

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

III. Estimating the Number and Proportion of Genetic Deviates by the Partitioning Method of Genetic Analysis

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The partitioning method of genetic analysis (5)² provides a means of estimating the numbers and proportion of genetic deviates in random mating populations. The population geneticists may be interested in number or proportion of individuals falling in certain classes of the frequency distribution because of their genotypes, while the plant breeder is interested in those individuals which occur in the upper classes of the frequency distribution. The latter must be reasonably sure that such superior individuals are not chance fluctuations from the mean of the population but are in the upper portion of the frequency distribution because of their genotype. Previous papers (1, 2) have presented the data on heterosis, combining ability and genetic variation when five diverse varieties of sugar beets were crossed in a diallel series. The purpose of this paper is to present the number of superior genetic deviates found in the varieties and their intercrosses using the partitioning method of genetic analysis.

Materials and Methods

Details of the experimental design and variety descriptions are included in a previous paper (1). The statistical analyses of the data presented in this paper are essentially those described by Powers (3, 4, 5) for the partitioning method of genetic analysis.

Frequency distribution tables were prepared for both root weight and sucrose percent for each entry in the experiment. These included the 5 monogerm varieties, their 10 intercrosses, 2 single crosses and the multigerm check. The frequency interval for root weight was .4 pound with a range from .4 to 6.4 pounds. The range for percent sucrose was from 7.50% to 18.00% at .75% frequency intervals.

The expected number of beets in each class interval was calculated (5) by projecting a normal distribution based on the population mean and standard error of the single cross which

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² Numbers in parentheses refer to literature cited.

estimated the environmental variance. For root weight, the standard error used to calculate the expected frequency distribution of any particular entry was the square root of the total variance for the single cross used to estimate its genetic variance. The mean of the two standard errors for the single crosses was used to calculate the expected frequency distribution for percent sucrose.

The frequency distributions were partitioned into three groups based on the change of the expected from the observed according to the partitioning method. Homogeneity chi square calculations indicate that the obtained populations for all entries except the nonsegregating populations vary from the expected. These calculations indicate that genetic deviates occur in all the populations except the nonsegregating populations. The plants located in the higher partition were considered genetically superior and the number of those plants in the population calculated.

Experimental Results

The partitioning method of genetic analysis enables the plant breeder to mathematically select the genetic deviates which fall into the upper classes of the frequency distribution. Based on the frequency data, Table 1 shows the number of genetic deviates for root weight that the plant breeder could expect of find per 10,000 plants. The table includes the five varieties and their ten intercrosses that were tested in this experiment. The percentage of these genetic deviates in the population vary from 5.9 to 17.5%. The average number of genetic deviates in 10,000

Table 1.—Number of genetic deviates per 10,000 plants for weight of root for five varieties and their intercrosses (parental populations in parentheses).

Populations	57-807	SP 5832-0	58-412	SLC 24	58-411
57-807	(375)	1375	1406	594	1469
SP 5832-0		(1187)	1000	1250	1750
58-412			(1594)	1719	1625
SLC 24				(656)	1312
58-411					(1094)

Table 2.—Number of genetic deviates per 10,000 plants for percent sucrose for five varieties and their intercrosses (parental populations in parentheses).

Populations	57-807	SP 5832-0	58-412	SLC 24	58-411
57-807	(125)	425	750	188	531
SP 5832-0		(62)	750	688	188
58-412			(375)	938	625
SLC 24				(219)	375
58-411					(312)

beets for the varieties is 981.2 while the average for the intercrosses is 1,350.0.

Table 2 presents the number of genetic deviates per 10,000 plants for percent sucrose. The percentage of the genetic deviates in the five populations and their intercrosses range from 0.62 to 9.38%. The average number of deviates for the varieties is 218.6 plants while the average for the intercrosses is 545.8 plants.

The number of genetic deviates per 10,000 plants for both root weight and sucrose percent are included in Table 3. The percent of plants superior in both weight and sucrose percent ranged from .03 to 5.67%. The average number of these plants in the varieties is 24 while 122.2 is the average of their intercrosses.

The obtained and estimated number of plants occurring above the .01% level of probability for each population are included in Table 4. These genetically-superior individuals are of particular interest to the plant breeder. Based on the calculations he can be reasonably sure that these plants were not in the higher frequency classes due to chance but are genetically superior.

Twelve genetically-superior plants were obtained, all found in the intercross populations, with 42 expected from the combined populations.

Table 3.—Number of genetic deviates expected per 10,000 plants based on the percentage of genetic deviates identified for root weight and percent sucrose.

Populations	57-807	SP 5832-0	58-412	SLC 24	58-411
57-807	(5)	567	105	11	78
SP 5832-0		(7)	75	86	33
58-412			(60)	116	102
SLC 24				(14)	49
58-411					(34)

Table 4.—Obtained and estimated number of genetically superior individuals for both high root weight and sucrose percent.

Populations		57-807	SP 5832-0	58-412	SLC 24	58-411
57-807	O	(0)	4	2	0	0
	E	(0)	18	4	0	2
SP 5832-0	O		(0)	0	0	0
	E		(0)	2	3	1
58-412	O			(0)	5	0
	E			(2)	4	3
SLC 24	O				(0)	1
	E				(2)	2
58-411	O					(0)
	E					(1)

Discussion

A greater number of genetic deviates were found for root weight than for sucrose percent. This data would indicate that if the plant breeder were mass selecting for tonnage, fewer plants would be necessary than if he were selecting for sucrose percent. Selection for both sucrose percent and weight of root would require an even greater number of plants than for either factor separately. The selection of 50 genetically-superior plants would require even a greater number of individuals. Considering all the populations, 3,840 plants were observed with 12 or 0.31% being genetically superior. If the plant breeder considered that 50 beets were sufficient to maintain genetic variability in the selected population, approximately 16,130 beets would be needed to insure the selection of this 50-beet sample.

No genetically-superior individuals were identified in the parental varieties. The 12 superior individuals for both root weight and sucrose percent were all found in the intercross populations. These data would suggest that the genetically-superior individuals are the result of hybridization and represent superior heterozygotes. Due to segregation during advanced generations, the original mean yield of the mother beets would be difficult to maintain. However, if the gametes which produced these genetically-superior individuals could be isolated and maintained by inbreeding, the original yield could be reproduced by hybridization.

Several of the populations studied appeared to have good genetic variability with a high probability of selecting genetically superior individuals. However, the mean yield and genetic variability of the populations need to be considered before subjecting them to selection. A population with a low mean yield and high genetic variability may be greatly improved by mass selection. However, the resulting increase in the mean yield may not equal a population with a high mean yield and low genetic variability before the variability in the population under selection is drastically reduced.

In our study population, 58-412, would be the best variety for advanced breeding; either mass selection or recurrent selection. The mean yield for both sucrose percent and root weight was high with good genetic variability present in the populations. No genetically superior individuals were identified in this population, however, two were expected.

The intercross 58-411 \times 58-412 appears to be the best varietal hybrid to select within following several generations of open-

pollination. Based on the mean yield, heterotic responses and genetic variability, these two varieties, 58-411 and 58-412, would also be the two best varieties to incorporate into a reciprocal recurrent selection program. Inbreeding with the synthetic populations produced by this cycling process should isolate gametes (inbred lines) that when hybridized would result in a population of genetically superior individuals.

Summary

The proportion of genetic deviates and number of genetically superior individuals were studied in five open-pollinated populations and their intercrosses by the partitioning method of genetic analysis. The number of genetic deviates identified in the higher classes of the frequency distribution was greater for root weight than for sucrose percent. Twelve genetically superior individuals were isolated for the populations with forty-two expected.

Literature Cited

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