

## Genetic basis of some quantitative traits in upland cotton (*Gossypium hirsutum* L.)

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### Abstract

Five cotton cultivars were crossed in a complete diallel to study the inheritance of different polygenic traits. Genotypic differences were found to be significant ( $P < 0.01$ ) for all the characters. Adequacy tests disclosed that data of all the parameters were fully adequate for genetic analysis except bolls per plant, staple length, fibre strength, and fibre fineness, which was partially or not adequate. Additive component of genotypic variation (D) was significant and predominant for plant height, sympodia per plant, staple length and fibre strength, while dominance effects ( $H_1$  and  $H_2$ ) were main controlling factors for of monopodia per plant, number of bolls, lint percentage and seed cotton yield. More dominant genes were revealed in the parents for sympodia per plant, lint percentage and seed cotton yield. The values of  $H_2/4H_1$  demonstrated asymmetrical and unequal distribution of dominant genes in the parents for all characters. Plant height, sympodia per plant, staple length and fibre strength exhibited high narrow sense heritability ( $h^2$  n.s) due to the presence of additive gene action, whereas, monopodia per plant, number of bolls, lint percentage and seed cotton yield possessed low heritability. The genetic analysis suggested that plant height, sympodia per plant, staple length and fibre strength could be improved through sib family, pedigree and progeny selection, while exploitation of heterosis would be necessary to attain the genetic advancement in monopodia per plant, number of bolls, lint percentage and seed cotton yield.

**Keywords:** Additive-dominance model; components of variation; multigenic traits; *Gossypium hirsutum*

### Introduction

Despite of substantial progress made in other sectors, agriculture, by part, still has the pivotal position in the economy of Pakistan (Ali & Khan 2007b). Amongst the crops, upland cotton (*Gossypium hirsutum* L.) is very important. It sustains a lot of peoples in various fields such as textile mills, agriculture fields, ginning factories, small-to-large scale business and trade. Cotton accounts for 8.6% of the value added in agriculture and about 1.8 percent to GDP

(Anonymous 2007). The crop was sown on the area of 3.075 million ha, 0.9 percent less than last year. The production of cotton is provisionally estimated at 13.0 million bales for 2006-07, lower by 0.1 percent over the last year's production of 13.019 million bales. Lower production was attributed primarily to the 11 percent decline in area sown in Sindh due to excessive rains and floods (Anonymous 2007). It means that area under cotton cultivation is shrinking

day by day due to many factors like rains and floods, water logging and salinity and industrialization (Ali & Khan 2007a).

Accordingly, the Ministry of Food, Agriculture & Livestock has prepared a long term Cotton Vision 2015 for sustained growth in cotton sector and the possible improvement in the quality of raw cotton. This vision includes the production of 20.7 million bales at the yield of 1,060 kgs ha<sup>-1</sup>, 20.1 million bales for local consumption, 0.6 million bales as exportable cotton surplus and improved yarn recovery rate 92% of from current average of 84% through clean/contamination free cotton production (Anonymous 2007). Because of the importance of this crop for the country's economy and to meet the challenge of Cotton Vision 2015, efforts have been placed on various aspects of the cotton production to increase its production. As the area under this crop is dwindling in future, so, the production of high yielding cultivars would be the answer to the problem.

In order to breed high yielding varieties of cotton, the genetic information on different quantitative traits may help cotton breeders in improving genetic architecture of the plant in particular direction for maintaining and improving the proper crop production level (Nadeem & Azhar 2004, Ali & Khan 2007b, Abbas et al. 2008). For this purpose, the use of already existing genetic variability in the breeding material as well as, the creation of new variability along with its genetic understanding is of crucial importance in a breeding program. In order to introduce this genetic variability, diallel crossing techniques have been widely utilized by the breeder (Iqbal et al. 2003, Basal & Turgut, 2005, Abbas et al. 2008, Ali et al. 2008, Ali & Awan 2009).

In past many scientists remained interested in studies to identify the inheritance pattern of metric traits. For example, the investigations of Khan et al. (2003), Ahmad et al. (2003), Nadeem & Azhar (2004), Basal & Turgut (2005), Ali & Khan (2007b) and Ali & Awan (2009) revealed additive type of gene action with partial dominance in most of the traits under study. However, some other scientists reported the presence of genes showing over-dominance for number of monopodia and sympodia (Ahmad et al. 2000), lint percentage (Basal & Turgut 2005) and seed cotton yield (Haq & Azhar 2004). May & Green (1994), Iqbal et al. (2003) and Haq & Azhar (2004) reported additive type of gene action for fibre length and fibre strength. Khan et al. (2001) and Ahmad et al. (2003) investigated non-additive

type of gene action for staple length whereas; they reported additive effects for fibre strength. The purpose of this experiment was also to unwind the genetic information about some metric traits in upland cotton following Mather & Jinks (1982).

## **Materials and methods**

### ***Genetic material and green house experiment***

The present studies were conducted at the experimental farms of the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the years 2005-07. The experimental material for these studies was developed by crossing five parental genotypes namely S12, MS-84, NIAB-78, LRA-5166 and CIM-109 in all possible combinations. The seeds of these five parents were sown in earthen pots placed in greenhouse during November 2005. During germination and growth, optimum conditions (light and temperature) were possibly provided and required agronomic practices were followed. At the time of flowering the parental lines were crossed in a complete diallel fashion (5x5) to generate 20 F<sub>1</sub> crosses (direct and reciprocal) and 5 selfs. All necessary precautionary measures were taken to avoid contamination of genetic material at the time of crossing and selfing. The plants were properly managed up to the maturity. At maturity, crossed and selfed bolls were picked and seed cotton of each cross was ginned separately using single roller electric ginner.

### ***Field experiment and laboratory testing***

The F<sub>0</sub> seed from all crosses along with their selfed parents were sown in the field in a Randomized Complete Block Design with three replications during June-2006. In a replication each of 25 entries was planted in a single row having 15 plants with plant to plant and row to row distances of 30cm and 75cm respectively. All the recommended agronomic practices and crop protection measures were applied from sowing till harvesting of crop. At maturity, the data were recorded for plant height (cm), number of monopodia, number of sympodia, and number of bolls per plant, lint percentage, seed cotton yield (g) from 10 randomly selected plants from each entry, both in field as well as laboratory on individual plant basis.

**Table 1.** Estimates of Mean Square for the multigenic traits in cotton

Parameters	Mean squares	
	Genotypic	Error
Plant height	290.57**	6.850
Monopodia per plant	4.4005**	0.045
Sympodia per plant	16.061**	0.677
Number of bolls	113.13**	1.942
Lint percentage	75.841**	2.216
Seed cotton yield	527.76**	19.80
Staple length	3.4985**	0.540
Fibre strength	5.8390**	0.721
Fibre fineness	0.2591**	0.008

For fibre analysis of staple length (mm), fibre strength (g/tex) and fibre fineness ( $\mu\text{g}/\text{inch}$ ), the seed cotton of all the plants in each entry were subjected to ginning by a single roller electrical gin in the laboratory on individual plant basis. Lint so obtained was placed at 65% humidity and 18-20°C temperature in an air conditioned room using humidifier before fibre testing (Ali et al. 2008). High Volume Instrument (HVI-900-SA; Zelwiger, Uster, UK) was used for fibre analysis.

#### **Statistical Analysis**

The data collected was subjected to standard techniques of analysis of variance (Steel et al. 1997) to establish the level of genotypic differences for the plant traits under study. The characters showing significant genotypic differences were further analyzed genetically following additive-dominance (AD) model of genetic analysis developed by Mather & Jinks (1982) and followed by Singh & Chaudhary (1985). The adequacy of the additive-dominance model and validity of some of the assumptions were assessed by using joint regression analysis and analysis of variance of  $(W_r + V_r)$  and  $(W_r - V_r)$ . These adequacy tests were followed by the calculation of estimate four genetic components of variation, D (additive effects of genes), H1 and H2 (dominance effects of genes), F value (an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variation in the dominance over the loci) E (the role of environmental effects) and  $h^2$  n.s (the heritability in narrow sense) for each character.

#### **Results and discussion**

##### ***Genotypic variation among the genotypes and assessment of the data for AD model***

Preliminary analysis of variance (ANOVA) following Steel et al. (1997) indicated significant differences ( $P \leq 0.01$ ) for all the characters among genotypes (Table 1). The results of the regression analysis for all the characters were presented in (Table 2). The regression analysis revealed that regression coefficient for all the traits departed significantly from zero and not from unity except fibre fineness, suggesting no non-allelic interaction. Iqbal et al. (2003), Nadeem & Azhar (2004), Basal & Turgut (2005) and Ali & Khan (2007) found similar results. The  $(b = 0.99 \pm 0.43)$  concerning fibre fineness did not depart significantly both from unity as well as zero, which indicated, non-additive variation included epistasis or multiple allelism. Hence, the data for fibre fineness did not fulfill the diallel assumptions and were unfit for additive-dominance model. Thus, the additive-dominance model offered reasonable foundation for interpreting the results. This property of the regression coefficient specified that intra-allelic interaction, meaning thereby, that genes were distributed independently among the parental lines, and was independent in action. The unit slope of the regression lines suggested that all the diallel assumptions have been met (Mather & Jinks, 1982). The suitability of the model data analysis was also tested with the analysis of variance of  $(W_r + V_r)$  and  $(W_r - V_r)$  (Table 3). Which detailed that there was no evidence of dominance effects as the mean square

**Table 2.** Test of Regression Coefficient for various characters in *Gossypium hirsutum* L.

Parameters	Regression Coefficient (b)	Standard error for b	t value for b-0	t value for 1-b	t <sup>2</sup> value
Plant height	1.06	0.19	5.44*	-0.29 <sup>ns</sup>	0.35 <sup>ns</sup>
Monopodia per plant	0.99	0.10	9.93*	2.35 <sup>ns</sup>	0.016 <sup>ns</sup>
Sympodia per plant	1.12	0.09	12.29*	-1.31 <sup>ns</sup>	2.33 <sup>ns</sup>
Number of bolls	0.93	0.10	8.63*	0.26 <sup>ns</sup>	0.20 <sup>ns</sup>
Lint percentage	0.95	0.23	4.04*	0.63 <sup>ns</sup>	0.20 <sup>ns</sup>
Seed cotton yield	0.95	0.16	5.90*	0.20 <sup>ns</sup>	0.003 <sup>ns</sup>
Staple length	0.84	0.15	5.29*	0.02 <sup>ns</sup>	0.45 <sup>ns</sup>
Fibre strength	0.96	0.21	4.48*	0.16 <sup>ns</sup>	0.025 <sup>ns</sup>
Fibre fineness	0.99	0.43	2.29 <sup>ns</sup>	0.99 <sup>ns</sup>	0.39 <sup>ns</sup>

between arrays for  $W_r + V_r$  was non-significant for staple length, fibre strength and fibre fineness, while the mean square between arrays for  $W_r - V_r$  was also non-significant, thus emphasizing partial adequacy of additive dominance hypothesis for staple length, fibre strength and full inadequacy for the data of fibre fineness for the model. The similar types of findings were also reported by Basal & Turgut (2005) and Ali & Khan (2007), who advocated the full fitness of the data for additive dominance model for these characters. Significant differences at 0.01 percent probability level for ( $W_r + V_r$ ) of lint percentage revealed the presence of dominance, while the  $W_r - V_r$  for  $F_1$  also highly significant, and this significance was the result of the presence of non-allelic interactions thus rendering the data of this trait partially fit for the additive dominance model as regression coefficient ( $b=0.95 \pm 0.23$ ) for the trait was significantly deviating from zero and non-significantly from unity. All the characters except lint percentage, staple length and fibre strength exhibited full adequacy for additive-dominance model suggested by Mather & Jinks (1982).

#### ***Genetic components of variation for the metric traits***

With regard to the genetic components estimated by the diallel analysis (Table 4), the additive component (D) was significant at the 0.05 level for number of bolls, lint percentage, seed cotton yield, staple length and fibre strength, however it was highly significant ( $P<0.01$ ) for plant height, monopodia and sympodia per plant. This confirmed the additive effects of the genes. Effect of additive genes was more prominent in the genetic control of plant height, sympodia per plant, staple length and fibre strength in which the

additive component was greater than the dominance component. This advocated that selection can be helpful for the improvement of these traits. Khan et al. (2003), Ahmad et al. (2003), Iqbal et al. (2003), Haq & Azhar (2004), Nadeem & Azhar (2004), Basal & Turgut (2005) and Ali & Khan (2007) also reported additive genetic effects for these parameters.

Dominance components ( $H_1$  and  $H_2$ ) were significant for all the characters except staple length, which showed dominance effects of genes are predominant for all the quantitative parameters (Table 4). This also suggested that the genetics of staple length was controlled mainly by additive genes (Haq & Azhar 2004). However,  $H_1$  and  $H_2$  components were higher than additive one (D) for monopodia per plant, number of bolls, lint percentage and seed cotton yield. This revealed that genetics of these characters were primarily handled by dominance effects. Preponderance of dominance effects for monopodia per plant, number of bolls, lint percentage and seed cotton yield suggested that exploitation of hybrid vigour might be advantageous for the betterment of the characters (Ahmad et al. 2000, Khan et al. 2001, Ahmad et al. 2003, Haq & Azhar 2004). The positive values of the F component for sympodia per plant, lint percentage and seed cotton yield indicated the excess of dominant alleles were present in the genetic material. On the other hand plant height, monopodia per plant, number of bolls, staple length, and fibre strength showed negative F value suggesting the presence of additive genes in the parental material. The significance for the component  $h^2$  in plant height number of bolls lint percentage and seed cotton yield confirmed that dominance was unidirectional. The ratio  $(H1/D)^{0.5}$  measured the overall degree of dominance, which was in the range

**Table 3.** Heterogeneity test for (Wr+Vr) and (Wr-Vr) estimates

Parameters	d.f.	Plant height	Monopodia per plant	Sympodia per plant	Number of bolls	Lint percentage	Seed cotton yield	Staple length	Fibre strength	Fibre fineness
Wr+Vr between arrays	4	5140**	0.87**	37.66**	111.4**	4368.5**	44040.8**	1.67 <sup>ns</sup>	4.24 <sup>ns</sup>	0.006 <sup>ns</sup>
Wr+Vr within arrays	10	449.09	0.078	4.57	33.01	65.69	1355.13	1.27	2.05	0.003
Wr-Vr between arrays	4	110.0 <sup>ns</sup>	0.006 <sup>ns</sup>	0.344 <sup>ns</sup>	1.90 <sup>ns</sup>	177.15**	777.94 <sup>ns</sup>	0.081 <sup>ns</sup>	0.077 <sup>ns</sup>	0.0003 <sup>ns</sup>
Wr-Vr within arrays	10	134.73	0.022	0.219	13.85	26.39	285.65	0.58	0.44	0.0002

**Table 4.** Components of variation for metric traits in cotton

Components of variation	Plant height	Monopodia per plant	Sympodia per plant	Number of bolls	Lint percentage	Seed cotton yield	Staple length	Fibre strength
D	69.52±5.18**	0.73±0.03**	10.4±0.25**	3.97±0.53*	26.1±6.08*	51.54±12.29*	0.89±0.08*	2.10±0.15*
F	-0.93±12.94 <sup>ns</sup>	-0.11±0.09 <sup>ns</sup>	6.83±0.62*	-5.02±1.34 <sup>ns</sup>	43.3±15.2*	102.4±32.2*	-0.67±0.21 <sup>ns</sup>	-0.64±0.4 <sup>ns</sup>
H <sub>1</sub>	51.8±14.00*	0.91±0.99*	3.15±0.65*	47.9±1.45**	77.1±16.4*	567.3±34.8**	0.05±0.22 <sup>ns</sup>	1.36±0.43*
H <sub>2</sub>	49.18±12.69*	0.84±0.90*	1.85±0.61*	35.2±1.31**	54.3±14.9*	479.3±31.6**	0.013±0.20 <sup>ns</sup>	1.33±0.40*
h <sup>2</sup>	24.30±8.57*	-0.01±0.06 <sup>ns</sup>	-0.11±0.41 <sup>ns</sup>	47.2±0.88*	40.2±10.1*	811.9±21.4**	0.04±0.14 <sup>ns</sup>	-0.01±0.2 <sup>ns</sup>
E	2.50±2.11 <sup>ns</sup>	0.02±0.15 <sup>ns</sup>	0.25±0.10*	0.77±0.21*	0.89±2.48 <sup>ns</sup>	7.40±5.27 <sup>ns</sup>	0.20±0.034*	0.26±0.06*
(H1/D) <sup>0.5</sup>	0.86	1.11	0.54	3.47	1.71	3.31	0.23	0.80
H2/4H1	0.23	0.23	0.14	0.18	0.17	0.21	0.18	0.24
(4DH <sub>1</sub> ) <sup>0.5</sup> +F/(4DH <sub>1</sub> ) <sup>0.5</sup> -F	0.98	0.87	3.92	0.69	2.86	1.85	0.72	0.67
h <sub>2</sub> (n. s)	0.71	0.66	0.77	0.53	0.16	0.12	0.75	0.69

of over dominance for monopodia per plant, number of bolls, lint percentage and seed cotton yield while it was in the range of partial dominance for other traits. This confirmed that these characters were controlled by dominant genes. The ratio  $H_2/4H_1$ , estimated the frequency of negative versus positive alleles at loci showing dominance, it was less than 0.25, which indicated that the additive components did not contain all the dominance effects in all the traits.

Estimates for the ratio of dominance to recessive genes in the parents  $((4DH_1)^{0.5}+F/(4DH_1)^{0.5}-F)$  for all the characters were less than 1.0 except sympodia per plant, lint percentage and seed cotton yield, which indicated the presence of an excess of dominant genes for each trait in the parents. While other parameters showed lower than 1.0 value, indicated the presence of an excess of recessive genes for this trait in the parents.

The range of narrow sense heritability was between low to high. The traits controlled by additive gene action (plant height, sympodia per plant, staple length and fibre strength) exhibited higher estimates (Basal & Turgut 2005, Ali & Khan, 2007). However, monopodia per plant, number of bolls, lint percentage and seed cotton yield showed lower estimates of narrow sense heritability which was due to the presence of dominant genetic effects (Ahmad et al. 2003, Haq & Azhar 2004). High estimates of heritability in narrow sense represents fixable, additive heritable variation, which indicated that response to selection, should be rapid for these characters. This offers a lot of scope for improvement of the characters through individual plant selection. Hayman (1957) reported that epistasis can decrease or increase degree of dominance which in turn effect on heritability estimates.

## Conclusion

It concluded that the preponderance of additive gene action coupled with high estimates of narrow heritability in plant height, sympodia per plant, staple length and fibre strength advocated that pedigree and recurrent selection might be a key option for the improvement of these traits. While, monopodia per plant, number of bolls, lint percentage and seed cotton yield which showed dominance genetic behavior along with lower estimates of narrow sense heritability could be boosted through heterosis for this group of genotypes.

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