



Full Length Article

Identification of Superior Parents and Hybrids for Yield and its Components in Cotton (*Gossypium hirsutum*)

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ABSTRACT

The purpose of this study was to identify superior parental combinations based upon general and specific combining abilities in order to exploit their potential for increasing seed cotton yield. Five cotton lines (NIAB 111, NIAB 999, CIM 448, MNH 93 & FH 901) and three testers (LRA Blight, CP 15/21 & 289 F-1) were crossed according to line × tester mating system. Data on 23 genotypes were recorded on monopodial and sympodial branches, number of bolls, boll weight, seed index and seed cotton yield. The variation due to general combining ability of the parents and specific combining ability of the hybrids for plant yield and its components were estimated by line × tester analysis. Result showed that MNH 93 was the best combiner for most of the traits studied. Variance components analysis indicated that except boll weight, all other characters were predominantly influenced by dominance properties of genes. Three varietal combinations NIAB 999 × CP 15/21, CIM 448 × LRA Blight and MNH 93 × 289 F-1 expressed high specific combining abilities for all characters. Results suggest that the parents may be used in the hybridization program aiming to develop hybrid cotton.

Key Words: *Gossypium hirsutum*; Combining ability; Line × tester analysis

INTRODUCTION

Extensive efforts were made by the breeders to exploit its potential for increasing cotton production due to the immense role of cotton crop in the economy of Pakistan. As a result, a galaxy of high yielding varieties with better quality characteristics were evolved for general cultivation in varying ecological zones of the cotton belt of the country. Due to wider adaptability of the recently bred varieties total production of the country increased considerably and during the crop year 2005 Pakistan had achieved the record production of 14.618 million bales (Anonymous, 2005). In order to meet the increasing demand for raw fibre in the local textile industry and for earning more foreign exchange through exportable surplus, the efforts must be made to keep pace, with the increasing demand of fibre and oil. Cotton improvement program may be more effective if information on the genetic mechanism controlling economic characters are available to the breeders. In addition, in order to develop promising plant material through hybridization, availability of superior parents is essential.

The estimates of general combining ability are important to determine the value of genotypes in hybrid combinations. Further differences in general combining abilities of varieties/lines were attributed to additive, additive × additive and higher-order additive interactions, whereas differences in specific combining ability were attributed to non-additive genetic variance (Falconer & Mackey, 1996).

One of the biometric methods used to collect such information is line × tester analysis. This mating design provides information about the general and specific combining abilities of the parents and also genetic basis of variation in different plant characters. Therefore, in order to gather such information about the germplasm available the present study was undertaken on eight varieties of cotton (*Gossypium hirsutum* L.).

MATERIALS AND METHODS

The material for the present studies comprised five female parents (lines) namely, NIAB 111, NIAB 999, CIM 448, MNH 93 and FH 901 and three male parents (testers), LRA Blight, CP 15/21 and 289 F-1. These eight parents were grown in 30 × 30 cm earthen pots in a green house. The temperature in glass house was maintained between 21°C (night) and 37°C (day) using steam as well as electric heaters. The seed parents (lines) were hand emasculated in evening and pollinated with testers the following morning to produce enough F1 hybrid seed. Extreme precautionary measures were taken to avoid pollen contamination of the genetic material during selfing and crossing operations.

Seeds of 15 F1 hybrids along with their selfed parents were field planted during the crop season 2005 with 75 cm row-to-row and 30 cm plant-to-plant distance and there were ten plants in each row. Experimental design was randomized complete block design with three replications. At maturity

data on middle eight plants per replication were recorded for yield of seed cotton (g), number of bolls, boll weight (g), monopodial branches, sympodial branches and seed index. Genetic analysis of the data was done following line \times tester technique (Kempthorne, 1957) in order to assess general and specific combining abilities of the parents for the characters under study. The Microsoft Excel computer program was used to statistically analyze the data. The general (GCA) and specific (SCA) combining abilities were estimated using the following formulae:

$$\begin{aligned} \text{GCA lines} &= (X_{i.}/tr) - (X_{...}/ltr) \\ \text{GCA testers} &= (X_{.j}/lr) - (X_{...}/ltr) \\ \text{SCA} &= (X_{ij}/r) - (X_{i.}/tr) - (X_{.j}/lr) + (X_{...}/ltr) \end{aligned}$$

Where $X_{i.}$ is the sum of columns; $X_{.j}$ is the sum of rows; X_{ij} is the total value of hybrids over replications; $X_{...}$ is the grand total and l, t and r are the number of lines, testers and replications.

RESULTS

The mean squares obtained from analysis of variance of number of monopodial and sympodial branches, number of bolls, boll weight, seed index and seed cotton yield showed highly significant ($P \sim 0.01$) genotypic differences for all the characters (Table I). Further partitioning of genotypes showed that females (lines) and males (testers) did not differ significantly from each other for the traits studied; however, lines \times testers interaction appeared to differ significantly for all the characters, suggesting the presence of significant amount of variation in these characters except boll weight (Table I). Mean squares revealed that eight parents and 15 crosses differed significantly ($P \sim 0.01$) for number of monopodial and sympodial branches, number of bolls, seed index and seed cotton yield, whilst mean squares were reduced to non-significant ($P > 0.05$) for boll weight (Table I). Mean squares resulting from interaction among parent vs crosses were also highly significant for all the characters, showing substantial variation among them.

Assessment of combining ability studies of the parents. Estimates of general and specific combining abilities of the eight parents were made and given in Table II and III, respectively.

General combining abilities. In order to reduce number of monopodial branches negative general combining ability of parents is desirable. Analysis of the data showed that NIAB 999, FH 901 and CIM 448 among males and CP 15/2 1 among females were revealed to be the potential parents, scoring values as -0.18, -0.32, -0.13 and -0.376, respectively (Table II). For sympodial branches, the parents NIAB 111, MNH 93 and CIM 448 among males and CP 15/2 1 among the females exhibited positive whilst NIAB 999, FH 901, LRA Blight and 289F-1 displayed negative GCA for the character. Two parents i.e., NIAB 999 and LRA Blight were the best general combiners for number of bolls, whilst NIAB 111 was the poorest in this respect. However, NIAB 111

(0.045), MNH 93 (0.476) and CIM 448 (0.169) had best general combining abilities and among the females LRA Blight and CP 15/21 were best general combiners for boll weight. For improved seed index, positive general combining ability is important. Here NIAB 111, CIM 448 and CP 15/2 1 were the potential parents for this purpose, whereas highest negative general combining ability was recorded in FH 901. For seed cotton yield, NIAB 999 with value of 11.357 exhibited the best general combining ability followed by LRA Blight (8.390 numerical value), whilst FH 901 with -7.645 displayed poor GCA for seed cotton yield.

Specific combining abilities. Estimates of specific combining abilities of various crosses combinations are presented in Table III and it was shown that about 47% of the crosses showed negative SCA for number of monopodial branches (Table III). The crosses CIM 448 \times LRA Blight and NIAB 999 \times 289 F-1 with negative values i.e., -0.544 and -0.414, respectively were revealed to be good combinations. For number of sympodial branched, the cross NIAB 111 \times CP 15/21 scored higher estimate for specific combining ability. It was revealed that for more number of sympodial branches the crosses MNH 93 \times 289 F-1, CIM 448 \times LRA Blight and NIAB 999 \times LRA Blight may be used in further breeding programme, because they had values 0.912, 0.571, 0.559, respectively.

For number of bolls four crosses i.e., NIAB 999 \times LRA Blight, NIAB 999 \times CP 15/21, MNH 93 \times 289-F1 and CIM 448 \times CP-15/21 scored higher positive values for SCA and thus were best specific combinations for the character. For boll weight, crosses MNH 93 \times LRA Blight (0.460) and CIM 448 \times CP 15/21 (0.432) possessed better SCA and GCA than the other crosses. MNH 93 \times 289 F-1 (0.177), FH 901 \times LRA Blight (0.138) and NIAB 111 \times CP 15/21 (0.136) possessed best SCA for seed index. For seed cotton yield positive SCA was 53%. NIAB 999 \times CP 15/2 1, MNH 93 \times 289 F-1 with higher values 11.33 and 10.49 were better than crosses FH 901 \times LRA Blight, CIM 448 \times 289 F- 1, which scored only 3.80 and 3.71 numerical values, respectively.

Genetic variances. The estimates of variance due to general combining ability (δ^2 GCA), specific combining ability (δ^2 SCA), additive variance (δ^2 A), dominance variance (δ^2 D), ratios of δ^2 GCA/ δ^2 SCA, and degree of dominance ($[\delta^2 H/\delta^2 D]^{1/2}$) for six characters are given Table IV. Dominance effects were more important for monopodial and sympodial branches, number of bolls, seed index and seed cotton yield. Ratio of δ^2 GCA/ δ^2 SCA and degree of dominance with more than unity indicated that the genes had over-dominance for these traits. The predominance of additive gene action for boll weight indicated by δ^2 GCA/ δ^2 SCA and degree of dominance, which was lesser than one.

DISCUSSION

Analysis of the data following combining ability approach revealed that variation in number of monopodial and sympodial branches, number of bolls, boll weight, seed

Table I. Mean squares obtained from partitioned analysis of variance of various plants in cotton

Source of variation	d. f	Monopodial branches	Sympodial branches	Number of bolls	Boll weight	Seed index	Seed cotton
Replications	2	0.0216 ^{NS}	0.0097 ^{NS}	0.0290**	1.1483 ^{NS}	0.0147 ^{NS}	2.4844 ^{NS}
Genotypes	22	1.1530**	4.2458**	62.993**	1.3629**	0.1471**	633.80**
Parents	7	2.7694**	2.8718**	92.435**	1.9521**	0.2630**	1218.9**
Crosses	14	0.9223**	4.6067**	49.291**	0.6461 ^{NS}	0.0827**	376.82**
Parents vs crosses	1	0.9887**	8.8102**	48.707**	7.2736**	0.2361**	135.05**
Lines (females)	4	1.0219 ^{NS}	5.0739 ^{NS}	30.044 ^{NS}	1.1486 ^{NS}	0.0680 ^{NS}	472.76 ^{NS}
Testers (males)	2	1.6897 ^{NS}	10.8446 ^{NS}	93.639 ^{NS}	0.713 ^{NS}	0.1000 ^{NS}	856.95 ^{NS}
Lines × testers	8	0.6806**	2.8137**	47.828**	0.3781 ^{NS}	0.0858**	208.82**
Error	44	0.0083	0.0050	0.0049	0.3706	0.0046	1.3154

*, ** reveal differences highly significant at 5% and 1% probability levels, whilst “NS” shows non-significant differences.

Table II. Estimates of General combining ability of parents of various plant traits in cotton

Parents	Monopodial branches	Sympodial branches	No. of bolls	Boll weight	Seed index	Seed cotton
				Lines		
NIAB 111	0.54	0.75	-2.525	0.045	0.072	-4.659
NIAB999	-0.18	-0.57	2.480	-0.258	-0.029	11.357
MNH 93	0.089	0.55	0.122	0.476	-0.038	0.978
FH 901	-0.32	-0.99	0.596	-0.432	-0.109	-7.645
CIM 448	-0.13	0.257	-0.674	0.169	0.104	-0.031
SE	0.0305	0.0237	0.0233	0.0203	0.0228	0.382
				Testers		
LRA Blight	0.107	-0.68	2.609	0.101	-0.053	8.390
CP 15/21	-0.376	0.952	-2.370	0.149	0.094	-6.389
289 F-1	0.270	-0.270	-0.238	-0.250	-0.040	-1.956
SE	0.0236	0.0183	0.0180	0.1572	0.0176	0.2961

Table III. Estimate of SCA of crosses for various plant traits in cotton

Crosses	Monopodial branches	Sympodial branches	No. of bolls	Boll weight	Seed index	Seed cotton
NIAB 111 × LRA Blight	0.087	-0.220	0.274	0.114	0.097	3.194
NIAB 111 × CP 15/21	-0.237	1.422	-0.979	-0.177	0.136	0.539
NIAB 111 × 289 F-1	0.150	-1.201	0.705	0.0623	-0.233	-3.734
NIAB 999 × LRA Blight	-0.151	0.559	2.635	-0.028	0.041	-1.439
NIAB 999 × CP 15/21	0.565	-0.508	4.982	0.176	-0.143	11.33
NIAB 999 × 289 F-1	-0.414	-0.0516	-7.167	-0.147	0.102	-9.893
MNH 93 × LRA Blight	0.682	-1.107	0.394	0.460	-0.127	0.286
MNH 93 × CP 15/21	-0.402	0.195	-3.00	-0.478	-0.051	-10.78
MNH 93 × 289 F-1	-0.280	0.912	2.608	0.018	0.177	10.49
FH 901 × LRA Blight	-0.073	0.196	-0.397	-0.326	0.138	3.800
FH 901 × CP 15/21	-0.057	-0.212	-1.403	0.046	-0.046	-3.22
FH 901 × 289 F-1	0.131	0.0151	1.800	0.279	-0.091	-0.577
CIM 448 × LRA Blight	-0.544	0.571	-2.906	-0.22	-0.149	-5.840
CIM 448 × CP 15/21	0.132	-0.897	0.403	0.432	0.104	2.132
CIM 448 × 289 F-1	0.413	0.326	2.503	-0.212	0.045	3.709
SE	0.0528	0.0411	0.0404	0.3515	0.0395	0.6622

Table IV. Estimates of variance due to GCA (δ^2_{GCA}), SCA (δ^2_{SCA}), additive (δ^2_A), dominance (δ^2_D), ratio of ($\delta^2_{GCA} / \delta^2_{SCA}$) and degree of dominance ($[\delta^2_H / \delta^2_D]^{1/2}$) for various plant traits of cotton

Genetic components	Monopodial branches	Sympodial branches	Number of bolls	Boll weight	Seed index	Seed cotton
Cov H.S (lines)	0.038	0.251	-1.976	0.085	-0.002	29.362
Cov H.S (tester)	0.067	0.535	3.054	0.022	0.0009	43.208
Cov H.S (Aveg)	0.008	0.063	0.051	0.009	-0.0001	5.9393
Cov F.S	2.67	16.17	128.95	1.114	0.1677	1346.18
$\delta^2_{GCA} = [(1+F)/4] \delta^2_A$	0.008	0.063	0.051	0.009	-0.0001	5.9393
(a) with F = 0, δ^2_A	0.034	0.254	0.207	0.038	-0.0004	23.757
$\delta^2_{SCA} = [(1+F)/2] \delta^2_D$	0.224	0.936	15.94	0.002	0.0270	69.171
(b) with F = 0, δ^2_D	0.896	3.745	63.76	0.009	0.1082	276.68
$\delta^2_{GCA} / \delta^2_{SCA}$	0.0357	0.0673	0.0032	4.5	-0.004	0.086
$[\delta^2_H / \delta^2_D]^{1/2}$	5.29	3.84	17.67	0.471	0.00	3.41

index and seed cotton yield, were genetically manifested. Moreover, total genetic variability observed in each of the characters was partitioned into various causal components i.e., GCA and SCA (Kempthorne, 1957), which revealed that both additive and dominance properties of the genes were responsible in the inheritance of these characters. However, the relative contribution of the i.e., variance components provided some better understanding on the genetic control of the characters. Non additive genetic effects were important to control yield of seed cotton, number of sympodial branches, number of monopodial branches, number of bolls per plant and seed index as already had been reported (Hassan *et al.*, 1999; Rajan *et al.*, 1999; Pavasia *et al.*, 1999; Subhan *et al.*, 2000; Neelima *et al.*, 2004), whilst additive genetic components appeared to be predominant for boll weight and was supported by the results of Carvalho *et al.* (1995), Ahmad *et al.* (1997), Khan *et al.* (1999). It was suggested that the characters controlled by non-additive properties of genes may have low heritability (Falconer & Mackey, 1996), suggesting that the segregating population are not amenable to selection pressure and breeder will have to be careful and imaginative, while selecting the desired plants from segregating population. By contrast, variation in boll weight might have high heritability, as this character was controlled by the genes acting additively (Table IV). Therefore, plants having good boll weight easily be identified from the subsequent generations.

Parents having good GCA for a particular character are expected to yield good hybrids (Ayub *et al.*, 1991; Khan *et al.*, 1991; Irfanullah *et al.*, 1994) and this behavior of parents was found to be valid in the inheritance of monopodial branches, sympodial branches, number of bolls, boll weight and seed cotton yield per plant. By contrast, varieties FH 901 and LRA Blight showed poor general combining ability for number of sympodial branches but they produced best cross combination, FH 901 × LRA Blight (Table III). For number of bolls varietal combinations CIM 448 × 289 F-1 and NIAB 111 × 289 F-1 were the promising one and these crosses had originated from hybrids of parents having poor general combining ability. For seed index FH 901, LRA Blight and MNH 93 were revealed to have negative numerical value but they yielded best cross combination. For seed cotton yield, varietal combinations CIM 448 × 289 F-1 and CIM 448 × CP 15/21 were the promising one (Table III) and these crosses had originated from hybrids of parents having low general combining ability. Thus it is not always necessary that good hybrids are the result of combination of parents having high GCA, sometimes parents with poor GCA may nick well as had been observed here. Thus the selection of the parents merely on the basis of best general combining ability is not necessarily an important criterion as had been advocated by Baloch and Chang (1970) and Azhar and Rana (1993) in their studies.

Information on GCA and SCA may provide guideline to breeders for the exploitation of the potential existed in the eight parental lines examined here. These results suggest that F2 population may be used advantageously for bringing improvement in boll weight as the breeding population is amenable to selection, as variation is additively manifested. However, characters controlled by non-additive properties of genes may have low heritability and thus the breeder will have to be careful and imaginative, while selecting the desired plants from segregating population. It is concluded from the nature of genetic material, that the plant material developed here could be used by the cotton breeders for the development of hybrid cotton.

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