



## Research Article

# Estimation of Combining Ability for Within-Boll Yield Components in Upland Cotton (*Gossypium hirsutum*)

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**Abstract** | In this study, three varieties Tarzon-05, FH-342, and VH-329 were crossed in line × tester fashion with three testers CIM-595, CRS-2, and BS-80 during the 2021–2022. The F<sub>1</sub> hybrids and their parents were planted in the fields, Plant Breeding and Genetics department, University of Agriculture Faisalabad using two replications with randomized complete block design (RCBD). Results of ANOVA revealed that all the genotypes were highly significant for most of the plant height, sympodial branches/plant, monopodial branches/plant, first fruiting nodes, number of bolls per plant, boll weight, number of seeds per boll, seed cotton yield/plant, lint index, lint percentage, seed index, seed density, seed volume, fiber fineness, fiber strength, and fiber length. For plant height, fibre strength, and seed density, Tarzon-05 stood out among the lines as a very effective general combiner. For the number of bolls per plant, the number of sympodial and monopodial branches, the number of nodes on the first fruiting branch, seed cotton yield and the lint percentage, VH-329 demonstrated good general combining ability. For boll weight, the FH-342 was proven to be an effective combiner. CIM-595 stood out among the testers as a good general combiner in terms of number of bolls per plant, monopodial branches, number of first fruiting branch node, seed cotton yield, and lint%. For fibre fineness, BS-80 was identified to be a good general combiner. A good specific combining ability was shown by the F<sub>1</sub> hybrids Tarzon-05×BS-80 for plant height and fibre length, VH-329×CIM-595 for the quantity of bolls per plant, VH-329×BS-80 for the quantity of sympodial branches per plant and Tarzon-05×CRS-2 for the quantity of monopodial branches per plant and fibre strength. For the number of nodes for first fruiting branch, boll weight, fibre length, and seed cotton yield/plant, VH-329×CRS-2 was determined to be a good specific combiner, and FH-342×CIM-595 shown good specific combining ability for seed density and fibre strength. For seed volume, all of the parents and their hybrids displayed non-significant GCA and SCA values. All attributes, with the exception of seed index, were governed by non-additive gene action. The information related to GCA, SCA and gene action obtained from this research will be helpful for plant breeders in future breeding programs.

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**Keywords** | Cotton, F<sub>1</sub>, Combining ability, Gene action



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## Introduction

The usage of inferior cotton cultivars is one of the key causes of Pakistan's low cotton production per unit area (Zafar *et al.*, 2021a; Laghari *et al.*, 2022). Cotton production may be increased by developing high-yielding varieties and hybrids with higher yield potential, good fiber quality, and disease resistance (Chaudhry *et al.*, 2022). All of the yield-related traits in cotton are linked to one another (Zafar *et al.*, 2020). Any modification in one feature has a significant impact on the others. It is quite beneficial for breeders to have all qualitative and quantitative data related to the development of good yielding cultivars (Hassan *et al.*, 2022).

Combining ability analysis helps the breeders to collect information about the potential of inbred lines (Zafar *et al.*, 2022). The combining ability is utilized in plant breeding programs to assess the performance of lines in the development of hybrid combinations (Perviz *et al.*, 2016). The performance of a line through a series of crosses is referred to as general combining ability (GCA), whereas the hybrid performance through a specific combination of genetic factors is referred to as specific combining ability (Tulu *et al.*, 2021). GCA is induced by additive genes, whereas specific combining ability is caused by non-additive genes that influence traits (Baloch *et al.*, 1993; Manan *et al.*, 2022).

Introduction of new cultivars with modified genetic base is very important step in plant breeding. The lower genetic base creates problem for researchers (Qin *et al.*, 2008). Therefore, it is very important for a breeder to have knowledge about the variations and inheritance of different traits. The Line×Tester analysis is also helpful to provide knowledge about GCA and SCA of parents and crosses (Manan *et al.*, 2022). A thorough investigation of the genetic process for controlling cotton plant properties under various environmental situations is also required for achieving these goals. Given the foregoing, a research project was designed to examine the genetic potential of several genotypes in the Faisalabad, Pakistan, climate.

The experiment was performed to achieve the following objectives:

- To evaluate the GCA of the parents as well as determine the hybrid which gives good results for

within-boll yield components.

- To study the gene action involved in the inheritance of the traits.

## Materials and Methods

The research was carried out in the Department of Plant Breeding and Genetics field area at the University of Agriculture, Faisalabad, Pakistan in 2020-21. The plant material for research was collected from the department. The experimental material consisting of three testers (CRS-2, BS-80, and CIM-595) and three lines (FH-342, VH-329, and Tarzan-05) were sown in November 2020 in a glasshouse to produce the F<sub>1</sub> generation. All the genotypes were sown at optimum conditions like the temperature, proper light, and humidity in a glasshouse for a maximum germination. The seed was sown in earthen pots. Three lines were crossed with three testers at the time of flowering. Six parents along with nine crosses were planted in May 2021 in the field in two replications by using a randomized complete block design with 75cm spacing between lines and 30cm spacing between plants. All the precautionary measures were made to avoid the contamination of genetic material. For data collection, 5 plants of each genotype from each replication were selected randomly. Proper agronomic practices like weeding, thinning, hoeing, proper irrigation, and plant protection measures were applied from sowing to picking. The list of parents and crosses is given below:

At maturity, data was collected from each replication for following traits on the individual plant bases in the field and laboratory. PH: plant height (cm), SB/P: sympodial branches/plant, MB/P: monopodial branches/plant, FFN/P: first fruiting nodes, NB/P: number of bolls per plant, BW: boll weight (g), NS/B: number of seeds per boll, SCY/P: Seed cotton yield/plant (g), LI: lint index (g), L%: lint percentage (%), SI: seed index (g), SD: seed density (g/cm<sup>3</sup>), SV: seed volume (cm<sup>3</sup>), FF: fiber fineness (µg/inch), FS: fiber strength (g/tex), and FL: fiber length (mm).

### Statistical analysis

The collected data were analyzed through analysis of variance (Steel *et al.*, 1997) by using statisticx 8.1 to determine the significant differences among genotypes under study. For the estimation of combining ability effects, the analysis was carried out by following Kempthorne (1957) by DOS Box.

Table 1: Combined ANOVA of cotton genotypes.

SOV	DF	PH	SB/P	MB/P	FFN/P	NB/P	BW	SCY/P	NS/B	L%	LI	FF	FS	FL	SI	SV	SD
Replication	1	16.896	0.100148	0.008333	2.427259	14.934	0.018476	512.3267	0.524481	3.60166	0.02176	0.04800	0.033	0.0403	0.028213	0.3000	0.000618
Genotypes	14	205.82**	35.06407**	0.369481**	4.476386**	68.574*	0.221499**	822.1861**	8.701259**	7.92**	0.22197**	0.37143**	11.4310**	1.38562**	0.737549**	1.77619**	0.03595**
Error	14	10.83	2.998779	0.033651	0.450354	5.5487	0.046722	30.85281	0.860434	0.84524	0.04019	0.00657	0.0276	0.15105	0.26152	0.58571	0.004309

\*\* highly significant. PH: plant height; SB/P: sympodial branches/plant; MB/P: monopodial branches/plant; FFN/P: first fruiting nodes; NB/P: number of bolls per plant; BW: boll weight; NS/B: number of seeds per boll; SCY/P: seed cotton yield/plant; LI: lint index; L%: lint percentage; SI: seed index; SD: seed density; SV: seed volume; FF: fiber fineness; FS: fiber strength and FL: fiber length.

Table 2: Combined ANOVA for line × tester.

SOV	DF	PH	SB/P	MB/P	FFN/P	NB/P	BW	SCY/P	NS/B	L%	LI	FF	FS	FL	SI	SV	SD
Replication	1	32.4688	0.0963	0.0083	2.4254	14.8685	0.0183	512.2028*	0.5254	3.5158	0.0213	0.4083	0.1333	1.8253	0.0282	19.6830	0.0007
Genotype	14	201.1802**	35.0858**	0.3694**	4.4764**	68.5183**	0.2208**	822.1666**	8.7009**	7.9013**	0.2221**	1.8155**	0.3470**	9.0649**	0.7375**	21.1677	0.0358**
Cross	8	269.6903**	54.3362**	0.3617**	5.1375**	89.6530**	0.2411**	940.9795**	3.2192**	9.6009**	0.1961**	2.1806**	0.4947**	9.7763**	0.6457*	35.7301	0.0524**
Line (C)	2	487.6315**	128.7762**	0.2109*	8.5448*	118.1547**	0.4892**	815.8375**	2.9894*	31.3184**	0.2401*	2.0556*	0.7006**	0.2217	1.8085*	33.9089	0.0826**
Tester (C)	2	232.6815**	16.6722**	0.3888**	3.0608	74.7329**	0.2259*	327.9643**	1.2116	6.6165**	0.1920*	4.2222**	0.0572	4.5800*	0.3382	35.6822	0.0690**
L × T (C)	4	179.2241**	35.9482**	0.4236**	4.4722	82.8623**	0.1247	1310.0581**	4.3379**	0.2343	0.1761**	1.2222*	0.6106**	17.1517**	0.2181	36.6647	0.0290**
Parent	5	120.6846**	3.4400**	0.2555**	1.8533	17.4780**	0.2025**	426.4244**	10.8095**	6.7505**	0.2021**	1.5875**	0.1695**	5.8588**	0.9616**	0.3413	0.0144*
Line (P)	2	11.6762	5.6117	0.0200	2.2067	11.0867	0.1877*	4.0825	0.6650	1.2097	0.3391**	0.7917	0.2717**	3.2917	1.2117*	0.7400	0.0117
Tester (P)	2	259.1632**	1.3867**	0.5850**	0.5000	18.8067**	0.1331	417.7937**	18.7650**	15.3353**	0.1254*	3.1667*	0.0017	3.7617	1.1283*	0.0867	0.0206*
L (P) vs. T (P)	1	61.7440*	3.2033*	0.0675	3.8533	27.6033*	0.3710*	1288.3695**	15.1875*	0.6627	0.0817	0.0208	0.3008*	15.1875*	0.1281	0.0533	0.0075
Cross vs. Parent	1	55.5778	39.3121	1.0005*	12.3036	154.6422	0.1496	1850.3751**	42.0113**	0.0583	0.5306*	0.0347	0.0534	19.4045*	0.3520	8.8002	0.0106
Error	14	9.8207	2.9735	0.0337	0.4506	5.5503	0.0473	30.8573	0.8601	0.8335	0.0401	0.5512	0.0348	1.3118	0.2615	23.1066	0.0044

\* significant \*\* highly significant. For more details and abbreviation see Table 1.

### General combining ability effects

$$\text{Line } g_i = \{(x_{j..}/tr) - (x_{..}/l_{tr})\}$$

$$\text{Testers } g_t = \{(x_{j..}/lr) - (x_{..}/l_{tr})\}$$

Where, l= number of lines; t= number of testers; r= number of replications; xii= total number of F<sub>1</sub> resulting from i<sup>th</sup> lines with all testers; x... = total of all crosses.

### Estimation of SCA effects

$$S_i = \{(x_{ij.})/r - (x_{i..}/tr) - (x_{.j.}/lr) + x_{...}/l_{tr}\}$$

Where; X<sub>ij</sub> = total number of F<sub>1</sub> resulting from i<sup>th</sup> lines with all testers with j<sup>th</sup> tester; X<sub>i</sub> = total of all crosses of i<sup>th</sup> line with all testers; X<sub>j</sub> = total of all crosses of j<sup>th</sup> tester with all lines.

### Contribution of lines, testers and their interaction to total variance

$$\text{Contribution of lines} = \{SS(l)/SS(\text{crosses})\} \times 100$$

$$\text{Contribution of testers} = \{SS(t)/SS(\text{crosses})\} \times 100$$

$$\text{Contribution of interaction} = \{SS(l)/SS(l \times t)\} \times 100$$

## Results and Discussion

Genetic change in plant character through natural selection plays a crucial role to create genetic variation in traits (Bashir *et al.*, 2022). Results of ANOVA depicted that all the genotypes were significantly different for the most of the attributes under study (Table 1). Different components of genetic variation in characters hold valuable information that helps in the selection of the breeding population (Zafar *et al.*, 2021b; Yali, 2022). Results of line  $\times$  tester ANOVA manifested that FS, FL, BW, FF, L%, NB/P, FFN/P, MB/P, and SB/P exhibit significant differences among parents and their crosses that showed existence of genetic variability (Table 2). Kempthorne (1957) further categories the genetic variability into general combining ability (GCA) and specific combining

ability (SCA) that helps us to understand the genetic control of character.

For hybrid development combining ability studies is a useful tool for parental lines selection (Solongi *et al.*, 2019). Further, Neelima *et al.* (2004) revealed six parents for their general combining abilities for different characters in cotton. The results of this research work indicated that parent line Tarzon-05 proved to be a very good general combiner for PH and SD. VH-329 showed good general combining ability for number of SB/P and MB/P, NB/P, FFN/P, SCY/P and L%. The line, FH-342 found to be a good combiner for BW. These results indicated that these three lines Tarzon-05, VH-329 and FH-342 have desired traits for a breeder to exploit variability in the traits which are investigated here. Among the testers, CIM-595 proved to be a good general combiner for NB/P, MB/P, and FFN/P, SCY/P and L%. CRS-2 found to be good combiner for PH, BW, and SD (Table 3). Similarly, Munir *et al.* (2016) reported the same results as the parents proved to be good general combiners. The parents which have good GCA for a specific trait are expected to give good yield in cross combinations (Khan *et al.*, 2017). This trend is found in present studies for example Tarzon-05 from lines and CRS-2 from testers indicated good general combining ability for PH and produced desired hybrids. So, these parents are supposed to be used in future breeding programs. Results of SCA of all the crosses are presented in Table 4. Among crosses, Tarzon-05  $\times$  BS-80 proved to be very good hybrids for PH. Both type of gene actions i.e., additive and non-additive found to be important for PH (Khan, 2017; Mishra *et al.*, 2015). For MB/P non-additive type of gene action is more important than additive type of gene action. The same findings were reported by (Khan *et al.*, 2017; Khokhar *et al.*, 2018). These branches give bushy look to the plants which result in slow boll formation.

**Table 3:** Estimation of GCA effects of six parents in *Gossypium hirsutum* L.

Genotypes (Parents)	PH	SB/P	MB/P	FFN/P	NB/P	BW	SCY/P	NS/B	L%	LI	FF	FS	FL	SI	SV	SD
Tarzon-05	-10.23**	-3.06**	0.06	-0.28	-1.47	-0.02	-7.42**	-0.70	-0.11	0.18	-0.61	0.34**	-0.22	0.32	-2.74	0.10**
FH-342	3.42*	-2.27**	0.15*	1.31**	-3.52*	0.30**	-6.02*	0.71	-2.23**	-0.22*	0.06	-0.01	0.07	0.31	1.42	0.03
VH-329	6.80**	5.33**	-0.25**	-1.03**	4.99**	-0.28**	13.44**	-0.01	2.34**	0.04	0.56	-0.34**	0.15	-0.63	1.32	-0.13**
CRS-2	-3.80*	-1.77**	0.12*	-0.13	-1.04	0.21**	2.12	0.26	-0.67	-0.20	-0.11	0.11**	0.97	-0.04	-2.78	0.07*
CIM-595	7.19**	0.23	-0.29**	-0.64**	3.93**	-0.18*	6.10*	0.26	1.21**	0.15	-0.78	-0.04	-0.73	-0.22	1.79	0.05
BS-80	-3.38*	1.54*	0.17**	0.77**	-2.89*	-0.03	-8.22**	-0.52	-0.54	0.05	0.89*	-0.07*	-0.23	0.25	0.99	-0.12**

\* significant \*\* highly significant. For more details and abbreviation see Table 1.



**Table 4:** Estimation of SCA effects of crosses in *Gossypium hirsutum* L.

Crosses	PH	SB/P	MB/P	FF-N/P	NB/P	BW	SCY/P	NS/B	L%	LI	FF	FS	FL	SI	SV	SD
Tarzon-05 × CRS-2	6.80*	1.44	-0.48**	1.64**	-5.08*	-0.16	-20.93**	-1.60	0.33	0.24	-0.22	0.36**	-2.45**	0.19	-5.61	0.10
Tarzon-05 × CIM-595	2.49	3.19**	0.15	-1.39**	1.40	-0.02	5.76	0.60	-0.01	-0.24	-0.56	-0.24**	0.15	-0.36	2.48	-0.03
Tarzon-05 × BS-80	-9.29**	-4.64**	0.33**	-0.25	3.68	0.17	15.17**	1.00	-0.32	0.00	0.78	-0.11	2.30*	0.17	3.13	-0.07
FH-342 × CRS-2	-2.06	1.50	0.48**	-0.24	-2.97	-0.16	-1.94	1.49	-0.02	0.07	0.11	-0.09	-1.03	0.03	2.43	-0.12*
FH-342 × CIM-595	-7.97**	-1.45	-0.01	0.88*	-6.00*	0.11	-13.31**	-0.06	0.25	-0.11	-0.22	0.56**	1.77	-0.04	-1.74	0.12*
FH-342 × BS-80	10.00**	-0.06	-0.47**	-0.64	3.03	0.04	15.24**	-1.43	0.25	0.04	0.11	-0.46**	-0.73	0.01	-0.69	-0.00
VH-329 × CRS-2	-4.73	-2.95*	0.00	-1.40**	2.10	0.13**	22.87**	0.11	-0.30	-0.31	0.11	-0.26**	3.48**	-0.22	3.18	0.02
VH-329 × CIM-595	5.45*	-1.75	-0.15	-0.15	4.60*	-0.10	7.55*	-0.54	0.23	0.35	0.78	-0.31**	-1.92	0.40	-0.74	-0.09
VH-329 × BS-80	-0.71	4.69**	0.14	0.89*	-6.70**	-0.22	-30.42**	0.44	0.08	-0.04	-0.89	0.57**	-1.57	-0.18	-2.44	0.07

\* significant \*\* highly significant. For more details and abbreviation see Table 1.

**Table 5:** Combined table for estimation of GCA variance ( $\sigma^2 GCA$ ), SCA variance ( $\sigma^2 SCA$ ) and ratio of  $\sigma^2 GCA/\sigma^2 SCA$ .

	$\sigma^2 GCA$	$\sigma^2 SCA$	$\sigma^2 GCA/\sigma^2 SCA$	$\sigma^2 A$	$\sigma^2 D$
PH	7.5388	84.4974	0.089	30.1554	337.9895
SB/P	1.5323	17.1585	0.0893	6.1293	68.6339
MB/P	-0.0052	0.2056	-0.0253	-0.0206	0.8224
FFN/P	0.0554	2.1288	0.0260	0.2218	8.5153
NB/P	-0.0052	0.2056	-0.0253	-0.0206	0.8224
BW	0.0097	0.0536	0.1809	0.0388	0.2146
SCY/P	-30.7565	644.448	-0.04772	-123.0262	2577.791
NS/B	-0.0932	1.6553	-0.0563	-0.3729	6.6210
L%	0.7805	-0.2153	-3.6252	3.1222	-0.8610
LI	0.0017	0.0640	0.0266	0.0067	0.2559
FF	0.0799	0.2361	0.3384	0.3194	0.9444
FS	-0.0097	0.3028	-0.03203	-0.0386	1.2111
FL	-0.6146	7.7885	-0.0789	-2.4585	31.1547
SI	0.0356	-0.0280	-1.2714	0.1425	-0.1121
SV	-0.0779	-0.4685	0.1663	-0.3115	-1.8741
SD	0.0020	0.0121	0.1653	0.0078	0.0485

For more details and abbreviation see Table 1.

Results of GCA, SCA variances and their ratio is presented in Table 5. For SB/P non-additive type of gene action is important than additive type of gene action. Subhan *et al.* (2003) reported that non-additive type of gene action is more important for SB/P branches. More the SB/P more will be the fruiting, because plant enters into the fruiting stage earlier. The tester CIM-595 and parental line VH-329 indicated positive GCA values which revealed that the both parents are best general combiner for number of bolls per plant. For this trait non-additive genes are more important than additive genes. The findings of present

study related to the findings of (Lakho *et al.*, 2016; Khan *et al.*, 2017; Khokhar *et al.*, 2018). For FF non-additive genetic effects were more important which relate to the findings of (Khan *et al.*, 2017). FL was also controlled by non-additive genes which confirm the results of (Isong *et al.*, 2019). FS is mostly reported to be controlled by non-additive type of gene action which is also confirmed in the previous studies by the (Gungor and Efe, 2016; Vekariya *et al.*, 2017). Fiber properties are very important in outcome of spinning process. In some traits like PH and FL, the male (testers) contribution was found to be dominant and in case of SCY/P, SB/P and NB/P, the female (lines) contributions were found to be dominant which identical to the findings of (Khokhar *et al.*, 2018). The parental lines which showed good general combining ability for a specific trait expected to produce good hybrids (Khan *et al.*, 2017). In the present, study critical comparison of cross combinations gives some interesting information. Some crosses with one parent have good GCA value and other parent have low GCA value for a particular trait showed best combinations for that trait. For example, FH-342 and CIM-595 showed poor combining ability for PH but they produced best combination with highly significant SCA value for PH. FH-342 and CIM-595 cross combination was very good combination SD but this cross produced from parents with poor combining ability. So, it is cleared from these results that parents with poor combining abilities can produce desired hybrids for a specific trait which confirms the findings of (Solongi *et al.*, 2019).

Testers i.e., CIM-595 plays an important role towards variation in MB/P, FFN/P, NB/P, SCY/P, and FS. The SI is influenced by additive genetic variance (Sahin *et*

al., 2018). This showed similar results to this research about SI. The contribution of both parents was found to be greater for variation in PH, MB/P and SB/P, NB/P, BW, SCY/P, and SD which relate to the results of (Isong *et al.*, 2019).

## Conclusions and Recommendations

Cotton genotype VH-329 recorded maximum GCA effects followed by Tarzon-05, whereas the hybrid combination for the number of nodes for first fruiting branch, boll weight, fibre length, and seed cotton yield/plant. VH-329 × CRS-2 was determined to be a good specific combiner. Except seed index, all the characters of these genotypes of cotton indicated variance of SCA greater than variance of GCA, when variance of SCA is higher than variance of GCA it means non-additive gene action is dominant over additive gene action. So heterosis breeding will be more fruitful than varietal development. Selection must be delayed in breeding populations because non-additive genes have low heritability. Parents which have good general combining ability for specific traits and the cross combinations with good specific combining ability are supposed to be used in future breeding programs for the improvement of these traits in cotton.

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## Novelty Statement

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## Author's Contribution

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## Conflict of interest

The authors have declared no conflict of interest.

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