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IMPROVEMENT IN F_3 POPULATION OF UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) THROUGH HERITABILITY ANALYSIS

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ABSTRACT

Mean performance and heritability in morphological yield traits of eight cultivars (SLH-284, CIM-446, CIM-473, CIM-496, CIM-499, CIM-506, CIM-554 and CIM-707) of upland cotton (*G. hirsutum*) and their 56 F_3 diallel populations were studied at University of Agriculture, Peshawar, Pakistan during 2011. The experiment was laid out in RCBD with triplicate replications. The analysis of variance showed highly significant variability among 8 × 8 F_3 populations including their parents for all the studied characters except monopodia per plant which was found to have significant differences. Among parental genotypes, CIM-707 showed maximum performance for sympodia per plant, locules per boll, seeds per locule and seeds per boll. Among F_3 populations, cross CIM-473 × CIM- 446 revealed superior performance in case of seeds per locule, seeds per boll, sympodia per plant and locules per boll which were found comparatively good for seed cotton yield per plant. Highest heritability was noticed for sympodia per plant (0.79) and locules per boll (0.77). Our findings further confirmed that F_3 populations from SLH-284 × CIM-707, CIM-473 × CIM-496, CIM-554 × CIM-707 and CIM-506 × CIM-499 were promising and performed better for various morpho-yield traits. Majority of the studied traits were highly heritable indicating that selection may lead to improvement in mean value of corresponding traits and thus may be used as guidance in future cotton breeding programs.

KEYWORDS: *Gossypium hirsutum*; Cotton; genotypes; F_3 populations; heritability; agronomic characters; morphological yield traits; Pakistan.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the most important cash crop of Pakistan and considered as a backbone of the economy. It is known as “queen of the fiber plants” and “white gold” due to its lint and for so many other by-products (17). The contribution of cotton in overall foreign exchange earning is about

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60 percent. Apart from its share in foreign exchange, it also provides raw materials for textile and oil industries and ginning factories. Besides, it has a great share in animal feed in the form of cotton seed cake and edible oil which is 60 to 70 percent (8). Pakistan's economy being as an agricultural country is mainly dependent on cotton production. Cotton shares about 2 percent to GDP and 8.2 percent of value addition in agriculture and has leading role of around 70 percent share in edible oil industry of Pakistan (8). Pakistan is at fourth in the globe, but there are still some hurdles which are hindering the cotton yield per unit area. During 2010-11 the total area under cotton cultivation was 2.69 million hectares and its production was about 11.56 million bales with an average yield of 731 kg per hectare (2). In different crop breeding programs, heritability plays an important role in measuring the extent of phenotypic differences due to its genetic makeup (14). The selection process of a crop germplasm is directly proportional to the extent of genetic heritability of the crop (6). The present study was conducted to evaluate the genetic variability of F_3 diallel populations and their parents and to estimate heritability (broad sense) for various traits under the climatic conditions of Pakistan.

MATERIALS AND METHODS

The study was carried out at University of Agriculture, Peshawar, Pakistan during 2010-11. Peshawar lies between 34°, 02′ north latitude and 71°, 37′ east longitude. The breeding material comprised eight upland cotton genotypes i.e. SLH-284, CIM-446 CIM-473, CIM-496, CIM-499, CIM-506, CIM-544 and CIM-707 and their 56 F_3 populations. The parental genotypes and their F_3 seeds of corresponding 56 populations were sown during 2010 in RCBD with three replications. Each treatment comprised four rows having 5 meter length alongwith 30 and 75 cm plants and rows spacing, respectively. The crop was grown under uniform environmental conditions and cultural practices were carried out as per recommendations for cotton to minimize variations. Picking was done during the month of November, 2011.

The number of monopodial and sympodial branches and locules of selected bolls were counted. The seeds in each locule were counted in 10 bolls from each plant to get average seeds per locule. From each genotype, 10 bolls were separated and after counting the number of seeds in each boll, the average number of seeds per boll were calculated. The yield of seed cotton from each guarded plant was weighed on electronic balance.

All the data were subjected to analysis of variance (ANOVA) according to Steel and Torrie (16) to test the null hypothesis of no differences between various F_3 populations and their parental means. Least significant difference (LSD) test was used for means comparison and separation. The genetic and environmental variances and heritability were calculated according to Singh and Chaudhary (13).

$$\textit{Genetic variance (Vg)} = \frac{\textit{Genotypes mean square} - \textit{Error mean square}}{\textit{Number of replications}}$$

$$\textit{Environmental variance (Ve)} = \textit{Error mean square}$$

$$\textit{Phenotypic variance (Vp)} = Vg + (Ve/r)$$

Broad sense heritability (h^2bs) on entry mean basis was calculated as:

$$h^2\ (bs) = \frac{Ve}{Vp}$$

Where;

Vp = Phenotypic variance for a trait.
h^2 (bs) = Broad sense heritability for a trait.

RESULTS AND DISCUSSION

Results (Table 1) revealed that all genotypes vary significantly for economically important traits and maximum genotypic variation was observed in all parents and F_3 populations. Monopodia per plant varied from 0.1 to 1.7 among the parents and 0.2 to 2.2 among F_3 populations (Table 2).

Table 1. Mean squares for different morphological yield traits in upland cotton.

Parameters	**Replications**	**Genotypes**	**Error**
Monopodia per plant	3.232	0.338*	0.226
Sympodia per plant	24.694	9.240**	1.907
Locules per boll	0.102	0.077**	0.035
Seeds per locule	2.448	0.452**	0.212
Seeds per boll	91.275	7.500**	4.889
Seed cotton yield per plant	2288.019	447.649**	210.926

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$, respectively

The minimum monopodia per plant (0.2) were found in many cross combinations. Maximum monopodia per plant (2.2) were observed in cross

C_{39} which were at par with cross C_{40} and C_{45} (1.9) and parental cultivar P_6 (1.7) while all other cultivars showed average values for monopodia per plant. The genetic variance and environmental variance for monopodia per plant were 0.037 and 0.226, respectively, while heritability (bs) for monopodia per plant was 0.33 (Table 3). The improved genetic variation with inconsistent mean performance was reported for monopodia per plant among different cotton cultivars (1, 5). Monopodia per plant and seed cotton yield were studied by many researchers which showed negative correlation, therefore molecular breeders have keen interest to achieve low number of monopodia per plant.

Sympodia per plant varied from 10.4 to 14.8 among the parents and 8.4 to 17.4 among F_3 populations (Table 2). The maximum sympodia per plant were found in cross (CIM-473 × CIM-496) (17.40) and at par with four other F_3 populations varied from 16.60 to 17.40. Minimum sympodia per plant were found in cross CIM-506 × CIM-473 (8.4) and at par with nine other F_3 populations ranged from 8.4 to 10.00. All other cultivars showed medium values for sympodia per plant. Genetic and environmental variances for sympodia per plant were 2.44 and 1.907 respectively, while heritability (bs) for sympodia per plant was 0.79 (Table 3). Results revealed greater genetic variability for sympodia per plant among different cotton cultivars. Our findings are inline with those of Mustafa *et al.* (12) and Ahmad *et al*. (1) who observed high level of heritability for sympodia per plant in all tested upland cotton genotypes. Sympodia per plant have significant positive relationship to seed cotton yield and most of the previous studies revealed positive influence of fruiting branches on seed cotton yield (1, 12).

Locules per boll varied from 4.28 to 4.76 among the parents and 3.84 to 4.92 among F_3 populations (Table 2). Maximum locules per boll were noticed in cross CIM-554 × CIM-707 (4.92) closely followed by five other F_3 populations with range of 4.72 to 4.8 and one parental cultivar CIM-707 (4.76). Minimum locules per boll were found in cross CIM-473×CIM-499 (3.84) and at par with cross F_3 population C_{12} (4.00). Other cultivars showed medium values for locules per boll. Both the genetic and environmental variances for locules per boll were 0.042 and 0.035, respectively, while heritability (bs) estimates for locules per boll were 0.77 (Table 3). Khan (8) and Ahmad *et al*. (1) studied genetic variability and correlation in upland cotton and obtained high heritability for locules per boll.

Parental cultivars for seeds per locule ranged from 6.10 to 6.92 and 6.12 to 6.98 among F_3 populations (Table 2). Highest number of seeds per locule were observed in cross CIM-473 × CIM-446 (6.98), which were found at par

Table 2. Mean performance for different morphological yield traits of upland cotton.

Parents and their F_3 populations	Monopodia per plant	Sympodia per plant	Locules per boll	Seeds per locule	Seeds per boll	Seed cotton yield per plant (g)
P1 = SLH-284	0.6	13.0	4.36	6.80	30.04	94.73
P2 = CIM-446	0.8	12.4	4.52	6.84	31.04	62.14
P3 = CIM-473	0.4	10.4	4.48	6.58	29.60	60.61
P4 = CIM-496	0.6	14.6	4.40	6.38	32.16	76.69
P5 = CIM-506	0.1	13.8	4.48	6.40	28.76	73.94
P6 = CIM-506	1.7	14.0	4.28	6.66	28.72	50.86
P7 = CIM-554	0.1	11.0	4.40	6.10	27.04	100.20
P8 = CIM-707	1.0	14.8	4.76	6.92	33.16	83.80
C1= SLH-284 × CIM-446	0.6	13.4	4.40	6.80	30.04	94.73
C2= SLH-284 × CIM-473	1.0	13.6	4.36	6.84	31.04	62.14
C3= SLH-284 × CIM-496	0.8	12.0	4.24	6.58	29.60	60.61
C4= SLH-284 × CIM-499	0.3	12.8	4.48	6.38	32.16	76.69
C5= SLH-284 × CIM-506	0.4	10.4	4.44	6.40	28.76	73.94
C6= SLH-284 × CIM-554	0.6	12.0	4.40	6.66	28.72	50.86
C7= SLH-284 × CIM-707	0.4	09.0	4.52	6.12	28.02	100.40
C8= CIM-446 × SLH-284	0.6	14.0	4.40	6.98	34.46	83.80
C9= CIM-446 × CIM-473	0.4	10.6	4.64	6.80	30.04	94.73
C10= CIM-446 × CIM-496	0.6	08.6	4.32	6.84	31.04	62.14
C11= CIM-446 × CIM-499	0.4	08.4	4.40	6.58	29.60	60.61
C12= CIM-446 × CIM-506	0.2	08.8	4.00	6.38	32.16	76.69
C13= CIM-446 × CIM-554	1.4	10.6	4.52	6.40	28.76	73.94
C14= CIM-446 × CIM-707	1.2	10.2	4.36	6.66	28.72	50.86
C15= CIM-473 × SLH-284	0.4	12.4	4.32	6.12	28.02	100.40
C16= CIM-473 × CIM-446	0.3	16.6	4.64	6.98	34.46	83.80
C17= CIM-473 × CIM-496	0.2	17.4	4.52	6.80	30.04	94.73
C18= CIM-473 × CIM-499	1.2	09.4	3.84	6.84	31.04	62.14
C19= CIM-473 × CIM-506	0.4	16.4	4.36	6.58	29.60	60.61
C20= CIM-473 × CIM-554	0.3	13.4	4.52	6.38	32.16	76.69
C21= CIM-473 × CIM-707	0.3	17.4	4.52	6.40	28.76	73.94
C22= CIM-496 × SLH-284	1.0	14.8	4.44	6.66	28.72	50.86
C23= CIM-496 × CIM-446	1.2	13.0	4.48	6.12	28.02	100.40
C24= CIM-496 × CIM-473	0.3	12.2	4.16	6.98	34.46	83.80
C25= CIM-496 × CIM-499	0.3	13.8	4.72	6.80	30.04	94.73
C26= CIM-496 × CIM-506	0.2	10.2	4.16	6.84	31.04	62.14
C27= CIM-496 × CIM-554	0.4	11.0	4.64	6.58	29.60	60.61
C28= CIM-496 × CIM-707	0.2	12.6	4.28	6.38	32.16	76.69
C29= CIM-499 × SLH-284	0.4	15.4	4.68	6.40	28.76	73.94
C30= CIM-499 × CIM-446	0.2	10.8	4.80	6.66	28.72	50.86
C31= CIM-499 × CIM-473	0.2	10.8	4.76	6.12	28.02	100.40
C32= CIM-499 × CIM-496	0.2	12.0	4.48	6.98	34.46	83.80
C33= CIM-499 × CIM-506	0.2	10.6	4.40	6.80	30.04	94.73
C34= CIM-499 × CIM-554	0.3	14.8	4.45	6.84	31.04	62.14

Table Contd…

C35= CIM-499 × CIM-707	**0.3**	**14.4**	**4.36**	**6.58**	**29.60**	**60.61**
C36= CIM-506 × SLH-284	**0.8**	**17.0**	**4.60**	**6.38**	**32.16**	**76.69**
C37= CIM-506 × CIM-446	**0.6**	**14.8**	**4.76**	**6.40**	**28.76**	**73.94**
C38= CIM-506 × CIM-473	**1.2**	**08.4**	**4.68**	**6.66**	**28.72**	**50.86**
C39= CIM-506 × CIM-496	**2.2**	**11.6**	**4.64**	**6.12**	**28.02**	**100.40**
C40= CIM-506 × CIM-499	**1.9**	**14.4**	**4.40**	**6.98**	**34.46**	**83.80**
C41= CIM-506 × CIM-554	**0.4**	**12.8**	**4.52**	**6.80**	**30.04**	**94.73**
C42= CIM-506 × CIM-707	**0.8**	**10.0**	**4.68**	**6.84**	**31.04**	**62.14**
C43= CIM-554 × SLH-284	**0.3**	**11.0**	**4.48**	**6.58**	**29.60**	**60.61**
C44= CIM-554 × CIM-446	**0.4**	**10.0**	**4.68**	**6.38**	**32.16**	**76.69**
C45= CIM-554 × CIM-473	**1.9**	**11.8**	**4.64**	**6.40**	**28.76**	**73.94**
C46= CIM-554 × CIM-496	**1.2**	**09.4**	**4.24**	**6.66**	**28.72**	**50.86**
C47= CIM-554 × CIM-499	**0.8**	**09.8**	**4.60**	**6.12**	**28.02**	**100.40**
C48= CIM-554 × CIM-506	**0.2**	**13.8**	**4.56**	**6.98**	**34.46**	**83.80**
C49= CIM-554 × CIM-707	**0.3**	**11.8**	**4.92**	**6.80**	**30.04**	**94.73**
C50= CIM-707 × SLH-284	**0.2**	**10.2**	**4.72**	**6.84**	**31.04**	**62.14**
C51= CIM-707 × CIM-446	**0.3**	**10.4**	**4.68**	**6.58**	**29.60**	**60.61**
C52= CIM-707 × CIM-473	**1.0**	**10.8**	**4.40**	**6.38**	**32.16**	**76.69**
C53= CIM-707 × CIM-496	**0.4**	**11.6**	**4.52**	**6.40**	**28.76**	**73.94**
C54= CIM-707 × CIM-499	**1.0**	**10.8**	**4.68**	**6.66**	**28.72**	**50.86**
C55= CIM-707 × CIM-506	**1.2**	**12.8**	**4.68**	**6.12**	**28.02**	**100.40**
C56= CIM-707 × CIM-554	**1.2**	**14.0**	**4.56**	**6.98**	**34.46**	**83.80**
LSD0.05	**0.5950**	**1.728**	**0.2342**	**0.5763**	**2.767**	**18.18**

***P = Parent, C = Cross**

with other two combinations of F_3 populations which ranged from 6.80 to 6.84. Minimum seeds per locule were noticed in cross combination CIM-554 × CIM-499 (6.12) and were also found statistically at par with nine F_3 populations ranged from 6.38 to 6.58. Other genotypes showed medium values for seeds per locule. Genetic and environmental variances for seeds per locule were 0.08 and 0.212, respectively, while heritability (bs) for seeds per locule was 0.53 (Table 3). Ahmad *et al*. (1); Khan *et al*. (10, 11) also observed significant variations for seed traits.

Seeds per boll varied from 27.04 to 33.16 among the parents, while 28.02 to 34.46 in F_3 populations (Table 2). Maximum number of seeds per boll were recorded in F_3 cross CIM-473 × CIM-446 (34.46), which were found at par with seven F_3 populations which ranged from 29.60 to 32.16 and two parents CIM-496 (32.16) and CIM-707 (33.16). Minimum seeds per boll were noticed in cross combination CIM-473 × CIM-284 (28.02) which were also found at par with F_3 crosses (28.72). All the remaining genotypes showed medium values for seeds per boll. Both genotypic and environmental variances for seeds per boll were 0.87 and 4.889, respectively, while heritability (bs) for seeds per boll was 0.35 (Table 3).

Seed cotton yield per plant varied from 60.61 to 100.2 g among the parents, while 50.86 to 100.4 g in F_3 populations (Table 2). Maximum seed cotton yield was authenticated by parent CIM-554 (100.2 g) as compared to nine other F_3 populations which ranged from 82.50 to 94.73g and one parent CIM-707 (83.8). Lowest seed cotton yield was observed in cross CIM-446 × CIM-707 (50.86 g) that is similar to other fifteen F_3 populations were ranged from 50.86 to 62.14 g. All other tested genotypes showed moderate values for seed cotton yield per plant. The heritability (bs) of seed cotton yield per plant was 0.53 while both genetic and environmental variances for seed cotton yield per plant were 78.90 and 210.93, respectively (Table 3). Significant variations were observed among upland cotton genotypes for various morphological yield traits (3, 6).Similarly, Soomro *et al*. (15) reported that different cotton genotypes showed maximum level of variability for seed cotton yield.

Table 3. Heritability (bs) estimates for different characters of upland cotton.

Parameters	**Vg**	**Ve**	**Vp**	h^2
Monopodia per plant	0.037	0.226	0.11	0.33
Sympodia per plant	2.44	1.907	3.07	0.79
Locules per boll	0.042	0.035	0.054	0.77
Seeds per locule	0.08	0.212	0.15	0.53
Seeds per boll	0.870	4.889	2.50	0.35
Seed cotton yield per plant	78.90	210.926	149.20	0.53

Vg = genetic variance, Ve = environmental variance, Vp = phenotypic variance, h^2 = heritability (bs)

CONCLUSION

Genotypes showed significant variations for various traits. F_3 populations CIM 473 × CIM 446, SLH-284 × CIM-707, CIM-473 × CIM-496, CIM-554 × CIM-707 and CIM-506 × CIM-554 were promising and showed best performance for morphological yield traits. It was also concluded that number of sympodial branches, locules per boll, seeds per locule and seed cotton yield per plant were highly heritable, indicating a significant importance in further improvement through future breeding programs.

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Ali Muhammad,	**:**	**Conducted the experiment**
Shahid Ali Khan	**:**	**Contributed in data analysis and writeup**
Muhammad Sajid	**:**	**Helped in conducting experiment**
Haris Khurshid	**:**	**Helped in review of literature**
Javed Iqbal	**:**	**Carried out review of research**
Noor Saleem	**:**	**Helped in conducting experiment**