GENETIC ANALYSIS FOR VARIOUS TRAITS IN *GOSSYPIUM HIRSUTUM* L.

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ABSTRACT:-A 6 x 6 complete diallel mating design was used to study the inheritance of different plant traits in upland cotton (*Gossypium hirsutum* L.). Six genotypes viz., **BJA-592**, **ACALA-SJ-4**, **4-F**, **CP-15/2**, **CIM-497** and **PB-899** were included in diallel crosses. Results revealed that over-dominance type of gene action was controlling the inheritance of monopodial and sympodial branches plant height number of bolls and boll weight. The line CP-15/2 possessed maximum dominant genes for monopodial branches, plant height and boll weight, BJA-592 for sympodial branches and ACALA-SJ-4 has maximum dominant genes for bolls per plant. However the cultivar CIM-497 carried maximum recessive genes for monopodial branches and plant height, PB-899 for bolls per plant and sympodial branches while ACALA-SJ-4 has maximum recessive genes for boll weight.

Key Words: Cotton; Inheritance; Plant Traits; Gene Action; Diallel Crosses; Pakistan.

INTRODUCTION

Cotton (*G. hirsutum* L.) is the world's leading fibre crop with annual production of 20 mt and grown in more than 80 countries. It contributes 60% in the total foreign exchange through the exports of value added products (Iqbal et al., 2005). It is an important cash crop for Pakistan. Cotton accounts for 8.6% of the value added in agriculture and about 1.8% to GDP of Pakistan (Anonymous, 2010). Pakistan is the 4th largest cotton producing country in the world after China, USA and India, and 3rd largest consumer of cotton (Akhtar, 2005). Cotton is the major source of vegetable fibre and genetic improvement in its fibre quality, resistance against insect pests, durability and colour must be made to keep pace with changing circumstances. Besides being the world's fourth largest cotton producer, the third largest exporter of raw cotton, and a leading exporter of yarn, Pakistan's cotton yield per acre ranks 13th in the world (Ghazala and Rasul, 2010).

Cotton breeders have made remarkable efforts to improve genetic makeup of cotton plant for the improvement in its production potential and fiber quality traits through breeding. The use of genetic information in the development of efficient breeding programme has been advocated by Hayman (1954), Mather and Jinks (1982), McCarty et al. (2004a and b), Khan (2003), Mei et al. (2006), Wu et al. (2006), Khan et al. (2007). Since past several years, cotton yield has been stagnant, therefore, efforts are going on to improve cultivars yield to fulfill the growing demand of fibers. Any information on the inheritance of different plant characters along with general and specific combining ability may help breeders in their efforts in that direction.

Through complete knowledge and understanding of inheritance fashion of various morpho-yield traits is a pre-requisite for enhanced progress in breeding new varieties of cotton. The diallel analysis technique (Mather and Jinks, 1982) is a useful tool to obtain precise information about the type of gene action involved for the expression of various yield and fibre traits. It provides a systematic approach for the detection of appropriate parent and crosses superior in terms of the investigated traits.

The aim of this study was to determine the type of gene action involved by means

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of diallel analysis of different F_1 cotton hybrids to establish some genetic parameters and to decide either early selection is favorable or the delayed selection towards later generations may give good results for different parameters.

MATERIALS AND METHODS

The six genotypes i.e. ACALA-SJ-4, PB-899, BJA-592, CP-15/2,4-F and CIM-497 were crossed in a diallel fashion. The 30 F_1 progenies alongside with parents were grown in a randomized complete block design with three replications. The plant to plant and row to row distance was kept at 30 and 75 cm, respectively. Each genotype consisted of 10 plants in each replication. The five plants were selected for collection of data. The height of plants was recorded when apical growth of the main stem ceased. The monopodial and sympodial branches on individual plant were counted and recorded at the end of the picking. The total number of bolls picked at each pick was counted and cumulative record was maintained for each plant separately. The average number of bolls per plant was computed for each genotype. Average boll weight was calculated by dividing the total seed cotton yield per plant with the total picked number of bolls of the respective plant, for data analysis. The mean boll weight of family in each replication was calculated.

Data were subjected to analysis of variance (Steel et al., 1996) to determine significant differences among F_1 hybrids and their respective parents. The diallel cross technique developed by Hayman (1954) and Jinks (1954) modified by Mather and Jinks (1982) and adopted by Singh and Chaudhry (1985) was followed for genetic analysis of the data.

RESULTS AND DISCUSSION

Analysis of variance indicated significant differences among parental genotypes and populations for all the traits (Table 1). The results obtained from the diallel analysis are discussed herewith.

Plant height regression line intercepted the Wr-axis below the point of origin (Figure 1) indicating over-dominance type of gene action involved in the inheritance of plant height which means that the
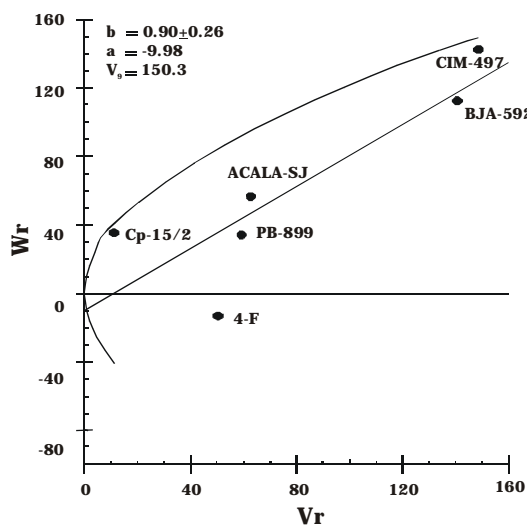

Figure 1. Vr/Wr graph for plant height

genotypes are efficient for producing hybrids and perform better for this parameter in hybrids. Similar results have been reported by Soomro (2000), Saravanan et al. (2003), Subhan et al. (2003), Mukhtar et al. (2005) and Naveed et al. (2005).

However, results differ from those of Ahmad et al. (2003), Inam and Azhar (2004), Nadeem and Azhar (2004) and Ahmed et al. (2006) who reported additive type of gene action for this character. This difference in the phenotypic manifestation could be

Table 1. Mean squares of various plant characters studied

SOV	df	Plant height	Monopodial branches	Sympodial branches	Bolls/ plant	Boll weight
Replications	2	49.88676	0.056759	4.130833	2.228981	0.093333
Genotypes	35	406.88480	0.366656	38.702360	216.943800	0.398381
Error	70	36.00333	0.032664	2.605119	1.921458	0.090095

due to different varieties tested under different environmental conditions. Non-allelic interaction was absent as the regression line did not deviate significantly from unit slope. From the varietal positions on regression line it was observed that variety CP-15/2 had maximum dominant genes being closest to the point of origin while variety CIM-497 had most of recessive genes being farthest from origin.

For monopodial branches the regression line passed through Wr-axis below the point of origin for number of monopodial branches (Figure 2), it signified that inheritance of this trait was controlled
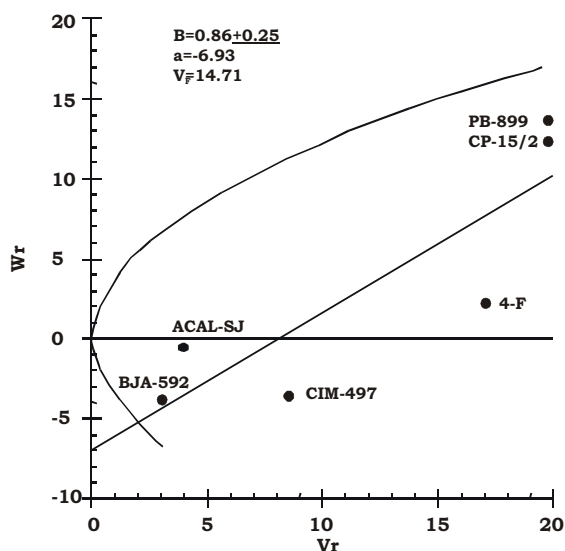

Figure 2. Vr/Wr graph for monopodial branches

by over dominance type of gene action and reveals that the character may be observed better in hybrids for these varieties. Results are similar to those of Neelima et al. (2004), Mukhtar et al. (2005) and Naveed et al. (2005) while differ from Khan et al. (2000) and Nimbalkar et al. (2004) who reported additive type of gene action for this character. As the regression line did not deviate significantly from unit slope, therefore, there is no evidence of non-allelic interaction of this trait. From the position of array points on the regression line it was clear that the variety CP-15/2 occupied the nearest position from The point of origin and had maximum dominant genes whereas variety CIM-497 that occupied the farthest position from the point of origin possessed most of recessive ones.

Over-dominance type of gene action was controlling the inheritance of sympodial branches as the regression line intercepted the Wr-axis below the point of origin (Figure 3) will be useful if used for hybrids for these varieties which may perform better. The results are compatible
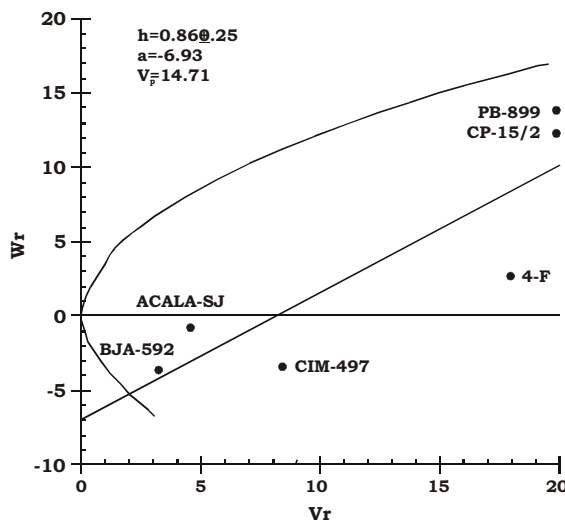

Figure 3. Vr/Wr graph sympodial branches

with the findings of Soomro (2000), Mukhtar et al. (2005) and Naveed et al. (2005) while Khan et al. (2000), Ahmad et al. (2003) and Baloch et al. (2004) reported additive type of gene action involved in the phenotypic expression of this trait. As the regression line did not deviate significantly from unit slope, so, epistasis was absent. From the position of array points on regres-
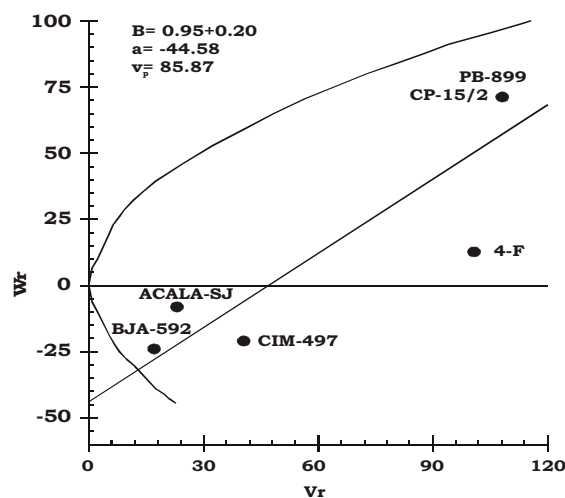

Figure 4. Vr.Wr graph for bolls per plant

sion line it was observed that variety ACALA-SJ-4 being closer to the origin had maximum dominant genes while PB-899 being away from origin carried maximum recessive genes.

The graphical representation for number of bolls showed that regression line (b) intercepted the Wr-axis below the point of origin (Figure 4) indicating over-dominance type of gene action involved in the expression of this character and it will be observed better if selection in hybrid for these varieties is delayed until late generations. Similar results have been reported by Shakeel et al. (2001), Saravanan et al. (2003), Inam and Azhar (2004), Neelima et al. (2004), Murtaza (2005) and Ahmed et al. (2006) while Ahmad et al. (2001 and 2003), Baloch et al. (2004), Nadeem and Azhar (2004), Azhar and Khan (2005), Mukhtar et al. (2005) and Naveed et al. (2005) reported additive type of gene action with partial dominance. The distribution of the array points on the regression line indicated that the variety ACALA-SJ-4 received maximum dominant genes being closest to the point of origin whereas the variety PB-899 being farthest from point of origin received maximum recessive genes.

A perusal of Figure 5 illustrated overdominance type of gene action controlling for the inheritance of boll weight supports the idea of better performance for this char-
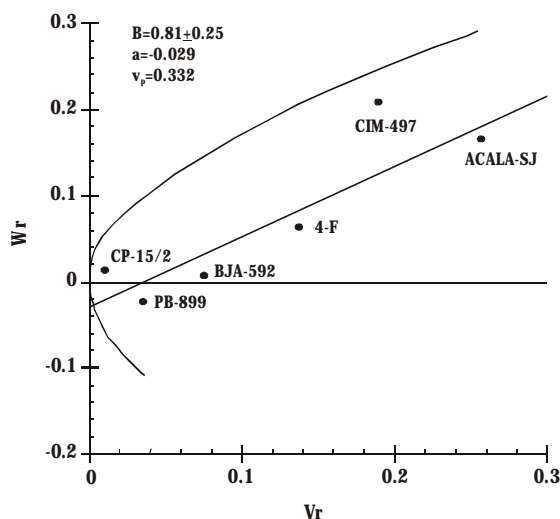
acter in hybrids of these varieties as the regression line intercepted the Wr-axis below point of origin. The results differ from those of Banumathy and Patil (2000), Ahmad et al. (2001) and Shakeel et al. (2001) while Saravanan et al. (2003), Subhan et al. (2003) and Tuteja et al. (2003) who reported additive type of gene action with complete dominance involved in the phenotypic manifestation of this trait. It confirmed the absence of epistasis. As far as the position of array points on regression line is concerned variety CP-15/2 received maximum dominant genes and variety ACALA-SJ-4 secured maximum recessive genes because of their closer and farther positions from the origin respectively.

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Figure 5. Vr/Wr graph for boll weight

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