

Variety Crosses in Sugar Beets (*Beta vulgaris* L.)

II. Estimation of Environmental and Genetic Variances for Weight Per Root and Sucrose Percent

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Received for publication February 8, 1963

The primary purpose of this variety crossing program was to thoroughly evaluate several monogerm varieties originating from diverse sources. The information obtained would enable the plant breeder to re-evaluate the converted monogerm and serve to guide his decisions when designing a breeding program. The implications of the general and specific combining ability, together with the heterotic responses were discussed in a previous report (3)². The estimations of the environmental and genetic variances for the parental varieties and their intercrosses will be included in this paper.

Materials and Methods

A detailed description of the varieties and the testing technique were included in a previous article (3). In addition to the five parental varieties and their intercrosses previously reported, two single-cross hybrids and a commercial multigerm, American #2 Check were included in the field plots. The single-cross hybrids, (NB₁ × NB₄) were produced by Dr. McFarlane and 58-9061 (52-430 × 52-407) produced by Dr. Powers were used to obtain the estimates of environmental variation. The check variety was included to compare the relative performance of monogerm and multigerm seed. The data included in this article are on an individual plant basis. The methods of statistical analysis are essentially those outlined by Powers (1,2).

Estimating Environmental Variances

Two single crosses were included in this study to estimate the environmental variances. Table 1 gives the means and within-population variances for root weight and sucrose percent for these nonsegregating populations. The within-population variances are essentially the environmental variances. No problem exists when only one nonsegregating population is included in the experiment because its within-population variance is the only estimate of the environmental variance available. When two or more nonsegregating populations are included, the ex-

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² Numbers in parentheses refer to literature cited.

perimenter hopes that these estimates will be fairly uniform and that he can use the mean to estimate the environmental variance. An examination of the within-population variances for the non-segregating populations included in this experiment indicated that considerable differences existed between the two populations for root weight, Table 1.

Table 1.—Means and within population variances for root weight and sucrose percent for the nonsegregating populations.

Nonsegregating populations	Root weight		Sucrose percent	
	Mean	Within-population variances	Mean	Within-population variances
NB ₁ × NB ₄	2.38	0.695	10.20	2.177
58-9061	2.80	1.241	12.18	2.019
Regression of means and Variances	67.2%		58.2%	

Powers (2) reported that a linear relationship exists between population means and the within-plot variances for root weight. He was able to show that the mean weight per root accounted for 99.7% of the sums of squares for variances. Based on these results and the apparent positive association between the means and variances in these data the regression of the within-plot variances on the means was calculated. The 40 replications for each nonsegregating population were divided into four groups, i.e., replication 1-10, 11-20, 21-30 and 31-40. The means of each group were used to calculate the regression.

The "t" test indicated that the regression value 0.8188 was significantly different from zero at the one percent level. (D.F. = $n - 2 = 6$.) Thus a true relationship existed between the means and the variances for root weight. The mean weight per root, however, accounted for only 67.2% of the sums of squares for variance, the remaining 32.8% of the variance was due to the interactions. This failure to account for a greater percentage of the variation seriously questioned the advisability of using regression to estimate the environmental variances of the entries in this test.

Several alternative methods for estimating the genetic variances were considered. These included the mean of the two estimates, the lower or higher estimate, either estimate as long as constant and the variance associated with the mean closest to the mean of the entry. Because the "t" test had indicated an association between the means and variances, the within-population variance for the single cross whose mean was closest to

the mean of the variety or intercross mean was used to estimate its genetic variance.

The regression of the means and within-plot variances were calculated for sucrose percent using the method employed for weight of root. The regression value of $-.3978$ was significantly different from zero at the one percent level. The relationship differed from the regression value for root weight in that it was a negative value. The mean sucrose percent accounted for 58.2% of the sums of squares for variances, the remaining 41.8% was due to the interactions. This also prohibited the use of regression to estimate the environmental variances for sucrose percent.

The within-population variances for sucrose percent of the two single-cross populations differed only by 0.158 and were considered to be estimates of the same effect. The mean of the two environmental estimates, 2.098, was used to estimate the genetic variances associated with the varieties and hybrids for sucrose percent.

Genetic Variances for Root Weight

The genetic variances for root weight of the parental populations and their F_1 intercrosses are included in Table 2. Brief descriptions of these varieties together with relative estimates of their genetic variability based on the knowledge of the breeding history have been included in a previous paper (3).

Variety 58-411 was considered to have a broad genetic base when compared to the other varieties under test. The estimate of the within-population genetic variance of 1.452 was the highest calculation for the five varieties which verifies this previous assumption. Varieties 58-412 and 57-807 were believed to moder-

Table 2.—Within population genetic variance for root weight of the parental populations (parentheses) and their F_1 intercross together with the average genetic variance for each variety based on the intercross performance (320 beets per population except where noted).

Parents	57-807	SP 5832-0	58-412	SLC 24	58-411	Mean
57-807	(0.721)	0.902 ¹	1.048	0.312	1.226	0.872
SP 5832-0		(1.055)	0.795 ¹	0.632 ¹	1.124 ¹	0.863
58-412			(1.149)	1.508	1.988 ¹	1.335
SLC 24				(0.799)	1.111 ¹	0.891
58-411					(1.452)	1.362

¹ 160 beets per population

σ^2 Variety $\bar{X} = 1.035$

σ^2 Cross $\bar{X} = 1.065$

ate genetic variability with varieties SP 5832-0 and SLC 24 having low variability. This assumption is apparently true for variety 58-412 because the genetic variance of 1.149 was the second highest of the five varieties. The genetic variance for variety 57-807 was the lowest of the five varieties disputing the assumption that this variety had a relative broad genetic base. Variety SP 5832-0 produced from eight monogerm progenies had the third largest genetic variance.

As shown in Table 1 the mean variances for varieties were approximately the same as the mean variances for crosses. In general the genetic variance for a specific intercross was higher when the genetic variances of the two parents were high than when their variances were low.

Genetic Variances for Sucrose Percent

The within-population genetic variances for percent sucrose are included in Table 3. Variety 58-411 considered to have a broad genetic base, had the largest genetic variance for percent sucrose when compared with the other varieties. The American #2 variety, 58-412, which had a high genetic variance for root weight was fourth for sucrose percent. The second highest variance was for variety SP 5832-0 which was considered to have a limited genetic base. The ranking of the genetic variances for varieties 57-807 and SLC 24 were third and fifth respectively.

The mean genetic variance for varieties was little different from the mean variance associated with crosses. This observation for percent sucrose was identical to the results obtained for weight of root.

Table 3.—Within population genetic variances for percent sucrose of the parental populations (parentheses) and their F_1 intercrosses together with the average genetic variance for each variety based on the intercross performance. (320 beets per population except where noted.)

Parents	57-807	SP 5832-0	58-412	SLC 24	58-411	Mean
57-807	(1.829)	1.623 ¹	2.269	0.701	1.669	1.566
SP 5832-0		(2.125)	1.731 ¹	1.001 ¹	2.584 ¹	1.735
58-412			(1.336)	2.637	-.108 ¹	1.632 2.212 ²
SLC 24				(1.141)	1.172 ¹	1.378
58-411					(2.444)	1.329 1.808 ²

¹ 160 beets per population σ^2 Variety $\bar{X} = 1.775$
² Negative variance deleted σ^2 Cross $\bar{X} = 1.740$

The genetic variation of the cross 58-412 \times 58-411 was a negative value. Examination of the frequency distribution of this cross revealed that the sucrose determinations for individual plants were grouped quite closely around the mean of 13.02%, verifying that the genetic variation was low. The heterotic response of this cross for sucrose percent was 106.2% of the mid-parent value indicating considerable heterosis for this intercross. Two theories may be advanced to explain the lack of genetic variance in this cross. Several assumptions are necessary to substantiate these theories. The first theory assumes that heterosis has increased the sucrose yield of the hybrid considerably but that unknown limiting factors have suppressed the sucrose of the better genotypes. This ceiling has tended to force the population variability into a rather narrow range. The second theory assumes complete dominance of the high sugar variety, 58-412, for sucrose percent when combined with variety 58-411. However, this dominance is not evident in the other intercrosses of 58-412.

Discussion

The most critical part of an experiment of this type is the estimation of the environmental variance. There appears to be a close association between the means and variances for root weight. Thus, the regression method of estimating the environmental variances for each entry would be highly accurate providing enough estimates were available to establish that a true relationship exists between the means and variances. Another possibility would be the development of a series of inbreds and single crosses which encompass a wide range for both root weight and sucrose percent. Such a series could be utilized to measure the environmental effects by using the means and variances of the inbred or single cross which closely correspond to the means of the entry.

The genetic variances of varieties and intercrosses for root weight were estimated using the total variance of the single cross whose mean was closest to the mean of that particular entry. The regression method was calculated but not used because 32.8% of the variation was due to interactions, i.e., means and variances were interacting. The genetic variances for root weight could be slightly bias for those entries whose means were diverging from the single cross means.

The estimates of the environmental variances for sucrose percent were nearly identical varying only by .158. The mean of the two estimates was considered to be a good measure of the

environmental variance, thus, resulting in a quite accurate and comparable estimate of the genetic variances of percent sucrose.

A variety is considered to be a randomly segregating population with a balanced genetic constitution. Intercrosses between varieties should respond as F_2 and be segregating for genotypes. The estimations of genetic variation are actually measurements of the degree of segregation. One would expect that the average genetic variation for the crosses would be greater than the average variation for the varieties. However, the genetic variation means for crosses versus varieties were approximately equal for both root weight and sucrose percent. Examination of the data and frequency distribution showed that the genetic variation of certain crosses were less than the variation of the parental populations involved in the cross. A reaction of this type is difficult if not impossible to justify genetically. Several theories to explain these data are plausible. Two of the crosses which resulted in low genetic variation estimates involve the variety SP 5832-0. This variety was considered to have a narrow genetic base, however, the estimates of the genetic variation were higher than expected. A previous paper (3) presented data from reciprocal crosses which indicated that variety SP 5832-0 was self-fertile. This population could be composed of two types of material; plants resulting from selfing and plants resulting from crossing. A population of this type would tend to have a high genetic variation due to the two extreme breeding types. The frequency distribution for this variety indicates two populations exist, but the population boundaries are not as apparent as in the cases of reciprocal crosses (3).

Another explanation of the similarity in the genetic variation of crosses versus varieties would be the lack of equilibrium in the intercrosses following hybridization. The intercross populations are essentially the first generation following crossing. Perhaps the genetic variation in later generations would be greater after the populations reached their genetic equilibrium. The advisability of selecting in the first generation after a variety cross is certainly open to question.

The results of the 57-807 \times SLC 24 intercross are difficult to explain. The genetic variation for this intercross was considerably below either of the parental populations for both root weight and sucrose percent. The actual yield was also below that of the parents (2). The type of gene action that would cause this reduction in yield and genetic variation defies logical explanation.

The data generally follow a logical pattern and were considered to be reliable. However, the genetic estimates are relative only to the varieties and intercrosses under test and are possibly subject to yearly interactions.

Summary

Estimates of the genetic variation among five diverse monogerm varieties and their diallel intercrosses are presented for root weight and sucrose percent. The average genetic variation of the intercrosses was approximately equal to the average genetic variation of the varieties for both root weight and sucrose percent.

Certain irregularities in the results were discussed along with the method of estimating environmental variance.

Literature Cited

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