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GENETICS OF OIL AND PROTEIN PERCENTAGE IN UPLAND COTTON

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A 6 x 6 diallel cross experiment was laid out to study heterosis and gene action for oil and protein percentage in six cultivars of *G. hirsutum* L. Heterosis was pronounced in all the crosses. Oil percentage was found to be controlled by additive gene action with partial dominance, while protein percentage was conditioned by overdominance.

Key words: Heterosis, Heterobeltiosis, Variance, Co-variance.

Introduction

Besides fibre, cotton (*G. hirsutum* L.) provides food in the form of edible oil and feed in the form of cotton seed cake. Therefore, the genetic improvement in edible oil contents and protein percentage alongwith different parameters of cotton plant will go a long way to make it more remunerative and competitive. There is little information available for understanding the genetic mechanism of the control of oil and protein percentage in the cotton crop. So the present work was undertaken to obtain some basic information on the manifestation of heterosis and to investigate the genetic systems controlling these chemical characters of cotton plant. Varying degrees of heterosis and additive and non-additive type of gene action have been reported earlier [2,3,9,12,14,16] for oil and protein percentage.

Materials and Methods

Six upland cotton cultivars *viz.* HL 1, SRT 1, E 288, Acala 1517V, Coker 201 and CIM 70 (local) were crossed during Nov. 1985 under greenhouse conditions in a complete diallel fashion. The temperature in the greenhouse was maintained between 60-100°F. The seeds from six parental lines and thirty F_1 hybrids including reciprocals were sown in the field during June 1986 in quadruplicated randomized complete block design. Each genotype comprised a single line of 10 plants spaced 30 cm apart, keeping 75 cm inter-row spacing. Standard production technology was followed from sowing till harvesting of the crop for all the plots. After the crop was harvested and ginned, the seed samples taken from the experimental trial were analysed for percentage of oil and protein by standard Soxhlet and kjeldahls methods [11] respectively. The data collected were subjected to the Fisher's analysis of variance as described by Steel and Torrie [13].

The values of direct and reciprocal crosses were averaged to satisfy the diallel assumptions [1]. Analysis of gene action was done using the technique developed by Hayman [1] and Jinks [6–8]. Standard error for the regression line was estimated according to Snedecor [4].

Heterosis and heterobeltiosis was calculated as percent increase or decrease exhibited by F_1 hybrids over mid and better parental values, respectively. Significance of heterosis and heterobeltiosis was tested according to Wynne *et al.* [5] and Khan [10], respectively.

Results and Discussion

A perusal of analysis of variance given in Table 1 revealed highly significant genotypic variation for both oil and protein percentage. Sum of squares for genotypes were further partitioned into parents, crosses and parents versus crosses to test their individual differences.

Highly significant variation was observed among parents and among crosses while variation for parents versus crosses was non- significant for the studied triats. The rejection of null hypothesis or significance of Fisher's ratio in case of analysis variance (F-test), indicates the difference only between two means of the experimental material. But if the entries are more in number, like 36 in the present study, then only this information is unsatisfactory. Further partition of the genotypic variation into various components helps to elaborate the results.

Percentage of oil. Nine out of fifteen hybrids exceeded their mid parental values and seven exceeded their better parental values for oil percentage (Table 4). The magnitude of positive heterosis and heterobeltiosis ranged from 0.85%

TABLE 1. ANALYSIS OF VARIANCE FOR OIL AND PROTEIN PERCENTAGE.

SOV	DF	Mean square	
		Oil (%)	Protein (%)
Replications	3	15.36**	1.09^{NS}
Genotypes	35	22.56**	15.08**
Parents	5	8.39**	7.92**
Grosses	29	13.42**	6.17**
Parents vs crosses	1	0.75^{NS}	9.99^{NS}
Error	105	0.32	2.05

** = Significant at 1% level of probability; NS = Non- significant.

(SRT 1 x Acala 1517V) to 14.58% (CIM70 x SRT1) and 0.052% (SRT 1 x E 288) to 7.44% (HL 1 x CIM 70), respectively. Heterosis was highly significant in eight crosses, and in the HL1 x E 288 cross it was significant only (Table 4). However, nine crosses showed highly significant and another cross (HL 1 x Acala 1517V) showed only significant heterobeltiosis [2,3,9,12,14,16].

Analysis of variance of Wr + Vr and Wr - Vr is given in Table 2, while Vr/Wr and Wr+Vr/p graphs are provided in Figs 1 and 2. Figure 1 showed that the regression line passed through Wr-axis above the origin. It indicated additive type of gene action with a little dominance as the line made a tangent with the parabola. On inspection of Fig. 2, and regression coefficient ($b = 0.56 \pm 0.12$) it became clear that gene interaction was not involved in the determination of this character. The mean squares between arrays for Wr-Vr is non-significant when tested against that within arrays and indeed is smaller than it. There is thus no evidence of any non-allelic interaction in the phenotypic manifestation of this character. From the position of array points on the regression line (Fig. 1), it seems that E 288 has the maximum dominant genes while SRT 1 has the recessive ones being nearest and farthest from the origin, respectively. As the correlation between array (Wr+Vr) is positive (+0.2478), therefore, E 288 containing maximum dominent genes has the highest covariance value. This in turn shows that dominant genes are not responsible for high oil percentage. Such observations for percentage of oil have also been reported by Boghra *et al.* [2], Voitenok *et al.* [3], While Khan *et al.* [9], and Singh *et al.* [12], Rakhmanov *et al.* [14] and . Sokolova *et al.* [16], have reported non-additive gene effects controlling this trait. Different genotypes and even the same genotype may show different type of gene action under different environments [15].

TABLE 2. ANALYSIS OF VARIANCE OF Wr + Vr FOR OIL PERCENTAGE.

Items	DF	SS	MS	Vr	r	b
Between arrays Wr + Vr	5	-60.7116	12.1432	NS	0.2478	0.2449 ± 0.42
Within arrays	6	76.8571	12.8095		0.3535	0.4892 ± 0.64
Between arrays Wr-Vr	5	0.4485	0.897	NS	-0.4244	-0.1335 ± 0.16
Within arrays	6	1.1885	0.1981		-0.6369	-0.2805 ± 0.16

TABLE 3. ANALYSIS OF VARIANCE OF Wr + Vr FOR PROTEIN PERCENTAGE.

Items	DF	SS	MS	Vr	r	b
Between arrays Wr + Vr	5	-7.76	-1.552	NS	-0.7102	-0.9939 ± 0.49
Within arrays	6	39.55	6.5916		-0.2424	-1.159 ± 2.32
Between arrays Wr-Vr	5	-4.69	-0.938	NS	-0.2925	-0.0405 ± 0.07
Within arrays	6	5.007	0.8345		-0.4215	-0.1997 ± 0.21

TABLE 4. ESTIMATION OF HETEROSIS AND HETEROBELTIOSIS FOR PERCENTAGE OF OIL.

Crosses	Mother parent	Pollen parent	Mid parent	F_1 hybrid	Ht. %	Hbt %
HL 1 x CIM 70	22.98	22.74	22.86	24.69	8.01**	7.44**
HL 1 x SRT 1.	22.98	19.36	21.17	22.68	7.14**	-1.31
HL 1 x E 288	22.98	18.65	20.82	20.13	-3.31*	-12.40**
HL 1 x Acala 1517v	22.98	20.77	21.88	23.82	8.87**	3.66*
HL 1 x Coker 201	22.98	22.18	22.58	23.17	3.94**	2.13
CIM 70 x SRT 1	22.74	19.36	21.05	24.12	14.58**	6.09**
CIM 70 x E 288	22.74	18.65	20.69	20.08	-2.95	-11.69**
CIM 70 x Acala 1517V	22.74	20.77	21.76	22.99	5.65**	1.10
CIM 70 x Coker 201	22.74	22.18	22.46	23.94	6.59**	5.28**
SRT 1 x E 288	19.36	18.65	19.01	19.37	1.98	0.052
SRT 1 x Acala 1517	19.36	20.77	20.07	20.24	0.85	-2.55
SRT 1 x Coker 201	19.36	22.18	20.77	20.43	-1.64	-7.89**
E 288 x Acala 1517v	18.65	20.77	19.71	19.22	-2.49	-7.46**
E 288 x Coker 201	18.65	22.18	20.42	20.40	-0.098	-8.03**
Acala x Coker 201 1517v	20.77	22.18	21.48	20.12	-6.33**	-9.29**

Ht % Heterosis.,Hbt% Heterobeltiosis. *, ** Significant at 5% and 1% level of probability.

Percentage of protein. Data pertaining to heterotic effects and analysis of variance of Wr + Vr for percentage of protein are presented in Table 3 and 5, respectively. The graphic representation for Vr/Wr and Wr + Vr/P is made in Figs. 3 and 4.

It may be observed from the data given in Table 5 that all but one (CIM 70 x Coker 201) crosses exhibited positive heterosis. This ranged from 3.24% for HL1 x SRI 1 to 20.97% for HL 1 x Acala 1517 v. Heterobeltiosis was observed in 10

TABLE 5. ESTIMATION OF HETEROSIS AND HETEROBELTIOSIS FOR PERCENTAGE OF PROTEIN.

Crosses	Mother parent	Pollen parent	Mid parent	F_1 hybrid	Ht. %	Hbt %
HL 1 x CIM 70	18.89	22.82	20.86	21.55	3.31	-5.57
HL 1 x SRT 1.	18.89	20.59	19.79	20.40	3.24	-0.92
HL 1 x E 288	18.89	19.79	19.34	20.98	8.48	6.01
HL 1 x Acala 1517v	18.89	17.45	19.17	21.98	20.79**	16.36*
HL 1 x Coker 201	18.89	19.42	19.16	21.56	12.53**	11.02*
CIM 70 x SRT 1	22.82	20.59	20.71	22.37	8.02	-1.97
CIM 70 x E 288	22.82	19.79	21.31	22.31	4.69	-2.23
CIM 70 x Acala 1517V	22.82	17.45	20.15	23.83	18.38**	4.43
CIM 70 x Coker 201	22.82	19.42	21.12	20.79	-1.56	-8.89*
SRT 1 x E 288	20.5	19.79	20.19	23.9	18.38**	16.08**
SRT 1 x Acala 1517	20.59	17.45	19.02	21.91	15.19**	6.41
SRT 1 x Coker 201	20.59	19.42	20.00	23.26	16.24**	12.79**
E 288 x Acala 1517v	19.79	17.45	18.62	21.76	16.86**	9.95
E 288 x Coker 201	19.79	19.42	19.61	21.62	10.25*	9.25
Acala x Coker 201 1517v	17.45	19.42	18.45	20.99	13.89**	8.08

Ht % Heterosis.,Hbt% Heterobeltiosis. *, ** Significant at 5% and 1% level of probability.

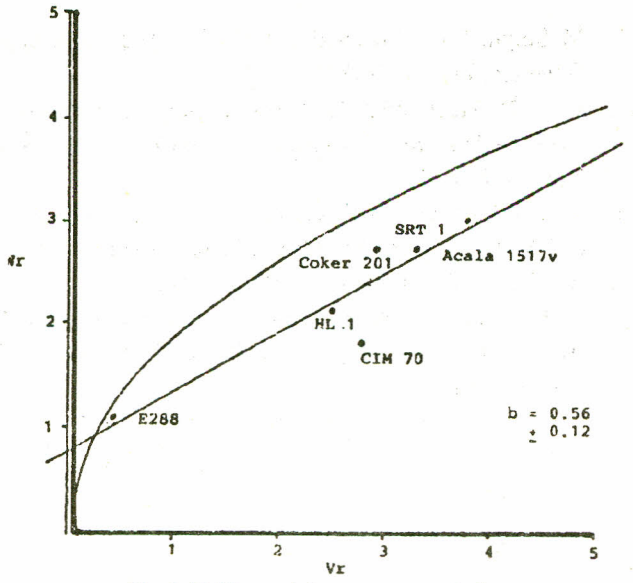

Fig. 1. Vr/Wr graph for percentage of oil.

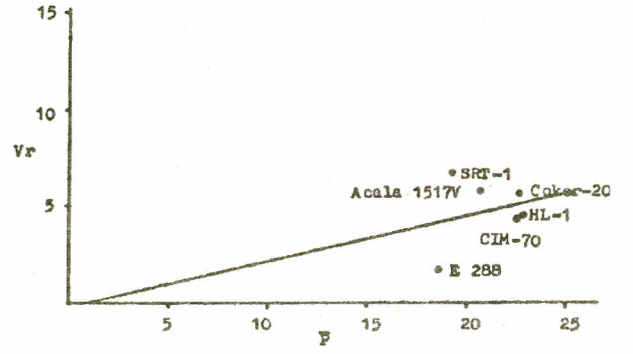

Fig. 2. Wr + Vr/P- graph for percentage of oil.

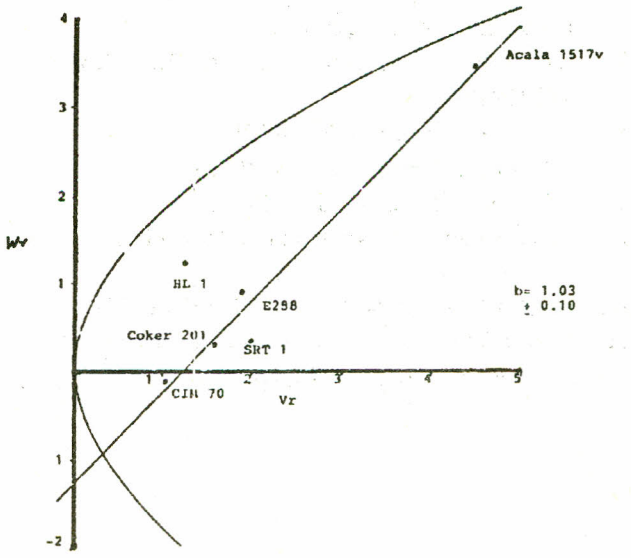

Fig. 3. Vr/Wr graph for percentage of protein.

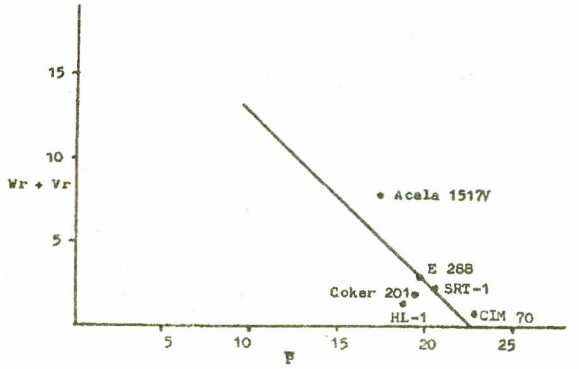

Fig. 4. Wr+Vr/P- graph for percentage of protein.

out of 15 crosses. Maximum positive heterobeltiosis occurred with HL 1 x Acala 1517 V (16.36) and the minimum (4.43%) with the cross CIM 70 x Acala 1517V.

A thorough probe into Table 5 revealed highly significant heterosis in eight crosses, while E 288 x Coker 201 showed only a significant level of heterosis. Three crosses, HL1 x Acala 1517V, SRT 1 x E288 and SRT 1 x Coker 201 manifested highly significant heterobeltiosis while HL 1 x Coker 201 and CIM 70 x Coker 201 exhibited only significant heterobeltiosis. Khan *et al.* [9] and Singh *et al.* [12] have also reported heterosis for this character.

The gene action for this trait appeared to be overdominance because the regression line cut the Wr-axis below the origin (Fig. 3). Regression line (b = 1.03 + 0.10) indicated unit slope. This had been confirmed by the MS between arrays of Wr-Vr (Table 3), which was non-significant when tested against that within arrays. It signified the absence of non-allelic interaction as far as percentage of protein is concerned. From the position of the array points along the regression line it is evident that CIM 70 with its position nearest to the origin possesses the maximum dominant genes, whereas Acala 1517V being away from the origin has recessive genes for this character (Figs. 3 and 4). As between arrays the value of "r" - 0.7102 (Table 3) is negative, so the variety CIM 70 having dominant genes was responsible for a higher percentage of protein. These results are in accordince with those of Khan *et al.* (9) and Singh *et al.* (12).

It is concluded that the cross HL 1 x Acala 1517v, with its significant heterotic effects for both chemical traits could be utilized for simultaneous improvement of protein and oil percentage.

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