Relationships of Four Yield Characters with Five Chemical Characters in Sugar Beets[1]

RICHARD J. HECKER, W. T. FEDERER, LEROY POWERS AND MERLE G. PAYNE[2,3]

Received for publication November 15, 1966

Following suggestions and leads in papers by Powers et al. (4)[4] and Payne et al. (3), it was decided to investigate the relationships of each of four yield characters with five thin juice chemical characters in sugar beets (*Beta vulgaris* L.). The four yield characters considered were weight per root, percentage sucrose, percentage apparent thin juice purity and gross sugar per root. The five thin juice chemical characters considered were potassium, glutamic acid, sodium, betaine and total nitrogen. The purpose of this study was to investigate methods of describing the mutual response of these four yield characters and the five thin juice chemical characters within populations of sugar beets as they are affected by their environment and from this response estimate values for the thin juice chemical characters at which the yield characters are maximized. One direct application is increased objectivity in the decision-making of management and cultural practice. The variability studied is primarily environmental, involving differences between replications within populations. The variability in each population is treated in a separate analysis. This permits the measurement and establishment of environmental relationships within populations, unaffected by genetic differences between populations.

Materials and Methods

The four yield characters are considered as dependent variables in this study and are designated as follows: weight per root in pounds (Y_1), percentage sucrose (Y_2), percentage apparent

---

[1] Joint contribution of the Crops Research Division, Agricultural Research Service, U. S. Department of Agriculture, the Colorado Agricultural Experiment Station, and the Beet Sugar Development Foundation. Colorado Agricultural Experiment Station Scientific Series No. 1078.

[2] Research Geneticist, Crops Research Division, Agricultural Research Service, U. S. Department of Agriculture, Professor of Biological Statistics, Cornell University, Ithaca, N. Y., Principal Geneticist, Crops Research Division, Agricultural Research Service, U. S. Department of Agriculture, and Professor of Chemistry, Colorado State University, Fort Collins, Colo., respectively.

[3] The authors are indebted to the Western Data Processing Center, University of California, Los Angeles, Calif. for analysis of portions of the data, Job No. 1081

[4] Numbers in parentheses refer to literature cited.

purity (Y_3) and gross weight of sugar per root in pounds (Y_4). The thin juice chemical characters are considered as independent variables and are designated as follows: potassium (X_1), glutamic acid (X_2), sodium (X_3), betaine (X_4) and total nitrogen (X_5). Glutamic acid, betaine and total nitrogen are expressed in milligrams per 100 milliliters of thin juice equated to a refractive dry substance of ten. Sodium and potassium are expressed in parts per million. Gross sugar per root is the product of Y_1 and Y_2. The design and details of the experiment have been discussed in other papers on these data, particularly Powers et al. (4). Briefly, the experiment consisted of six populations (three segregating and three non-segregating), two nitrogen fertility levels and 40 replications within each treatment. In the final analyses the nitrogen fertility levels were pooled, resulting in 80 replications per population. The experiment was conducted in 1956. As regards the populations, A54-1 is a commercial variety; A54-1BB is a genetically broad-based population resulting from the use of A54-1 as a female parent with 22 pollinators; 50-406BB was developed in the same manner, with the use of inbred 50-406 as the female parent; 50-406 and 52-307 are inbreds; and the F_1 hybrid resulted from crossing these two inbreds. The entire experimental area received a uniform application of 250 pounds of P_2O_5 per acre prior to planting. The fertilized treatment received two 100-pound applications of nitrogen, one prior to planting and the other about 75 days after planting. Residual nitrogen was considered to be fairly high, and the results indicate a definite nitrogen gradient down the field in the direction of irrigation water flow.

The 10-foot single-row plots were bordered by a common competitor to provide uniform competition. Spacings were 22 inches between rows and about 10 inches between plants within rows. Data were taken on eight plants per plot at harvest. The stands were nearly perfect. Only three observations on certain characters were not available in the entire experiment [see Dudley and Powers (1)]; in these cases the mean of the remaining seven was inserted for the missing value to simplify analyses on plot totals.

Regression Equations

In this study five regression equations are used to attempt a description of the dependent characters Y_h in terms of polynomial equations in the independent characters X_i on an "among-plot" basis. The variation among plots for a single population is mostly environmental; i.e., the expected value of the among plots mean square is $(\sigma_g^2 + \sigma_p^2 + 8\sigma_e^2)$ where σ_e^2 (the variance among

plots) is large relative to σ_g^2 and σ_p^2 because of the wide range of environments for the 80 plots [see Powers et al. (4)] and σ_p^2 (the variance among plants within a plot) is about the same size as σ_g^2 (the total genetic variance in the population). The variance within plots is about half genetic variance, σ_g^2, and about half environmental variance, σ_p^2. Hence, for management and cultural practices guides, a study of the regression equations for plot totals will yield the desired information. The fact that certain of the independent variables can be regulated, both through breeding and cultural practice, has been amply demonstrated. Since this is so, it would be desirable to have an estimate of the values of the independent variables, X_i, yielding maximum values for the dependent variables, Y_h.

Although it is rather improbable that the selected regression equations represent the true relationship between the independent and dependent variables, it was believed that at least one of the regression equations would be a good approximation and would result in usable estimates of the threshold values for independent variables (points at which each of the dependent variables is maximized).

The computational procedures for the regression equations involved ordinary multiple regression analysis. High speed computers were utilized to obtain the desired computations. Existing programs were adapted to the needs of the study.

The six regression equations considered were:

$$Y_{hj} = a_h + \sum_{i=1}^{5} b_{hi}X_{ij} + \sum_{i=1}^{5} c_{hi}X_{ij}^2 + \epsilon_{hj} \qquad [1]$$

$$Y_{hj} = \sum_{i=1}^{5} b_{hi}X_{ij} + \sum_{i=1}^{5} c_{hi}X_{ij}^2 + \epsilon_{hj} \qquad [2]$$

$$Y_{hj} = a_h + \sum_{i=1}^{5} b_{hi}X_{ij} + \sum_{i=1}^{5} c_{hi}X_{ij}^2 + \sum_{i=1}^{5} d_{hi}X_{ij}^3 + \epsilon_{hj} \qquad [3]$$

$$Y_{hj} = \sum_{i=1}^{5} b_{hi}X_{ij} + \sum_{i=1}^{5} c_{hi}X_{ij}^2 + \sum_{i=1}^{5} d_{hi}X_{ij}^3 + \epsilon_{hj} \qquad [4]$$

$$\log_e Y_{hj} = a_h + \sum_{i=1}^{5} b_{hi}\log_e X_{ij} + \sum_{i=1}^{5} c_{hi}X_{ij} + \epsilon_{hj} \qquad [5]$$

$$\log_e Y_{hj} = \sum_{i=1}^{5} b_{hi}\log_e X_{ij} + \sum_{i=1}^{5} c_{hi}X_{ij} + \epsilon_{hj} \qquad [6]$$

Equations [1] through [6] will hereafter be referred to as models 1 through 6. Models 1, 2, 3, and 4 are standard polynomial regression equations, with models 2 and 4 passing through the origin. Models 5 and 6 result when the functional relationship between Y_h and X_i is of the form:

$$Y_{hj} = a_h \prod_{i=1}^{5} X_{ij}^{b_{hi}} e^{c_{hi} X_{ij} + \epsilon_{hj}} \qquad [7]$$

where e is the Naperian base 2.71828 • • • , and its exponent is $c_{hi}X_{ij} + \epsilon_{hj}$. Equation [7] implies a multiplicative relation between the X_i and a polynomial relation of X_i to $\log_e Y_h$. (The use of $\log_{10}$ instead of $\log_e$ is permissible since this involves multiplication of both sides of models 5 and 6 by a constant.) All b_{hi} are inherently positive and all c_{hi} are inherently negative in models 2 and 4. Also, all X_{ij} are positive values.

Estimated threshold values, $\hat{X}_{hi}$, are obtained by taking the derivatives of each regression equation, setting the derivative equal to zero, and solving for $\hat{X}_{hi}$ in terms of the estimated regression coefficients for each value of h and i. The $\hat{X}_{hi}$ values for the six regression models are:

$$\text{Models 1 and 2: } \hat{X}_{hi} = -b_{hi}/2c_{hi} \qquad [8]$$

$$\text{Models 3 and 4: } \hat{X}_{hi} = \frac{-c_{hi} \pm \sqrt{c^2_{hi} - 4b_{hi}d_{hi}}}{2d_{hi}} \qquad [9]$$

$$\text{Models 5 and 6: } \hat{X}_{hi} = -b_{hi}/c_{hi} \qquad [10]$$

The appropriate root in equation [9] has to be a positive quantity and a maximum value for the curve; minimum, negative, and imaginary values are not acceptable. All $\hat{X}_{hi}$ are inherently nonnegative, so that any estimated $\hat{X}_{hi}$ which is negative is inadmissible biologically.

The $\hat{X}_{hi}$ from models 1, 2, 3, and 4 are directly comparable to those from models 5 and 6. When differentiation is performed and the resulting equation set equal to zero, one finds that value, $\hat{X}_{hi}$, of the X_i which maximized $Y_h = f(X_i)$ = a function of the X_i. Confidence intervals for $\hat{X}_{hi}$ from models 1 and 2 may be computed as described by Kenney and Keeping (2).

For many situations, and perhaps for the present data, it may be desirable to incorporate interaction terms in models 1 through

6. In the first two, such terms as X_1X_2, $X^2_1X_2$, $X_1X^2_2$, $X^2_1X^2_2$, $\cdots$, X_4X_5, $X^2_4X_5$, $X_4X^2_5$, $X^2_4X^2_5$, etc., could be added to account for interactions between the independent variables. Similar interaction terms may be included in models 3, 4, 5, and 6 as $X_1X^3_2$, $X^2_1X^3_2$, $X^3_1X^3_2$, or (log X_1) X_2, X_1 log X_2, etc. Also, additional powers of the X_i could be included in the exponent of e in equation [7]. Whether or not the additional parameters in the regression equations would yield a better fit to the data would need to be determined empirically on a large set of data such as those used for the present study.

Results

The relationships of the dependent with the independent variables were investigated for each dependent variable. All six multiple regression models were compared in each dependent variable analysis within each population.

The means for all dependent and independent variables within populations are listed in Table 1. For certain of the characters there are relatively large differences beteen populations. The differences for weight per root and percentage sucrose were discussed extensively by Powers et al. (5). Although not shown, it is generally true for all characters that the treatment and population variances were, by far, the largest. In order of magnitude of the mean squares, these two sources of variation were followed by replicates and the population by treatment interaction. These four sources of variation are large compared to the remaining first and second order interactions. Similar

Table 1.—Means of dependent (Y_h) and independent (X_i) variables within populations.

Variate	Population					
	A54-1	A54-1BB	50-406BB	50-406	F_1 hybrid	52-307
Weight per root (Y_1), lbs.	2.26	2.17	1.72	0.89	1.88	0.87
Percentage sucrose (Y_2), %	17.3	17.3	17.1	16.8	17.6	16.6
Percentage purity (Y_3), %	94.6	94.8	95.8	94.3	96.4	95.7
Gross sugar per root (Y_4), lbs.	0.39	0.37	0.30	0.15	0.33	0.14
Potassium (X_1), ppm	1279	1221	1059	1132	989	1031
Glutamic acid (X_2), mg. per 100 ml.	46.5	24.5	26.1	12.7	10.7	6.5
Sodium (X_3), ppm	374	373	255	255	267	346
Betaine (X_4), mg. per 100 ml.	103.2	100.3	88.0	99.3	76.3	91.2
Total nitrogen (X_5), mg. per 100 ml.	32.8	30.9	23.1	22.9	15.6	14.8

Table 2.—Simple correlation coefficients from untransformed data.

Population and variate	Sucrose %	Purity %	Gross sugar	K	Glutamic acid	Na	Betaine	N
A54-1								
Root weight	—0.42	—0.59	0.93	0.54	0.60	0.48	0.63	0.60
Sucrose %	1.00	0.74	—0.06	—0.56	—0.66	—0.83	—0.52	—0.78
Purity %		1.00	—0.34	—0.73	—0.85	—0.89	—0.78	—0.93
Gross sugar			1.00	0.35	0.39	0.19	0.48	0.33
Potassium				1.00	0.58	0.68	0.60	0.68
Glut. acid					1.00	0.72	0.78	0.92
Sodium						1.00	0.66	0.85
Betaine							1.00	0.82
A54-1BB								
Root weight	—0.42	—0.65	0.94	0.50	0.60	0.53	0.65	0.65
Sucrose %	1.00	0.70	—0.08	—0.68	—0.58	—0.86	—0.37	—0.75
Purity %		1.00	—0.43	—0.76	—0.76	—0.86	—0.75	—0.95
Gross sugar			1.00	0.28	0.42	0.24	0.55	0.41
Potassium				1.00	0.51	0.73	0.61	0.76
Glut. acid					1.00	0.68	0.56	0.77
Sodium						1.00	0.54	0.88
Betaine							1.00	0.77
50-406BB								
Root weight	0.09	—0.60	0.97	0.46	0.34	0.28	0.76	0.49
Sucrose %	1.00	0.33	0.31	—0.06	—0.47	—0.79	—0.11	—0.54
Purity %		1.00	—0.50	—0.45	—0.73	—0.67	—0.78	—0.85
Gross sugar			1.00	0.41	0.22	0.08	0.69	0.34
Potassium				1.00	0.46	0.31	0.44	0.55
Glut. acid					1.00	0.63	0.60	0.89
Sodium						1.00	0.46	0.76
Betaine							1.00	0.75
50-406								
Root weight	—0.31	—0.34	0.95	0.47	0.19	0.26	0.55	0.38
Sucrose %	1.00	0.75	—0.02	—0.65	—0.74	—0.90	—0.63	—0.89
Purity %		1.00	—0.13	—0.71	—0.53	—0.79	—0.78	—0.85
Gross sugar			1.00	0.30	—0.04	—0.01	0.40	0.13
Potassium				1.00	0.50	0.65	0.83	0.77
Glut. acid					1.00	0.75	0.46	0.82
Sodium						1.00	0.54	0.89
Betaine							1.00	0.77
F_1 hybrid								
Root weight	—0.01	—0.48	0.96	0.38	0.28	0.21	0.61	0.39
Sucrose %	1.00	0.56	0.27	—0.57	—0.68	—0.76	—0.24	—0.68
Purity %		1.00	—0.29	—0.77	—0.86	—0.78	—0.79	—0.92
Gross sugar			1.00	0.20	0.07	—0.02	0.50	0.18
Potassium				1.00	0.72	0.68	0.65	0.79
Glut. acid					1.00	0.72	0.64	0.97
Sodium						1.00	0.49	0.80
Betaine							1.00	0.74
52-307								
Root weight	—0.09	—0.55	0.98	—0.26	0.55	0.51	0.69	0.63
Sucrose %	1.00	0.23	0.09	0.24	—0.23	—0.53	0.18	—0.25
Purity %		1.00	—0.47	0.18	—0.74	—0.79	—0.69	—0.84
Gross sugar			1.00	—0.24	0.48	0.38	0.70	0.55
Potassium				1.00	—0.03	—0.19	—0.05	—0.08
Glut. acid					1.00	0.70	0.72	0.91
Sodium						1.00	0.54	0.80
Betaine							1.00	0.82

results for covariances were obtained. The large treatment, replicate, and treatment by replicate mean squares as compared to a relatively small within-plots mean square, verifies an earlier statement that the environmental variance among plots was large relative to the environmental and genetic variance within plots.

The simple correlation coefficients of all variates in the experiment are presented in Table 2. In general the correlations of root yield and gross sugar are negative with percentage sucrose and purity, and positive with the thin juice chemical characters. In the case of percentage sucrose and purity, the correlations with chemical characters are, with three exceptions, negative. Among all the independent variables, betaïne has the highest simple correlation with root weight and gross sugar in all cases, except one, where it has the same correlation with root weight as does total nitrogen. In all populations, percentage sucrose is most highly correlated with sodium, whereas purity is most highly correlated with total nitrogen. Among the 216 simple correlations 190 are significant at $P = 0.05$, each having 78 degrees of freedom.

All six multiple regression models were applied to the data for each yield character and the five thin juice chemical characters in each population. The multiple correlation coefficients of the yield characters with the five X_i and their squares, cubes, and/or logs for each population are presented in Table 3. Those

Table 3.—Multiple correlation coefficients (R) with the four yield characters, using only those models where deviations are measured from the mean.

Population	Regression model	Multiple correlation coefficients (R)			
		Weight per root (Y_1)	Percentage sucrose (Y_2)	Percentage apparent purity (Y_3)	Gross sugar (Y_4)
A54-1	1	0.79	0.88	0.96	0.77
	3	0.81	0.89	0.96	0.79
	5	0.81	0.90	0.94	0.79
A54-1BB	1	0.81	0.89	0.96	0.77
	3	0.86	0.90	0.96	0.82
	5	0.83	0.90	0.95	0.79
50-406BB	1	0.79	0.88	0.95	0.79
	3	0.83	0.90	0.96	0.82
	5	0.80	0.90	0.94	0.80
50-406	1	0.62	0.94	0.93	0.59
	3	0.64	0.95	0.94	0.60
	5	0.64	0.95	0.91	0.59
F_1 hybrid	1	0.84	0.90	0.91	0.84
	3	0.86	0.91	0.93	0.87
	5	0.86	0.92	0.89	0.86
52-307	1	0.78	0.82	0.88	0.78
	3	0.83	0.84	0.90	0.83
	5	0.82	0.83	0.87	0.82

multiple correlation coefficients shown are only from those models where deviations in Y_h are measured from the mean. In the remaining models where the intercept is zero, about 99% of the variability is accounted for by regression in every case. These multiple correlation coefficients are of little analytic value.

All the multiple correlation coefficients in Table 3 are significant at $P = 0.01$; and 35 to 92% of the variability in Y_h is accounted for by regression. In most cases, model 3 has accounted for the greatest portion of the variability followed in order by 5 and 1, except for purity, where model 3 is followed by 1 and

Table 4.—Estimated threshold values ($\hat{X}_i$) for maximum root weight (Y_1).

Population	Regression model	Thin juice chemical character				
		Potassium (ppm) ($\hat{X}_1$)	Glutamic acid (mg./100ml.) ($\hat{X}_2$)	Sodium (ppm) ($\hat{X}_3$)	Betaine (mg./100ml.) ($\hat{X}_4$)	Nitrogen (mg./100ml.) ($\hat{X}_5$)
A54-1	1			320	129	55
	2		105	420	92	68
	3			350	20	38
	4					38
	5	4790		360		45
	6			360		43
A54-1BB	1		50	500	111	150
	2		59	330	117	101
	3	1860	69		111	43
	4		17		108	43
	5		97	260	104	86
	6		106	260	104	82
50-406BB	1				71	45
	2				92	47
	3	1400	148	20	108	31
	4				108	31
	5				81	59
	6				81	55
50-406	1			70		32
	2	1300		100		30
	3	780	64	130	227	28
	4	460			249	27
	5			70		31
	6	1070		80		32
F_1 hybrid	1	1090		300		27
	2			260	125	33
	3		12	270	121	17
	4	870			119	19
	5	1820	15	160		28
	6		15	150	292	29
52-307	1	320	7	440	128	
	2		7	50	136	
	3	910	6	700	161	65
	4	790			138	106
	5	860	7	410	122	
	6		7	410	131	

5. Of the four Y_h, apparent purity (Y_3) has the greatest portion of its variability accounted for by the X_1 followed by sucrose, root weight and gross sugar.

The threshold values ($\hat{X}_{hi}$) computed from equations [8], [9], and [10] for each population are presented in Tables 4 through 7 for the dependent variables Y_1 through Y_4, respectively. The blanks in the tables have resulted when the computed threshold estimates were negative, not maxima, or not real. There is a potential of six estimates for each threshold point. Model 3 provides a threshold estimate in 102 of the 120 cases,

Table 5.—Estimated threshold values ($\hat{X}_i$) for maximum percentage sucrose (Y_2).

Population	Regression model	Thin juice chemical character: Potassium (ppm) ($\hat{X}_1$)	Glutamic acid (mg./100ml.) ($\hat{X}_2$)	Sodium (ppm) ($\hat{X}_3$)	Betaine (mg./100ml.) ($\hat{X}_4$)	Nitrogen (mg./100ml.) ($\hat{X}_5$)
A54-1	1	1630			156	
	2	1420			114	
	3	1580	941	150	122	
	4	1340			123	
	5	1430		160		10
	6	1990		170		16
A54-1BB	1	660			125	
	2	1210			119	
	3	920	70		123	24
	4	1070			123	18
	5	960		70	550	20
	6			30		26
50-406BB	1	1070			117	
	2	1050			129	
	3	990	12	140	88	60
	4	980	8		92	86
	5	1000	3	140	130	
	6		1	140	513	
50-406	1	1230			70	
	2	1200	11		35	
	3		428	100	77	37
	4	1190			77	37
	5	1230		100	76	
	6			90	82	1
F_1 hybrid	1	1110			116	
	2	1080			445	
	3		102	100	111	
	4				111	
	5	1170		130		7
	6			120	101	14
52-307	1				183	
	2	1120			209	
	3	1230	30	160	138	
	4	760			160	
	5			140		4
	6			140		4

followed by 74, 68, 68, 62, and 59 for models 5, 2, 6, 4, and 1, respectively. A few of the threshold estimates are admittedly unrealistic but are in general sufficiently consistent to indicate population differences.

Threshold estimates were also calculated within fertility levels within populations; these are not included in the text. However, in most cases where all threshold estimates were available, the across-treatment estimate was found to be between the corresponding estimates made from the within-treatment analyses. This logically suggests that the estimates in Tables 4 through 7 are probably more accurate than estimates within treatments, since

Table 6.—Estimated threshold values ($\hat{X}_1$) for maximum percentage apparent purity (Y_3).

Population	Regression model	Thin juice chemical character				
		Potassium (ppm) ($\hat{X}_1$)	Glutamic acid (mg./100ml.) ($\hat{X}_2$)	Sodium (ppm) ($\hat{X}_3$)	Betaine (mg./100ml.) ($\hat{X}_4$)	Nitrogen (mg./100ml.) ($\hat{X}_5$)
A54-1-1	1	1140				
	2	1370			104	
	3				79	7
	4	1220			80	60
	5	1210			103	
	6	1160			97	
A54-1BB	1	340				
	2	1290	21	10	103	
	3	1050	24	670	116	98
	4	1120			94	
	5	1140	18		96	
	6	1120	19		99	
50-406BB	1	730			49	
	2	1100	32	210	85	
	3	1170	77	640	57	5
	4	1000		920	64	
	5	1020	2		68	
	6	1020	3		69	
50-406	1	1790	144			-
	2	1210	41			
	3	1390	93	500	40	15
	4	1100	34	70	22	17
	5	1430				9
	6	1320				7
F_1 hybrid	1		14			
	2	1030				
	3	930	19	800	111	39
	4	930			116	33
	5	1050	15			
	6	1040	15			
52-307	1	1450	11			
	2	1050				11
	3	1150	10	80	221	12
	4	1010			58	12
	5	1080	6			
	6	1110	6			3

there are twice as many observations on which the regression is calculated and the range of data across treatments is greater than the range of data within either treatment.

Table 8 lists the number of analyses in which certain necessary conditions are fulfilled. In models 1, 2, 5, and 6 conditions necessary for a maximum are $b_{hi} > 0$ and $c_{hi} < 0$, but are not of themselves necessary conditions in models 3 and 4.

In determining which of the six multiple regression models provides the best fit, four factors are considered: number and realism of the threshold estimates; proportion of the total variability accounted for by regression; fulfillment of necessary con-

Table 7.—Estimated threshold values ($\hat{X}_i$) for maximum gross sugar (Y_4).

Population	Regression model	Thin juice chemical character				
		Potassium (ppm) ($\hat{X}_1$)	Glutamic acid (mg./100ml.) ($\hat{X}_2$)	Sodium (ppm) ($\hat{X}_3$)	Betaine (mg./100ml.) ($\hat{X}_4$)	Nitrogen (mg./100ml.) ($\hat{X}_5$)
A54-1	1	1990	126	280	102	47
	2		105	310	97	48
	3			310		34
	4					34
	5	2340		280		33
	6			290		33
A54-1BB	1		57	170	119	104
	2		6	170	122	89
	3	1840	68		114	43
	4				113	43
	5		92	190	112	67
	6		877	180	118	58
50-406BB	1				98	50
	2				97	50
	3	1670	174	80	108	36
	4				108	36
	5	1030		70	90	216
	6			60	95	80
50-406	1			10	244	30
	2	1270		20	272	30
	3	890	64	120	72	28
	4	420				28
	5			90	113	31
	6			90	112	32
F_1 hybrid	1	1110		230	1362	25
	2			140	122	89
	3		6	180	118	16
	4	1510			116	18
	5	1030		70	90	216
	6		14	140	130	27
52-307	1		7	420	148	
	2		7	420	153	
	3	890	6	380	155	36
	4	710			144	40
	5	880	7	380	148	
	6		7	380	164	

ditions; and relative proportion of the variability accounted for by individual variables. From these evaluations it was concluded that model 3 provides the best fit for all dependent variables followed by models 4 and 1, except in the case of purity, where model 3 is followed by model 5.

Table 8.—Enumeration of analyses in which necessary conditions are fulfilled.

Yield character and model	Condition				
	$b_{hi}>0$	$c_{hi}<0$	Significant[1] $b_{hi}<0$	Significant[1] $c_{hi}>0$	Positive and real X_i
Root weight					
1	22	20	1	1	18
2	21	20	1	1	19
3					26
4					15
5	22	22	0	0	19
6	20	20	0	1	18
Percent sucrose					
1	11	20	0	0	11
2	13	23	3	3	13
3					24
4					15
5	21	19	1	1	19
6	17	16	3	4	16
Percent purity					
1	9	14	9	1	9
2	15	16	7	6	15
3					27
4					19
5	15	23	3	1	14
6	16	24	5	1	15
Gross sugar					
1	22	23	1	1	21
2	21	22	3	2	20
3					25
4					13
5	24	23	0	0	22
6	21	20	1	2	19
Desired number	30	30	0	0	30

[1] P = 0.05

In considering the threshold estimates in this study there are six regression analyses on each population for each dependent variable. There is, therefore, some choice of model from which the best threshold estimate may be calculated even though model 3 in general provided the best fit. In order to remain objective, it is possible, as each variable is considered within each population, to compare among models 1, 3, and 5 (in which a particular X_i is maximizing) the additional variability in Y_h accounted for by each X_i or its log. Due to a difference in computer program and output peculiar to this study a similar comparison is not

possible for the $\hat{X}_i$ from models 2, 4, and 6. Therefore selection of the most likely correct threshold estimates from all analyses cannot be entirely objective. But by also considering the general fit of the models for each case and fulfillment of necessary conditions for individual X_i the threshold estimates most likely to be correct have been selected from the six possible choices, and are listed in Table 9. These are estimates of concentrations of the thin juice chemical characters at which the individual yield characters are maximized and, hence, the point at which the yield characters commence to be depressed.

Table 9.—The best estimates of concentrations of the thin juice chemical characters at which the yield characters are maximized and in parentheses the model from which it was calculated.

Population and yield character	Thin juice chemical character				
	Potassium (ppm)	Glutamic acid (mg./100ml.)	Sodium (ppm)	Betaine (mg./100ml.)	Nitrogen (mg./100ml.)
A54-1					
Root weight	4790(5)	105(2)	350(3)	92(2)	55(1)
Percent sucrose	1580(3)	941(3)	150(3)	122(3)	10(5)
Percent purity	1210(5)	—— *	—— *	79(3)	7(3)
Gross sugar	1990(1)	105(2)	310(3)	102(1)	34(3)
A54-1BB					
Root weight	1860(3)	69(3)	330(2)	111(3)	43(3)
Percent sucrose	920(3)	70(3)	70(5)	123(3)	24(3)
Percent purity	1050(3)	24(3)	10(2)	94(3)	98(2)
Gross sugar	1840(3)	68(3)	170(1)	114(3)	43(3)
50-406BB					
Root weight	1400(3)	148(3)	20(3)	108(3)	31(3)
Percent sucrose	990(3)	12(3)	140(3)	88(3)	60(3)
Percent purity	1170(3)	32(2)	210(2)	57(3)	5(3)
Gross sugar	1670(3)	174(3)	80(3)	108(3)	50(1)
50-406					
Root weight	780(3)	64(3)	130(3)	227(3)	28(3)
Percent sucrose	1190(4)	11(2)	100(3)	77(3)	37(3)
Percent purity	1390(3)	34(4)	70(4)	40(3)	9(5)
Gross sugar	890(3)	64(3)	120(3)	72(3)	28(3)
F_1 hybid					
Root weight	1090(1)	15(5)	270(3)	121(3)	27(1)
Percent sucrose	1080(2)	102(3)	100(3)	111(3)	7(5)
Percent purity	930(3)	19(3)	800(3)	111(3)	33(4)
Gross sugar	1110(1)	14(6)	180(3)	118(3)	25(1)
52-307					
Root weight	910(3)	6(3)	440(1)	128(1)	65(3)
Percent sucrose	1230(3)	30(3)	160(3)	138(3)	4(5)
Percent purity	1150(3)	10(3)	80(3)	58(4)	12(3)
Gross sugar	890(3)	6(3)	380(3)	155(3)	36(3)

* No estimate possible.

Discussion

Although plot totals were used in these analyses, plot means could also be used. Using plot totals for the multiple regression analyses within populations results in estimates of environmental

regression of the four yield characters on the five chemical characters, since the genetic variation in the plot totals is very small compared to the environmental variation. Hence, these regressions may be considered to be estimates of the environmental relationships among characters for each population. Certain genetic comparisons are afforded by across population comparisons.

Relatively large treatment, replicate, and treatment by replicate mean squares, when compared with the within-plots mean square, make these data well suited to a curve-fitting study. Since the population by treatment mean square was quite large, it is also possible that year and population by year effects could be of considerable importance with respect to the best fitting multiple regression model. This possibility has not been investigated. Similar analyses of the within-plot variability, which is in large part genetic, would be of considerable interest for breeding purposes. These within-plot analyses have not been made.

Among the simple correlation coefficients it is of some interest that betaine is the best single predictor of both root weight and gross sugar in all populations except A54-1BB where it is the same as total nitrogen. For percentage sucrose and purity, sodium and total nitrogen have the highest simple correlations without exception. In spite of this, there are indications among the non-segregating populations of some genetic differences in the association of the chemical characters as they affect the yield characters. Therefore, the effect of environment on the relationship between the yield characters and thin juice chemical characters might be modified by breeding.

Comparisons of multiple correlation coefficients can be made among those from models 1, 3, and 5. Those from models 2, 4, and 6 are extremely high because those models account for such a high proportion of the total variability. This is due to deviations being measured from zero. Hence the multiple correlation coefficients from models 2, 4, and 6 are of little comparative value. Those from models 1, 3, and 5 are indicative of the "fit" to the model being considered. In Table 3, in 70 of 72 cases, model 3 accounts for as much variability or more than models 1 and 5. Of course it should be remembered that model 3 cannot account for less variability than model 1. The proportion of variability accounted for in percentage purity is very high, particularly among the segregating populations, 88 to 92%. The reason why model 1 accounts for more variability in percentage purity than model 5 is not clear. This is true in all populations and is contrary to the results for the other three yield characters.

Models 1, 3, and 5 are generally considered to provide a creditable "fit" to the data.

It is apparent, upon reviewing the threshold estimates in Tables 4 through 7 that all six models tested leave something to be desired. Model 3 provides a threshold estimate in 85% of all cases, but these are not necessarily all resulting from functions of the same form. The other five models are not greatly different and provide threshold estimates in 49 to 62% of the cases. For root weight and gross sugar, threshold estimates of betaine and nitrogen are most frequently estimated, compared to betaine and potassium for percentage sucrose and purity. The conditions of this experiment appear to have fairly well straddled the nitrogen level and possibly the level of betaine precursors at which root and gross sugar yields are maximized. The same thing can be said for betaine and potassium in the cases of percentage sucrose and purity. Threshold estimates for these chemical characters can be expected to arise less frequently as a result of extrapolation.

The fulfillment of necessary conditions is not a very satisfactory comparison of performance of all six models but does give some worthwhile comparisons among models 1, 2, 5, and 6. In models 3 and 4 $b_{hi} > 0$ and $c_{hi} < 0$ are not applicable as necessary conditions. Hence in Table 8, fulfillment of these conditions and the statistical significance of $b_{hi} < 0$ and $c_{hi} > 0$ are not noted for models 3 and 4.

In considering the threshold estimates of the five thin juice chemical characters there are six regression analyses within each population for each yield character. As a routine it would not be practical to calculate a number of analyses and have a choice of threshold estimates. Ideally one model would be applied in all cases. Many models other than the six in this study could be generated. However among these six, model 3 provides the best fit for all yield characters across all populations. This third degree polynomial, in general, satisfies more of the necessary criteria of a good fit than any of the other models. Models 2, 4, and 6, in which the function has been forced through the origin, do not fit as well as anticipated. Since model 3 has been determined to be the most satisfactory, it is assumed that it should result in the most accurate threshold estimates. This is borne out in Table 9 where 83 of the 118 most likely correct threshold estimates have resulted from the use of model 3.

Since very little could be done under the conditions of this experiment to control the thin juice concentration of potassium, glutamic acid, sodium, and betaine except as they are related to nitrogen, the threshold values for total nitrogen are of principal

interest. In Table 9, most of the threshold estimates calculated to be the best estimates of concentrations of the thin juice chemical characters at which the yield characters commence to be depressed, appear to be biologically reasonable.

The accuracy of some estimates can be pointed out. In Table 9 root weight for population A54-1 is supposed to maximize at 55 milligrams of nitrogen. This corresponds to the estimate made by Powers et al. (5) where they found by examination of means that in this population the maximum root weight was reached with a concentration of total nitrogen lying somewhere between 46.8 and 62.9 milligrams per 100 milliliters of thin juice. In considering percentage sucrose and percentage purity in this same population the threshold values are 10 and 7, respectively. This concentration of total nitrogen in the thin juice would be attainable by this population only under an extreme nitrogen deficiency; but it is reasonable to expect that any increase in this nitrogen concentration would result in some decrease in percentage sucrose and percentage purity, since in the data of this study, all increases of nitrogen in the thin juice were accompanied by some decrease in sucrose and purity. It appears that a gradual, slight decrease occurs in percentage sucrose and percentage purity with increasing nitrogen from about 10 milligrams to some point between 46.8 and 62.9 where, as Powers et al. (6) point out, there is a sharp reduction in sucrose and purity. This may also be true for other characters where gradual decreases change into abrupt and drastic decreases. In such cases, threshold values would be of little value of themselves but could be of some value when considered along with means. The relation of total nitrogen to root weight, percentage sucrose, and percentage purity is a good example of this. Maximum percentage sucrose in population A54-1 is attained at about 10 milligrams of nitrogen, but at this point root weight would be very low. An increasing concentration of nitrogen from 10 milligrams to about 55 results in a tolerable decrease in percentage sucrose and percentage purity because it results in a marked increase in weight per root. This then represents among these economic characters a compromise which is necessary in most genotypes. Powers et al. (6) have presented evidence that in certain genotypes this compromise need not be so great. They pointed out that the F_1 hybrid in this study had a lower concentration of total nitrogen in the thin juice than A54-1. From Table 9, the F_1 hybrid apparently also has a lower threshold value than A54-1, 27 milligrams of nitrogen compared to 55. For total nitrogen then, the threshold estimates would indicate that, even though the F_1 has a lower concentration of total

nitrogen in the thin juice, root weight is maximizing at a lower point on the nitrogen scale. Hence concentrations of total nitrogen in the thin juice in relation to their effects on root yield may not be directly comparable. In this same F_1 population the maximum percentage sucrose should be achieved at about 7 milligrams of nitrogen. This, as in A54-1, probably represents a nitrogen concentration attainable only under nitrogen deficient conditions and would result in low weight per root. An examination of the means over a range of fertility levels would be necessary to establish the nitrogen concentration at which sucrose reached the point of diminishing total sugar.

Not all the threshold estimates, however, are biologically reasonable, a notable exception being the case of A54-1BB where 98 milligrams of nitrogen is supposed to maximize purity. Other less striking instances can be noted.

In considering gross sugar which is a product character of weight per root and percentage sucrose, it is generally maximized somewhere between that concentration of a thin juice chemical character which leads to maximum root weight and that concentration which leads to maximum sucrose or at the same point as root weight. This is biologically reasonable.

An interaction of genotypes with years, locations, or both could also affect threshold estimates as developed in this study. This possibility is not investigated in this experiment. If interactions affecting the threshold estimates are not highly important, the threshold estimates established for a particular genotype or population should be of considerable value in determination of the most productive fertility levels for the dependent variables and in determination of the fertility level leading to the highest total sugar production.

Threshold values as developed in this study would likely be of greatest value in determining the points on the axes of the independent variables at which a particular population achieved maximum root weight and maximum total sugar. Then an examination of the means in a range of fertility levels would indicate the fertility level at which this maximum is being achieved. Since different genotypes at the same fertility level have been demonstrated to have different levels of chemical characters in the thin juice, it would be necessary to examine each population in a manner such as this in order to determine the concentrations of the characters of interest at which root weight and gross sugar are maximizing. The threshold values are not likely to be of great value in studying percentage sucrose or percentage purity unless accompanied by a comprehensive examination of a range of treatment means.

It would appear that threshold estimates such as these might be of greater value in dealing with F_1 hybrids (from crossing two inbreds) where the within population variability would be entirely environmental.

Summary

The environmental interrelationships and the mutual response of five chemical characters in the thin juice with four yield characters were studied in three segregating and three non-segregating populations of sugar beets. The thin juice chemical characters were potassium, glutamic acid, sodium, betaine, and total nitrogen. The four yield characters were weight per root, percentage sucrose, percentage thin juice purity, and gross sugar per root.

Six multiple regression models were used in an attempt to describe the response function of each of the four yield characters on the five thin juice chemical characters. From these regression analyses comparisons were made of the means, partial regression coefficients, simple correlation coefficients, and multiple correlation coefficients. Threshold estimates of the five chemical characters were calculated for each of the yield characters. These were estimates of the concentration of a particular thin juice chemical character at which a particular yield character was maximized. This is the maximum with respect to each independent variable in the regression function. In certain cases the function is minimizing or else the maximum does not exist.

Among the six threshold estimates for each chemical character the most likely correct estimates were determined. These are based on variability accounted for, fulfillment of necessary conditions, and other factors. Most of these threshold estimates appear to be biologically reasonable and, where comparable, are within the range established by a study of the means. The threshold values for maximum root weight and gross sugar yield, in general, occur in a range attainable under commercial field conditions, this being particularly true for total nitrogen. Threshold values for maximum percentage sucrose and purity occur at such a low point on the total nitrogen scale that they are likely to be of little value.

Among the six models used, the third degree polynomial, including the mean, satisfies more of the criteria of a good fit than any of the others.

Application of methods such as these could be of value in determining the thin juice concentrations of various quality components, particularly nitrogen, at which a particular population achieved maximum root yield and total sugar yield.

Literature Cited

(1) DUDLEY, J. W., and LEROY POWERS. 1960. Population genetic studies on sodium and potassium in sugar beets (*Beta vulgaris* L.). J. Am. Soc. Sugar Beet Technol. 11: 97-127.

(2) KENNEY, J. F., and E. S. KEEPING. 1951. Mathematics of Statistics, Part 2. 2nd Ed. D. Van Nostrand Co., N. Y.

(3) PAYNE, MERLE G., LEROY POWERS, and E. E. REMMENGA. 1961. Some chemical genetic studies pertaining to quality in sugar beets (*Beta vulgaris* L.). J. Am. Soc. Sugar Beet Technol. 11:610-628.

(4) POWERS, LEROY, D. W. ROBERTSON, R. S. WHITNEY, and W. R. SCHMEHL. 1958. Population genetic studies with sugar beets (*Beta vulgaris* L.) at different levels of soil fertility. J. Am. Soc. Sugar Beet Technol. 9:637-676.

(5) POWERS, LEROY, W. R. SCHMEHL, W. T. FEDERER, and MERLE G. PAYNE. 1963. Chemical genetic and soils studies involving thirteen characters in sugar beets. J. Am. Soc. Sugar Beet Technol. 12:393-448.