narrow sense,

$$h^2 = \frac{\sigma^2_g}{\sigma^2_P} = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_d + \sigma^2_i + \sigma^2_e + \sigma^2_j}$$

When vegetative propagation is used, the effects of dominance and epistasis are passed on to the next generation because the genotypes of individuals are transfered unchanged. So the term heritability may be employed in its broad sense,

$$h^2 = \frac{\sigma^2_h}{\sigma^2_P} = \frac{\sigma^2_g + \sigma^2_d + \sigma^2_i}{\sigma^2_g + \sigma^2_d + \sigma^2_i + \sigma^2_e + \sigma^2_j}$$

There are several methods of estimating heritability, but the method of separating out the σ^2_g or σ^2_h by an analysis of variance of open-pollinated or vegetative progenies from single mother trees appears to be the most suitable for our material. By this method however, the heritability of common characters which are the most important from the practical point of view, cannot be estimated until the trial plantation becomes rather old, although that of a character observable in the nursery or in a young plantation can be estimated in a shorter period. It is really desirable to get some information about the heritability of common characters as earlier as possible, so the author has attempted a very rough estimation in Cryptomeria by comparing the variance in a stand planted with seedlings with that in another stand established from cuttings of a native vegetative race. The reliability of the estimation is naturally very low but it still seems to be useful as a primary standard.

Materials and Methods

The first stand was established with three-year-old seedlings in 1914 and the stand was 42 years old at the time of survey in April 1956. A sampling strip 175 meters long and 5 meters wide was laid out in this stand practically along the slope of the ground (*Fig.* 1). The heights and some other quantitative characters of all 49 individuals growing within this strip were measured. The sample included an elite tree[2]) which had already been registered, so it cannot strictly be considered as a random sample. But as there was no special factor determining the direction of the sample strip we will consider it to be a random sample.

The second stand was a plantation in the Hita district of a native vegetative race called "Insugi". Rooted cuttings were planted in 1918, and in October 1956 at the time of the survey the stand had completed 39 seasons of growth. Seven points were chosen at random in the stand and the seven individuals nearest to each point constituted the sample (*Fig.* 2).

We have already started to propagate these sample trees by cuttings and open-pollinated seedlings from single trees in order to growing up experimental materials for estimating the heritability by the method of analysis of variance. At the same time, the author tried to obtain a rough estimation of the heritability in the broad sense by comparison of these two populations.

As mentioned above, the phenotypic variance of the seedling population ($\sigma^2_{P_1}$) is the sum of the genetic variance ($\sigma^2_{h_1}$) and the environmental variance (σ^2_E). Similarly the phenotypic variance of the native

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[2]) The term "elite tree" is employed for a phenotypically outstanding tree in Japan. In the forestry practice it is not necessary nor desirable to distinguish "plus tree" and "elite tree".

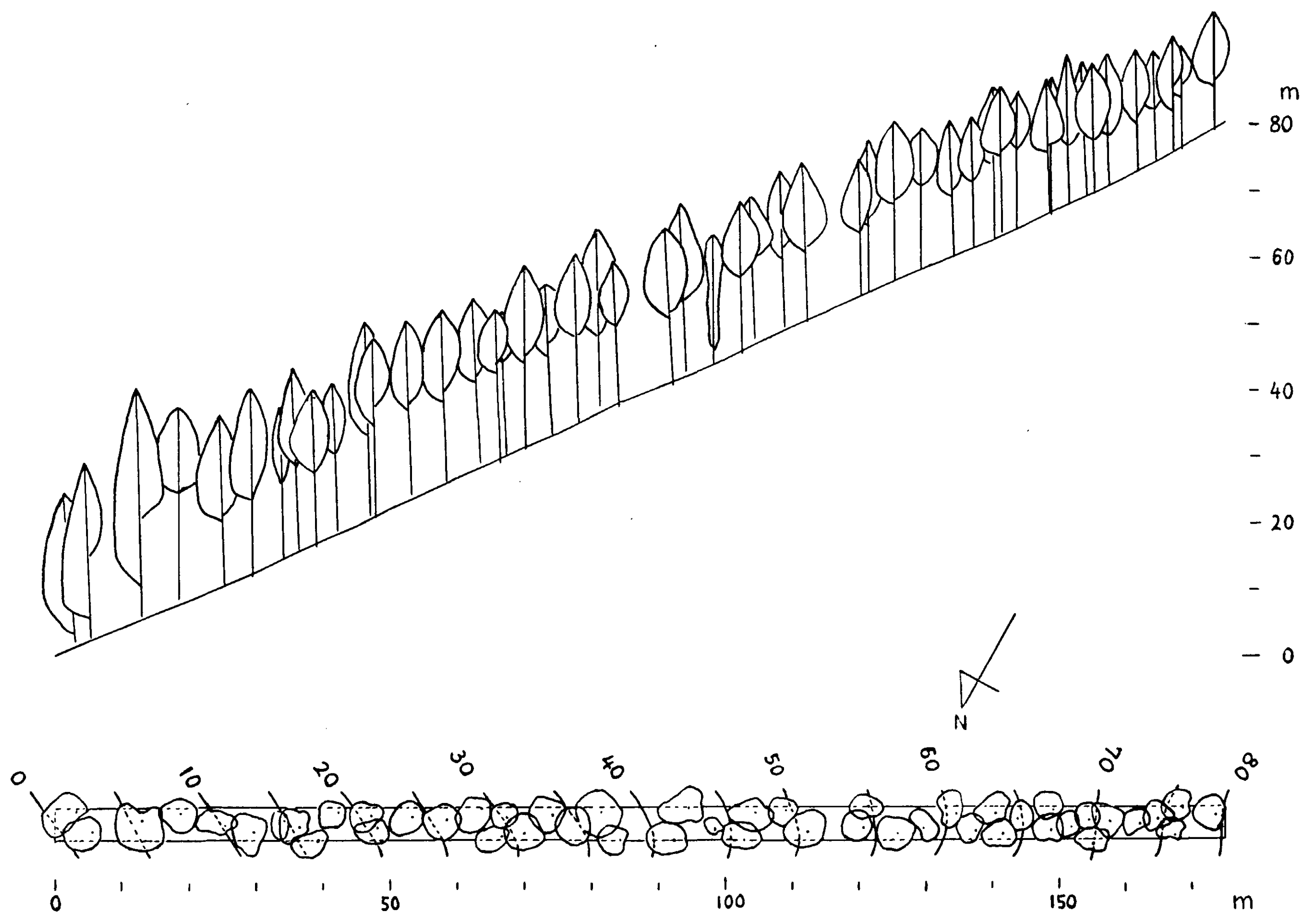

Fig. 1. — The sample of the seedlings population. Forty nine trees were measured in a sample strip 175 m. long and 5 m. wide. The third tree from the left is an elite tree which had already been registered.

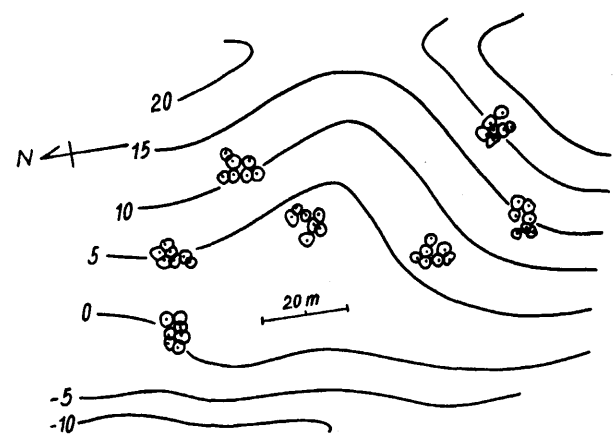

Fig. 2. — The sample of the Insugi population, a native vegetative race of *Cryptomeria*. Seven points were selected in the stand and the seven nearest trees were measured. This stand has a much heavier density than the stand of seedling origin.

race Insugi ($\sigma^2_{P_2}$) is also divided into genetic ($\sigma^2_{h_2}$) and environmental variance (σ^2_E). After excluding macroscopic environmental variation by calculation, σ^2_E is considered as being almost the same for the two populations. As "Insugi" is one of the most homogeneous races, the genetic variance ($\sigma^2_{h_2}$) should be very small compared with that of the seedling population ($\sigma^2_{h_1}$). So the difference between the phenotypic variances is

$$\Delta\sigma^2_P = \sigma^2_{P_1} - \sigma^2_{P_2} = \sigma^2_{h_1} + \sigma^2_E - \sigma^2_{h_2} - \sigma^2_E = \sigma^2_{h_1} - \sigma^2_{h_2} \doteqdot \sigma^2_{h_1}$$
$$(\sigma^2_{h_1} \gg \sigma^2_{h_2})$$

Accordingly, the heritability in the broad sense in the seedling population is estimated as follows:

$$h^2 = \frac{\sigma^2_{h_1}}{\sigma^2_{P_1}} \doteqdot \frac{\Delta\sigma^2_P}{\sigma^2_{P_1}} = \frac{\sigma^2_{P_1} - \sigma^2_{P_2}}{\sigma^2_{P_1}}$$

Results

Estimations were attempted for the following characteristics: —

(1) Tree height

From the data, mean values of 23.0 meters and 23.2 meters were obtained for the heights of the seedlings and Insugi respectively, the standard deviations being 3.63 meters and 1.74 meters. However, the effect of macroscopic environmental variation must be excluded from these deviations. For this purpose the author tried an

Table 1. — Analysis of Variance of Tree Height

Source of Variation	Sum of Squares	Degrees of Freedom	Mean Square	F
Seedlings				
Total	631.24	48		
Blocks	438.32	6	73.05	15.91**
Individuals	192.92	42	4.59	
Insugi				
Total	145.96	48		
Blocks	83.91	6	13.99	9.45**
Individuals	62.05	42	1.48	

**) Hyghly significant.

analysis of variance by dividing the samples into seven blocks of seven individuals each. The results are shown in *Table 1*, where the differences between blocks were highly significant. So the mean squares due to individual variation become the phenotypic variances of the populations, and the coefficients of variation are calculated as 9.3 per cent for the seedlings and 5.3 per cent for Insugi.

(2) Stem girth

Stem girth was measured at a height of 1.2 meters. The macroscopic environmental effect was eliminated by the same way as for tree height. The results are shown in *Table 2*. The differences between blocks were not significant in the Insugi stand, but the effect was still excluded from the total variance, because it is well known that growth conditions greatly affect girth and the existence of an environmental difference has already been demonstrated by the analysis of height variance. So, the net standard deviations of stem girth are 19.0 centimeters for the mean value of 103.7 centimeters in the seedlings and 9.2 centimeters for the mean value of 77.0 centimeters in Insugi. These give coefficients of variation of 18.3 per cent and 11.9 per cent, respectively.

Table 2. — Analysis of Variance of Stem Girth

Source of Variation	Sum of Squares	Degrees of Freedom	Mean Square	F
Seedlings				
Total	23083	48		
Blocks	7929	6	1321.5	3.66**
Individuals	15154	42	360.8	
Insugi				
Total	4629	48		
Blocks	1112	6	185.3	2.21
Individuals	3517	42	83.7	

**) Hyghly significant.

(3) Stem taper

Stem girth at a height of 3.2 meters was measured and one half of the decrease in girth from that at breast height served as the measure of stem taper. The relation between taper and stem girth is shown in *Fig. 3*. It is

Fig. 3. — The relation between taper and girth at breast height. Taper is expressed as one half of the difference between measurements of girth at 1.2 m and 3.2 m height. ⊙ and × represent the seedlings and Insugi respectively.

evident that there is regression between these two characters, so the total variance was at first reduced by the variance due to this regression and then analyzed by means of blocks (*Table 3*)[3]. There is no significant difference between blocks, so the residual variance from the regression forms the net phenotypic variance. The net standard deviations are, therefore, 1.5 centimeters for the mean of 4.6 centimeters in the seedlings, and 0.74 centimeters for the mean of 4.4 centimeters in Insugi. These represent coefficients of variation of 32 per cent and 17 per cent respectively.

Table 3. — Analysis of Variance of Stem Taper

Source of Variation	Sum of squares	Degrees of Freedom	Mean Square	F
Seedlings				
Total	168.1	48		
Regression	66.6	1		
Residue	101.5	47	2.16	
{ Blocks	{ 6.8	{ 6	1.13	
{ Individuals	{ 94.7	{ 41	2.31	
Insugi				
Total	41.9	48		
Regression	16.3	1		
Residue	25.6	47	0.54	
{ Blocks	{ 2.9	{ 6	0.48	
{ Individuals	{ 22.7	{ 41	0.55	

(4) Crown diameter

The relation between the logarithmic values for crown diameter and stem diameter at breast height is shown in *Fig. 4*. There is a marked regression between these two characters. The effects of this regression were taken from the total variance and the residual variance was analyzed

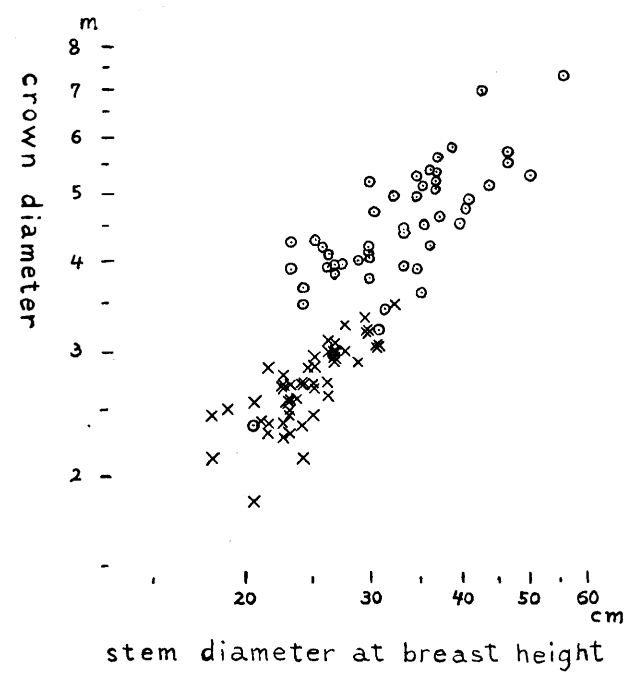

Fig. 4. — The relation between crown and stem diameters. They are arranged on a logarithmic scale. ⊙ and × represent the seedlings and Insugi respectively. Insugi has more slender crowns than the seedlings.

[3]) In his comment, Dr. J. D. MATTHEWS of Alice Holt Lodge pointed out that this analysis is in fact analysis of covariance. This is not actually analysis of covariance but the author agree with him upon the fact that the data ought to have been analyzed by the method of analysis of covariance. The situation is the same for the analysis of the results for crown diameter, bark thickness and branch thickness.

Table 4. — Analysis of Variance of Crown Diameter

Source of Variation	Sum of Squares	Degree of Freedom	Mean Square	F
Seedlings				
Total	0.3760	48		
Regression	0.2191	1		
Residue	0.1569	47	0.0033	
(Blocks	(0.0366	(6	0.0061	2.08
(Individuals	(0.1203	(41	0.0029	
Insugi				
Total	0.1533	48		
Regression	0.0915	1		
Residue	0.0618	47	0.0013	
(Blocks	(0.0103	(6	0.0017	1.31
(Individuals	(0.0515	(41	0.0013	

between blocks *(Table 4)*. As the block effect is not significant, the residue from the regression is considered as the net value. The phenotypic variances are 0.0033 for the seedlings and 0.0013 for Insugi. In terms of standard deviation they are 0.058 and 0.036 respectively (in logarithmic value). There is no reason to calculate the coefficient of variation, because the size of the deviation does not vary in accordance with the size of the mean value.

(5) Bark thickness

The thickness of bark was measured at the breast height at two different positions. The relation with stem girth is shown in *Fig. 5*. There is a regression between them. The effect of this regression was excluded from the variance, and the residue was analyzed as usual *(Table 5)*. The block effect is highly significant in Insugi but is not significant in the seedlings. This seems to be mainly due to the fact that we failed to keep the knocking force constant when we measured the bark of Insugi trees with a beat-in scale, but there is some reason to suspect the existence of macroscopic environmental variation. The observations appear to show that the bark is thicker in a dry and well

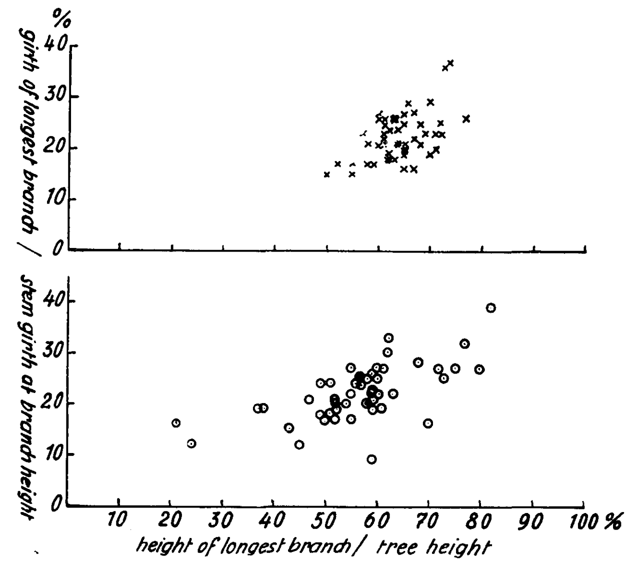

Fig. 6. — The relation between the branch thickness ratio and the ratio of the height of the longest branch to the height of the tree. The former is the ratio of the girth of the longest branch (5 cm from the stem) to the stem girth at the height of the branch (10 cm. below). ⊙ and × represent the seedlings and Insugi respectively. In Insugi, the height of the longest branch was not measured, so the height of the lowest living branch has been used.

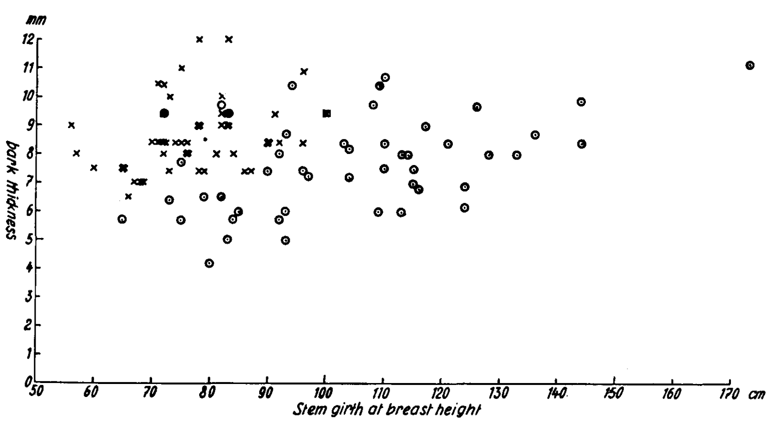

Fig. 5. — The relation between bark thickness and girth at breast height. The thickness of the bark was measured with a beat-in scale at breast height at two positions. ⊙ and × represent the seedlings and Insugi respectively.

aerated site. We shall, therefore, take the variance due to individual variation in the Table as the net phenotypic variance. Thus the standard deviations are calculated as 1.44 millimeters for the mean of 7.7 millimeters in the seedlings and as 0.92 millimeters for the mean of 8.7 millimeters in Insugi. Coefficients of variation are 18.6 per cent in the seedlings and 10.6 per cent in Insugi.

(6) Branch thickness

The girth of the longest branch was measured at a distance of 5 centimeters from the stem, and a percentage was calculated by dividing this figure by the girth of the stem at a distance of 10 centimeters below the branch. This ratio served as the measure of branch thickness. Obser-

Table 5. — Analysis of Variance of Bark Thickness

Source of Variation	Sum of Squares	Degrees of Freedom	Mean Square	F
Seedlings				
Total	134.4	48		
Regression	26.2	1		
Blocks	23.6	6	3.93	1.82
Individuals	84.6	41	2.06	
Insugi				
Total	73.0	48		
Regression	8.1	1		
Blocks	30.0	6	5.00	5.88**
Individuals	34.9	41	0.85	

**) Highly significant.

Table 6. — Analysis of Variance of Branch Thickness Ratio

Source of Variation	Sum of Squares	Degrees of Freedom	Mean Square	F
Seedlings				
Total	1494.7	48		
Regression	690.7	1		
Residue	804.0	47	17.11	
(Blocks	(81.5	(6	13.58	
(Individuals	(722.5	(41	17.62	
Insugi				
Total	1085.3	48		
Regression	341.3	1		
Residue	744.0	47	15.83	
(Blocks	(137.7	(6	22.95	1.55
(Individuals	(606.3	(41	14.78	

vations showed that the ratio varied with the height of the branch and against the height of the tree. The relation between two ratios, the branch thickness ratio and the ratio of the height of the longest branch to the height of the tree is shown in *Fig. 6*. In this figure, the relative height of the longest branch in Insugi is replaced with that of the lowest living branch, because we did not measure the height of the longest branch. In *Fig. 6*, we see a marked regression between these two ratios. The variance was analyzed in the usual way *(Table 6)*. There is no significant difference between blocks, and the variances are 17.11 in the seedlings and 15.83 in Insugi. In terms of standard deviation, they are 4.14 per cent and 3.98 per cent respectively for the same mean value of 22.2 per cent. These two deviations are directly comparable as the mean value is the same, so the coefficients of variation were not calculated. The variation in Insugi is probably over-estimated because the effect of the regression is not completely excluded.

(7) The angle of the longest branch

The angle was measured at the same position as the girth on the longest branch by means of a clinometer. Branch angle has apparently no relation with any other character, and the result of the analysis of variance showed no differences between blocks *(Table 7)*. The standard deviations are therefore calculated directly from the measurements and are 9.0° and 4.8° respectively for the mean value of 79.9° in the seedlings and 76.0° in Insugi. It is not necessary to calculate the coefficients of variation because the deviation does not vary in proportion to the mean.

The heritability in the broad sense in the seedling population and the expected effect of selection can be estimated from the variation which has been studied above. The results of the calculations of variation are summarized in *Table 8*. Variation is always larger in the seedlings than in Insugi, and the differences are highly significant except for branch thickness where the variation of Insugi has probably been over-estimated. F-values were calculated with ordinary variances (i. e. the squares of the standard deviations) for some characters for which the deviations did not vary in proportion to the mean values, and, in other characters, with relative variances (i. e. the squares of the coefficients of variation).

For those characters which showed significant differences in variance, the heritability and the effect of selection were calculated. The effect of selection can be obtained as a percentage of the mean by dividing the expected gain, i. e. the product of the standard deviation, the heritability and the selection differential, by the mean value. The selection differential is the mean deviation of the selected portion from the population mean in the normally distributing population of the standard measure. It can be read in the table of the statistics of the normal distribution and the values corresponding to the selection

Table 7. — Analysis of Variance of Branch Angle

Source of Variation	Sum of Squares	Degrees of Freedom	Mean Square	F
Seedlings				
Total	3845.8	48	80.12	
Blocks	393.1	6	65.52	
Individuals	3452.7	42	82.21	
Insugi				
Total	1083.9	48	22.58	
Blocks	155.6	6	25.93	1.28
Individuals	928.3	42	20.18	

Table 8. — Comparison of Variation between Seedlings and Insugi

Character	Population	Mean	Standard Deviation	Coefficient of Variation	Variance or Relative Variance	Degree of Freedom	F
Tree Height	Seedlings	23.0 m	2.14 m	9.3 %	86.49	42	3.13**
	Insugi	23.2 m	1.22 m	5.3	27.67	42	
Stem Girth	Seedlings	103.7 cm	19.0 cm	18.3	334.89	42	2.36**
	Insugi	77.0 cm	9.2 cm	11.9	141.61	42	
Stem Tager	Seedlings	4.6 cm	1.5 cm	32	1024	47	3.54**
	Insugi	4.4 cm	0.74 cm	17	289	47	
Crown Diameter	Seedlings	0.649 log. m	0.058 log. m		0.0033	47	2.53**
	Insugi	0.430 log. m	0.036 log. m		0.0013	47	
Bark Thickness	Seedlings	7.7 mm	1.44 mm	18.6	345.96	41	3.08**
	Insugi	8.7 mm	0.92 mm	10.6	112.36	41	
Branch Thickness	Seedlings	22.2 %	4.14 %		17.11	47	1.09
	Insugi	22.2 %	3.98 %		15.83	47	
Branch Angle	Seedlings	79.9 °	9.0 °		80.12	48	3.55**
	Insugi	76.0 °	4.8 °		22.58	48	

**) Highly significant.

Table 9. — Heritability and Expected Effect of Selection in the Seedling

Charakter	Variance in Seedlings $\sigma^2_{P_1}$	Variance in Insugi $\sigma^2_{P_2}$	Difference $\Delta\sigma^2_P$	Heritability $\frac{\Delta\sigma^2_P}{\sigma^2_{P_1}}$	Effect of Selection Top 5%	Effect of Selection Top 1%
Tree Height	86.49	27.67	58.82	68%	13%	17%
Stem Girth	344.89	141.61	193.28	58	22	28
Stem Taper	1024	289	735	72	48	62
Crown Diameter	0.0033	0.0013	0.0020	61	18	24
Bark Thickness	345.96	112.36	233.60	68	26	34
Branch Angle	80.12	22.58	57.54	72	13 °	17 °

of top 5 per cent and 1 per cent of the population are 2.06 and 2.67 respectively. The effect of selection for branch angle is shown as the expected gain itself. As the standard deviation of crown diameter is given as a logarithmic value, the effect of selection is computed as follows: — calculate the expected gain as a logarithmic value, and subtract 1 from the corresponding common number. This gives the effect of selection as a percentage of the mean diameter of crown.

The results are shown in *Table 9*. Considerable effects are demonstrated in the table.

Discussion

(1) The reliability of the estimation

First we must emphasize the fact that the sample from the seedling population is not a strictly random one. As mentioned above, this sample contains an elite tree. As a result of this there was an enlarged sample variance, and thus the heritability would be over-estimated in those characters which concern growth rate. Indeed, a recalculation of tree height excluding the block in which the elite is found, shows the heritability to have fallen to 53 per cent and the effect of selection to ca. 8 per cent.

On the other hand the genetic variance in Insugi is not zero because the race is not a real clone but probably a mixture of several clones of very similar appearance (TODA, 1952). For this reason, the heritability is underestimated, but the degree of the under-estimation cannot be determined with our present knowledge.

Beside these, there is another source of error. It was assumed that the environmental variance is the same for both these populations. But we do not know if it is really the same or not. In fact we have some reason to believe that the environmental variance is smaller in Insugi because this race is believed to be highly site-adaptable and this could mean that the growth of Insugi trees is not so much affected by poorer site quality as compared with trees of other races. This fact decreases the environmental variance and becomes a cause of over-estimation of heritability.

In short, it will be best to assume that the values of heritability have been over-estimated and be careful in applying the results.

(2) Effect of selection

Although the heritability values must be treated with care because of the possible over-estimation, the effect of selection is still very remarkable. Assuming that an 8 per cent improvement is expected in tree height, and 15 per cent in girth, 43 per cent increase of volume can be expected by selection of the top 5 per cent of trees. Beside this, decrease of stem taper and decrease of bark thickness will contribute greatly to the increase of the volume of timber produced by single stems, and the decrease of crown diameter will contribute to an increase of production per unit area. Of course it will be very difficult to find trees which show a high superiority in all the characters mentioned, but if we could really find several such trees, tremendous improvement would be possible.

It must be emphasized here that this effect is that expected from mass selection. Merely select a number of phenotypically superior trees in the seedling population, propagate them by cuttings and plant the cuttings in mixture without any clonal test. Then we can expect such an improved production with the new population. If properly planned clonal test is laid down and we select clones as a result of the test, the effect of the selection must be considerably greater. Heritability based upon the mean of N plants is given as follows:

$$\frac{h^2}{h^2 + \frac{1-h^2}{N}}$$

where h^2 is the heritability on a single plant basis. So, for example, the heritability of tree height based upon a clonal test of 10 plants increases to 96 per cent from 68 per cent on a single plant basis, and the effect of selection becomes 18 per cent instead of 13 per cent.

(3) Heritability in the narrow sense

Heritability is studied here in its broad sense, and it can be applied only when the material is propagated by cuttings or by other vegetative means. When the material is propagated from seed, the effect of selection must be estimated from heritability in the narrow sense.

Unfortunately we have no means of estimating this from our own material at present, but some German data for Scots pine enables us to make a rough estimation of it. The calculation is presented below.

After STERN (1953), the standard deviation of tree height in Scots pine is ca 3 per cent smaller in single stem progenies on average than in a bulk population. So, the difference in variances is $(1.00)^2 - (0.97)^2 = 0.0591$, that is nearly 6 per cent of the variance of the bulk population. This value corresponds to one fourth of the heritability in the narrow sense which is, therefore, easily calculated as 24 per cent.

If the heritability in Cryptomeria also has a similar value, the heritability of tree height in the narrow sense is about one third of that in the broad sense. So the effect of selection will be decreased at the same rate. When selected trees are propagated through elite seed orchards, ca. 3—4 per cent improvement can be expected by selecting the top 5 per cent of the population.

The author expresses his hearty thanks to Dr. J. D. MATTHEWS for his kindly reading and correcting the manuscript. The author also appreciates his valuable comments very much.

Summary

(1) Heritability in its broad sense, i. e. the relative amount of total genetic variance in phenotypic variance, was estimated in a seedling population by means of a comparison with a population of a native vegetative race of *Cryptomeria*.

(2) Heritabilities of tree height, stem girth, stem taper, crown diameter, bark thickness and angle of the longest branch were all high, and thus remarkable increases of timber production will be possible by the mass selection of the top 5 per cent or 1 per cent of a population and their propagation by cuttings. Clonal selection will greatly accelerate improvement.

(3) Heritability in its narrow sense, i. e. the relative amount of additive genetic or genic variance instead of total genetic variance, cannot be estimated directly from the present material. But some German data in Scots pine permits a rough estimation of heritability in the narrow sense, and if that in *Cryptomeria* is similar to that in Scots pine it will be about one third of the heritability in the broad sense. So the effect of selection will also be decreased to the same extent when the selected trees are propagated by means of elite seed orchards.

Résumé

Titre de l'article: *Variation et héritabilité pour quelques caractères de Cryptomeria.* —

1) L'héritabilité au sens large, c'est-à-dire le rapport de la variance génétique totale à la variance phénotypique, fut estimée dans une population issue de semis en la comparant avec une population représentant une race de *Cryptomeria* multipliée végétativement.

2) L'héritabilité de la hauteur, de la grosseur et de la décroissance du fût, du diamètre de la couronne, de l'épaisseur de l'écorce et de l'angle d'insertion de la plus longue branche est très élevée; il est donc possible d'accroître considérablement la production par la sélection massale des meilleurs 5 ou 1 pour cent d'une population suivie de propagation par boutures. La sélection clonale permettra d'accélérer beaucoup l'amélioration.

3) L'héritabilité au sens précis de valeur relative de la variance additive génétique ou génique au lieur de la variance génétique totale ne peut être estimée avec le matériel envisagé. Mais certaines données allemandes concernant le pin Sylvestre permettent une estimation approchée de l'héritabilité au sens étroit du mot, et si ces données peuvent être étendues du pin Sylvestre au *Cryptomeria,* elle serait environ un tiers de l'héritabilité au sens large. Ainsi, l'effet de la sélection est diminué dans la même proportion lorsque les arbres sélectionnés sont multipliés par l'intermédiaire des vergers à graines.

Zusammenfassung

Titel der Arbeit: *Variation und Heritabilität einiger quantitativer Merkmale bei Cryptomeria.* —

1. Die Heritabilität im weiteren Sinne (d. h. die relative Höhe der gesamten genetischen Varianz innerhalb der phänotypischen Varianz) wurde in einer Sämlingspopulation durch Vergleich dieser mit einer vegetativ vermehrten einheimischen Population (race) von *Cryptomeria japonica* abgeschätzt.

2. Die Heritabilität der Höhe, des Stammumfanges, der Formzahl, der Kronenweite, der Rindenstärke und des Ansatzwinkels des längsten Astes war sehr hoch, und damit wird ein merklicher Anstieg der Holzproduktion durch die Massenselektion der obersten 5 oder 1 Prozent einer Population und ihre Vermehrung durch Stecklinge möglich. Klon-Auslesen werden die Fortschritte wesentlich beschleunigen.

3. Die Heritabilität im engeren Sinne (d. h. die relative Höhe der additiven genetischen oder genischen Varianz anstatt der genetischen Gesamtvarianz) kann bei dem vorliegenden Material nicht direkt bestimmt werden. Jedoch erlauben einige deutsche, an *Pinus silvestris* gewonnene Daten die grobe Ermittlung der Heritabilität im engeren Sinne. Und falls die Situation bei *Cryptomeria* der bei der Kiefer ähnelt, wird diese etwa ⅓ der Heritabilität im weiteren Sinne ausmachen. Auch der Selektionseffekt wird in demselben Maße herabgesetzt, wenn die ausgewählten Bäume durch Samenplantagen vermehrt werden.

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