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GENE ACTION FOR SOME QUANTITATIVE CHARACTERS IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.)

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The study, includes a six-parent complete diallel cross of varieties/lines viz. CRIS-15, TH-3/83, TH-28/83, CRIS-9, NIAB-78 and Rehmani of *Gossypium hirsutum* L. It was initiated to determine the genetics of lint weight, seed index, staple length and seed cotton yield per plant. The WrVr graph showed that, lint weight and seed cotton yield were conditioned by over-dominance, while seed index and staple length by partial-dominance type of gene action. CRIS-9 and NIAB-78 x CRIS-9 appeared to be best general and specific combiners, respectively. Hence, they are recommended for future breeding programme.

Key words: Gene action, Genetics of cotton, Breeding potential.

Introduction

Cotton is one of the most important cash crop of Pakistan. It has played a pivotal role in the improvement of the economy of the country which cannot be ignored. Although, great advancements have been made in regard to improve the quality and yield of this crop, still there is a great potential in bringing the new varieties with better quality, high yield and better adaptability. Keeping these facts in mind, great responsibility falls upon plant breeders to work out plans for increasing the yield of cotton.

The success of plant breeding programme aiming at evolution of high yielding, better quality, responsive to high doses of fertilizer, disease and insect pest resistant varieties of cotton crop depends upon the selection of suitable parents to be utilized in any hybridization programme. Hence, the present study was under taken to determine the genetic system, affecting the economic traits of cotton plant, in order to facilitate to frame breeding strategy.

Materials and Methods

To assess the genetic architecture in upland cotton present studies were undertaken at the Agriculture Research Institute, Tando Jam during 1999-2000. Four cultures and two varieties of *Gossypium hirsutum* L., CRIS-15, TH-3/83, TH-28/83, CRIS-9, NIAB-78, and Rehmani were used.

Crosses were attempted in complete diallel fashion during 1998-99. The F_1 seeds along with their parents were sown in the field during kharif season of 1999-2000 in RCBD with 5 replications. Thirty and seventy-five centimeters distances were kept within and between the rows respectively. Recommended agronomic practices were performed at proper time. The data, regarding different characters were arranged and subjected to statistical analysis. Fisher's standard techniques of analysis of variance were applied to determine the differences among the treatments (Fisher 1958). Only the characters for which the genotypes showed diversity were assessed for genetics analysis. It includes diallel technique developed by Hayman (1954) and Jinks (1954 - 1956).

All the crosses were arranged into arrays in the form of diallel table and two statistics, the variance of arrays (Vr) and covariance of arrays and parental values (Wr) were calculated from the diallel table.

Information on gene interaction was obtained by plotting the covariance (Wr) of each array against its variance (Vr). The slope and position of regression line were fitted to array points within a limiting parabola.

Results and Discussion

The data presented in Table 1 revealed that the mean squares of all the traits, studied were highly significant, which indicated different heritage of genotypes.

Table 2 revealed that the CRIS-9 with the highest array mean (40.97 g) appeared to have better general combining ability for lint weight followed by CRIS-15 with array mean of (36.90 g)

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and within array, the cross NIAB-78 x CRIS-9 gave the highest value (51.2 g), indicating better specific combining ability.

Figure 1 shows that the regression line intersected the Wr-axis below the origin, showing over dominance type of gene action. From the position of the array points along the regression line revealed that NIAB-78 being nearest to the origin possessed maximum dominant genes for lint weight, while TH-28/83 had maximum recessive genes due to its farthest position. These results got support from the findings of White (1966), Verhalen *et al* (1971), Baker and Verhalen (1973). The results were in disagreement with those of Gururaja *et al* (1977), who reported that the character was controlled by partial dominance.

A perusal of Table 3 showed that the TH-28/83 with the highest array mean (8.26 g) appeared to have better general combining ability for seed index followed by CRIS-9 with array mean of (8.13 g) and within array, the cross Rehmani x TH-3/83 gave the highest value (138 g), indicating better specific combining ability.

Figure 2 indicates that the regression line intercepted the Wr-axis above the origin thereby, indicating partial type of gene action. The position of array points along the regression line, made it obvious that variety CRIS-9 had the maximum dominant genes due to its position closer to the origin, whereas,

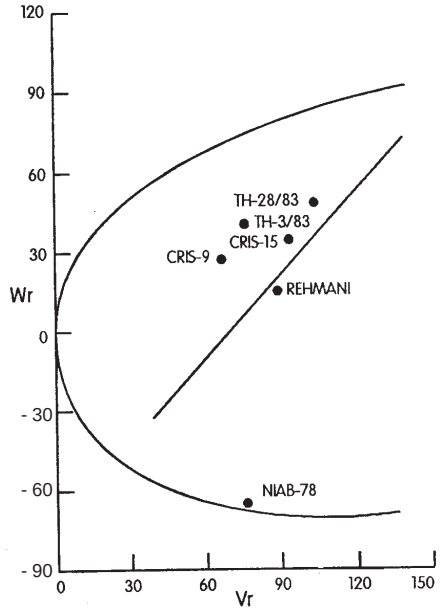

Fig 1. Wr/Vr graph for lint weight.

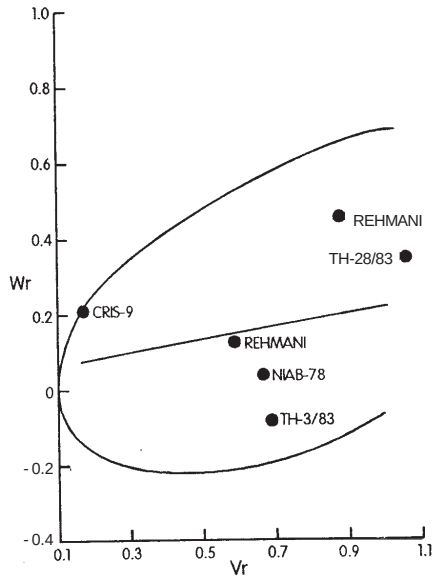

Fig 2. Wr/Vr graph for seed index.

Table 1

Analysis of variance (mean squares) for genotypes with respect to seed cotton yield and other traits in 6 x 6 diallel crosses of cotton

Source of variation	D.F	Lint weight	Seed index	Staple length	Seed cotton yield
Replication	4	509.53	1.44	0.655	3413.22
Treatments	35	404.58**	3.53**	3.54**	3030.89**
Error	140	192.7	0.93	1.46	1394.53

**Highly significant.

Table 2

6 x 6 Diallel. Average Lint weight (in grams) per plant variance (Vr) and covariance (Wr) for F_1 generation

Parents	CRIS-15	TH-3/83	TH-28/83	CRIS-9	NIAB-78	Rehmani	Wr	Vr
CRIS-15	42.22	33.32	35.44	50.00	32.86	44.54	35.71	84.23
TH-3/83	44.40	43.60	37.34	34.20	25.76	26.90	41.37	76.15
TH-28/83	26.50	25.10	17.58	31.30	49.80	26.30	49.81	114.48
CRIS-9	24.10	28.40	31.30	40.82	34.84	21.14	27.33	66.56
NIAB-78	47.60	42.20	49.96	51.20	32.20	40.70	- 64.61	76.00
Rehmani	36.60	46.10	28.52	38.28	43.80	38.44	15.14	88.96
Total	221.42	218.72	200.14	245.80	219.26	198.02	-	-
Array mean	36.90	36.45	33.36	40.97	36.54	33.00	-	-

TH-28/83 had the recessive genes due to its distant position. Gururaja *et al* (1977) and Sanyasi *et al* (1982) reported similar results. However, the study of Khan *et al* (1987) and Said Rehman and Khan (1988) was contradictory to these findings who reported complete or over dominance type of gene action for this character which might be due to differences in the genetic background of the parental varieties.

The highest array mean 28.55 mm was observed for Rehmani which proved better general combiner for staple length followed by CRIS-15, with array mean of 28.53 mm and within array, the cross CRIS-15 x Rehmani gave the highest value 29.6 mm, indicating better specific combining ability (Table 4).

The regression line intercepted the Wr-axis above the origin thereby, indicating partial type of gene action. The position of array points along the regression line made it obvious, that variety CRIS-9 had the maximum dominant genes due to its position closer to the origin whereas, NIAB-78 had the recessive genes due to its distant position. Findings of Verhalen and Murray (1969), are in accordance with these results. However, the studies of earliers (Verhalen and Murray 1967; Verhalen *et al* 1971; Chaudhry 1974; Gururaja *et al* 1977; Khan 1978; Khan *et al* 1980; Mirza and Khan 1984; Khan *et al* 1987; Khan *et al* 1990 and Shah 2000) are contradictory to these findings they reported complete or over dominance type of gene action for this character which might be due to differences in the genetic background of the parental varieties.

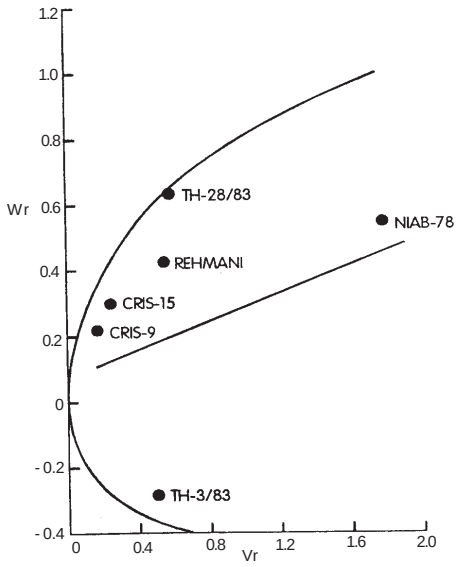

Fig 3. Wr/Vr graph for Staple length.

Table 3

6 x 6 Diallel. Average seed index (gm), variance (Vr) and covariance (Wr) for F_1 generation

Parents	CRIS-15	TH-3/83	TH-28/83	CRIS-9	NIAB-78	Rehmani	Wr	Vr
CRIS-15	8.02	8.56	9.56	7.46	7.80	7.92	0.4696	0.89
TH-3/83	8.16	7.74	8.80	8.00	8.06	8.72	-0.0897	0.70
TH-28/83	9.60	7.30	9.54	8.56	7.78	7.82	0.3559	1.68
CRIS-9	6.96	6.58	6.60	8.48	7.44	8.00	0.2172	0.18
NIAB-78	7.30	7.20	6.84	7.88	7.48	6.48	0.0487	0.67
Rehmani	8.58	8.74	8.20	8.38	9.64	8.40	0.1334	0.59
Total	48.62	46.12	49.54	48.76	48.20	47.34	-	-
Array mean	8.10	7.69	8.26	8.13	8.03	7.59	-	-

Table 4

6 x 6 Diallel. Average staple length (mm), variance (Vr) and covariance (Wr) for F_1 generation

Parents	CRIS-15	TH-3/83	TH-28/83	CRIS-9	NIAB-78	Rehmani	Wr	Vr
CRIS-15	28.80	28.10	28.60	27.90	28.50	29.60	0.30	0.25
TH-3/83	29.20	28.20	27.80	27.60	26.00	28.50	-0.79	0.52
TH-28/83	28.20	27.60	27.50	27.40	27.30	27.30	0.65	0.56
CRIS-9	28.00	27.70	27.50	27.80	26.60	28.40	0.22	0.17
NIAB-78	28.10	28.40	27.30	28.00	27.30	28.80	0.54	1.79
Rehmani	28.90	29.60	28.30	28.60	29.70	28.70	0.53	0.55
Total	171.20	169.60	166.00	167.30	165.40	171.30	-	-
Array Mean	28.53	28.27	27.67	27.88	27.57	28.55	-	-

Table 5

6 x 6 Diallel. Average yield of seed cotton per plant (in gm), variance (Vr) and covariance (Wr) for F_1 generation

Parents	CRIS-15	TH-3/83	TH-28/83	CRIS-9	NIAB-78	Rehmani	Wr	Vr
CRIS-15	115.08	94.00	90.44	136.70	88.30	112.56	405.56	560.86
TH-3/83	126.50	126.50	100.30	88.00	72.50	72.50	454.31	893.39
TH-28/83	74.20	61.40	48.70	82.30	125.20	69.70	415.30	695.87
CRIS-9	65.00	77.20	97.20	104.20	88.80	56.70	168.31	795.88
NIAB-78	102.92	116.40	128.70	148.80	89.80	11.00	-448.37	388.65
Rehmani	102.60	138.50	79.00	87.40	115.80	97.40	96.61	552.87
Total	586.30	614.00	544.34	647.30	580.40	519.86	-	-
Array mean	97.72	102.33	90.72	107.88	96.73	86.64	-	-

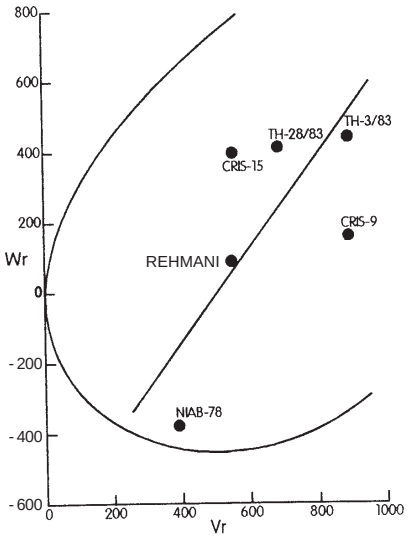

Fig 4. Wr/Vr graph for seed cotton yield.

A perusal of Table 5 showed that the CRIS-9 with the highest array mean (107.88) had better general combining ability for yield of seed cotton followed by TH-3/83, with array mean of (102.33 g) and within array, the cross NIAB-78 x CRIS-9 gave the highest value (148.8 g), indicating better specific combining ability. This showed that among the entire cross combinations studied these parents NIAB-78 x CRIS-9 had best specific combining ability. Hence, this combination might exhibit superior hybrids in later segregating generations for this character.

It is observed from the Fig. 4 that the regression line intercepted the Wr-axis below the origin, signifying the over dominance type of gene action. The position of array points along the regression line revealed that NIAB-78 had the maximum dominant genes being nearest to the origin, while TH-3/83 possessed the maximum recessive genes due to its farthest position. Similar results have been reported by the following (Marani 1961; Verhalen *et al* 1971; Mirza and Khan 1974; Patil 1977; Salem *et al* 1984; Sadykhova 1986; Jagtab and Kohle 1987; Said Rehman and Khan 1988; Khan *et al* 1990). However, White and Kohel (1964) and Ramey and Miller (1966) have reported partial dominance. The difference might be attributed to different genetic stock and ecology.

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