

Genetic Studies of Various Morphological Traits in Upland Cotton (*Gossypium hirsutum* L.)

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A complete diallel cross experiment was conducted involving five cotton (*Gossypium hirsutum* L.) genotypes viz. SLH-41, F-281, COKER-3113, LA-85-52-1 and H-88-8-J.69-J.70 to explore genetic effects controlling various quantitative traits. Data on major agronomic traits including plant height, number of monopodial branches, sympodial branches, number of bolls per plant and boll weight were recorded. All the genotypes were found to be significantly different from each other for the above mentioned traits. Joint regression analysis proved the validity of the data of all traits for additive-dominance model. All the traits almost showed over dominant type of gene action while the inheritance of number of sympodial branches was of additive type with partial dominance. Over dominance suggested heterosis breeding as an appropriate tool for improvement of these traits.

Key words: Diallel analysis; Cotton genetics; Yield parameters; Variation; *Gossypium hirsutum* L.

Cotton occupies a unique position in Pakistan's agriculture economy. Efforts on various aspects of cotton crop improvement have been under way to increase its overall production of the country. The economy of Pakistan mainly depends upon cotton production, back bone of foreign exchange earnings, exportable surplus of cotton fiber and fiber made products. The total share of cotton is about 69 % annually in foreign exchange and economy of the country. Its share in the GDP of agriculture is 1.6 % and also significant role in domestic oil production⁷. The crop not only meets

the need of the fiber of the local industry but also provides edible oil for cooking purpose and low grade oil for the soap manufacturing industries. Residual seed cake is a valuable protein concentrate that is used for livestock feed⁷.

The factor in the process of crop production is an essential and has always been a good variety of a crop³³. Breeders are trying to produce high yielding varieties by using new molecular techniques and their significant impact on improving the economy of the country. The main focuses of the plant breeder on crop variety improvement for the enhancement of yield, production and quality of the crop.

For a successful cross parents must be genetically diverse and physiologically efficient³³. Keeping this in view, an experiment was undertaken

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in the University of Agriculture, Faisalabad, Plant Breeding and Genetics department, to study the gene action in F_1 hybrids to select suitable parents for the evaluation of high yielding hybrids, well adaptive to the prevailing climatic conditions and having better quality. The current research work was carried out to analyze some important cotton cultivars to ascertain the relative performance regarding gene control for yield and its components.

The diallel analysis technique devised by Hayman¹⁴ and Jinks¹⁵ which was reviewed and studied by Mather and Jinks²⁰ is an important tool to obtain knowledge about the types of gene action that involved and expressed in various yield characters³⁸. Diallel analysis provides the information about the superiority of parents and crosses on the basis of various investigated traits. The present study was to obtain desirable genetic information on the basis of various morphological traits by using Hayman¹⁴ and Jinks¹⁵ approach through diallel fashion.

MATERIALS AND METHODS

The experiment was conducted at University of Agriculture, Faisalabad in the experimental area of Plant Breeding and Genetics department, during the years 2007-08. The experimental material consisted of five parental genotypes namely SLH-41, F-281, COKER-3113, LA-85-52-1 and H-88-8-J.69-j.70 representing a range of yield and fibre quality traits, was sown in earthen pots placed in greenhouse during November 2007. Various agronomic practices were followed during germination and other growth environmental conditions. In glass-house, temperature was maintained at 35-40°C throughout the period. At flowering, the parental lines were crossed in a complete diallel fashion (5×5) to generate 20 F_1 crosses (direct and indirect) along with 5 self-crosses. All the plants were ginned for further studies. The F_0 seed from all crosses along with their parents was sown in the field during June-2008 in RCBD with three replications. In a replication 25 entries were planted each in a single row having 10 plants with a distance of 30cm and 75cm within and between rows respectively. At maturity, the data were recorded for plant height, number of bolls per plant, boll weight, number of

monopodial branches and number of sympodial branches on five guarded plants from each entry, both in field as well as laboratory on individual plant basis. All the traits were analyzed by using techniques of analysis of variance³⁶ to study the plant and other genetic analysis by Hayman¹⁴ and Jinks¹⁵ approaches.

RESULTS AND DISCUSSIONS

Analysis of variance for plant height showed highly significant differences among the genotypes evaluated. Results of joint regression analysis (Table 2) indicated that data were fit for additive-dominance model. A perusal of (Fig 1) indicated that regression line intercepted the Wr-axis is fairly below the origin revealing that over dominant type of gene action was controlling this character. The regression line deviation from unit slope showed absence of non allelic interaction. The results were compatible with those of Pavasia *et al.*²⁸ and Khan *et al.*¹⁷. While some other scientists like Murtaza *et al.*²² and Bertini *et al.*⁹, Khan *et al.*¹⁶ and Shakeel *et al.*³⁵ reported additive type of gene action and Kumeresan *et al.*¹⁸ reported both type of gene action for this trait. The variety SLH-41 possessed maximum dominant genes due to very close to the array point's origin of distribution on regression line whereas the variety LA-85-52-1 had maximum recessive genes due to away from the point of origin (Fig-1).

The genotypes had highly significant differences for bolls number per plant. Results of joint regression analysis (Table-2) indicated that data were quite fit for additive-dominance model. The Fig-2 showed that regression line intercepted the Wr-axis below the origin showing over dominant type gene action. Over-dominance which is in accordance with Khan *et al.*¹⁶, Murtaza *et al.*²², Amin *et al.*⁵, Ahmad *et al.*², Ahmad and Mehra¹, Bertini *et al.*⁹ and Shakeel *et al.*³⁵, whereas, Carvalho *et al.*¹⁰, Saeed *et al.*³¹, Yingxin and Xiangming³⁹, Goudar *et al.*¹² and Subhan *et al.*³⁷ reported additive type of gene action also Kumeresan *et al.*¹⁸ and Rauf *et al.*³⁰ reported both type of gene action additive and non additive for this trait. Sambamurthy and Ranganadhacharyulu³⁴, Murtaza²³, Nadeem and Azhar²⁴ reported both additive and dominance gene action.

Table 1. Analysis of variance for agronomic traits in 20 crosses and 5 self-pollinated

SOV	d.f.	Plant height	No. of bolls per plant	Boll weight	Number of sympodial branches	Number of monopodial branches
Replication	2	0.39 ^{NS}	0.12 ^{NS}	0.32 ^{NS}	1.67 ^{NS}	1.07 ^{NS}
Genotypes	24	7.99**	483.27**	25.63**	19.41**	6.22*
Error	48					
Total	74					

NS= Non Significant, *= Significant at ± 0.05 , **=Significant at ± 0.01

Table 2. Results of Joint Regression Analysis

S. No.	Character	b	Remarks	Conclusions
1	Plant height	0.97 \pm 0.11	b value deviated significantly from zero but not from unity.	The data were adequate for simple additive-dominance model.
2	Number of bolls per plant	0.92 \pm 0.13	b value differed significantly from zero but not from unity.	The data were fit for additive-dominance model
3	Boll weight	0.89 \pm 0.92	b value differed significantly from zero but not from unity	The data were fit for additive-dominance model
4	No.of sympodial branches	1.11 \pm 0.16	b value differed significantly from zero but not from unity.	The data were adequate for genetic analysis.
5	No.of monopodial branches	0.98 \pm 0.22	b value differed significantly from zero but not from unity.	The data were fit for additive-dominance model

The variety H-88-8-J.69-J.70 obtained dominant genes being closest to the origin of regression line whereas the variety COKER-3113 had recessive genes being away from origin point (Fig-2). For boll weight significant differences existing among the genotypes were observed. Results of joint regression analysis (Table 2) indicated that data were fit for additive-dominance model. A perusal of (Fig-3) indicated that regression line intercepted the Wr-axis below the origin revealing over dominance type of gene action controlling this character.

The results seemed to be compatible with those of Murtaza *et al.*²² and Bertini *et al.*⁹ while Khan *et al.*¹⁶ and Shakeel *et al.*³⁵ while differed from Gururajan and Henry¹³ as they revealed the additive type of gene action and Nadeem and Azhar²⁴ reported additive dominance type of gene action was controlling this character. The variety F-281 having dominant genes being closest to the origin whereas the variety SLH-41 had maximum

recessive genes and vice versa for other traits. (Fig-3).

The analysis of variance for plant height indicated highly significant differences among the genotypes (Table-1). Results of joint regression analysis (Table 1) indicated that 'b' value (0.99 ± 0.10) deviated significantly from zero but not from unity showing that the data were adequate for additive-dominance model suggested by Hayman¹⁴ and Jinks¹⁵. The Vr/Wr graph (Fig. 4) indicated that this character is governed by over dominance type of gene action as the regression line intercepted Wr axis below the origin.

The results are in accordance with the findings of Ajmal *et al.*³, and Ahmad and Mehra¹, Saif *et al.*³², Shakeel *et al.*³⁵, Deshpande and Baig¹¹ and Naveed *et al.*²⁵ while Carvalho *et al.*¹⁰, Khan *et al.*¹⁶, Murtaza *et al.*²², Mukhtar *et al.*²¹ and Khan *et al.*¹⁷ reported additive type of gene action in phenotypic manifestation of this character. Figure 4 revealed that variety F-281 has maximum

dominant genes as it is nearest to the origin whereas H-88-8-J.69-J.70 has maximum recessive genes as it is the farthest from the origin.

Analysis of variance for number of sympodial branches showed highly significant differences existing among the genotypes evaluated (Table-1). Results of joint regression analysis indicated that data were fit for additive-dominance model (Table-2). A perusal of indicated

the partial and additive type of gene action was also involved for various character because the regression line intercepted the W_r -axis is fairly above the origin (Fig-5). On the other hand, the variety LA-85-52-1 possessed maximum dominant genes while the variety COKER-3113 obtained maximum recessive genes (Fig-5).

The results seemed to be compatible with those of Amin *et al* ⁵, Ajmal *et al.*³, Malek and

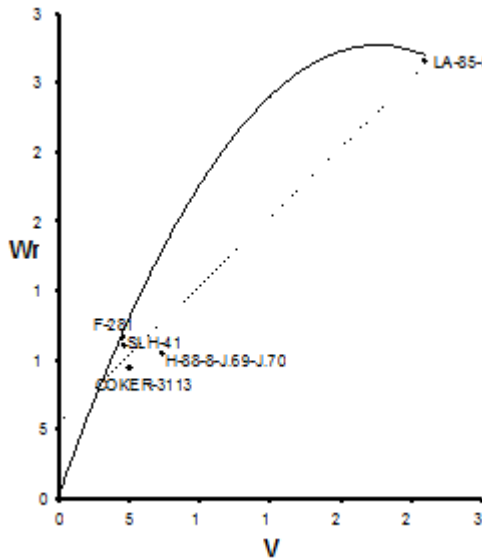


Fig. 1. Joint regression for plant Height

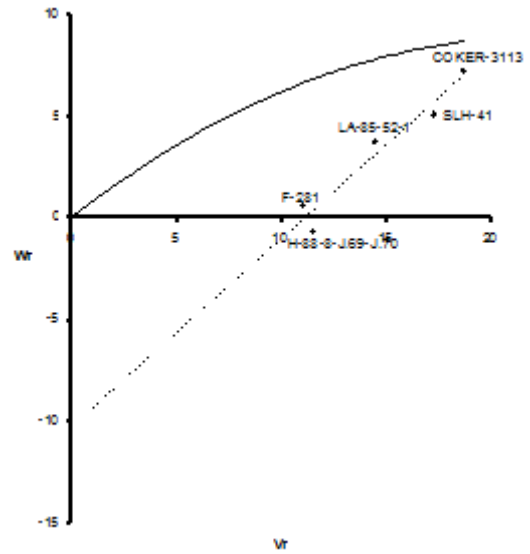


Fig. 2. Joint regression for number of bolls per plant

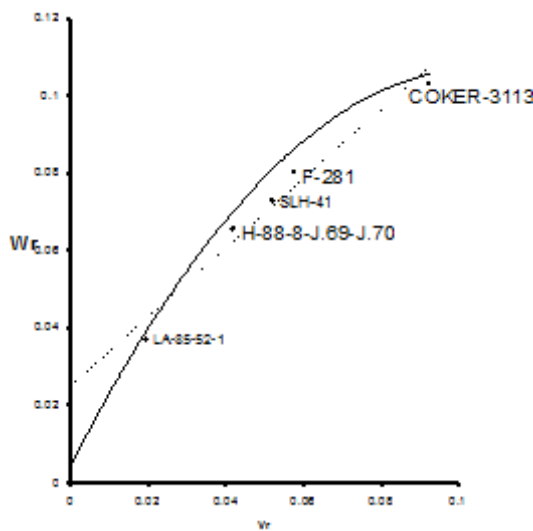


Fig. 3. Joint regression for boll weight

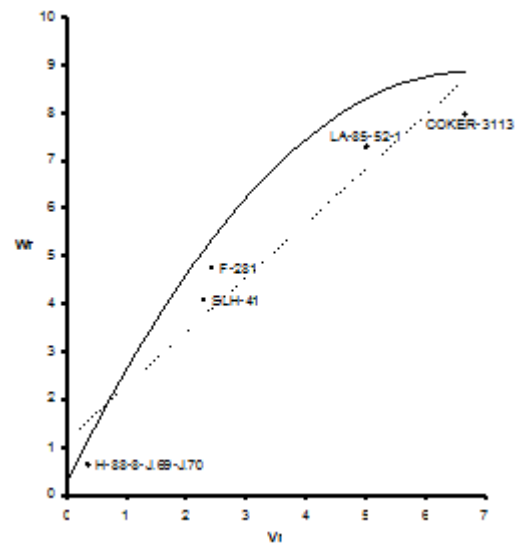


Fig. 4. Joint regression for sympodial branches

Shamsuddin¹⁹, Paxasia *et al.*²⁹, Ali *et al.*⁴, Banumathy and Patil⁸, Khan *et al.*¹⁷, Anisa *et al.*⁶, Neelima *et al.*²⁶, Nimbalkar *et al.*²⁷, while differed from Murtaza *et al.*²² and Bertini *et al.*⁹ while Khan *et al.*¹⁶ and Shakeel *et al.*³⁵ reported additive type of gene action also Ahmad *et al.*² and Rauf *et al.*³⁰ indicated both additive and non additive genetic variation.

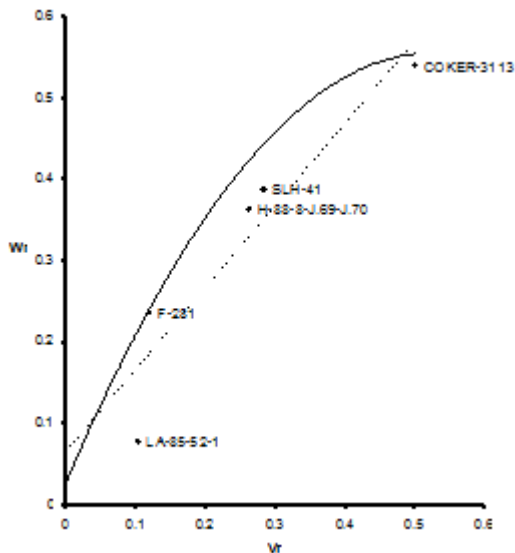


Fig. 5. Joint regression analysis for monopodial branches

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