International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print), 2222-5234 (Online)
http://www.innspub.net
Vol. 15, No. 2, p. 166-173, 2019

INNSPUB

RESEARCH PAPER OPEN ACCESS

Estimation of heterosis and combining ability for some quantitative parameters in *Gossypium hirsutum*

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Key words: Cotton; Fiber traits; Genetic effects; Hybrid vigour; SCA.

http://dx.doi.org/10.12692/ijb/15.2.166-173 Article published on August 09, 2019

Abstract

Cotton is an important oilseed andfiber crop in Pakistan as well as in world. Improvement can be madein yield and fiber characteristics of cotton crop after understanding the various mechanisms of gene actions controlling the yield contributingtraits.In the current study, four genotypes of cotton namely, NIAB-KIRN, FH-942, PB-896 and PB-76 were crossed in a random mating fashion. The parents and F_1 hybrids were planted in field in three replicationsfollowing randomize complete block design. At maturity, data were collected for yield and fiber related traits. Analysis of variance of mean valuesexhibitedthe presence of significant variations. This data were analyzed for their assessment of combining ability, where it is found that the genotype NIAB-KIRN has additive gene action for number of seeds/boll, seed index and seed cotton yield per plant. Thus, nominated as a good general combiner.Whereas PB-896 × PB-76 showed good specific combining ability for seed-cotton yield/ plant and cotton-seed yield per plant, while the combination of PB-896 × FH-942 has exhibited significantly high heterosis for fiber and seedcotton yield.Based on this information the parents and combinations have potential of genetic material for yield of seed cotton as well as fiber related parameters.

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Introduction

Cotton belongs to genus*Gossypium* andfamily Malvaceae. More than 50 speciesof genus *Gossypium* are reported till now. Amongst them, 45 are diploid and 5 are allotetraploid, where*Gossypium hirsutum* and *G.barbadense*which had both A and D sub-genomes arecultivated allotetraploid species (Chen *et al.*, 2007).Naturally *G. hirsutum* is a perennial, woody shrub plant with indeterminate type of growth habit (Cothren and Oosterhuis, 2010). Within species,genetic variation is necessary to start a breeding program for the improvement of particular trait of interest(Azhar *et al.*, 2009). The information about the extent and type of genetic variation relies on different methodologies used for its assessment (Bajracharya *et al.*, 2006). There are severaltypes of breeding methods that can be utilized to achieve the desired genetic variability in segregating populations. These methods include selection after hybridization and mutation (Esmail *et al.*, 2008). The breeding importance of different crops depends upon the combining ability and genetic variation in relation to traits(Ilyas *et al.*, 2007). For the assessment of combining abilities,diallel analysis has been used successfully in variousfield crops like cotton(Singh *et al.*, 2010), wheat(Mahpara *et al.*, 2017), rice(Shabbir *et al.*, 2018) and maize(Murtadha *et al.*, 2018). Combining ability analysis given byGriffing is beingthought-out to be valuablefor plant breeders(Griffing, 1956). Mating of genotypes inall possible combinations extent the genetic variation of filial generations and is supportive for the estimation of both combining abilities*i.e.* general and specific(Gilbert, 1958).Breeding tools which are utilized for hybrid production based upon high level of heterosis and specific combining abilities(Khan *et al.*, 2009). From breeding point of view, commercial heterosis is important because it is aimed to develop hybrids which are superior over existing cultivars in the market.Estimation ofboth combining abilities,*i.e.,* general and specific for fibre strength, fibre fineness, ginning turn out, fiber length and fiber uniformity ratio in previous studies suggested the idea of selection to improve these traits(Green and Culp, 1990;Zeng and Pettigrew, 2015; Kothari *et al.*, 2016;Zhang *et al.*, 2016;Zhang *et al.*, 2017). In another study, GCA effects werefound to be significantforfibrestrengh, fibre length and fiber uniformity ratio (Coyle and Smith, 1997).(Ekinci *et al.*, 2010)estimated the heterotic effect of yield related parameters in *G. hirsutum*, and found significant and positive effects for heterosis/hybrid vigour and heterobeltiosis for seed-cotton yield, lint percentage and boll weight. As both combining abilities *i.e.* general and specific as well as heterosis estimates are useful tools to determine gene action to achieve further breeding objectives. Therefore, this research was aimed to assess GCA, SCA and heterosis in available cotton cultivars and advance breeding lines for varioustraits to identify potential breeding material.

Materialsand methods

Development of F_1 hybrids and assessment in field conditions

The presentedresearchwas conducted during the year 2016-2018 at research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. The experimental site is situated at31.42° latitude and 73.08°longitudes. The planting material for this study was developed by crossing four genotypes, namely PB-76, PB-896, NIAB-KIRN and FH-942 in a complete diallel fashion. The parents were grown in earthen pots in glasshouse during October 2016. The optimal growing conditions *i.e.* temperature (25-35°*C*)and lightintensity (25,000-30,000 lux) was maintained for germination and growth of the plants in glasshouse. At the time of flowering, self, direct and reciprocals crosses were made between the genotypes. A large number of pollinations were made in order to produce sufficient quantity ofF_0seed.Cotton seed fromselfed and crossed bolls were picked at maturity and kept separately in cloth bags. Later on F_0seed along with their parents was sown in field in triplicates according to randomized complete block design by keeping 75 ×30 cm row and plant spacing. All the recommended agronomic practices were adopted including thinning and proper fertigation to have good plant population per unit area.

Data recording

At maturity, data were collected for yield and fiber traits.The traits involved wereplant height, number of bolls/ plant, boll weight, seed/ per boll, cotton seed yield/ plant, seed-cotton yield/ plant,lint index, seed index, fibre length, fibre strength, fibre fineness and fibre uniformity ratio. When epical growth of the main stem had ceased, the plant height startingfrom the zero node to epical bud of five guarded plants from each parent as well as progeny was measured by using measuring rod.All offully opened bolls from these plants werecounted and picked in cloth bags. Later on, numbers of seeds per boll were counted. Average boll weight was calculated by dividing the total seed cotton yield per plant with the number of pocked bolls of respective plant. The mean boll weight of plants in each replication was calculated, likewise cottonseed yield was also recorded for each plant for statistical analysis.Weight of lint in a sample and weight of seed cotton was determined to calculate ginning turn outby using formula,

$$\text{Lint percentage} = \frac{\text{Weight of lint in a samle}}{\text{Weight of seed cotton in a sample}} \times 100$$

While, lint index was recorded by using the following formula,

$$\text{Lint index} = \frac{\text{Seed index} \times \text{Lint \%}}{100 - \text{Lint \%}}$$

A high-volume instrument (modelUSTER® HVI 900 SA) available in the Department of Fiber Technology, University of Agriculture, Faisalabad was used to measure fiber quality parameters from clean sample of lint obtained from bolls of selected plants. This computerized instrument recorded fiber length (mm), fiber strength (g/tex), fiber fineness (µg/inch) and fiber uniformity ratio according to international standards.

Statistical analysis

The analysis of variance was employedas proposed by Steel *et al.* (1997)on recorded datato find the genotypic variation for selected traits by using Statistix 8.1 software(McCullagh, 2018).Once it was known that significant variation exist in the data set, then comining ability (Griffing, 1956) and heterosis estimates (Falconer and Mackay, 1996) were calculated by using Dial98 (Ukai,2006).

Results

Mean squares of various traits for genetic variability are described in Table 1 and 2. For all the studied traits including yield and fiber, significant variations were found in the germplasm genotypes. These differences indicated the suitability of genotypes for genetic studies.

Table 1. Analysis of variance in the form of mean squares of various traits for genetic variability.

SOV	DF	PH	NB/P	BW	NS/B	CSY/P	SCY/P	SI	LI	GOT	FL	FS	FF	FUR
Replications	2	27.82	1.06	0.04	16.45	58.6	41.08	0.44	1.36	64.35	1.1	0.41	0.09	18.43
Genotypes	15	308.53**	2.48*	4.76**	57.10**	116.32**	285.80**	0.51*	1.74**	71.54*	2.72**	6.15**	0.28*	53.80**
Error	30	31.18	1.2	1.25	22.77	53.14	14.35	0.14	0.53	21.23	1.31	1.3	0.03	11.35

Where, df stands for degree of freedom; * and **, denote difference significant at 5% and 1% probability levels, respectively.

It wasfound that NIAB-KIRNexhibited highest positive GCA effect for cottonseed yield (Table 3).Furthermore, PB-76 and FH-942 had maximum positive and significant GCA for number of seeds/boll and yield of cotton-seed respectively.PB-896 showed significant and maximum GCA for uniformity ratio of fibre.The cross among NIAB-KIRN × FH-942 exhibited positive SCA for plant height while its parental genotypes exhibited negative GCA for this trait.The hybridof PB-76×PB-896 revealed maximumeffects ofSCA for number of bollsper plant,fiber fineness and seed index. While hybrids namely, FH-942 × PB-76 and PB-896 × PB-76 showed negative SCA fornumber of boll per plant WhileFH-942×PB-76 revealed as good specific combiner for seed index and boll weight. PB-896 × FH-942 was proved to be best combination for uniformity ratio of fiber and seed/boll. For yield of seed cotton and GOT%, hybrid PB-896 × NIAB KIRNexhibited highest value for SCA.

Table 2. Analysis of variance in the form of mean squares of various traits for combining ability analysis.

SOV	DF	PH	NB/P	BW	NS/B	CSY/P	SCY/P	SI	LI	GOT	FL	FS	FF	FUR
GCA	3	8.66**	1.42*	0.20*	0.45*	63.67**	111.06**	0.02**	0.22^{ns}	11.02**	0.69*	0.80*	0.06*	12.45**
SCA	3	216.51**	0.97*	2.72**	3.65**	33.85**	83.01**	0.13*	1.05*	25.28**	1.69*	4.00**	0.14*	14.87*
Reciprocals	6	15.73*	0.77*	0.84*	0.96*	13.44*	55.87*	1.45*	0.56*	6.78*	2.77**	3.66*	0.58**	6.76*
Error	30	2.09	0.19	0.45	1.53	2.84	23.66	2.04	1.38	7.34	2.65	1.73	0.45	3.87

Note: List of abbreviations has been provided.

The cross of FH-942 × NIAB KIRN displayed positive significant SCA for fiber length. The cross among NIAB KIRN × PB-76 showed positive SCA for fiber strength.These findingsindicated the existence of non-additive gene behavior ingoverning theseparameters.

In addition to combining ability, the heterotis percentages for all of traits are briefed out in Table 4.The hybrid of NIAB-KIRN × FH-942 exhibited maximum heterosis for plant height while indirect cross of these accessions exhibited highly significant heterosis for number of bolls per plant. For number of seeds per boll and boll weight, PB-896 × FH-942 showed highest heterosis estimates.Heterosis %age was ranged from 2.01% to 26.23% for plant height.Nine out of twelve hybrids displayed maximum positive and significant heterosis. PB-76 × FH-942 showed highest hybrid vigor for boll weightwhile the hybrid PB-896 × PB-76 exhibited highest heterosis estimate for seed present per boll and yield of seed-cotton.

The heterosis was ranged from 2.43 to 56.74% for seed-cotton yield per plant.Maximum heterosis %age for fibre length (11.89%) and fibre strength (8.4%) were exhibited by hybrids PB-896 × PB-76 and PB-76 × FH-942, respectively.

Table 3. General and specific combining ability effects data for all traits.

Crosses	PH	NB/P	BW	NS/B	CSY/P	SCY/P	SI	LI	GOT	FL	FS	FF	FUR
P1	0.80*	0.69 **	0.08	0.92	-0.44	-0.26	-0.03	0.20	-1.58	-0.04	0.40	0.11 *	1.42
P2	1.20*	-0.44	-0.07	1.72*	-0.61	1.47	-0.06	-0.27	1.72	-0.46	-0.49	-0.14 **	-0.62
P3	-0.65*	-0.07	-0.22	1.42	4.45 **	5.95 *	0.07	0.03	0.06	0.27	0.06	0.03	0.92
P4	-1.35*	0.18	0.21	0.62	3.39 *	4.23*	0.03	0.04	-0.20	0.23	0.03	-0.01	-1.72 *
P1 × P2	-14.55**	-1.68 **	-1.72 **	-0.40	10.61**	15.78 **	0.49 **	-1.19 **	2.75*	-2.32**	-3.82 **	-0.74 **	-0.40
P1 × P3	6.65	-0.24*	0.94 **	-3.09 **	-2.37	-2.58	0.35**	0.51 **	5.05**	0.24	0.12	-0.13 *	-3.09 **
P1 × P4	-12.33 *	-0.73 *	-1.36 **	6.43 **	2.59	4.0	0.34**	-0.12	-4.37**	0.48	-0.28	-0.03	6.43 **
P2 × P1	0.34	2.21*	2.75*	4.55**	2.34*	0.65	3.28*	3.11**	0.65	1.98*	0.045	3.43**	4.55**
P2 × P3	-10.21	0.29 *	-1.45 **	3.36 **	-4.22 *	-7.36 *	-0.07	1.17 **	2.8*	0.23^{ns}	1.68 **	0.25 **	3.36 **
P2 × P4	9.09	0.77*	0.82 *	-1.03	-3.85 *	-2.58	0.19*	-1.20 **	-3.87**	-0.79 *	1.08 **	0.05	-1.03
P3 × P1	2.45*	-0.43 *	-0.39	-3.45**	0.46	0.76*	-2.11*	-1.83	2.87**	-0.34	0.34	-2.43*	-3.45**
P3 × P2	-0.24	0.32 *	-2.67*	2.65*	-3.45*	-1.89	0.30	0.44	-3.67**	2.76*	3.45**	1.63	2.65*
P3 × P4	20.64 **	0.37 *	-1.70 **	2.39 *	3.31	7.79 *	-0.02	0.21	-5.14**	-0.86 *	0.16	-0.08	2.39 *
P4 × P1	-1.54*	0.42 *	0.03	-1.33	-2.31	6.87*	-3.21*	-2.56*	0.38	-3.38**	-2.98**	0.03	-1.33
P4 × P2	0.34	-2.64*	3.45*	0.27	5.34*	-5.34	3.45*	-0.55	-0.45	-1.75	-0.34	0.31	0.27
P4 × P3	-0.45	3.45**	0.29	2.12*	0.045	2.45	0.54	1.56	0.29	4.28**	-0.31	0.45	2.12*

Where, P1= PB-896, P2= PB-76, P3-=NIAB-KIRN, P4= FH-942.

Discussion

Genetic improvement in vegetative and reproductive traits of cotton relies on the magnitude of genetic variation that exists in germplasm. Therefore, plant breeders are keen to know about the genetic component of variation for the concerned trait. Biometrical data showed significant variation for all parameters observed in this research. The genetic component of variation is thanadditionally divides into two elements*i.e.* GCA and SCA.These components provide appropriate understanding about genetic control of plant traits. LowerGCA to

SCA ratios revealed theprevalence of non-additive gene action for studied traits. These findings were in conformitywith (Aslam *et al.*, 2015;Maqboool *et al.*, 2017;Khokhar *et al.*, 2018).However, Rauf*et al.* (2005) reported that the involvement of both additive and non-additive genetic effects for fiber traits. Parental lines with maximumSCA estimates are expected to produce productive hybrids by crossing with suitable testers.Significant GCA effects for parents indicated the possibilities of transferring these traits to progenies(Samreen *et al.*, 2008). The use parents either with positive or negative GCA depends upon the nature of traits and target of breeding programs. For example, parents showing positive GCA for yield of seedcotton can be used to enhance yield through breeding while for plant height and fiber fineness, parents with negative GCA are suitable as lower or medium values for these traits are desirable(Ashokkumar *et al.*, 2010).

Table 4. Heterosis percentages data for all studied traits.

Crosses	PH	NB/P	BW	NS/B	CSY/P	SCY/P	SI	LI	GOT	FL	FS	FF	FUR
P1 × P2	-21.50	-7.93	-64.20**	64.39*	58.98*	56.74*	14.56**	-36.40**	10.56^{ns}	11.89**	-20.98**	-19.83**	2.09^{ns}
P1 × P3	2.52	3.96	-3.47^{ns}	2.75^{ns}	20.22^{ns}	25.56^{ns}	-6.09	18.74*	18.16*	-0.88^{ns}	-1.58^{ns}	6.36*	-4.12^{ns}
P1 × P4	-21.11	0.03	52.59**	53.45**	6.17^{ns}	15.33	18.77**	-12.20^{ns}	-17.14*	-0.71^{ns}	-4.26^{ns}	-4.85^{ns}	24.72**
P2 × P1	7.23	0.23	25.34^{ns}	-14.47^{ns}	21.67^{ns}	23.21^{ns}	2.33^{ns}	12.39*	17.24*	1.02^{ns}	2.01^{ns}	2.02^{ns}	22.56**
P2 × P3	2.56	0.28	32.73^{ns}	4.28^{ns}	12.34*	16.52	3.70*	10.34^{ns}	17.22^{ns}	3.11*	4.21^{ns}	11.02*	12.89*
P2 × P4	-17.39	0.01	-62.66**	21.32^{ns}	-10.34^{ns}	8.49	-0.57^{ns}	35.02*	9.83^{ns}	-2.01^{ns}	8.49*	-2.95^{ns}	11.55^{ns}
P3 × P1	5.67	2.07	-7.18^{ns}	35.56**	3.22^{ns}	2.43^{ns}	8.77*	38.80**	-15.51*	-6.19^{ns}	4.65^{ns}	-1.32^{ns}	3.99^{ns}
P3 × P2	26.23*	15.23	2.03^{ns}	-12.34^{ns}	-26.20^{ns}	-14.23*	1.88^{ns}	10.21^{ns}	13.22*	0.23^{ns}	3.12^{ns}	23.88**	-3.55^{ns}
P3 × P4	2.01	1.02	14.23^{ns}	23.37^{ns}	2.76^{ns}	-6.90	7.54*	34.32*	12.32*	3.22^{ns}	2.21^{ns}	2.93^{ns}	0.45^{ns}
P4 × P1	14.21	-2.20^{ns}	23.43*	14.21**	34.12^{ns}	2.54	2.76^{ns}	2.87^{ns}	10.23^{ns}	4.22^{ns}	2.01^{ns}	3.23^{ns}	4.23^{ns}
P4 × P2	13.44	21.43*	12.11^{ns}	4.75^{ns}	33.59^{ns}	-11.54	0.03^{ns}	12.23*	13.22*	3.02^{ns}	3.12^{ns}	2.04^{ns}	2.01^{ns}
P4 × P3	21.13*	2.20^{ns}	-64.27**	3.75^{ns}	19.32*	43.83^{ns}	-0.20^{ns}	9.81^{ns}	-18.66*	-4.28^{ns}	3.95^{ns}	-1.63^{ns}	13.74*

Where, P1 = PB-896, P2= PB-76, P3= NIAB-KIRN, P4= FH-942.

Present study displayed significant heterosis for fiber and yield parameters. Results regarding heterotic effects for seed cotton yield/plant suggested that five F_1 hybrids displayed positive and significant heterosis.Comparison between the observed heterosis of hybrids and the GCA effects of their parents revealed the range of heterosis. Most of the productive hybrids*i.e.* (NIAB-KIRN×PB-896) and(PB-76 × PB-896)were the results of crosses between parents exhibiting high and low GCA estimates(Arain *et al.*, 2015). Generally, high heterosis(Bilwal *et al.*, 2018)was observed in those crosses where one of the two parents had quite lower GCA estimate as compare to others. Some of hybrids were observed with high heterosis values from the crosses between two parents having high GCA estimates(Patil, 2018). In many cases, the crosses between parents possessing high GCAs for a given traits results into inferior hybrids(Jatoi and Memon, 2016). Thus, based upon the results, the hybrid PB-896 × PB-76 exhibited superior SCA for yield of seedcotton and cottonseed yield per plant while the hybrid PB-896 × FH-942 exhibited highly significant heterosis for yield of seed cotton and fibre related parameter. The mentioned results are in accordance with (Kannan and Saravanan, 2016;Tigga *et al.*, 2017;Balakrishna *et al.*, 2017).The genetic components are highly influenced by environmental conditions, so potential of these hybridscould be assesses after cultivation in multi-location trials in the cotton belt of Pakistan.

Conclusion

The investigations found in this study opened the avenues for exploitation of parents and their hybrids for heterosis breeding for various traits. The higher values of GCA, SCA and heterosis indicate that there is great chance to select the potential genotype for certain traits which can be exploited in future for advancement of yield and fiber related parameters.

List of abbreviations

GCA, general combining ability, SCA, specific combining ability, PH, plant height; NB/P, number of bolls/plant; BW, boll weight; NS/B, number of seed/ boll; CSY/P, cotton seed yield/ plant; SCY/P, seed cotton yield/plant; SI, seed index; LI, lint index; GOT, ginning out turn; FL, fiber length; FS, fiber strength; FF, fiber fineness; FUR, fiber uniformity ratio.

Declaration of interest

Not applicable.

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