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COMBINING ABILITY ESTIMATES FOR SEED COTTON YIELD AND ITS RELATED TRAITS USING LINE × TESTER MATING DESIGN IN UPLAND COTTON

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ABSTRACT

Combining ability study of cotton varieties were conducted using a line × tester design with six hybrids, 2 testers (male) and 3 lines (females) for the characters seed cotton yield and related traits. The experiment was conducted in randomized complete block design with three replicates during 2018-19. Data were recorded for seed cotton yield and its related traits. Mean squares from analysis of variance showed large dissimilarity between lines, testers and their crosses for different yield related characters representing the occurrence of heritable variability. The tester variety NIA-Noori and line CRIS-342 had exhibited comparatively higher array mean and proved to be the better general combiners. SCA dominant gene effects in CRIS-342 × NIA-Noori showed the potential for increasing the number of bolls plant^{-1}, boll weight and seed cotton yield plant^{-1}. In cotton breeding programme these selected parent can be used to develop high yielding cotton varieties and hybrids with better seed cotton yield and its related characters.

Keywords: *Gossypium hirsutum* L., combing ability, gene action, hybrids, lines × testers

INTRODUCTION

Cotton being a white gold is an important cash crop of Pakistan. Thus, it has turn out to be very important for Pakistan to enhance it's per acre yield. In Pakistan there are numbers of causes for low yield in cotton crop. Such as high cost of crop growing inputs (seeds, fertilizers and pesticides), high incidence of pest and CLCV disease assault, lack of good quality seeds, insufficiency of water for irrigation, lack of advanced technologies and alertness about expert principles, and adulteration in pesticides, fertilizers and seeds. To modify the varieties to meet the ever changing need of the society, cotton breeders all over the world have been exploiting the available genetic resource.

Testing the general and specific combining ability (GCA and SCA) of available genetic resources is important for effective cotton breeding programs. GCA refers to the average performance of a line in a chain of crosses whereas SCA shows the variation in the performance of crosses based upon the average performance of line involved in the cross combination. Sprague and Tatum (1942) explained that largely additive gene effects involved in general combining ability. To identify potentially superior parent and hybrids, combining ability helps in identifying the gene action and effects in the expression of quantitative characters (Abro *et al.*, 2009). Line × tester analysis is most important biometrical tool which gives combining ability variances and effects (Sajjad *et al.*, 2016). This analysis helps in identifying and selecting the best general combiner and specific combiners. Different researchers have carried out combining ability studies by means of line × tester analysis for identifying the suitable parents. Some investigators reported non-additive gene action for yield and related traits (Baloch and Bhutto, 2003; Sawarkar *et al.*, 2015 and Usharani *et al.*, 2016) as well as fibre quality parameters (Seoudy et al., 2014; Ashok *et al.*, 2014 and Sivia *et al.*, 2017) for different cotton genotypes. Keeping in view the above facts, this study was carried out for evaluating the GCA, SCA and also genetic variation due to GCA and SCA for studied cotton genetic resources. The work reported in this study provides some basic information for the cotton breeders regarding selection of parents to be used in future cotton breeding programme.

MATERIALS AND METHODS

During 2018, two genotypes NIA-Noori and LRA-5166 were used as a tester (male) and three genotypes NIA-Ufaq, Haridost and CRIS-342 as lines. For the line × tester (male) analysis study, six line × tester (male) full-sib progenies of hybrid F_0 seeds were collected from the crosses. The experiment comprised of six hybrids along with their 2 testers (male) and 3 lines was conducted in randomized complete block design in triplicate. In this experiment, the row to row and plant to plant spacings were kept at 75 cm and 30 cm, respectively. All recommended cultural practices were carried out whenever needed. Five plants from each genotype per replication were randomly tagged for field observations. Data on phenological (plant height and number of sympodial branches/plant) and yield traits (number of bolls and seed cotton yield/plant) were recorded among each line, tester (male) and hybrids were recorded. The recorded data for each parameter were analyzed by following Steel *et al*. (1997). The mean square from line × tester (male) design, combining ability variances and effects were computed according to the procedure given by Kempthorne (1957) and practiced by different researchers (Baloch and Bhutto, 2003 and Aslam *et al.,* 2015).

RESULTS AND DISCUSSION

Line × tester analysis is an important biometrical tool which shows the ability of genotypes to combine in general and specific cross combinations and provides information on GCA & SCA variances and effects (Sajjad *et al.,* 2016). Line × tester analysis helps to recognize and select best general and specific combiner. The mean squares of GCA presented in Table 1 revealed significant difference for all the traits. Sivia *et al.* (2017) also computed the mean squares from line × tester (male) design and GCA and SCA variances and observed significant differences among studied traits. The mean performance of parents and their hybrids from present study are presented in Table 2 which indicates that pollinator NIA-Noori when crossed with female line Haridost gave tall plant (138 cm) which means the line (female) Haridost has good additive gene effect to increase the height. While, the lowest GCA effect was shown in line (female) CRIS-342 and tester NIA-Noori. When NIA-Noori tester crossed with female line (female) CRIS-342 produced dwarf plants. The highest number of sympodial branches (23.3) and boll weight (3.9 g) were recorded with hybrid NIA-Ufaq × NIA-Noori. Tester NIA-Noori when crossed with line (female) CRIS-342 gave higher seed cotton yield (156 g/plant).

Combining Ability (Variance and Effects)

Plant Height (cm)

Line (female) Haridost indicated higher GCA estimates and proved good combiner having additive gene effect to control the plant height (Table 3). Therefore, haridost could be chosen as general parent to be crossed with any pollinator to control the height. Whereas, in the same character, plant height, the pollinator NIA-Noori when crossed with line (female) CRIS-342 and pollinator LRA-5166 crossed with Haridost gave higher SCA (11.67 & 22.83) than the GCA (Table 4). Both the pollinators formed good combinations for height having predominant gene effect to pollinators control the height. Both pollinators could be given priority in hybridization programme with the prediction of choice improvement in height of cotton because both pollinators possesses dominant gene. Whereas, CRIS-342 × NIA-Noori and NIA-Ufaq × LRA-5166 crosses have dominant gene to reduce the height to dwarfism in plant. The results are in accordance with the results of Baloch and Bhutto (2003) and Usharani *et al.* (2016). Kalwar *et al.* (1998) and Khan *et al.* (2003) reported non-additive gene action for plant height. Lukonge *et al.* (2008) opposed these results by reporting additive gene action for this trait. Khan et al. (2015) also observed such contradictory results. Jatoi *et al.* (2010) and Patel et al. (2014) results also revealed non-additive and additive type of gene action for plant height.

Sympodia Branches/Plant

Results presented in Table 3 suggested that among the lines (female) NIA-Ufaq and NIA-Noori tester (male) exhibited maximum GCA effects indicated good combiners having additive gene effect to improve the number of sympodial branches/plant. If the parent NIA-Noori is used in the hybridization programme, the promising progenies could be developed and selected to increase number of sympodial branches per plant. Whereas, among the hybrids the NIA-Noori tester (male) crossed with NIA-Ufaq and LRA-5166 with CRIS-342 and NIA-Ufaq lines (female) resulted higher magnitude of SCA revealed that both pollinators have dominant genes and proved as best specific combiners (Table-4), suggested that both the hybrids could be used in breeding programme to increase sympodial branches/plant. These findings are in accordance with those of Abro et al. (2009), Sayal *et al*. (1999), Zia-ul-Islam (2001) and Baloch (2004).

Boll Weight (g)

The results revealed that line (female) CRIS-342 and NIA-Noori tester (male) showed higher GCA for boll weight, and could successfully be improved through selection from segregating populations (Table 3). While, among hybrids, higher SCA effects were showed by the NIA-Noori tester (male) crossed with Haridost and CRIS-342 for traits boll weight (Table 4). Dominant gene is responsible for expression of these traits and also insinuating the feasibility of hybrid improvement in this study. Where, the cross NIA-Noori tester (male) with NIA-Ufaq showed positive SCA. It is evident that the character is controlled by dominant genes affect for this trait. These findings are coinciding with the results of (Baloch and Baloch 2005, Baloch *et al*., 2008, Iqbal *et al*., 2004, Meena *et al*., 2001 and Zia ul Islam *et al*., 2001). The results are in accordance with the findings of Usharani *et al.* (2016), Kalwar *et al.* (1998) and Khan *et al.* (2003) who reported non-additive type of gene action for boll weight.

Table 1. Mean squares from analysis of variance (ANOVA) of quantitative and qualitative characters for line × tester analysis in cotton genotypes.

Source of variance	**D.F**	**Plant height (cm)**	**Symp. Branches /plant (No.)**	**Bolls Plant^{-1} (No.)**	**Boll wt. (g)**	**Seed cotton yield/plant (g)**
Replications	2	88.84	9.8485	30.2121	0.33091	71.27
Genotypes	10	493.14**	14.6242**	91.8970**	0.25085**	1416.05**
Parents	4	503.93 **	22.567**	106.567**	0.34333**	536.600ns
P vs.C	1	285.88**	8.3639**	241.536**	0.02571**	5200.1**
Crosses	5	525.96**	9.5222ns	50.2333**	0.22189**	1362.80**
Lines (female)	2	1086.9**	11.556ns	108.500**	0.12056ns	2121.50**
Tester (male)	1	0.89ns	16.056ns	6.722ns	0.6806**	2048.00**
Line × Tester	2	227.56**	4.2222ns	13.722ns	0.0206ns	261.500**
Pooled error	20	0.348	1.4152	1.1788	0.0086	27.27

Table 2. Mean performance of hybrids and parents for quantitative and qualitative characters line × tester analysis in cotton genotypes.

Genotypes	**Plant height (cm)**	**Symp. Branches /plant (No.)**	**Bolls Plant^{-1} (No.)**	**Boll wt. (g)**	**Seed cotton yield/plant (g)**
NIA-Ufaq x NIA-Noori	129.67c	23.3 a	32.0c	3.90 a	125 bc
Haridost x NIA-Noori	138.00 a	20.3b	33.0c	3.60 c	119 cd
CRIS-342 x NIA-Noori	101.00 i	19.0b	38.7a	3.80 b	156 a
NIA-Ufaq xLRA-5166	123.00e	19.7b	27.3e	3.30 e	92 f
Haridost x LRA-5166	131.33b	18.7b	35.0b	3.20f	112 d
CRIS-342 x LRA-5166	115.67 g	18.7b	37.7a	3.40 d	132 b
NIA-Ufaq	125.67 d	22.7a	24.0f	3.57 c	84 f
Haridost	131.00 b	19.7b	37.7a	3.40 d	102 e
CRIS-342	119.33 f	18.7b	29.0de	3.40 d	129 b
NIA-Noori	112.3 h	18.7b	23.0f	3.90a	113 d
LRA-5166	97.67 j	15.0c	32.0c	2.90 g	87 f

Similar letters are non significant in each row according to Duncam Multiple Range Test at $p < 0.05$.

Table 3. Estimates of GCA effects for quantitative and quality traits in five Parents data based on F_1 generation in cotton.

Genotypes	**Plant height (cm)**	**Symp. Branches /plant (No.)**	**Bolls plant^{-1} (No.)**	**Boll wt. (g)**	**Seed cotton yield /plant (g)**
NIA-Ufaq	3	1.66	-4.67	0.07	-14.17
Haridost	11.5	-0.33	-0.67	-0.13	-7.17
CRIS-342	-14.5	-1.33	5.33	0.07	21.33
NIA-Noori	-0.33	0.66	0.67	0.23	10.67
LRA-5166	0.33	-0.66	-0.67	-0.23	-10.67

Table 4. Estimates of SCA effects for quantitative and qualitative traits in F_1 hybrids of cotton genotypes.

Hybrids	**Plant height (cm)**	**Symp. branches /plant (No.)**	**Bolls plant^{-1} (No.)**	**Boll wt. (g)**	**Seed cotton yield/plant (g)**
NIA-Ufaq x NIA-Noori	3.33	1.3	1.3	0.1	5.8
Haridost x NIA-Noori	11.67	-0.3	3.7	0.2	21.2
CRIS-342 x NIA-Noori	-33.17	-2.7	6.3	0.2	29.8
NIA-Ufaq x LRA-5166	-11.83	0.7	-5.3	0.1	-12.8
Haridost x LRA-5166	22.83	-0.7	-5.7	-0.6	-42.7
CRIS-342 x LRA-5166	7.167	1.7	-0.3	0.0	-1.3

Number of Bolls/Plant

Results for number of bolls/plant (Table 3) indicated that the line CRIS-342 (female) and NIA-Noori tester (male) showed higher GCA for bolls/plant suggested that these traits are controlled by additive genes and could successfully be improved through selection from segregating populations. If these parents, be used in the hybridization programme, this will increase number of bolls/plant. While, among hybrids higher SCA effects were showed by the NIA-Noori tester (male) crossed with Haridost and CRIS-342 for traits bolls/plant (Table 4). These findings are in accordance with those of Abro et al. (2009), Sayal et al. (1999) and Zia-ul-Islam (2001).

Seed cotton yield/plant

Table 3 indicated that the line CRIS-342 (female) and NIA-Noori tester (male) showed higher GCA for seed cotton yield/plant suggesting that this trait was controlled by additive genes and could successfully be improved through selection. While among hybrids higher SCA effects were showed by the NIA-Noori tester (male) crossed with Haridost and NIA-Noori for traits seed cotton yield (Table 4). Dominant gene is responsible for expression of these traits and also insinuating the feasibility of hybrid improvement in this study. Whereas the cross of NIA-Noori tester (male) with NIA-Ufaq showed positive SCA and dominant gene effect for this trait. These results are coinciding with the results of Usharani *et al.* (2016), Kalwar *et al*. (1998) and Khan *et al*. (2003).

Conclusions

From present study, it was concluded that the tester variety NIA-Noori and line CRIS-342 had exhibited comparatively higher array mean and proved better general combiners among the testers and lines for most of yield and yield contributing traits under study. SCA, dominant gene affects in hybrid CRIS-342 × NIA-Noori among the crosses for increasing the yield and related traits.

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