



Research Article

Estimation of Heterosis and Combining Ability for Yield and Fibre Related Traits in *Gossypium hirsutum* L.

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Abstract | The combining ability and heterosis analysis are the important biological phenomenon that has been used to select the top performing parents and hybrids in different crop plants. In cotton, heterosis of morphological and yield related traits using line × tester design is very important to identify best performing parents in future cotton breeding program. Therefore, in this study five lines (MNH-1020, MNH-1035, FH-152, CIM-632 and BS-20) were crossed with three testers (CEMB-100, RH-662 and NIAB-5) using line × tester crossing design, which resulted 15 F₁ hybrids. The analysis of variance found significant variation between the parents and hybrids, demonstrating the presence of genetic diversity. For several traits including plant height, number of nodes per plant, number of bolls, boll weight, yield per plant, percentage of ginning outturn (GOT%), fiber length, micronaire value and fiber strength, the ratio of general combining ability (GCA) variance to specific combining ability (SCA) variance (2 GCA/2 SCA) indicated the prevalence of non-additive gene action. In addition, lines FH-152, CIM-632 and BS-20 showed a strong GCA impact for majority of the studied traits. Significant GCA effects were seen among the testers for most of the qualities in NIAB-5. Further, the hybrids FH-152 × NIAB-5 and CIM-632 × NIAB-5 displayed strong SCA effects, positive heterosis, and heterobeltosis for different important traits.

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Introduction

Cotton is the most important fibre crop in the world, and it is cultivated in more than 50 nations (Smith, 1999). Cotton belongs to family *Malvaceae* and genus *Gossypium* which contain

more than 50 species including 45 diploid and 5 allotetraploid species. Among them; the two mostly growing allotetraploid species are *Gossypium hirsutum* and *G. barbadense*, having both A and D sub-genomes (Chen *et al.*, 2007). Currently, cotton is an important cash crop in various countries including the United

States, China, India, Pakistan, Uzbekistan, Australia, and Africa (AICCIP Annual Report, 2018-19). China is second in terms of cotton production and consumption in the world (Li *et al.*, 2022), with a yield of 462 kg/ha in 2021.

Pakistan is the third-biggest cotton consumer around the globe after China and India and the sixth-largest cotton producer in terms of area and output (Ahmad *et al.*, 2014). Cotton and cotton related products contribute 10 percent to gross domestic product (GDP) and 55 percent to the foreign exchange earnings of the country (Pakistan Agriculture Research Council, 2021-22). Pakistan's cotton productivity is lower than that of other nations, hence in order to increase output, new high yielding cultivars with appropriate fibre quality criteria must be developed (Jatoi *et al.*, 2011; Akhtar *et al.*, 2014). Worldwide cotton growing area has been decreased in recent years, mostly as a result of high production costs and fierce market rivalry with other commodities (Mei *et al.*, 2013). One of the effective phenomenon used in cotton breeding efforts is heterosis. Heterosis, also known as hybrid vigor, is a frequently seen biological phenomenon that has been used to produce crops including canola, corn, sorghum, and rice. One of the goals of cotton breeders has long been to use heterosis to boost lint output, and both intraspecific and interspecific heterosis has been seen in cotton (Li *et al.*, 2022). Identification of parents that exhibit good heterosis upon crossing and the creation of high yielding hybrids are important requirements for the economic utilization of heterosis in cotton (Komala *et al.*, 2019). The degree of heterosis varies depending on the genetic distance between the parents, their reproductive mode, the traits (Zhou *et al.*, 2012), the plant development stages being studied (Groszmann *et al.*, 2013), and the environment. Estimating the heterotic effect of yield-related parameters in *G. hirsutum*, (Ekinici and Basbag, 2015) discovered substantial and favorable effects for heterosis/hybrid vigour and heterobeltiosis for seed-cotton yield, lint%, and boll weight. In addition, hybrid production using pedigree breeding and heterostic gene combinations in developing inbred lines with beneficial gene combinations have shown the importance of parents with good combining abilities (Jatoi *et al.*, 2011).

Estimation of both general and specific combining ability for fiber strength, fiber fineness, ginning turn

out, fibre length, and fibre uniformity ratio, raised the possibility of selection to enhance these characteristics (Zhang *et al.*, 2017). Breeding techniques like reciprocal selection for enhancing combining ability can be implemented by segregating populations based on various pairings of genotypes (Patil *et al.*, 2011).

The current study was designed to assess the general combining ability (GCA) impacts of parents and the specific combining ability (SCA) effects of various cross combinations using Line \times Tester mating design, keeping in mind the appropriate relevance of cotton's yield and fibre quality attributes. Further, the heterosis potential of the various economic yield-contributing and fibre quality features will also be evaluated.

Materials and Methods

The experiment was conducted in the experimental fields of The Islamia University of Bahawalpur in 2021 and 2022. In this experiment, five lines (MNH-1020, MNH-MNH-1035, FH-152, CIM-632, and BS-20) and three testers were employed (CEMB-100, RH-662, NIAB-5). Each of the 5 lines was crossed with 3 testers separately in a line-tester model, resulting in 15 different cross combinations. Genotypes of the lines and testers were raised. Using traditional hand emasculation and pollination, the crosses, which are intra specific between the genotypes of upland cotton, were created. Following this, we raised F_1 offspring from crosses and collected parental seed. Next year in 2022, the F_1 seed of 15 hybrids and their 8 parents were raised. A randomized complete block design (RCBD) was used to generate fifteen crosses in three replications, with each cross being raised in double rows of 450 cm in length, with 90 cm between rows and 40 cm between plants, in order to maintain five plants per row. In order to assess their combining ability, the parents were also grown in a nearby block with a double row for each entrance and a spacing of 90 by 40 cm. In order to achieve good crop stand, recommended agronomic methods and need-based plant protection measures were implemented. To record the biometrical observations of nine yield attributes, five competitive plants for each genotype from parents and F_1 were randomly chosen within each replication and were tagged with tags. Afterwards different morphological, yield and quality related attributes such as plant height (PH) in cm, nodes per plant (NPL), boll per plant (BP), Boll weight (BW)

in gm, yeild per plant (YPL) in gm, GOT %, fiber Length (FL) in mm, micronaire value(MIC) in $\mu\text{g}/\text{inch}$ and fiber strength (FS) in g/tex . The information on the parameters given above was statistically examined using the analysis of variance method (Steel *et al.*, 1997). Combining ability analysis was carried out in accordance to Kempthorne (1957) combining ability study. According to Fehr (1987), heterosis was measured as a percent increase (+) and decrease (-) of the F_1 hybrids compared to their mid parent and better parent heterosis values.

Results and Discussion

The analysis of variance using mean squares for the line into tester showed significant differences at 0.01 and 0.05 level of probability among the genotypes, parents, crosses, parent vs crosses, lines and testers for plant height, nodes per plant, boll per plant, boll weight, yield per plant, ginning outturn percentage, fiber length, micronaire value and fiber strength. The results showed a notable degree of diversity in the studied traits (Table 1).

General combining ability effects

As in data BS-20 shows the highest positive GCA for plant height in lines and MNH-1035 shows the highest negative value of GCA for plant height. BS-20 is best general combiner and MNH-1035 is the poor general combiner for plant height. Whereas from testers NIAB-5 shows highest positive combining ability value and RH-662 shows highest negative value as in Table 2. For NPL from lines BS-

20 is good general combiner while FH-152 is poor general combiner. While in NIAB-5 is good general combiner and CEMB-100 is poor general combiner for NPL. BPP is a significant that trait which contribute in increasing yield of cotton. For BPP BS-20 showed maximum positive GCA values and MNH-1020 shows maximum negative values. While in testers RH-662 is a good combiner and CEMB-100 is bad combiner for BPP trait. For the trait YPL we conclude that CIM-632 is a good combiner for YPL and MNH-1020 is bad combiner. While in testers NIAB-5 is a good combiner and CEMB-100 is a bad combiner for YPL. Among the lines BS-20 displayed maximum positive effects for GOT% and MNH-1035 displayed maximum negative effects for the trait GOT%. While in testers NIAB-5 has maximum positive GCA effect and RH-662 has maximum negative GCA effect for GOT%. For trait FL among lines CIM-632 is good combiner and MNH-1020 is bad combiner for the given trait. While in testers NIAB-5 is a good combiner and CEMB-100 is a poor combiner for the trait FL. Among the parents, the line MNH-1020 has maximum positive GCA value and the line CIM-632 has maximum negative value for GCA for MIC. While from tester NIAB-5 showed maximum positive effect and RH-662 maximum negative effect for GCA for MIC. For FS trait among parents, CIM-632 is best combiner and MNH-1020 is poor combiner the given trait. In testers NIAB-5 is a good combiner for FS and CEMB-100 is bad combiner for the trait FS (Table 2).

Table 1: Analysis of variance indicating mean squares for different Traits in *Gossypium hirsutum* L.

SOV	DF	PH	NPL	BPP	BW	YPL	GOT%	FL	MIC	FS
Rep	2	140.10**	4.47ns	10.73ns	0.01ns	126.83ns	0.23ns	0.00ns	0.04ns	0.08ns
Gen	22	444.50**	33.20**	237.28**	0.78**	3104.57**	43.47**	13.85**	0.58**	14.46**
cross	14	448.27**	35.02**	204.50**	0.78**	3476.23**	34.96**	8.18**	0.58**	8.78**
LINE(c)	4	614.91**	57.74**	132.05**	1.77**	5386.44**	83.18**	18.68**	1.29**	20.03**
TEST(c)	2	324.26**	57.15**	80.68**	0.67**	2983.27**	10.61*	0.20*	0.28**	1.05**
LXT (c)	8	395.96**	18.12**	271.68**	0.30**	2644.36**	16.95*	4.94**	0.30**	5.08**
P	7	482.09**	32.73**	246.66**	0.81**	1498.91**	8.28*	10.74**	0.17**	10.90**
L (p)	4	608.23**	28.23**	252.23**	0.73**	1747.25**	9.19**	11.07**	0.17**	11.20**
T (p)	2	192.11**	58.11**	312.33***	0.38**	1372.80**	8.44**	0.30*	0.06ns	0.27*
L(P)vT(P)	1	557.51**	0.01ns	93.02**	2.01**	757.77*	4.33*	30.33**	0.42**	30.98**
CrovsPAR	1	128.62**	11.01ns	630.58**	0.62**	9141.09**	408.93**	114.83**	3.40**	118.82**
Error	44	482.09	5.09	9.9	0.03	146.86	0.62	0.06	0.02	0.06
Total	68									

Table 2: General combining Ability effects for different plant traits in *Gossypium hirsutum* of line and testers.

Parents	PL	NPL	BPP	BW	YPL	GOT%	FL	MIC	FS
Lines									
MNH-1020	2.87 *	-2.80 **	-5.44 **	-0.45 **	-30.42 **	-0.98 **	-1.75 **	0.59 **	-1.81 **
MNH-1035	-10.91 **	1.31 ns	-2.67 **	-0.27 **	-17.41 **	-3.01 **	-1.04 **	0.05 ns	-1.09 **
FH-152	3.76 **	-1.58 *	2.67 **	-0.15 **	3.22 ns	-2.34 **	0.39 **	0.02 ns	0.38 **
CIM-632	-5.69 **	-0.58 ns	2.67 **	0.66 **	31.25 **	2.32 **	1.95 **	-0.37 **	2.01 **
BS-20	9.98 **	3.64 **	2.78 **	0.21 **	13.36 **	4.02 **	0.45 **	-0.28 **	0.51 **
SE	1.3387	0.6626	0.8999	0.0524	3.2171	0.3149	0.1031	0.0477	0.1039
Tester									
CEMB-100	-2.13 *	-0.31 ns	-2.64 **	-0.21 **	-15.51 **	0.47 ns	-0.04 ns	-0.00 ns	-0.01 ns
RH-662	-3.20 **	-1.78 **	1.69 *	-0.00 ns	3.47 ns	-0.97 **	-0.09 ns	0.14 **	-0.26 **
NIAB-5	5.33 **	2.09 **	0.96 ns	0.21 **	12.04 **	0.50 *	0.13 ns	-0.14 **	0.27 **
SE	1.0369	0.5132	0.6971	0.0406	2.492	0.2439	0.0799	0.0369	0.0805

Specific combining ability

The combinations MNH-1020 x RH-662 and FH-152 x NIAB-5 are good specific combiner for the trait plant height and MNH-1020 x NIAB-5 and BS-20 x NIAB-5 bad specific combiner. For trait NPL the cross MNH-1020 x NIAB-5 and FH-152 x NIAB-5 showed maximum positive value of SCA while MNH-1020 x NIAB-5 and FH-152x RH-662 showed maximum negative values for SCA. For the trait BPP the hybrid combinations CIM-632 x NIAB-5 and BS-20 x RH-662 showed maximum SCA effect for the trait BPP and the hybrid combinations CIM-632 x RH-662 and BS-20 x NIAB-5 indicated maximum negative SCA effects for the trait studied. For BW FH-152 x NIAB-5 and CIM-632 x RH-662 hybrids are good specific combiner for BW. The hybrid combinations FH-152 x RH-662 and CIM-632 x RH-662 are poor specific combiner. For trait YPL the hybrids FH-152 x NIAB-5 and BS-20 x RH-662 showed maximum positive effects for SCA for YPL while the hybrids FH-152 x RH-662 and CIM-632 x RH-662 displayed maximum negative SCA effects for the trait YPL. Hybrids MNH-1035 x CEMB-100 and FH-152 x NIAB-5 are good specific combiners while the hybrids MNH-1035 x NIAB-5 and FH-152 x RH-662 are bad specific combiner for GOT% trait. For trait FL hybrid combinations FH-152 x NIAB-5 and CIM-632 x RH-662 having maximum positive values for SCA effects while the hybrids combinations MNH-1020 x NIAB-5 and MNH-1035 x CEMB-100 having maximum negative values for SCA for the trait under study. For trait MIC the cross combinations CIM-632 x RH-662 and BS-20 x NIAB-5 are good specific combiner and the cross combinations CIM-632 x NIAB-5, FH-152 x

RH-662 and BS-20 x RH-662 are poor combiners for the given trait. Hybrids FH-152 x NIAB-5 and CIM-632 x RH-662 displayed maximum positive values for SCA for trait FS and while hybrids MNH-1020 x NIAB-5 and FH-152 x CEMB-100 showed maximum negative value for the given trait (Table 3).

The SCA variance is greater than the GCA variance for all the traits under study, this suggests that the non-additive genetic effects are more important. This means that the performance of the offspring cannot be predicted solely based on the genetic values of the parents, and the interactions between specific pairs of parents are crucial to determining the trait's expression (Table 4).

Heterosis and heterobeltosis

Heterosis and heterobeltosis for the trait plant height is positively significant. The combinations FH-152 x NIAB-5 showed maximum positive heterosis and cross MNH-1020 x RH-662 is at second number in heterosis while the same combinations displayed maximum heterobeltosis for the trait which is studied. For trait NPL the combinations FH-152 x NIAB-5 displayed maximum heterosis followed by CIM-632 x RH-662 and the hybrid BS-20 x NIAB-5 showed maximum heterobeltosis and CIM-632 x RH-662 is at second number in heterobeltosis. For trait BPP the hybrid BS-20 x RH-662 showed maximum positive heterosis and the hybrid CIM-632 x NIAB-5 is at second while the cross same crosses displayed maximum significant positive heterobeltosis for the trait which is under study. The hybrids CIM-632 x NIAB-5 showed maximum heterosis for the trait BW and the hybrid CIM-632 x RH-662 followed it while

Table 3: Specific combining ability effects for 15 hybrids of different plant traits in *Gossypium hirsutum*.

Crosses	PL	NPL	BPP	BW	YPL	GOT%	FL	MIC	FS
MNH-1020 x CEMB-100	-2.20 ns	0.20 ns	0.64 ns	0.27 **	11.78 *	-0.84 ns	1.20 **	0.21 *	1.21 **
MNH-1020 x RH-662	15.20 **	3.00 *	0.31 ns	-0.01 ns	1.46 ns	0.14 ns	0.01 ns	-0.13 ns	0.02 ns
MNH-1035 x NIAB-5	-13.00 **	- 3.20 **	-0.96 ns	-0.26 **	-13.24 *	0.70 ns	-1.21 **	-0.09 ns	-1.22 **
MNH-1035x CEMB-100	3.58 ns	-1.24 ns	0.53 ns	0.02 ns	3.87 ns	2.69 **	-0.85 **	0.09 ns	-0.84 **
MNH-1035 x RH-662	1.64 ns	-0.11 ns	0.87 ns	0.11 ns	7.18 ns	0.03 ns	0.17 ns	0.08 ns	0.17 ns
MNH-1035 x NIAB-5	-5.22 *	1.36 ns	-1.40 ns	-0.14 ns	-11.05 ns	-2.71 **	0.68 **	-0.18 *	0.66 **
FH-152 x CEMB-100	-9.76 **	-0.69 ns	3.53 *	-0.17 ns	2.17 ns	-0.65 ns	-0.95 **	0.22 *	-0.98 **
FH-152 x RH-662	-5.36 *	-2.22 ns	-8.13 **	-0.27 **	-32.22 **	-2.91 **	-0.70 **	-0.22 *	-0.73 **
FH-152 x NIAB-5	15.11 **	2.91 *	4.60 **	0.44 **	30.05 **	3.55 **	1.65 **	-0.01 ns	1.71 **
CIM- 632 x CEMB-100	3.36 ns	-0.02 ns	1.87 ns	-0.28 **	-4.46 ns	-1.07 ns	-0.60 **	-0.02 ns	-0.59 **
CIM-632 x RH-662	0.76 ns	1.44 ns	-10.13 **	0.41 **	-22.41 **	0.97 ns	1.34 **	0.24 **	1.35 **
CIM-632 x NIAB-5	-4.11 ns	-1.42 ns	8.27 **	-0.12 ns	26.87 **	0.10 ns	-0.74 **	-0.22 *	-0.76 **
BS-20 x CEMB-100	5.02 *	1.76 ns	-6.58 **	0.17 ns	-13.36 *	-0.14 ns	1.20 **	-0.51 **	1.21 **
BS-20 x RH-662	-12.24 **	-2.11 ns	17.09 **	-0.24 *	45.98 **	1.77 **	-0.82 **	0.02 ns	-0.81 **
BS-20 x NIAB-5	7.22 **	0.36 ns	-10.51 **	0.08 ns	-32.62 **	-1.64 **	-0.38 *	0.49 **	-0.39 *

Table 4: Variance due to general combining ability and specific combining ability for different traits.

	PH	NPL	BPP	BW	YPL	GOT%	FL	MIC	FS
Var of GCA	1.8495	0.5973	2.3751	0.0167	29.4094	0.637	0.1149	0.0098	0.1307
Var of SCA	126.6108	4.7257	88.1333	0.0946	850.4058	5.3529	1.6148	0.0956	1.6633
GCA/SCA	0.0146	0.1263	0.0269	0.0176	0.0345	0.119	0.0711	0.1024	0.0785

Table 5A: Mid parental and better parental heterosis of crosses.

Crosses	PH		NPL		BPP		BW	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
MNH-1020 x CEMB-100	-3.08 ns	-3.50 ns	-14.00 **	-14.00 *	-50.00 **	-50.00 **	-5.39 ns	-8.14 ns
MNH-1020 x RH-662	13.29 **	7.22 **	-1.64 ns	-10.00 ns	-29.28 **	-42.59 **	-16.30 **	-21.43 **
MNH-1035 x NIAB-5	-4.43 *	-5.69 **	-20.57 **	-23.85 **	-39.79 **	-46.30 **	-7.32 ns	-11.63 *
MNH-1035x CEMB-100	-11.37 **	-14.55 **	-6.47 ns	-6.93 ns	-31.54 **	-45.06 **	-13.48 **	-20.62 **
MNH-1035 x RH-662	-8.93 **	-16.39 **	1.09 ns	-7.92 ns	3.52 ns	1.98 ns	-11.79 **	-12.24 **
MNH-1035 x NIAB-5	-11.47 **	-15.37 **	3.81 ns	0.00 ns	-16.44 **	-25.98 **	-2.86 ns	-12.37 **
FH-152 x CEMB-100	-1.86 ns	-7.06 **	-6.45 ns	-13.00 *	-21.11 **	-29.63 **	-20.63 **	-30.56 **
FH-152 x RH-662	6.03 **	5.64 *	-7.69 ns	-9.30 ns	-19.30 **	-27.56 **	-24.27 **	-27.78 **
FH-152 x NIAB-5	21.88 **	16.40 **	7.69 ns	-3.67 ns	0.79 ns	0.79 ns	13.98 **	-1.85 ns
CIM- 632 x CEMB-100	-4.95 **	-5.26 *	-3.16 ns	-8.00 ns	-15.83 **	-32.72 **	5.49 ns	-4.95 ns
CIM-632 x RH-662	-2.55 ns	-7.68 **	6.36 ns	2.22 ns	-13.13 ns	-14.85 ns	23.62 **	21.78 **
CIM-632 x NIAB-5	-4.11 *	-5.26 *	-4.52 ns	-12.84 *	24.11 **	9.45 ns	26.82 **	12.38 **
BS-20 x CEMB-100	-0.51 ns	-6.92 **	5.26 ns	0.92 ns	-37.08 **	-48.15 **	-7.25 *	-23.81 **
BS-20 x RH-662	-7.54 **	-17.50 **	-2.08 ns	-13.76 **	63.11 **	60.00 **	-19.64 **	-28.57 **
BS-20 x NIAB-5	6.32 **	-1.35 ns	3.67 ns	3.67 ns	-28.45 **	-34.65 **	3.92 ns	-15.87 **

the same crosses displayed maximum heterobeltosis but the cross CIM-632 x RH-662 showed more heterobeltosis than cross CIM-632 x NIAB-5 (Table 5A).

For the trait yield per plant the cross CIM-632 x NIAB-5 showed maximum positive heterosis followed by the cross BS-20 x RH-662 while the same crosses showed maximum positive heterosis

in the same order as heterosis. Out of 15 crosses the heterosis percentage started from 7.67 and ends at 60.26 and the heterobeltois percentage ranges from 7.24 to 59.51 for the given trait. For the trait GOT% FH-152 x NIAB-5 showed maximum heterosis and heterobeltois values followed by the cross BS-20 x NIAB-5. For Fiber length the hybrid FH-152 x NIAB-5 having maximum heterosis and heterobeltois values followed by CIM-632 x RH-6 (Table 5B). For trait Micronire value the hybrid MNH-1020 x CEMB-100 showed maximum heterosis value followed by FH-152 x CEMB-100 and for heterobeltois the hybrid MNH-1020 x CEMB-100 showed maximum positive value and the hybrid MNH-1020 x RH-662 is second number. For FS the hybrid BS-20 x NIAB-5 showed maximum heterosis and heterobeltois values followed by the cross FH-152 x NAIB-5 which is at second number (Table 5B).

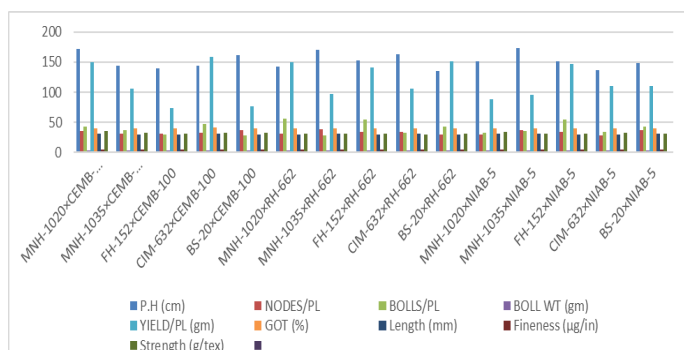


Figure 1: Mean performance of F_1 crosses.

Mean performance of traits

Mean performance of all traits is highly significant which indicates that there is variation present between them. This is an important for the breeding programs (Figure 1).

Genetic betterment of plant characters such as yield, disease resistance, and growth rate relies heavily on the availability and magnitude of genetic variability within the population. In this study, GCA to SCA ratio indicates that non-additive activity of genes has a greater effect on plant height, nodes per plant, boll per plant, boll weight, yield per plant, GOT%, fiber length, micronaire value and fiber strength. Present results are according to the results of Usharani *et al.* (2016) and Khokhar *et al.* (2018). But, Lukonge *et al.* (2008) and Khan *et al.* (2015) calculated additive gene action which is not in accordance to present results Patel *et al.* (2014) also calculated additive and non-additive both gene actions for attributes we are studied. Imran *et al.* (2012) and Monicashree *et al.* (2017) both found non-additive gene action for boll weight and boll numbers per plant which is in accordance to our results. The current study's findings correspond with those of YanalAlkuddsi *et al.* (2013) showed that non-additive genetic effects on seed cotton yield and GOT %. According to recent research, fiber strength and fiber length are major indicators of fiber quality attributes and are significantly influenced by non-additive genetic factors. These results appear to

Table 5B: Mid parental and better parental heterosis of crosses.

Crosses	YPL		GOT%		FL		MIC		FS	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
MNH-1020 x CEMB-100	-52.89 **	-54.10 **	-12.48 **	-12.66 **	-7.60 **	-13.52 **	27.71 **	26.19 **	-8.01 **	-13.93 **
MNH-1020 x RH-662	-39.70 **	-48.50 **	-16.97 **	-20.22 **	-12.52 **	-18.84 **	22.40 **	21.43 **	-13.37 **	-19.56 **
MNH-1035 x NIAB-5	-44.42 **	-52.47 **	-10.85 **	-13.08 **	-15.33 **	-21.13 **	13.62 **	11.45 **	-14.96 **	-20.49 **
MNH-1035x CEMB-100	-39.78 **	-48.14 **	-12.73 **	-16.13 **	-14.04 **	-17.58 **	13.47 **	13.01 **	-14.08 **	-17.94 **
MNH-1035 x RH-662	-8.69 ns	-10.16 ns	-25.14 **	-25.28 **	-11.86 **	-16.25 **	16.26 **	15.32 **	-12.42 **	-17.00 **
MNH-1035 x NIAB-5	-17.80 *	-19.25 *	-26.88 **	-28.10 **	-9.12 **	-13.28 **	0.40 ns	-3.05 ns	-8.53 **	-12.69 **
FH-152 x CEMB-100	-36.33 **	-37.37 **	-17.15 **	-18.76 **	-10.23 **	-13.52 **	23.48 **	15.45 **	-10.71 **	-13.93 **
FH-152 x RH-662	-39.04 **	-47.52 **	-28.75 **	-30.07 **	-10.50 **	-14.56 **	15.15 **	7.26 *	-11.47 **	-15.32 **
FH-152 x NIAB-5	15.00 **	-0.86 ns	37.62 **	26.27 **	6.99 **	1.04 **	10.08 **	0.00 ns	5.53 **	1.14 **
CIM- 632 x CEMB-100	-8.90 ns	-20.66 **	-5.81 **	-6.37 **	-9.15 **	-10.54 **	3.36 ns	0.00 ns	-9.16 **	-10.42 **
CIM-632 x RH-662	7.57 ns	7.24 ns	-8.05 **	-10.97 **	4.96 **	4.36 **	12.97 **	8.87 *	-4.90 **	-5.45 **
CIM-632 x NIAB-5	60.26 **	59.51 **	6.21 **	5.85 **	-9.51 **	-10.44 **	-8.13 **	-13.74 **	-8.87 **	-10.07 **
BS-20 x CEMB-100	-38.97 **	-39.02 **	2.37 ns	1.13 ns	-4.28 **	-6.81 **	-8.26 **	-9.76 **	-4.06 **	-6.97 **
BS-20 x RH-662	30.94 **	14.26 *	-0.55 ns	-5.37 ns	-11.63 **	-14.76 **	7.82 *	5.65 ns	-11.83 **	-15.17 **
BS-20 x NIAB-5	-23.75 **	-33.37 **	6.59 *	3.92 **	-9.14 **	-11.97 **	9.60 **	4.58 ns	15.19 **	8.04 **

study showed a variety of heterosis and heterobeltosis for different plant characteristics. The current findings agree with those presented by Patil *et al.* (2011). Combinations FH-152 × NIAB-5 demonstrated the most heterosis while the hybrid BS-20 × NIAB-5 revealed the most heterobeltosis. These findings are according to the results of Monicashree *et al.* (2017). For trait BPP, the hybrids BS-20 × RH-662 and CIM-632 × NIAB-5 showed the most positive heterosis, respectively, and the same crosses also showed the most significant positive heterobeltosis. Vineela *et al.* (2013) showed similar results for F1 cotton hybrids. The hybrids CIM-632 × NIAB-5 is at top for the trait BW. The findings of Seoudy *et al.* (2014) are consistent with the characteristic under investigation in the current study. For the trait YPL the cross CIM-632 × NIAB-5 proved to be at top due to its positive and maximum heterosis and heterobeltosis values. The findings here are consistent with those of Tyagi *et al.* (2014). The trait GOT% FH-152 × NIAB-5 had the highest levels of heterosis and heterobeltosis and established itself as the greatest new cross combination. For the lint percentage, reported a decent level of heterosis and heterobeltosis present findings are aligning with his results. The hybrid FH-152 × NIAB-5 has the highest heterosis and heterobeltosis values for fiber length, followed by CIM-632 × RH-662. The current results correspond with those of Baloch *et al.* (2014). The results of the current study are consistent with those of Sajjad *et al.* (2016) and Maqbool *et al.* (2017). The findings of parental contributions in hybrid offspring, as seen in the current study, are further supported by the findings of Saleh and Ali (2012) and Khokhar *et al.* (2017). The micronaire value's decline is a sign of finer fiber. The findings of earlier investigations (Usharani *et al.* 2016) are consistent with the discoveries found in the current study. The hybrid BS-20 × NIAB-5 displayed the highest levels of heterosis and heterobeltosis for FS.

Conclusions and Recommendations

It was concluded the tester NIAB-5 and three lines, namely BS-20, FH-152, and CIM-632, displayed favorable traits as general combiners for both yield and fibre attributes. In addition, both yield and fiber-related attributes were found to be well-performed by the F1 hybrids FH-152 × NIAB-5 and CIM-632 × NIAB-5 showing that these particular combinations produced promising results in future cotton breeding

program to improve yield and fibre quality traits. For sustainable cotton production, this research can aid in improving breeding techniques and creating high-yielding cultivars through targeted hybridization.

Novelty Statement

This research endeavors to elucidate the dynamics of these genetic phenomena, shedding light on optimizing upland cotton cultivation for improved productivity and quality.

Author's Contribution

Javaria Ashraf: Conducted research and analysis.

Ali Hassan: Write-up and data analysis.

Salman Wahid and Kamran Alyas: Helped in data collection.

Sadia Kanwal and Sadia Kanwal: Results interpretation.

Amna Bibi, Samaria Nisar and Rameen Nawaz: Helped in literature review and proofreading.

Conflict of interest

The authors have declared no conflict of interest.

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