Research article

Genetic analysis of morphological and yield contributing traits in upland cotton (*Gossypium hirsutum* **L.**)

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Abstract
The use of already existing genetic variability in the breeding material as well as the creation of new variability along with the genetic understanding of various agronomic traits is of crucial importance to develop potential sources of cotton. The 5x5 complete diallel cross experiment was carried out in order to determine gene action as well as general and specific combining ability consisting of five parental genotypes namely MNH-700, BH-162, CIM-499, FH-634 and Sarmast. All the traits were controlled by additive type of gene action with partial dominance. Maximum numbers of dominant genes were observed in FH-634 for plant height and number of sympodial branches. Variety CIM-499 has maximum number of dominant genes for number of bolls, number of sympodial branches and seed cotton yield while SARMAST has maximum number of dominant genes for boll weight. MNH-700 was good general combiner for boll weight and number of bolls, CIM-499 for seed cotton yield and number of sympodial branches while BH-162 and FH-634 for plant height and number of monopodial branches, respectively. From above results it was suggested that these characters can be improved through appropriate selection procedure because all these characters are controlled by additive type of gene action with partial dominance while the parents with good specific combining abilities for certain traits can be used for hybrid development.
Key words: Cotton, genetic analysis, morphological traits, yield traits.

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Introduction

Cotton is a warm climate crop grown in 80 countries worldwide. It is cultivated from 45^0 North to 32^0 South by over 20 million farmers. Over 90 percent of cotton in the world is *Gossypium hirsutum* L. or upland cotton, while about 10 percent of cotton in the world is related to species *G. barbadense* L. [1]. Cotton (*Gossypium hirsutum* L.) is of great economic importance for Pakistan as it plays a vital role in agriculture, industrial development, employment generation and earning of foreign exchange through export of its raw material as well as finished products. This crop also is of a major concern to our textile industry as it provides basic raw material needed in its expansion. Cotton seed is an important source of edible oil too. It contributes 65-70% to the local edible oil production. Low grade oil is utilized in soap and lubricant manufacturing. Residual seed cake is a valuable protein concentrate used for livestock feed [2]. Efforts on various aspects of the crop have been under way to increase its overall production. The most important factor in the production process has always been a good variety of any crop. Cotton breeders managed to produce high yielding varieties through various genetic manipulations and breeding approaches and consequently, a significant progress was achieved in this connection. As the improvement in yield and quality in agricultural crops is a continuous process,

therefore, the breeders are busy all the time in adopting different techniques and approaches for improving the production of the crops based on the information generated through genetic analysis of the varieties and/or species. The first step in a successful breeding program is to select appropriate parents to be used. The diallel analysis technique devised by Hayman [3] that was reviewed and studied by Mather and Jinks [4] is a useful tool to obtain precise information about the type of gene action involved for the expression of various plant characters. It provides a systematic approach for the detection of appropriate parents and crosses superior in terms of the investigated traits. The present research work was launched to obtain the genetic information for some economic plant traits in cotton by using diallel techniques. This type of information may help the plant breeders to launch a breeding program for cotton improvement.

Material and Methods

The present experiment was carried out at experimental area of the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the years 2007-2009. The experimental material consisting of five parental genotypes namely MNH-700, BH-162, CIM-499, FH-634 and SARMAST, representing a range of morphological and yield contributing traits, were

sown in earthen pots placed in glasshouse during November, 2007. During germination and growth, environmental conditions were possibly controlled and recommended agronomic practices were carried out. In glasshouse, temperature was maintained at 40^oC along with 65% relative humidity throughout the growth period. The plants were exposed to natural sunlight also supplemented with artificial sun light for a total period of sixteen hours. At flowering stage, the parental lines were crossed in a complete diallel fashion (5 x 5) to generate 20 F_1 crosses (including reciprocals) along with 5 selfs.

At maturity, selfed and crossed bolls were picked and cotton seeds were ginned with single roller ginning machine. The F_0 seeds from all crosses along with their parents were sown in the field during June, 2008 following triplicate Randomized Complete Block Design (RCBD). In each replication 25 entries were planted. Nine seeds were sown per row with a distance of 30 cm and 75 cm within and between rows, respectively. All recommended agronomic practices and crop protection measures were carried out from sowing to harvesting of the crop. All P_2O_5, K_2O and 1/3 of the nitrogen fertilizer were applied at the time of sowing. At maturity, the data were recorded from the 5 guarded plants on individual plant basis for plant height, number of monopodial branches, number of sympodial branches, number of bolls, boll weight and seed cotton yield. The data thus collected was subjected to analysis of variance technique in order to determine the genetic differences for characters under study [5]. The characters showing significant genotypic differences were further analyzed genetically, following the additive dominance model of genetic analyzed developed by Hayman [3] and Mather and Jinks [4]. SPSS version 11.5 statistical software (SPSS, Chicago, USA) was used for detailed analysis.

Result and Discussion

All the genotypes for all the traits showed highly significant results for genetic component of variation (Table 1), thus data could be further analyzed by additive dominance model. Array values and mean value of array of 5x5 diallel (Table 2-6) were used to estimate general and specific combining abilities of various traits studied respectively. The Vr/Wr graphs of the analyzed data are shown in Fig. 1-6. Results

are discussed in detail, as under:

Plant height

The values of variances (Vr) and co-variances (Wr) were calculated and Vr/Wr graph in Fig. 1 shows that an additive type of gene action with partial dominance was involved in the inheritance of plant height as the regression line intercepted the Wr-axis above the point of origin. Epistasis was absent as the regression line did not deviate significantly from unit slope. The results were in accordance with Steel et al. [5] and Laxman and Ganesh [6] while were differed from the results of some other researchers [7] who reported dominance type of gene action for this character. From the varietal positions on the regression line, it was observed that FH-634 being closer to the point of origin had maximum dominant genes and Sarmast being away from origin possessed most of the recessive genes. Table-2 indicated that variety BH-162 with maximum array mean value (188.03) had the best general combining ability while the cross CIM-499 x BH-162 indicated the best specific combining ability for plant height.

Number of monopodial branches

The Vr/Wr graph in Fig. 2 shows that an additive type of gene action with partial dominance was involved in the inheritance of number of monopodial branches as the regression line intercepted the Wr-axis above the point of origin. The results supported the observations of Naveed et al. [11] and Nimbalkar et al. [12], while were differed from Iqbal et al. [10] and Laxman and Ganesh [6] who observed dominant type of gene action for this character. From the varietal positions on the regression line, it was observed that BH-162 being closer to the point of origin had maximum dominant genes and MNH-700 being away from the point of origin possessed maximum recessive genes. Table-2 indicated that variety FH-634 with maximum array mean value (3.64) had the best general combining ability while the cross Sarmast x FH-634 indicated the best specific combining ability for number of monopodial branches.

Number of sympodial branches

The Vr/Wr graph in Fig. 3 shows additive type of gene action with partial dominance was involved in

Table 1 Mean squares of analysis of variance of different cotton characters.

SOV	DF	Height (cm)	MB	SB	No. of bolls	Bolls (g)	Yield (g/plant)
Genotype	24	752.6250**	0.981339**	9.26698**	87.59428**	0.391185**	932.1523**
Replication	2	107.3807	0.022198	0.66490	0.559575	0.003601	13.89742
Error	48	105.7862	0.016888	1.09956	2.488103	1.584791	14.08230

**=Highly significant at 5%, DF = degree of freedom, MB = Monopodial branches, SB = Sympodial branches, SOV = source of variation

the inheritance pattern of number of sympodial branches as the regression line intercepted the Wr-axis above the point of origin. Epistasis was absent as the regression line did not deviate significantly from unit slope. The results were in accordance with Steel et al. [5], Nimbalkar et al. [12] and Laxman and Ganesh [6] while differed from Ahmad et al. [8] and Iqbal et al. [10] and Naveed et al. [11] who reported dominance type of gene action for this character. From the varietal positions on the regression line it was observed that CIM-499 being closer to the point of origin had maximum dominant genes and Sarmast being away from the point of origin possessed most of recessive ones.Table-3 indicated that variety CIM-499 with maximum array mean value (21.83) had best general combining ability while the cross MNH-700 x CIM-499 indicated the best specific combining ability for number of sympodial branches.

Number of bolls per plant

The Vr/Wr graph in Fig. 4 shows that the regression line intercepted the Wr-axis above the point of origin indicating additive type of gene action with partial dominance was controlling the

expression of this character. The results were in accordance with Iqbal et al. [10] and Abbas et al. [13] while differed from the results of some other researchers [9, 14, 15] who reported dominance type of gene action for number of bolls. The distribution of array points on the regression line indicated that the variety CIM-499 being closest to the point of origin possessed maximum dominant genes while the variety MNH-700 being farthest from the point of origin possessed maximum recessive genes. Table- 3 showed that the variety MNH-700 possessed maximum array mean value (26.26) thus seemed to be the best general combiner while the cross FH-634×MNH-700 possessed maximum value (28.83) indicating the best specific combining ability for this trait.

Boll weight

The Fig. 5 shows that an additive type of gene action with partial dominance controlled the inheritance pattern of this trait as the regression line intercepted the Wr-axis above the point of origin. The results were similar to those of Murtaza [16] and

Table 2 5x5 diallel Table for plant height and number of monopodial branches.

Varieties	MNH-700		BH-162		CIM-499		FH-634		SARMAST	
	Plant height (cm)	Monopodial /plant	Plant height (cm)	Monopodial /plant	Plant height (cm)	Monopodial /plant	Plant height (cm)	Monopodial /plant	Plant height (cm)	Monopodial /plant
MNH-7OO	173.62	2.14	184.18	2.98	175.90	2.81	181.93	3.56	162.10	2.68
BH-162	184.18	2.98	196.24	3.03	194.82	3.06	188.61	3.34	176.31	3.17
CIM-499	175.90	2.81	194.82	3.06	182.26	3.05	182.32	3.56	164.27	3.01
FH-634	181.93	3.56	188.61	3.34	182.32	3.56	185.70	3.92	178.47	3.80
SARMAST	162.10	2.68	176.31	3.17	164.27	3.01	178.47	3.80	140.68	3.02
Total	877.73	14.2	940.16	15.6	899.57	15.5	917.03	18.2	821.83	15.7
Mean	175.54	2.83	188.03	3.12	179.91	3.10	183.41	3.64	164.37	3.14

Table 3 5x5 diallel Table for number of sympodial branches and number of bolls.

Varieties	MNH-700		BH-162		CIM-499		FH-634		SARMAST	
	Sympodia /plant	Number of bolls	Sympodia /plant	Number of bolls	Sympodia/ plant	Number of bolls	Sympodia/p lant	Number of bolls	Sympodia/p lant	Number of bolls
MNH-7OO	21.90	34.92	20.83	23.63	22.13	20.29	21.67	28.83	19.86	23.63
BH-162	20.83	23.63	18.83	19.83	21.97	18.53	19.48	18.81	18.13	17.18
CIM-499	22.13	20.29	21.97	18.53	22.28	15.25	20.99	18.85	21.79	19.47
FH-634	21.67	28.83	19.48	18.81	20.99	18.85	21.28	18.17	20.67	15.72
SARMAST	19.86	23.63	18.13	17.18	21.79	19.47	20.67	15.72	17.01	11.83
Total	106.39	131.3	99.24	97.98	109.16	92.39	104.09	100.3	97.46	87.83
Mean	21.28	26.26	19.85	19.60	21.83	18.48	20.82	20.08	19.49	17.57

Table 4 5x5 diallel Table for boll weight (g) and cotton seed yield (g).

| Varieties	MNH-700		BH-162		CIM-499		FH-634		SARMAST	
	Boll weight (g)	Seed yield (g)	Boll weight (g)	Seed yield (g)	Boll weight (g)	Seed yield (g)	Boll weight (g)	Seed yield (g)	Boll weight (g)	Seed yield (g)
MNH-7OO	3.32	95.17	3.11	74.73	2.83	48.85	2.82	70.85	2.71	61.14
BH-162	3.11	74.73	3.15	63.18	2.88	43.99	2.93	51.51	2.25	44.85
CIM-499	2.83	48.85	2.88	43.99	2.67	40.73	2.62	44.11	2.25	35.83
FH-634	2.82	70.85	2.93	51.52	2.62	44.11	2.80	50.21	2.33	31.78
SARMAST	2.71	61.14	2.25	44.85	2.25	35.83	2.33	31.78	2.09	25.55
Total	14.79	350.74	14.32	278.27	13.25	213.51	13.5	248.47	11.63	199.15
Mean	2.96	70.15	2.86	55.65	2.65	42.70	2.70	49.69	2.33	39.83
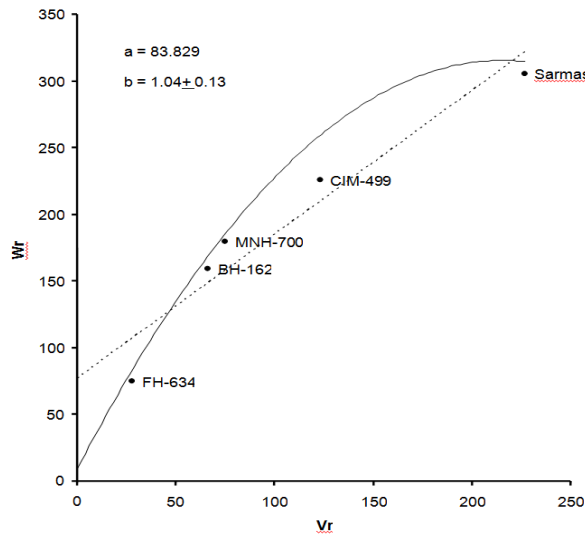
Fig. 1 Plant height
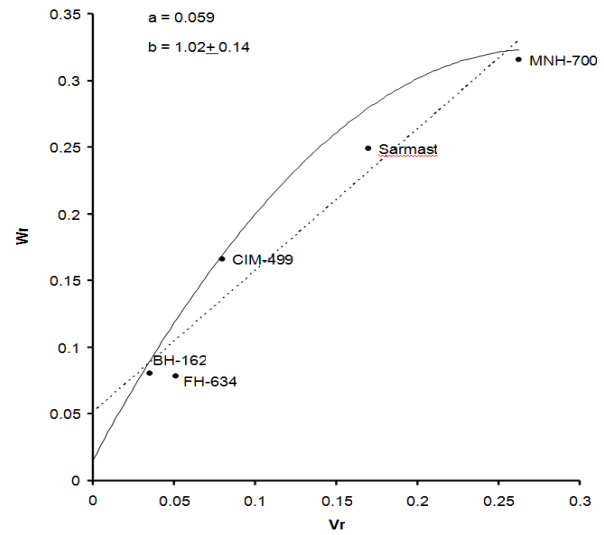

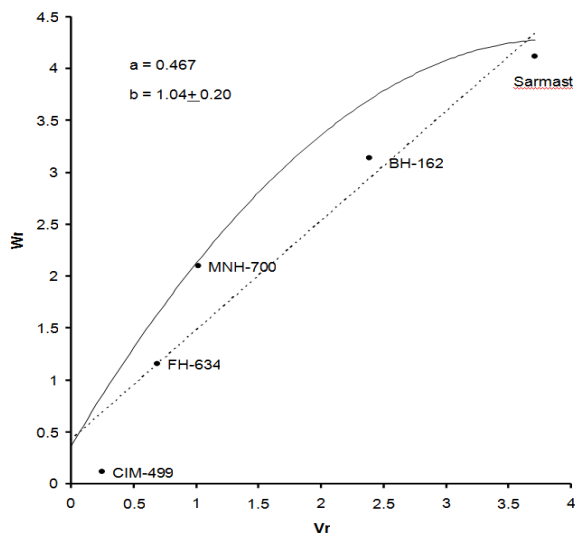**Fig. 2** Number of Monopodial branches

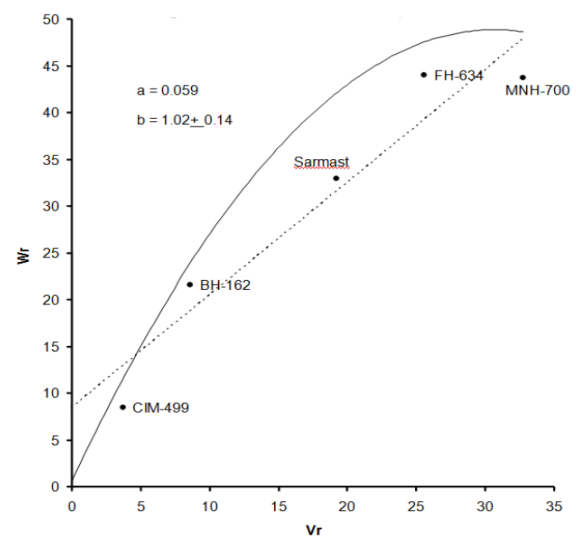**Fig. 3** Number of symbodial branches
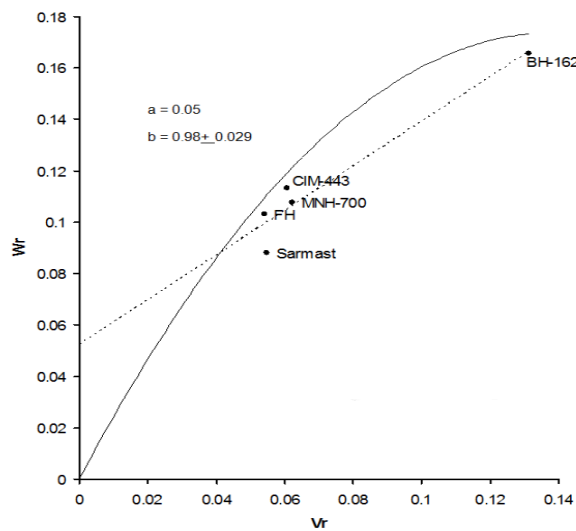

Fig. 4 Numbere of bolls
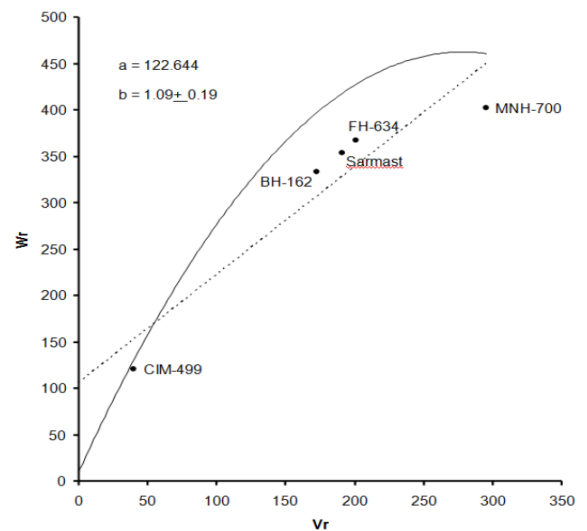

Fig. 5 Boll weight

Fig. 6 Cotton seed yield

Basal and Turgut [15]. While differed from Esmail [1] and Khan et al. [2] who reported dominance as well as over dominance type of gene action for this trait. From the varietal position on the regression line it was observed that Sarmast being closest to the point of origin possessed maximum number of dominant genes while BH-162 being farthest to the point of origin possessed maximum number of recessive genes. The data in Table 4 revealed that the variety MNH-700 with highest array mean value (2.96) proved to be best general combiner while the crosses BH-162 x MNH-700 showed the good specific combining ability with value (3.11) for boll weight.

Seed cotton yield

An additive type of gene action with partial dominance was involved in the inheritance of seed cotton yield as the regression line intercepted the Wr-axis above the point of origin (Fig. 6). Epistasis was absent as the regression line did not deviate significantly from unit slope. The results were similar to those of Abbas et al. [13] and Ming-bao et al. [17] while differed from the results of other researchers [1, 2, 6] who reported dominance type of gene action for this character. From the varietal positions on regression line, it was observed that that variety CIM-499 being closest to the point of origin possessed the maximum number of dominant genes while MNH-700 being away from the point of origin possessed maximum number of recessive genes. Table 4 indicated that variety MNH-700 with maximum array mean value (70.15) had best general combining ability, while the cross BH-162 x MNH-700 indicated the good specific combining ability with highest value (74.73) for seed cotton yield.

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