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ESTIMATING GENETIC PARAMETERS OF AGRONOMIC AND QUALITY TRAITS IN A DIALLEL CROSS OF SUGARBEET

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ABSTRACT

Knowledge of genetic characters of agronomic and quality traits and their heritability in sugarbeet (*Beta vulgaris* L.), is the most important requirement for breeding high yielding varieties and good processing of this strategic crop. For this reason, fifteen hybrids from a diallel cross of six multigerm, diploid inbred lines (S_4) of sugarbeet were studied to determine the combining ability, gene action, heterosis, and heritability of thirteen technological and agronomical characteristics. Six parental lines and their F_1 s (twenty one genotypes) were evaluated in a randomized complete block design with four replications in Kooshkak Agricultural Research Center in 1996. Data were analyzed with method II and mix-model B of Griffing. Hayman's method was also used for graphical and genetical analysis. Significant differences were observed between genotypes for all traits except alkalinity. General combining ability (GCA) mean squares were significant for all traits. However, specific combining ability (SCA) mean squares were significant only for root yield, sugar percentage, impure sugar yield, recoverable sugar yield and white sugar yield, Significant ratio of GCA/SCA mean squares for sugar percentage showed that additive variance was more important. Non- sucrose components were controlled by additive gene action and had the maximum additive variance. Additive variance accounted for 54% and 75% of total genetic variance for root yield and sugar percentage, respectively. A significant negative correlation was observed between yield and technological characters. Test for validity of diallel

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assumptions showed epistasis effect for root yield, impure sugar yield, white sugar yield, recoverable sugar yield, potassium and mollasses sugar percentages. The frequency of dominant genes was more than the recessive genes in sugar percentage, purity, recoverable sugar percentage, white sugar and potassium percentage. Broad-sense heritability varied between 0.38 for white sugar yield to 0.73 for potassium percentage. White and recoverable sugar percentage, and white and recoverable sugar yield showed similar genetic expression. Parent 6 had more recessive genes, while , parents 1, 2 and 5 had more dominant genes.

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برآورد پارامتر های ژنتیکی صفات زراعی و کیفی در یک تلاقی دای آلل چغندر قند

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به ترتیب دانشجوی سابق کارشناسی ارشد، و استادیار بخش زراعت و اصلاح نباتات دانشکده کشاورزی دانشگاه شیراز، شیراز، ایران.

چکیده

آگاهی از ویژگی های ژنتیکی صفات زراعی و کیفی چغندر قند (*Beta vulgaris* L.) وشیوه توارث آن ها، مهمترین شرط دستیابی به تهیه ارقامی با عملکرد بالا همراه با فرآوری مطلوب این محصول مهم و استراتژیک می باشد. برای این منظور، ۱۵ هیبرید حاصل از طرح تلاقی دای آلل با ۶ رگه اینبرد مولتی ژرم دیپلوئید (S_4) برای مطالعه قابلیت ترکیب، نوع عمل ژن، در صد هتروزیس و ماهیت توارث پذیری ۱۳ صفت مهم زراعی و تکنولوژیک چغندر قند مورد بررسی قرار

گرفت. شش رگه والدینی به همراه نتاج F_1 حاصل از آن ها در قالب بلوک های کامل تصادفی با ۴ تکرار در مزرعه مقایسه شدند. ارزیابی داده ها بر اساس روش II و مدل مخلوط گریفینگ انجام شد. روش هیمن نیز برای تجزیه و تحلیل گرافیکی مورد استفاده قرار گرفت. تجزیه واریانس مقدماتی نشان داد که تفاوت ژنوتیپ ها از نظر کلیه صفات به جز ضریب قلیائیت معنی دار بود. میانگین مربعات GCA تمام صفات معنی دار گردید. در حالیکه میانگین مربعات SCA فقط برای عملکرد ریشه، درصد قند، عملکرد قند ناخالص، عملکرد قند قابل استحصال و عملکرد قند سفید معنی دار بود. نسبت میانگین مربعات GCA به SCA برای درصد قند معنی دار بود بنا براین سهم واریانس افزایشی در تظاهر آن مهمتر می باشد. اجزاء غیر قندی تحت کنترل اثرات افزایشی ژن بوده و دارای بیشترین واریانس افزایشی بودند. واریانس افزایشی عملکرد ریشه و درصد قند به ترتیب ۵۴٪ و ۷۵٪ کل واریانس ژنتیکی بود. همبستگی صفات مربوط به عملکرد و صفات کیفی منفی و معنی دار بود. آزمون فرضیات دای آلل حاکی از وجود اثرات اپیستازی برای صفات عملکرد ریشه، عملکرد قند ناخالص، عملکرد قند سفید، عملکرد قند قابل استحصال، مقدار پتاسیم و در صد قند ملاس بود. ژن های غالب در صفات درصد قند، درجه خلوص، درصد قند قابل استحصال، درصد قند سفید و مقدار پتاسیم فراوانی بیشتری نسبت به ژنهای مغلوب داشتند. وراثت پذیری عمومی بین ۳۸٪ برای عملکرد قند سفید تا ۷۳٪ برای درصد پتاسیم برآورد گردید. درصد قند سفید و قابل استحصال، و عملکرد قند سفید و قابل استحصال کنترل ژنتیکی مشابهی را نشان دادند. والد شماره ۶ دارای ژن های مغلوب بیشتر ولی والد های ۱، ۲ و ۵ دارای ژن های غالب بیشتری بودند.

INTRODUCTION

Sugarbeet (*Beta vulgaris* L.) is one of the predominant crops in Iran. Many economically important characters in sugarbeet are quantitative and are influenced by environmental conditions. Plant breeders look for quantitative approaches to combine desirable characters. One of the most common approaches is the use of diallel crossing system first proposed by Yates (13). This method was modified and used in many crop species, but little work has been done in sugarbeets.

Combining ability and type of gene action controlling 11 sugarbeet characters were studied by Smith *et al.* (10). They concluded that additive genetic variance was predominant for components of purified juice. Significant non-additive gene effects were found for non - sucrose components. Skaracis and Smith (9) demonstrated that dominance and additive gene effects were most important for root yield, while sucrose content and juice purity were controlled by additive effects. Srivastava *et al.* (12) stated the importance of additive effects for gross sugar.

Doney and Theurer (1) showed that general and specific combining ability effects were significant for cell division rate in roots of sugarbeet. They concluded that cell division rate was conditioned largely by non-additive gene effects and that root heterosis was due primarily to increases in cell number rather than cell size. A significant heterosis was reported for root yield and sugar percentage by Doney *et al.* (2). Kornienkov and Bychkova (6) concluded that hybrids with significant heterosis for sugar content were those in which both, or at least one of the parental lines showed predominance of non-additive over additive effects in the control of the character. Hybrids with high heterosis for root yield could be obtained by crossing lines with predominace of additive effects to lines in which non-additive effects predominated. Some additional diallel analyses have been conducted on bolting (5), seed germination (11) and cytoplasmic male sterility (7). However, very limited number of studies in combining ability, heterosis, and kind of gene action have been conducted in Iran.

The objectives of this study were: first to determine the general and specific combining ability, gene action, heterosis and nature of inheritance in 13 agronomic and technological characters, and second to estimate genetic components and heritability for these characters.

MATERIALS AND METHODS

Fifteen F_1 diallel hybrids and their 6 multigerm diploid inbred parents were grown in Kooshkak Agricultural Research Center, 60 km north of Shiraz, in 1996. The six S_4 parental lines (hereafter called lines 1, 2, 3, 4, 5, and 6) showed wide diversity for agronomic characters and were obtained from Sugarbeet Seed Institute, Karaj, Iran. Line 2 was originally from Netherlands but others were from Iran. Plots consisted of two rows 60 cm apart and 9 m long. Each entry was bordered on each side by a medium vigor common competitor (cultivar IC 6203) row. Plants within rows were spaced 25 cm apart. The experimental design was a randomized complete block with 4 replicates. All cultural practices were in accordance with standard agronomic practices recommended in the location.

At harvest, plants in a 50 cm section at each end of the rows were discarded to eliminate the possible border effects and root weight (t ha^{-1}), percent sugar, purity, impure sugar yield (t ha^{-1}), recoverable sugar yield (t ha^{-1}), white sugar yield (t ha^{-1}), nitrogen, sodium, and potassium content (meq 100 g^{-1}), alkalinity, and mollasses sugar percentage were measured. Quality characters were measured by Betalyser (8).

Analysis of variance was performed for each of the characters. Griffing's method II for mixed models (3) was then employed to estimate the general combining ability (GCA) and specific combining ability (SCA). The Hayman (4) analysis of diallel crosses was also used (assuming diploid segregation, no difference between reciprocal crosses, independent action of nonallelic genes, no multiple allelism, homozygous parents, and independent distribution of genes between the parents) to partition the genetic variance and determine heritability. The method of moments was used to estimate the variance components .

RESULTS AND DISCUSSION

Genotypes were significantly different with respect to all characters except alkalinity, thus GCA and SCA mean squares were determined for all characters except alkalinity (Table 1). GCA variances were highly significant for all characters, indicating the importance of additive gene effect in controlling them. However, SCA mean squares were only significant for root yield, percent sugar, impure sugar yield, recoverable sugar yield, and white sugar yield. To determine the relative importance of additive and non-additive gene effects, the significance of GCA/SCA was tested for characters in which both GCA and SCA were significant (Table 1). The non-significant ratio of GCA/SCA in root yield, impure sugar yield, recoverable sugar yield and white sugar yield suggested that non-additive rather than additive gene actions were probably more important in their expression. However, the GCA/SCA ratio in sugar percentage was significant, indicating that additive gene effect was more important in this character. These results are in agreement with others (9, 10) on sugarbeets. GCA effects were variable for different characters among parents (Table 2). The positive (or negative) GCA effects for any parent indicate the possibility of increasing (or decreasing) the character in the progenies produced by that parent.

The SCA effects for parent 1 with regard to root yield, impure sugar yield, recoverable sugar yield and white sugar yield, and for parent 5 with regard to sugar percent were significant (Table 3). The positive significant SCA effect for any hybrid suggests that the mean of the hybrid was greater than expected, based on the mean performance of the lines involved.

Estimates of specific combining ability variances associated with each parent for all characters are given in Table 4. Low variance indicates low variability among crosses involving the associated parent. Negative variances may be interpreted as estimates of zero variance, while a high positive variance indicates that not all combinations of that parent would produce a uniform pattern for that character. However, in choosing parents with higher potential, the SCA variance associated with each parent must be considered. The GCA effect for lines 1 and 2 with respect to root yield, for example, were positive and significant (Table 2). Thus lines 1 and 2 could transmit higher root yields to all of their crosses, however, Table 4 shows that line 1 has a larger SCA variance compared to line 2. Therefore, line 2 may

Table 1. Mean squares for general combining ability (GCA) and specific combining ability (SCA) effects for the characters measured.

Sources of variation	d.f.	Root yield	Percent sugar	Purity	Impure sugar yield	Recoverable sugar	Recoverable sugar yield	White sugar	White sugar yield	Nitrogen	Sodium	Potassiur	Molasses sugar
GCA	5	148.46**	0 .66**	6.43**	3.80**	1.41**	2.31**	1.41**	2.11**	0.22**	0.08**	0.63**	0.15**
SCA	15	43.82*	0 .10*	0.39	1.56*	0.14	1.19*	0.14	1.11*	0.07	0.01	0.04	0.01
Error	60	21.56	0. 06	0.43	0.75	0.09	0.57	0.09	0.53	0.06	0.02	0.04	0.01
GCA/SCA		3.39	6.48**		2.44		1.95		1.91				

* and ** Significant at 0.05 and 0.01 probability levels, respectively.

Table 2. Estimates of GCA effects for 12 characters.

Parents	Root yield (t ha^{-1})	Percent sugar	Purity (%)	Impure sugar yield (t ha^{-1})	Recoverable sugar (%)	Recoverable sugar yield (t ha^{-1})	White sugar (%)	White sugar yield (t ha^{-1})	Nitrogen (meq 100^{-1}g)	Sodium (meq 100^{-1}g)	Potassium (meq 100^{-1}g))	Mollasses sugar (%)
1	3.46*	0.08	0.30	0.75**	0.12	0.71**	0.13	0.69**	-0.11	0.06	-0.17**	-0.05
2	7.17**	-0.58**	-1.80**	0.99**	-0.85**	0.65**	-0.85**	0.60**	0.30**	0.15**	0.56**	0.27**
3	-2.16	0.15*	0.12	-0.32	0.16	-0.26	0.16	-0.24	-0.02	0.01	-0.03	0.00
4	-3.38*	0.04	0.37*	-0.62*	0.10	-0.52*	0.11	-0.50*	-0.19**	-0.01	-0.13*	-0.07*
5	-2.98*	0.15*	0.43*	-0.48*	0.21*	-0.37	0.21*	-0.36	-0.02	-0.12**	-0.05	-0.06*
6	-2.1	0.16*	0.57**	-0.31	0.26**	-0.21	0.26**	-0.20	-0.01	-0.09*	-0.18**	-0.09**
S.E. (g_i)	1.50	0.08	0.21	0.28	0.10	0.24	0.10	0.23	0.08	0.04	0.06	0.03
S.E. (g_i-$g_{'i}$)	2.32	0.12	0.33	0.34	0.15	0.38	0.15	0.36	0.12	0.06	0.09	0.05

* and ** significant at 0.05 and 0.01 probability levels, respectively.

Table 3. Estimates of SCA effects for 12 characters.

Parents and crosses	Root yield (t ha^{-1})	Percent sugar	Purity (%)	Impure sugar yield (t ha^{-1})	Recoverable sugar (%)	Recoverable sugar yield (t ha^{-1})	White sugar (%)	White sugar yield (t ha^{-1})	Nitrogen (meq 100^{-1}g)	Sodium (meq 100^{-1}g)	Potassium (meq 100^{-} g)	Mollasses sugar (%)
1	-7.40*	0.16	0.16	-1.37*	0.18	-1.21*	0.18	-1.17*	-0.07	-0.03	0.00	-0.02
2	-3.79	-0.27	-0.39	-0.97	-0.29	-0.93	-0.29	-0.91	0.00	0.00	0.07	0.02
3	-5.26	-0.25	0.16	-1.22	-0.19	-1.07	-0.19	-1.04	-0.15	0.11	-0.25	-0.06
4	-3.83	-0.05	-0.19.	-0.77	-0.09	-0.70	-0.09	-0.68	0.02	0.07	0.03	0.03
5	-0.19	-0.41*	-0.38	-0.31	-0.43	-0.33	-0.43	-0.33	0.21	0.05	-0.04	0.02
6	-5.33	0.23	0.55	-0.92	0.32	-0.77	0.32	-0.74	-0.01	-0.05	-0.20	-0.09
1x2	-2.03	0.04	0.29	-0.34	0.08	-0.26	0.08	-0.25	0.12	0.05	-0.20	-0.04
1x3	6.73*	0.00	-0.67	1.30*	-0.13	1.05*	-0.13	1.02*	0.33*	0.00	0.27*	0.13
1x4	8.37**	0.12	0.79	1.72**	0.26	1.64**	0.26	1.59**	-0.08	-0.22**	-0.16	-0.14*
1x5	0.84	0.00	-0.38	0.19	-0.07	0.12	0.07	0.11	-0.09	0.13	0.10	0.07
1x6	0.88	-0.49**	-0.31	-0.13	-0.50*	-0.14	-0.5*	-0.14	-0.13	0.09	-0.03	0.00
2x3	-1.27	0.25	-0.06	-0.03	0.20	-0.03	0.20	-0.02	0.12	-0.08	0.21	0.06
2x4	6.45*	-0.39*	-0.47	0.98	-0.43*	0.81	-0.43*	0.78	-0.04	0.22**	-0.10	0.04
2x5	-2.51	0.61**	.28**	-0.04	0.77**	0.16	0.77**	0.17	-0.49**	-0.17*	-0.17	-0.16*
2x6	6.95*	0.03	-0.26	1.38*	-0.03	1.18*	-0.03	1.14*	0.28*	-0.02	0.11	0.06
3x4	7.27*	-0.05	-0.46	1.42*	-0.13	1.21*	-0.13	1.17*	0.26*	-0.03	0.20	0.08
3x5	1.11	0.07	0.39	0.27	0.14	0.29	0.14	0.28	-0.32*	-0.08	-0.04	-0.08
3x6	-3.32	0.24	0.48	-0.51	0.31	-0.39	0.31	-0.37	-0.08	-0.03	-0.15	-0.07
4x5	-9.82**	0.40*	0.50	-1.73	0.46	-1.51**	0.46	-1.46	0.18	-0.07	-0.15	-0.06
4x6	-4.61	0.02	0.03	-0.84	0.02	-0.74	0.02	-0.71	-0.35*	-0.04	0.14	0.00
5x6	10.77**	-0.27	-1.04*	1.94**	-0.44	1.62**	-0.44*	1.56**	0.31*	0.09	0.33*	0.17*

* and ** Significant at 0.05 and 0.01 probability levels, respectively.

be preferred to line 1, because of its uniformity in transmitting higher root yield. Meanwhile, line 2 has a negative and significant GCA effect with respect to sugar percent. The correlation coefficient between root yield and sugar content was negative and significant (r = -0.49).

GCA and SCA variances and the proportion (%) of the total genetic variance counted for additive and non-additive genetic variaces are presented in Table 5. GCA and SCA variances permit comparisons of the additive and non-additive gene effects. Additive genetic variance is equal to twice the estimated GCA variance component, whereas non-additive variance is equal to SCA variance . It could be concluded that the additive component for all the characters except impure sugar yield, recoverable sugar yield, and white sugar yield were relatively higher than dominant component (Table 5). These results supported other studies that non-sucrose components are under genetic control (9, 10, 12).

Estimates of heterosis is expressed as the superiority of F_1 hybrids over their better parent. Negative heterosis values for any character indicate the decrease of that character in the F_1 generation relative to higher parent. Heterosis for root yield ranged from -17.72 (hybrid 4×5) to 23.90 (hybrid 5×6) (Table 6). The best performing cross for root yield, sugar percent, impure sugar yield, and recoverable sugar yield was 3×4. Line 2 was obtained from the Netherlands. The GCA for this line with respect to root yield, impure sugar yield, white sugar yield, recoverable sugar yield, percent nitrogen, sodium, potassium, and mollasses sugar were positive and significant. The crosses between line 2 and other lines also exhibited relatively large heterosis. This line may be recommended as a valuable parent for producing hybrids with better agronomic and technological characters. The test for validity of diallel assumptions showed that epistasis was a significant effect for root yield, impure sugar yield, white sugar yield, recoverable sugar yield, potassium and mollasses sugar percentage (Table 7). In each case one or two parents were eliminated to restore the desired rectilinear relationship (Fig. 1). From the genetic component of variation three important values were calculated: the mean degree of dominance $(H_1/D)^{1/2}$, the proportion of the genes with positive and negative effects

Table 4. Estimates of specific combining ability variances (σ_{si}^2) associated with parents based on the diallel analysis of characters studied.

Parents	Root yield	Percent sugar	Purity	Impure sugar yield	Recoverable sugar	Recoverable sugar yield	White sugar	White sugar yield	Nitrogen	Sodium	Potassiu	Mollasses sugar
1	3	0.023	0.014	0.646	0.018	0.553	0.017	0.521	-0.003	0.008	0.010	0.002
2	9.298	0.106	0.177	0.183	0.138	0.114	0.137	0.104	0.045	0.011	0.006	0.000
3	4	-0.009	-0.062	0.445	-0.021	0.278	-0.022	0.257	0.033	-0.007	0.018	0.000
4	5	0.042	-0.042	1.852	0.052	1.491	0.052	1.388	0.015	0.016	0.001	-0.001
5	9	0.111	2.960	1.166	0.189	0.837	0.188	0.773	0.076	0.005	0.016	0.009
6	9	0.052	1.160	1.106	0.067	0.763	0.067	0.705	0.039	-0.006	0.014	0.001

Table 5. Estimates of GCA and SCA variances and the proportion (%) of additive and dominance variance.

Variance	Root yield	Percent sugar	Purity	Impure sugar yield	Recoverable sugar	Recoverable sugar yield	White sugar	White sugar yield	Nitrogen	Sodium	Potassiu	Mollasses sugar
GCA	0	0.070	0.754	0.280	0.158	0.140	0.158	0.125	0.020	0.008	0.074	0.017
SCA	9	0.047	-0.041	0.811	0.052	0.622	0.052	0.580	0.010	-0.001	0.001	-0.003
Additive (%)	54.02	74.84	100	40.85	85.83	31.12	85.87	30.21	79.59	100	99.32	100
Dominant (%)	45.98	26.16	0.00	59.15	14.17	68.88	14.13	69.79	20.41	0.00	0.68	0.00

Table 6. Estimates of heterosis (%) relative to high parental values for characters studied.

Crosses	Root yield (t ha^{-1})	Percent sugar	Purity (%)	Impure sugar yield (t ha^{-1})	Recoverable sugar (%)	Recoverable sugar yield (t ha^{-1})	White sugar (%)	White sugar yield (t ha^{-1})	Nitrogen (meq 100^{-1} g)	Sodium (meq 100^{-1} g)	Potassium (meq 100^{-1} g)	Molasses sugar (%)
1x2	- 2.66	-3.96*	-2.21*	9.94	-6.07**	6.60	-6.27**	6.96	-13.98	- 2.29	-14.70**	-13.82**
1x3	13.67	-0.47	-1.14	12.90	-1.57	11.72	-1.60	11.67	24.78	- 4.21	7.21	6.85
1x4	14.33	-0.40	0.74	13.86	0.34	14.68	0.35	14.70	- 7.10	-19.51	- 4.17	7.30
1x5	2.89	-0.49	-0.46	2.53	-0.98	2.15	-0.98	2.15	-23.12	- 2.06	0.55	3.11
1x6	4.36	-4.04**	-1.25	1.44	-5.25*	1.29	-5.42*	1.19	-15.14	- 2.25	- 0.81	- 0.96
2x3	- 9.30	-1.14	-2.40*	- 2.78	-3.52	-0.02	-3.70	0.34	- 7.52	-14.54	- 6.52	- 8.82
2x4	- 0.44	-4.89**	-2.74**	2.48	-7.22**	5.18	-7.67**	5.42	-25.03	4.58	-12.77**	-11.64*
2x5	-12.11	1.53	-0.64	- 4.14	0.86	0.59	0.87	1.10	-37.84**	-28.60**	-12.59**	-18.82**
2x6	1.99	-4.43**	-3.51**	7.95	-8.01**	11.22	-8.28**	11.58	- 1.18	-16.99	-10.26**	-12.00*
3x4	21.27*	0.48	-0.58	22.54*	0.03	21.84*	0.04	21.85*	14.16	-11.54	5.16	3.90
3x5	3.76	1.64	0.51	6.89	2.23	7.55	2.29	7.68	-28.72	-23.99	0.46	- 3.42
3x6	3.68	-0.03	-0.58	3.75	-0.61	3.50	-0.63	3.49	- 2.99	-17.77	-0.99	- 4.60
4x5	-17.72	2.88*	0.85	-14.33	3.75	-13.62	3.87	-13.48	-12.08	-19.77	-3.46	- 4.31
4x6	- 1.06	-1.67	-0.81	- 2.29	-2.50	- 2.87	-2.57	- 2.93	-34.76	-14.54	-1.27	- 2.75
5x6	23.90*	-2.59	-1.92*	22.34*	-4.48	21.70*	-4.63*	21.72*	6.63	6.94	4.61	5.75

* and ** Significant at 0.05 and 0.01 probability levels, respectively.

Table 7. Estimates of the components of variation and their proportional values for 12 characters on the basis of Hayman' s test.

Components of variation	Root yield	Percent sugar	Purity	Impure sugar yield	Recoverable sugar	Recoverable sugar yield	White sugar	White sugar yield	Nitrogen	Sodium	Potassium	s sugar
D	21.18	0.39*	3.40*	-0.09	0.82*	-0.46	0.82*	-0.45	0.07*	0.02*	0.34*	0.07*
F	-63.02	0.17	0.45	-2.47	0.26	-2.03	0.26	-10.89	-0.04	-0.02	0.06*	0.00
H_1	41.76	0.21*	-0.01	1.32	0.24	0.77	0.24	0.71	0.12*	0.00	0.02	-0.01
H_2	61.82*	0.16	0.18	2.13	0.20	1.45	0.20	1.35	0.13*	0.01	0.03	0.00
h^2	75.46*	0.00	-0.36	3.79*	-0.04	3.08*	-0.04	2.90*	-0.03	-0.01	-0.01	-0.01
E	45.53*	0.09*	0.64*	1.58*	0.15*	1.28*	0.15*	1.20*	0.06*	0.02*	0.05*	0.02*
h^2_n	0.34	0.51	0.67	0.27	0.60	0.21	0.60	0.20	0.34	0.39	0.70	0.64
h^2_b	0.51	0.65	0.69	0.45	0.70	0.39	0.70	0.38	0.58	0.42	0.73	0.64
$(H_1/D)^{1/2}$	1.40	0.73	...	...	0.54	...	0.54	...	1.31	0.00	0.24	...
$H_2/4H_1$	0.37	0.19	...	0.40	0.21	0.47	0.21	0.48	0.27	...	0.37	0.00
$[(4DH_1)^{1/2}+F]$	...	0.99	...	...	1.59	...	...	1.59	0.20	...	1.01	...
$[(4DH_1)^{1/2}-F]$												

* Significant at 0.05 probability level.

D : Additive component of variance.

H_1, H_2 : Dominant component of variance, with no dominance $H_1 = 0$, with complete dominance $H_1 = D$, with overdominance $H_1 > D$.

F : Mean covariance of additive and dominance effects over all the arrays.

E : Expected environmental component of variance.

h^2 : Algebraic sum of the dominance effect over all loci in heterozygous phase in all crosses.

h^2_n : Narrow sense heritability.

h^2_b : Broad sense heritability.

in the parents (H_2 /$4H_1$), and the proportion of dominant to recessive genes in the parents ($([4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$) (Table 7). These values suggest that gene loci controlling root yield, and percent nitrogen have an overall measure of overdominance. The $H_2/4H_1$ ratio indicates some degree of asymmetry between positive and negative genes for recoverable sugar yield, percent sugar, percent potassium and nitrogen.

The proportion of dominant and recessive genes in the parents shows that for sugar, recoverable sugar, white sugar, and potassium percents, dominant genes are in excess. Hayman (2) lists a number of assumptions for reliable conclusions from such analysis. In the absence of information about all these assumptions, it is still possible to draw the (Vr, Wr) graph and estimate different genetic parameters including D,F, H_1, H_2 , and h^2. These estimates, however, need to be interpreted with caution.

The values of Wr and Vr for each array were calculated and regressed on each other (Fig. 1). The linear regression of Wr on Vr was tested for significance (β=0) and for deviation from unity (β=1) by the usual t-tests (as shown in Fig. 1). The position of Vr and Wr on the line reveals the relative proportions of dominant and recessive genes in the r parent. Completely recessive parents correspond to points at the upper ends and completely dominant parents to points at the lower end of limiting parabola. With complete dominance the line passes through the origin while with partial dominance the line lies above and with overdominance below the origin.

As a result parents 3 and 6 with respect to root yield, impure sugar yield, recoverable sugar yield and white sugar yield possess the most recessive genes, whereas, parents 1, and 5 with respect to root yield and parents 1 and 2 with respect to impure sugar yield, recoverable sugar yield and white sugar yield possess the most dominant genes. Parent 5 with respect to percent sugar, purity, white sugar percent, recoverable sugar percent, nitrogen, sodium, and potassium content, and mollasses sugar had more dominant genes, while parents 2 and 4 had more recessive genes in sugar percent, purity, percent recoverable and white sugar, and sodium content. Parent 6 with respect to nitrogen and potassium content, and parents 2 and 3 with respect to mollasses sugar possess more recessive genes.

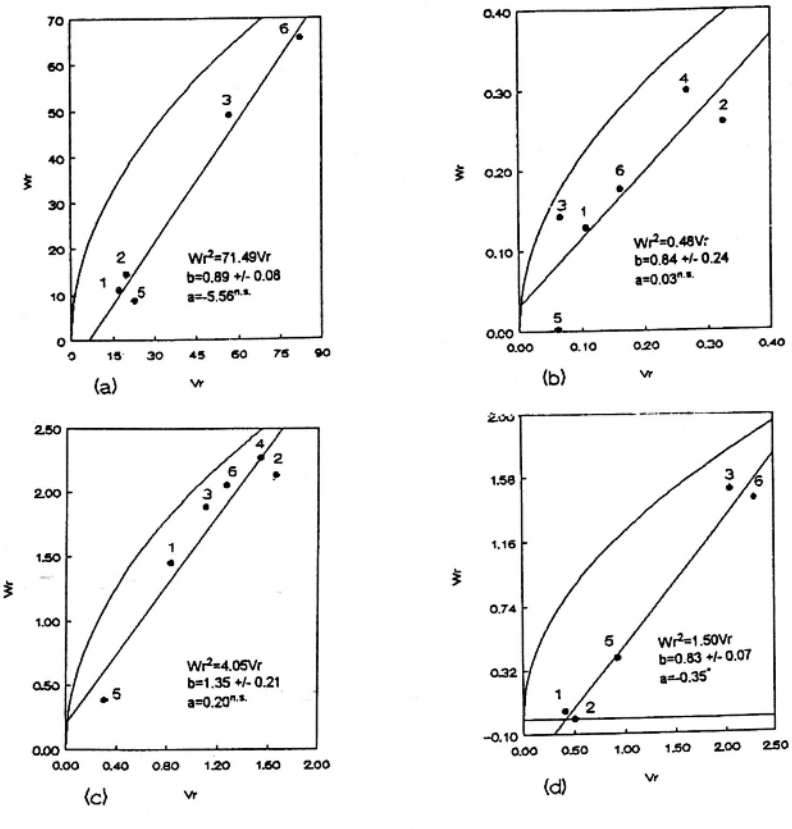

Fig. 1. Continued.

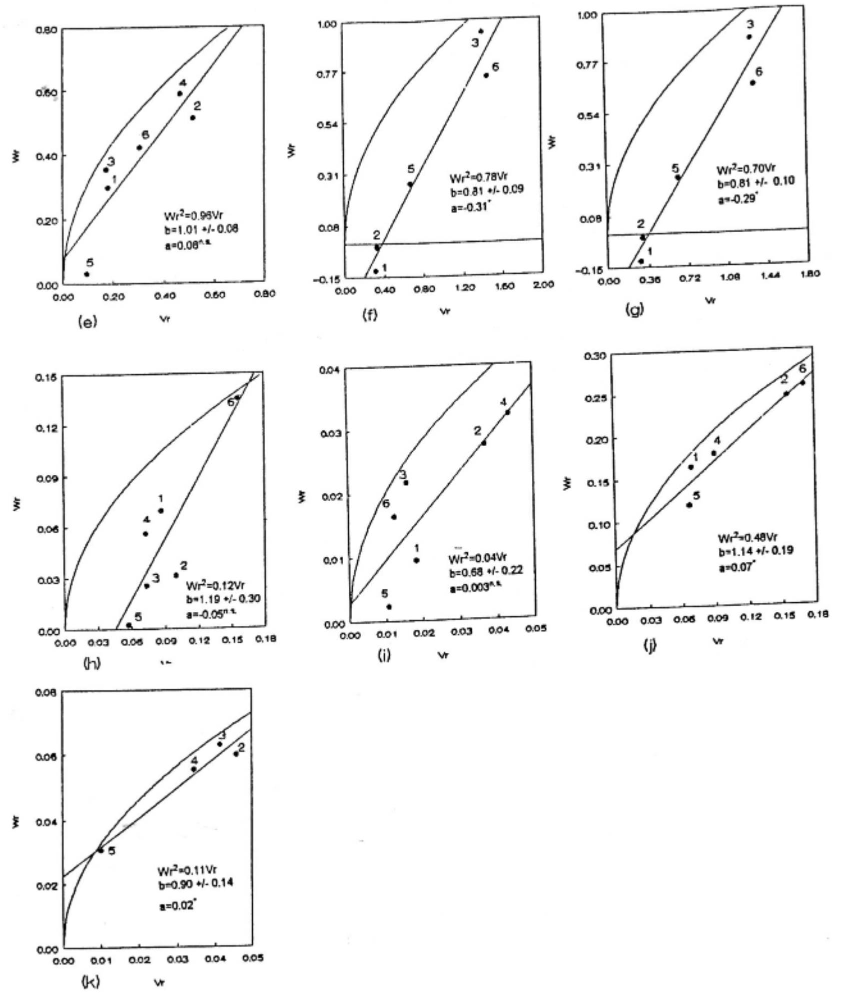

Fig. 1. The regression of Wr on Vr and the limiting parabola for (a) root yield, (b) sugar percent, (c) purity percent, (d) impure sugar yield, (e) recoverable sugar percent and white sugar percent, (f) recoverable sugar yield, (g) white sugar yield, (h) percent nitrogen, (i) percent sodium, (j) percent potassium, (k) mollasses sugar percent.

* Significant at 0.05.

n.s. Non-significant.

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