

Research Article

Combining ability estimates for yield and fibre quality traits in Bt and non-Bt upland cotton genotypes

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Abstract

The present studies were conducted during cotton season 2012 at experimental farm of Central Cotton Research Institute, Sakrand. Six non-Bt females viz. CRIS-342, BH-167, CIM-573, CRIS-134, FH-941 and Sadori and six males containing Bt gene (Cry1Ac) viz. FH-113, IR-NIBGE-1524, IR-NIBGE-3701, MG-6, AA-802 and Sitara-008 were crossed in 6 × 6 North Carolina Design II fashion, thus 36 crosses were developed for genetic analysis. The characters such as days to open 1st flower, seed cotton yield kg ha⁻¹, bolls plant⁻¹, sympodial branches plant⁻¹, lint %, staple length and fibre fineness were evaluated. The male × female interaction's significant differences clearly indicated the importance of specific combining ability (SCA) of hybrids and proposed the dominant genes involvement in the articulation of studied characters. The significant mean squares owing to both female and male parents determined the general combining ability (GCA) indicated predominant effect of the additive variances advocating the studied parameters. Higher values of σ^2_{SCA} against σ^2_{GCA} , greater ratio of $\sigma^2_{SCA}/\sigma^2_{GCA}$ than one, greater degree of dominance (σ^2_D/σ^2_A)^{1/2} than unity clearly revealed the foremost role of dominant gene effect. These results showed the prevalence of dominant gene action suggesting the achievability of hybrid crop development. General combining ability estimates designated that non- Bt females CRIS-134, CIM-573 and FH-941 and Bt males IR-NIBGE-3701, MG-6 and AA-802 were found as promising general combiners for earliness, seed cotton yield and fibre quality characters. Specific combining ability and heterotic effects are imperative estimates for deciding appropriateness of F₁ hybrid crop development. For SCA effects, thirteen hybrids out of thirty six were recognized as best specific combiners for seed cotton yield, earliness and fibre quality parameters.

Keywords: Bt and non-Bt cotton; Combining ability; Fibre traits; Yield

Introduction

For improving yield and fibre traits, the conventional methods require recognition of

potential parents in terms of their combining ability. The concept of combining ability plays a significant role in crop improvement,

since it helps plant breeder to corroborate the nature and importance of gene action influencing quantitative characters [1]. Combining ability analysis assists in the assessment of inbreds as regards their genetic value and choice of appropriate parents for either hybrid cotton or hybridization followed by selection. The better specific cross combinations may also be recognized by this method. Parents showing a high average combining ability in crosses with other parents are considered possessing good general combining ability (GCA) while if their potential is to combine well in particular crosses, such hybrids are considered as having good specific combining ability (SCA) [2]. Combining ability analysis offers adequate chance to cotton breeders in understanding the basis on which definite potential parental lines could be utilized for cotton breeding programmes [3]. For the recognition of best combining parents, combining ability analysis ultimately is used in the breeding programmes with better results [4]. The estimates of GCA and SCA are usually used for determining the potential of parents and their hybrids for improvement of crop production [5]. So parent's selection for hybridization can be done by reason of combining ability and *per se* performance. However, effects of GCA and SCA are more informative and reliable than *per se* values as they also provide information about the type of gene action; that is, additive or non-additive [6, 7]. Dominant gene action for uniformity ratio and yield while for ginning out turn % additive gene action were observed [8]. Non-additive gene action for all fibre traits was observed by [9]. Yield and its associated parameters in substitution lines were advocated by integrated effects of additive and non-additive genes, while ginning outturn% was chiefly advocated by additive genes, yet boll mass, total fruits

plant⁻¹, seed cotton and lint yields were largely governed by dominant genes [10]. Despite diallel design, factorial mating design or North Carolina mating design-II (NC-II) also use by breeders for evaluation of components of variance [11]; more number of parents is involved to generate a fewer crosses in comparison of diallel mating design. Genetic information produced by this mating design is utilized to estimate the general and specific combining ability of parents and their progenies respectively. In view of the importance of transgenic insect resistant cotton in controlling insect pests and increasing the yield with significant reductions in the use of chemical insecticides, present research work will undertake the study on nature of gene action of earliness, fibre traits and seed cotton yield from 6 × 6 NC-II crosses of cotton cultivars. This investigation is aimed at estimating combining ability of Bt and non-Bt cotton parents for yield and fibre traits. In addition, it will identify those parents and hybrids which possess superior combinations for desirable characters.

Materials and methods

The present research was conducted at experimental field of Central Cotton Research Institute, Sakrand, Pakistan. Six non-Bt female parents such as CRIS-342, FH-941, CRIS-134, BH-167, CIM-573 and Sadori and six Bt male parents viz., FH-113, IR-NIBGE-1524, IR-NIBGE-3701, MG-6 AA-802 and Sitara-008 were crossed in North Carolina Design-II fashion during 2011, hence thirty six cross combinations were developed for genetic variance analysis. The seed of twelve parents and thirty six F₁ hybrids were planted in a randomized complete block design in four replications during 2012. Each hybrid and parent in a replication was sown four rows of 6.0 m length with distance of 30.0 cm within plants and 75.0 cm within rows. One bag of diammonium phosphate was applied

before sowing at land preparation and three bags of nitrogen were applied in split doses. Field practices such as thinning and weeding were practiced. Insecticides such as acephate 250gram and diafenthiuron 200 ml/acre were sprayed to control the sucking insect pest population. Ten plants were tagged in each genotype per replication for recording the data for days to open 1st flower, bolls plant⁻¹, sympodial branches plant⁻¹, seed cotton yield, staple length (mm), micronaire ($\mu\text{g}/\text{inch}$) and lint %. The collected data were analyzed for determining general and specific combining ability variances and their effects in F_{1s}. The analysis of variance was determined following statistical procedures [12], whereas mean squares for general combining ability were estimated from males and females and specific

combining ability from male \times female interactions [13].

Results and discussion

Analysis of variance and mean performance of females and males

The analysis of variance of seven earliness, yield and fibre quality traits depicted in (Table 1) revealed that variances due to genotypes, parents, crosses and parents vs. crosses, were significant for all the characters studied. The average performance of female parents given in (Table 2) showed that CIM-573 took minimum days to open 1st flower, measured longest staple length and produced medium longer fibre; CRIS-134 set higher number of bolls plant⁻¹, produced highest seed cotton yield in kg ha⁻¹ and gave desirable micronaire value; BH-167 ginned higher lint %.

Table 1. Mean squares from analysis of variance for earliness, seed cotton yield and fibre quality traits of F₁ hybrids derived from six females and six males of cotton

Source of Variation	Degrees of Freedom	Days to 1 st Flower	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Seed cotton yield (kg ha ⁻¹)	Lint (%)	Staple length	Micro-naire
Replication	3	0.21	0.13	1.911	642.58	0.25	0.22	0.08
Genotypes	47	8.92**	24.16**	169.92**	625424.44**	13.59**	3.55**	0.46**
Parents	11	7.20**	31.81**	26.95**	170700.05**	13.94**	2.76**	0.62**
Crosses	35	4.06**	12.28**	72.63**	316775.12**	11.07**	3.26**	0.28**
P vs. C	1	198.11**	355.64**	5045.14**	16430119.12**	97.79**	22.52**	5.16**
Males (M)	5	9.76**	19.34**	113.53**	574650.95**	15.36**	4.20**	0.32**
Females (F)	5	8.63**	10.49**	100.76**	553107.58**	30.30**	7.27**	0.83**
M \times F	25	2.01**	11.22**	62.93**	217933.46**	6.37**	2.27**	0.16**
Error	141	0.41	1.37	10.12	244.71	0.31	0.19	0.03
Genetic components of variances								
δ^2_{gca}		0.21	0.38	2.31	12216.15	0.36	0.09	0.01
δ^2_{sca}		1.91	10.88	60.40	217872.29	6.29	2.22	0.15
δ^2_{A}		0.84	1.52	9.25	48864.58	1.43	0.37	0.04
δ^2_{D}		7.63	43.52	241.60	871489.14	25.16	8.89	0.62
$\delta^2_{\text{sca}} / \delta^2_{\text{gca}}$		9.10	28.63	26.15	17.83	17.47	24.67	15.00
$[\delta^2_{\text{D}} / \delta^2_{\text{A}}]^{1/2}$		3.02	5.35	5.11	4.22	4.18	4.97	3.87
Proportional contribution of males and females								
Males (M)		34.34	27.18	22.33	25.92	19.81	18.40	16.44
Females (F)		30.36	14.75	19.82	24.94	39.10	31.86	42.47
M \times F		35.30	78.90	61.89	49.14	41.09	49.74	41.08

** = Significant at 1% probability level

In general, the female parents like CIM-573, CRIS-134 and BH-167 performed superbly for earliness, seed cotton yield and fibre quality traits, thus these female parents may be exploited in hybridization and selection programmes for the development of pure lines or hybrids with higher yields and good fibre quality characters..Amongst six male Bt parents, IR-NIBGE-3701 took minimum days to open first flower, produced maximum seed cotton yield in kg ha⁻¹, high lint % and recorded desirable micronaire value. While MG-6 produced more number of sympodia plant⁻¹, formed maximum bolls plant⁻¹, higher seed cotton yield in kg ha⁻¹ with medium longer fibre. The AA-802

formed more bolls plant⁻¹ at maturity. By and large these three transgenic male parents such as IR-NIBGE-3701, MG-6 and AA-802 may be crossed with potential females to develop breeding material for higher yield, more lint % and longer fibre length (Table 2). Similarly, [14] reported that lines such as Chandi-95, NIA-Ufaq and Sadori performed better for boll weight, bolls per plant, sympodial branches per plant and seed cotton yield. [15] also observed that amongst four Egyptian cotton lines, Giza 92 gave the best performance for number of bolls per plant, seed cotton yield, lint yield, micronaire and staple length.

Table 2. Mean values for earliness, seed cotton yield and fibre quality traits of six female and six male parents evaluated by NC-II design

Females	Days to 1 st Flower	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Seed cotton Yield (kg ha ⁻¹)	Lint %	Staple Length (mm)	Micronaire (µg/inch)
CRIS-342	43.50	19.08	44.93	3919.50	36.20	27.35	4.65
CRIS-134	42.75	20.25	45.75	4148.25	36.05	27.30	4.68
Sadori	44.25	26.13	44.60	3830.25	38.34	27.55	4.75
BH-167	44.00	22.00	39.80	3402.25	40.75	28.80	4.45
CIM-573	41.75	23.28	41.65	3672.00	38.85	29.55	4.33
FH-941	45.25	25.38	43.70	3869.50	37.25	28.53	4.65
Average	43.58	22.68	43.40	3806.96	37.91	28.18	4.58
LSD (5%)	0.96	1.76	4.79	23.57	0.84	0.66	0.26
Males	Days to 1 st Flower	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Seed cotton Yield (kg ha ⁻¹)	Lint %	Staple Length (mm)	Micronaire (µg/inch)
FH-113	45.50	22.80	43.53	3922.75	38.81	27.40	5.33
IR-NIBGE-1524	45.25	27.03	44.10	3665.75	37.12	28.15	5.18
IR-NIBGE-3701	43.25	26.03	39.20	4062.50	41.55	27.95	5.48
MG-6	44.00	28.20	47.93	4038.50	38.28	28.78	5.40
AA-802	45.25	23.05	45.50	3694.50	38.26	26.63	5.25
Sitara-008	46.50	26.28	41.00	3840.00	35.37	27.45	5.05
Average	44.96	25.56	43.54	3870.67	38.71	27.73	5.28
LSD (5%)	0.96	1.76	4.79	23.57	0.84	0.66	0.26

Genetic analysis for combining ability estimates

The mean squares (Table 1) articulated significant variations amongst genotypes, parents, crosses, parent vs. crosses, males, females and male \times female interactions for all the characters studied in F_1 hybrids. These significant differences revealed that the data is valuable for combining ability analysis. The significance of variances both males and females established the importance of general combining ability (GCA), while significance of male \times female interactions suggested the value of specific combining ability (SCA), consequently the significance of dominant genes and heterosis breeding. These findings are in consonance with other researchers as they also noted significance of both GCA and SCA variances for fibre and yield traits [16-19].

Genetic analysis for determining GCA and SCA of parents for yield and fibre traits are very essential parameters for developing new breeding material. The GCA is important for hybridizations and selection programmes whereas SCA is rewarding for hybrid cotton development [20]. General combining ability analysis of female and male parents (Table 3) indicated that from six female parents, CIM-573 proved itself as good general combiner for earliness character i.e. days to open first flower due to their desirable negative GCA effects and from male parents AA-802, MG-6 and IR-NIBGE-1524 were also good general combiners by manifesting desirable negative GCA effects. [21] observed that lines H-1155 and ISR12 expressed significantly negative GCA estimates for days to 1st flower. For sympodial branches, female CRIS-134 and males AA-802 and IR-NIBGE-3701 by manifesting higher positive desirable GCA effects were observed as best general combiners, while for bolls plant⁻¹, female CRIS-134 and males IR-NIBGE-1524 and MG-6 with higher positive GCA

effects were found as good general combiners. Similar to our results, [22, 23] reported that in inheritance of characters of sympodia and bolls plant⁻¹ additive genes were involved. The females CRIS-134 and CIM-573 and males MG-6, IR-NIBGE-3701, IR-NIBGE-1524 have higher positive GCA effects desirable for yield kg ha⁻¹. [24] succeeded in identifying parents like NIAB-999, CIM-473 and Acala have good general combining ability for seed cotton yield. Regarding other traits like lint %, females BH-167 and Sadori and three males IR-NIBGE-3701, MG-6 and AA-802; for staple length females CIM-573 and FH-941 and males AA-802, MG-6 and IR-NIBGE-1524 established as good general combiners. [25] stated that though both SCA and GCA were significant, yet GCA was much greater than SCA, thus additive genes were prevailing in the control of lint%. While, [26] found that for 2.5% span length, additive genes were prevailing. For micronaire, females CIM-573 and CRIS-342 and males FH-113 and AA-802 depicted higher desirable negative GCA effects. These results, generally suggested that female parents CRIS-134, CIM-573 and FH-941 and males IR-NIBGE-3701, MG-6 and AA-802 were good combiners for nearly all studied characters; hence such parents are most suitable for hybridization programmes to develop superior hybrids or pure varieties.

Specific combining ability effects are rewarding for assessing the aptitude of inbreds to develop superior F_1 hybrids. In present research, thirty six F_1 hybrids were evaluated for SCA effects and given in (Table 4). The maximum significant enviable negative SCA effects were observed for days to open 1st flower in hybrids like CIM-573 \times IR-NIBGE-3701, CRIS-134 \times MG-6, FH-941 \times AA-802, FH-941 \times MG-6 and BH-167 \times MG-6. While maximum positive SCA effects for sympodial branches plant⁻¹ was observed in

hybrid FH-941 × AA-802 followed by CIM-573 × IR-NIBGE-3701, CRIS-134 × MG-6, BH-167 × IR-NIBGE-3701 and CRIS-342 × MG-6. Extremely higher SCA estimates for bolls plant⁻¹ were observed in hybrids such as CIM-573 × IR-NIBGE-3701, FH-941 × IR-NIBGE-3701, CRIS-134 × MG-6, FH-941 × AA-802 and CRIS-134 × IR-NIBGE-3701. For seed cotton yield, quite a number of hybrids such as CRIS-134 × MG-6, CIM-573 × IR-NIBGE-3701, CRIS-342 × IR-NIBGE-3701, CRIS-134 × IR-NIBGE-3701 and BH-167 × MG-6 manifested remarkable positive SCA estimates. Maximum positive SCA effects was also observed by CIM-573 × IR-NIBGE-3701 followed by FH-941 × AA-802, CRIS-134 × FH-113, BH-167 × FH-113 and BH-167 × MG-6. These high SCA scoring hybrids may be utilized for future cotton breeding programmes for obtaining higher lint %. For staple length, the maximum positive SCA estimates were manifested by FH-941 × MG-6 followed by CIM-573 × IR-NIBGE-1524, FH-941 × IR-NIBGE-3701, FH-941 × IR-NIBGE-1524 and FH-941 × FH-113. The desirable negative SCA estimates were observed by the hybrids such as BH-167 × IR-NIBGE-3701, BH-167 × Sitara-008, CIM-573 × IR-NIBGE-3701, Sadori × IR-NIBGE-1524 and CIM-573 × AA-802. From these results, it could be predicted that quite higher number of hybrids possibly suitable for hybrid cotton development with enhanced yield and fibre characters. Several previous researchers observed similar results like [20] reported greater GCA over SCA variances for traits such as plant height, bolls per plant, ginning outturn % and seed cotton yield though for sympodial branches plant⁻¹ and fibre length observed higher SCA than GCA variances. Greater value of SCA than GCA variances were observed for number of bolls per plant, seed cotton yield, fibre length and ginning outturn % exemplifying the importance of non-additive effects in

genetic control of these traits [27]. While for fibre quality traits, non-additive genes were involved [28, 29].

Additive and dominance variances (σ^2A and σ^2D)

The additive variances (σ^2A), dominance variances (σ^2D) and degree of dominance ($(\sigma^2D/\sigma^2A)^{1/2}$) for various characters (Table 1) revealed that dominance genetic variances were more prominent against additive. The greater values of dominance variance (σ^2D) for almost all studied traits indicated prevalence of non-additive type of genes advocating the heritage of studied traits. Variances due to general combining ability (GCA) in terms of additive variance (σ^2A), specific combining ability (SCA) in terms of dominance variance (σ^2D) and degree of dominance ($(\sigma^2D/\sigma^2A)^{1/2}$) of all traits under observation are shown in (Table 1). It is quite evident that genetic variances due to SCA were more important than SCA. Dominant gene actions were more effective than additive genes respectively in F₁s for days to open first flower (7.63 and 0.84), sympodial branches plant⁻¹ (43.52 and 1.52), bolls plant⁻¹ (241.60 and 9.25), seed cotton yield kg ha⁻¹ (871489.14 and 48864.58), lint % (25.16 and 1.43), staple length (8.89 and 0.37) and micronaire (0.62 and 0.04) which illustrated higher dominance variances against the additive ones. The supremacy of dominant gene action was further proved with degree of dominance ($(\sigma^2D/\sigma^2A)^{1/2}$) being greater than unity (1.0) showed over dominant genes for the studied traits. The preponderance ratio of σ^2SCA/σ^2GCA is also greater than unity which explained predominance of super-dominant gene effects in the expression of studied traits. Previous researchers [30, 31] also found high proportion of dominant variances for most of the traits they studied. [33] also corroborated that degree of dominance being greater than 1.0 revealed the existence of dominant genes controlling the characters

studied. [34] concluded that higher value of degree of dominance for all studied traits

was due to key function of dominant genes.

Table 3. General combining ability (GCA) effects for earliness, yield and fibre quality traits of six female and six males of cotton

Females	Days to 1 st Flower	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Seed cotton yield (kg ha ⁻¹)	Lint %	Staple Length	Micro-naire
CRIS-342	-0.24	-0.25	0.44	0.62	-1.69**	-0.16	-0.14**
CRIS-134	0.03	1.09**	2.38**	301.41**	-0.24*	-0.46**	0.22**
Sadori	0.49**	-0.81**	-3.67**	-96.17**	0.36**	-0.57**	0.11**
BH-167	-0.10	-0.36	-0.62	-94.30**	1.68**	-0.15**	-0.03
CIM-573	-1.19**	-0.03	1.04	52.81**	0.43	0.80**	-0.28**
FH-941	0.51**	-0.36	0.44	-58.76**	-0.54**	0.54**	0.12**
S.E.(gi.)	0.13	0.23	0.64	3.19	0.11	0.09	0.03
S.E. (gi-gj)	0.18	0.33	0.91	4.52	0.16	0.13	0.05
Males	Days to 1 st Flower	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Seed cotton yield (kg ha ⁻¹)	Lint %	Staple Length	Micro-naire
FH-113	0.64**	-0.42	-0.95	-123.38**	-0.47**	-0.18*	-0.14**
IR-NIBGE-1524	-0.17*	0.21	1.64*	77.33**	-0.78**	0.27**	0.17**
IR-NIBGE-3701	0.13*	0.62*	0.82	141.90**	1.07**	-0.01*	0.08*
MG-6	-0.59**	0.05	1.61*	182.83**	0.80**	0.29**	0.02
AA-802	-0.79**	1.06**	0.81	-84.01**	0.15**	0.37**	-0.11**
Sitara-008	0.78**	-1.52**	-3.93**	-194.67**	-0.76**	-0.74**	-0.02
S.E. (gi.)	0.13	0.23	0.64	3.19	0.11	0.09	0.03
S.E(gi-gj)	0.18	0.34	0.91	4.52	0.16	0.13	0.05

*, ** Declared significant when GCA effects were twice and thrice equal or greater than S.E.(gi.) respectively.

Proportional contribution of males, females and their interactions

The proportional contribution of female, male and their interactions indicated that male parents donated greater portion of paternal effect over maternal for days to open 1st flower, bolls plant⁻¹, sympodial branches plant⁻¹ and seed cotton yield kg ha⁻¹. On the other hand, the female parents contributed normal portion of variances for lint %, staple length and micronaire thus added fair amount of variance derivable to maternal effect. Similar to present findings, [35] found maximum proportional contribution to total variance of female parents for lint percentage, staple length,

fibre fineness and seed cotton yield. [36] reported that female parents contributed maximum portion of genetic variance for yield and fibre characters. Relatively higher portion of genetic variances for the traits like seed cotton yield kg ha⁻¹, sympodial branches plant⁻¹, bolls plant⁻¹, lint % and staple length was contributed by male × female interactions. Such variances revealed that the characters were advocated by both maternal and paternal influence with additive and dominant genes. Nonetheless, the involvement of male × female interaction was greater for some traits, which revealed predominance of both paternal and maternal influence for

characters studied. High proportional contribution of male \times female to total variance revealed higher SCA estimates for traits studied.

Table 4. Specific combining ability (SCA) effects for earliness, yield and fibre quality traits of thirty six F₁ hybrids of cotton

F ₁ Hybrids	Days to 1 st Flower	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Seed cotton yield (kg ha ⁻¹)	Lint %	Staple Length	Micro-naire
CRIS-342 \times FH-113	-0.70*	1.56*	5.60*	231.88**	0.13	0.35	0.12
CRIS-342 \times IR-NIBGE-1524	-0.53	-2.79**	-4.54*	-372.91**	-1.85**	0.60*	0.02
CRIS-342 \times IR-NIBGE-3701	-0.55	1.49*	5.71*	451.17**	-1.07**	0.01	-0.18*
CRIS-342 \times MG-6	-0.31	2.29**	1.76	303.30**	-1.27**	1.68**	0.04
CRIS-342 \times AA-802	0.30	1.56*	1.50	151.81**	-2.12**	-0.46*	0.19*
CRIS-342 \times Sitara-008	-0.57	-3.10**	-1.70	-21.24*	-1.11**	-2.05**	-0.18*
CRIS-134 \times FH-113	1.00**	1.13	-3.19*	206.17**	2.67**	-1.22**	-0.08
CRIS-134 \times IR-NIBGE-1524	-0.63	0.65	-1.83	-37.87**	1.16**	0.01	-0.14
CRIS-134 \times IR-NIBGE-3701	0.75*	0.51	7.02**	385.71**	1.37**	-0.56*	0.24*
CRIS-134 \times MG-6	-1.66**	2.51**	9.86**	752.59**	-0.79*	-0.47*	-0.04
CRIS-134 \times AA-802	0.60	0.35	-1.47	1.35	-1.07**	-1.01**	0.46**
CRIS-134 \times Sitara-008	0.73*	0.17	-5.99**	36.55**	-0.11	-2.47**	-0.14
Sadori \times FH-113	0.96**	-1.41*	-2.27	-317.15**	0.68*	-0.13	-0.05
Sadori \times IR-NIBGE-1524	-0.02	-1.86**	-4.99*	-450.69**	-1.84**	0.58*	-0.31**
Sadori \times IR-NIBGE-3701	-0.04	0.25	-2.86	-48.11**	0.06	-0.47*	0.32**
Sadori \times MG-6	0.80*	-2.38**	-4.91*	-76.48**	-0.94**	0.48*	0.12
Sadori \times AA-802	0.56	-0.03	-5.47*	-250.47**	-2.00**	-0.51*	0.14
Sadori \times Sitara-008	-0.06	-3.17**	-6.47**	-285.53**	-0.15	-1.97**	-0.06
BH-167 \times FH-113	1.20**	-4.31**	-8.46**	-588.83**	1.91**	-1.32**	0.22*
BH-167 \times IR-NIBGE-1524	0.25	-1.71*	-8.60**	-904.62**	0.55	0.18	0.06
BH-167 \times IR-NIBGE-3701	-0.27	2.50**	1.85	-238.79**	0.35	-0.32	-0.46**
BH-167 \times MG-6	-0.73*	1.42*	4.70*	363.84**	1.56**	-0.22	0.11
BH-167 \times AA-802	1.10**	1.32*	2.04	54.60**	0.23	-1.11**	0.21*
BH-167 \times Sitara-008	1.41**	-1.67*	-4.91*	-348.96**	0.66*	-2.49**	-0.44**
CIM-573 \times FH-113	-0.38	0.25	-0.81	-286.24**	0.38	0.36	-0.16
CIM-573 \times IR-NIBGE-1524	0.04	-1.30*	2.70	137.22**	-0.67*	2.34**	-0.13
CIM-573 \times IR-NIBGE-3701	-1.88**	2.64**	11.85**	616.50**	3.45**	1.12**	-0.36**
CIM-573 \times MG-6	-0.29	-2.34**	-1.00	14.18	-0.50	0.32	-0.08
CIM-573 \times AA-802	0.72*	-2.00**	-5.16*	-90.56**	0.10	-0.87**	-0.28**
CIM-573 \times Sitara-008	-0.15	-3.78**	-6.21**	-203.87**	-1.08**	-0.75**	-0.01
FH-941 \times FH-113	0.30	1.78**	0.78	10.17	1.51**	1.83**	-0.04
FH-941 \times IR-NIBGE-1524	0.07	1.68*	6.04**	284.38**	-0.58*	2.04**	0.20*
FH-941 \times IR-NIBGE-3701	-0.20	1.21*	10.19**	261.96**	0.12	2.22**	0.26**
FH-941 \times MG-6	-0.76*	0.94	2.94	305.34**	-3.28**	3.46**	0.15
FH-941 \times AA-802	-1.35**	5.33**	7.18**	-53.90**	3.16**	1.40**	0.30**
FH-941 \times Sitara-008	0.28	0.32	-0.92	7.55	0.45	-0.57*	-0.02
S.E. (s.e.)	0.32	0.59	1.59	7.82	0.28	0.22	0.08
Range of SCA effects	-0.02 to -1.88	0.17 to 5.33	0.78 to 11.85	1.35 to 752.59	0.06 to 3.45	0.01 to 3.46	-0.02 to -0.46

*, ** Declared significant when GCA effects were twice and thrice equal or greater than S.E. (g.i.) respectively

Conclusions

The significant variances among parents, F_{1s} , GCA and SCA revealed that the data was suitable for assessing inbreds' potentiality, hybrid evaluation, combining ability estimates and gene action. General combining ability estimates revealed that non-Bt females CRIS-134, CIM-573 and FH-941 and Bt males IR-NIBGE-3701, MG-6 and AA-802 were best general combiners for earliness, yield and fibre quality traits. Consequently, these parents with additive genes may be the choice parents for hybridization and selection programmes, while quite a number of hybrids were also identified with desirable specific combining ability, hence such hybrids can be exploited for hybrid cotton development. The degree of dominance $(\sigma^2D/\sigma^2A)^{1/2}$ was higher than 1.0 showing that over dominant gene action was predominant in advocating all the traits studied.

Authors' contributions

Conceived and designed the experiments: MJ Baloch, R Anjum, GM Baloch & Q Chachar, Performed the experiments: R Anjum, Analyzed the data: MJ Baloch & R Anjum, Wrote the paper: R Anjum & MJ Baloch.

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