

Full Length Research Paper

Study of heritable variation and genetics of yield and yield components in upland cotton (*Gossypium hirsutum* L.)

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Increase in seed cotton yield on a sustainable basis is a primary objective of cotton breeding programs, which is a result of an effective exploitation of quantitative (polygenic) traits. The diallel cross techniques is mainly applied for studying the nature of action and genetic constitution of cotton genotypes. Six cotton varieties were crossed in a complete diallel fashion to study the inheritance of seed cotton yield and its components, lint percentage and fiber length. Field evaluation of six parental genotypes and thirty F_1 was made in a randomized block design with three replications. Genotypes mean values differed significantly ($P \leq 0.05$) for all traits and greater than the dominance component (H_1 and H_2). The dominance effect H_1 and H_2 was non significant for number of bolls per plant and fiber length. The value of $H_2/4H_1$ indicated a symmetrical and unequal distribution of dominant genes in the parents for all traits except for lint percentage as the $H_2/4H_1$ value 0.24 is very close to 0.25, which indicated symmetrical and equal distribution of dominant genes in the parents for lint percentage. Estimates of narrow sense heritability ($h^2_{n.s}$) were higher for all the traits that are due to additive gene action. The results of the present study indicated that the pedigree of progeny selection will be helpful to improve these traits.

Key words: Cotton genotypes, diallel cross, *Gossypium hirsutum* L, heritability, seed cotton, genetic studies, yield components.

INTRODUCTION

Cotton (*Gossypium hirsutum* L) is the most important fiber crop in Pakistan and the world. Agriculture in Pakistan has a pivotal role in the economy (Ali and Khan, 2007). Cotton accounts for 8.20% of value added to agriculture and about 2.0% to GDP (Anonymous, 2010). Most of the traits for improving seed cotton yield are inherited in a quantitative manner. Quantitative traits are

modified by the change in environment and management strategies. The trait like seed cotton yield is the combined effect of many agronomic traits like number of bolls per plant, and boll weight which are controlled by many genes having direct or indirect effects.

The expression of an individual gene is often modified by expression of other genes. Linkage locks are difficult to breakup. Genotype in a given environment /management system may require accumulation of genes from diverse sources and the optimum genotype fit for any environment/management system will be different from another system (Meredith, 1984). Dudley and Moll (1969) stated that quantitative inheritance studies should be carried out for solving or classifying problem that are faced by breeders. In order to breed high yielding varieties of cotton, the genetic information on different yield contributing traits may help breeders in improving

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Abbreviations: H_1 and H_2 , Dominance component; ($h^2_{n.s}$), narrow sense heritability University; **UCA and ES**, College of Agriculture and Environmental Sciences; **ANOVA**, analysis of variance; **b**, regression coefficient; **D**, additive component.

genetic architecture of plant in particular direction for maintaining and improving the proper crop production level (Nadeem and Azhar, 2004; Ali and Khan, 2007; Abbas et al., 2008). Many investigations (Al-Rawi and Kohel, 1969; Baker and Verhalen, 1973; Murray and Verhalen, 1969; Verhalen et al., 1971) showed that a reasonable useful genetic variability is present in cotton. In order to exploit this genetic variability diallel crossing techniques have been widely utilized by breeders (Ashokkumar et al., 2010; Ali et al., 2008; Iqbal et al., 2003; Abbas et al., 2008; Ali and Awan 2009; Godoy and Palomo, 1999). Additive type of gene action with partial dominance in most of the traits has been reported by previous researchers (Ahmad et al., 2003; Iqbal et al., 2003; Ali and Awan, 2009). But some other scientists have reported the presence of genes showing over dominance for lint percentage (Basal and Turgut, 2005) and seed cotton yield (Haq and Azhar, 2004; May and Green, 1994) while Haq and Azhar (2004) also reported additive gene action for fiber length. The study was designed to investigate the inheritance of yield and yield components, lint percentage and fiber length in upland cotton by methods given by Mather and Jinks (1982).

MATERIALS AND METHODS

Genetic material

1. Neelam-121. It is a tall growing, heat susceptible and late maturing variety.
2. MNH-6070. It is an erect type bearing small leaf with light green color, early in maturity with high lint percentage and short fiber length.
3. ARS-802. It is heat susceptible, late in maturity and with small boll size.
4. MNH-786. It is an early maturing variety, moderately compact, very good boll size.
5. IUB-2009. It is a new strain of cotton having moderate bushy growth habit, early in maturity, medium boll size with good lint percentage.
6. IUB-11. It is also a new strain of cotton having a very good boll size, bushy in growth habit, slightly low lint percentage and good fiber length.

Field procedure

This study was initiated in 2009 under greenhouse at University College of Agriculture and Environmental Sciences (UCA and ES) by making all possible crosses (direct and reciprocal cross). The yield evaluation of six parents and their thirty F_1 's was made in 2009 at UAC and ES. A randomized complete block design with three replications was used. Each plot consisted of two rows of 20 plants each with plants spaced 30 cm apart in rows 75 cm apart. All the agronomic and plant protection strategies were adopted in standard fashion.

Collection of data

At maturity, data were recorded for number of bolls per plant, average boll weight (g), seed cotton yield per plant (g), lint percentage and fiber length (mm) from 10 consecutive guarded

plants from each genotype (parents, direct and reciprocal crosses).

Statistical analysis

The data collected was subjected to standard techniques of analysis of variance (ANOVA) to determine the level of genotypic differences for the plant traits under study (Steel and Torrie, 1981). The character showing significant genotypic differences were further analyzed genetically following model developed by Mather and Jinks (1982) and followed by Singh and Chaudhary (1985). This biometrical genetic model based upon several assumptions was tested, $r(Y, W_r + V_r)$ – a measure of direction of dominance is indicated by the correlation of the mean parental phenotype values (y) and ($W_r + V_r$) values. A correlation of +1 indicates that the recessive genes have positive effects while a value of -1 indicates that dominant genes have positive effects. Small correlation indicates that portions of the dominant genes have positive and negative effects (Hayman, 1954). D – component of variation due to additive effects of genes, F – an indicator of excess of dominant or recessive genes in the parent. A positive sign indicates an excess of dominant alleles of dominant effects on the parents while a negative sign indicates the same of recessive alleles. A value of $F = 0$ indicates that either no gene exhibited dominance or that the dominant and recessive alleles of each gene are distributed equally among the parents. H_1 and H_2 – components of variation due to the dominance effects of genes; h_2 – the summation of dominance deviation over all loci. When the frequency of dominant and recessive alleles is equal, then $H_1 = H_2 = h_2$. Significance of h_2 confirms that dominance is unidirectional. E – environmental component as estimated by the error mean square from the analysis of variance. $(H_1/D)_{1=2}$ – a weighted measure of the average degree of dominance at each locus with a value of zero indicating no dominance, a value of 1 indicating complete dominance and a value greater than 1 indicating over-dominance. Partial dominance results in a value between 0 and 1. The dominance component H_1 is used in this ratio because it has the same coefficient as D (Hayman, 1954). $H_2/4H_1$ – an estimator of the average frequency of negative versus positive alleles at loci exhibiting dominance. It has a maximum value of 0.25 when $p = q = 0.5$. Value less than 0.25 indicate that the additive components do not contain all dominance effects. Therefore, the above ratio of average degree of dominance would not be accurate (Mather and Jinks, 1971). $KD/DR = (4DH_1)_{1=2} + F / (4DH_1)_{1=2} - F$. A ratio of the total number of dominant to recessive genes in all parents. The formula of Crumpacker and Allard (1962) was used to estimate heritability.

$$\text{Heritability } D .1 = 4D / \dots = 4DC \dots = 4H_1 - 1 = 4FCF /$$

The above estimators were calculated only when the genetic components in the respective ratios were significantly different from zero.

RESULTS

The results of ANOVA indicated the significant differences at 0.05 level for number of bolls per plant, boll weight, seed cotton yield, lint percentage and fiber length (Table 1). Table 2 contains average values for number of bolls/plant, boll weight, seed cotton yield, lint percentage and fiber length of breeding material under study. Data showed that MNH-6070 had the highest lint percentage (42.3%), IUB-11 and MNH-786 had highest boll weight,

Table 1. Mean squares for yield and its components, lint percentage and fiber length in 6X6 diallel experiment.

SOV	d.f	Number of bolls per plant	Boll weight (g)	Seed cotton yield	Lint (%)	Fiber length (mm)
Rep	2	2.37	0.142*	7.924*	3.38*	0.053*
Genotype	35	50.26*	1.173*	13.161*	4.43*	2.662*
Error	70	3.67	0.12	0.145	0.078	0.015

Significant at 0.05 level.

Table 2. Mean for yield and its components, lint percentage and fiber length for the parental lines.

Genotype/Variety	Number of bolls per plant	Boll weight (g)	Seed cotton yield (kg ha ⁻¹)	Lint (%)	Fiber length (mm)
Neelam-121	40.3	3.13	3433	37.9	26.8
MNH-6070	41.3	3.15	4345	42.3	26.2
ARS-802	46.4	2.81	3092	39.5	27.4
IUB-11	44.1	4.86	4850	38.6	30.1
IUB-09	53.5	3.72	4909	40.7	27.5
MNH-786	42.3	4.16	4763	39.9	28.3

4.86 and 4.16 g, respectively. While genotype IUB-2009 had highest (53.5) number of boll per plant. The same genotype had highest seed cotton yield 4909, 4850 and 4763 kg ha⁻¹ for IUB-2009, IUB-11 and MNH-786, respectively. Opposite results obtained with genotypes MNH-6070 and ARS-802 which had the lowest seed cotton yield of 3433 and 3093 kg ha⁻¹, respectively. The genotype IUB-11 had the highest fiber length (29.6mm). On the other hand MNH-6070 and Neelam-121 had lowest fiber length 26.2 and 26.8 mm, respectively. The regression coefficient (b) for all the traits under study was significantly different from zero and non significantly different from one (Table 3). The a values for all these traits indicated that regression line cut the Wr axis on positive side very close to zero except for number of bolls per plant.

With regard to genetic components estimated by the diallel analysis, the additive component (D) was significant at 0.05 level for number of bolls per plant, boll weight, seed cotton yield, lint percentage and fiber length. Dominance component (H₁ and H₂) was significant for number of bolls per plant, boll weight, seed cotton yield and lint percentage. Non significant (H₁ and H₂) were observed for fiber length and number of bolls per plant. The computed value of F component was negative for all traits under study. The value of h² was significant for boll weight, seed cotton yield, lint percentage and fiber length. The ratio (H₁/D)^{1/2} was 0.661, 0.809, 0.556, 0.839 and 0.678 for boll weight, number of bolls per plant, lint percentage, fiber length and seed cotton yield respectively. The ratio H₂/4H₁ was less than 0.25 for all the traits under study except lint percentage whose value was 0.24 (Table 3). The estimates for the ratio of dominance of recessive genes in the parents [(4DH₁)^{1/2}+F]/ [(4DH₁)^{1/2}-F] was less than one for all traits (Table 3). The minimum computed value of heritability in

broad sense and narrow sense was 78% (Table 3).

DISCUSSION

Yield increase in cotton is a result of an effective exploitation of quantitative characters. The diallel cross techniques developed by Hayman (1954, 1958) and Jinks (1954, 1956) are handy techniques to study the nature of gene action, genetic constitution of cotton varieties for allelic or non allelic interactions. In test of (Vr, Wr) regression co-efficient for each trait is expected to be significantly different from zero but not significantly different from one, if all diallel assumptions hold true. The results presented in Table 3, showed fitness of adequacy of the additive dominance model (Mather and Jinks, 1982) for all characters studied. The results of this test indicated that all assumptions are valid for all traits under study within this breeding material. As regression value for all characters deviated significantly from zero and showed non significant differences from unity. The (a) value indicated that all the traits under study are governed by additive dominance gene action.

The D was significant which confirmed the effect of additive gene was more prominent for all the traits under study, as the additive component was greater than the dominance component. This indicated that the selection in segregating generation can be helpful for the improvement of these traits. Many other scientists Khan et al. (2003), Iqbal et al. (2003), Haq and Azhar (2004), Basal and Turgut (2005), Ali and Khan (2007), and Ali et al. (2009) also reported additive effects for these parameters. Significant H₁ and H₂ showed dominance effect of genes or pre-dominant for all quantitative parameters under study except fiber length and number of bolls per plant. This also indicated that the genetics of

Table 3. Genetic component of variation, associated ratio and standard error for seed cotton yield and its component, lint percentage and fiber length.

Factor	Boll weight (g)	Number of bolls per plant	Seed cotton yield (kg ha ⁻¹)	Lint (%)	Fiber length (mm)
r(Y., Wr+Vr)	-0.89223	0.320914	-0.84558819	0.0797	-0.49807
t	0.109	2.567	0.310	0.870	0.061
a	0.084	7.838	0.811	0.557	0.200
b	0.988±0.108	0.429±0.143	0.977±0.145	0.826±0.138	0.851±0.247
b=0	9.143*	2.997*	6.730*	5.967*	3.443*
b=1	0.108ns	3.993*	0.162ns	1.256ns	0.600ns
E	0.005±0.008	1.213±1.731	0.121±0.091	0.057±0.043	0.005±0.071
D	0.592±0.021	21.516±4.579	5.889±0.240	2.398±0.112	1.456±0.188
F	-0.176±0.051	-6.982±11.187	-2.347±0.587	-0.557±0.275	-0.058±0.460
H ₁	0.259±0.053	14.083±11.625	2.709±0.610	0.740±0.286	1.025±0.478
H ₂	0.277±0.047	12.100±10.385	2.023±0.545	0.710±0.255	0.940±0.478
h	1.231±0.032	-0.326±6.990	4.013±0.367	1.777±0.172	1.370±0.288
(H ₁ /D) ^{1/2}	0.661	0.809	0.678	0.556	0.839
H ₂ /4H ₁	0.219	0.215	0.187	0.240	0.229
1/2F/[D(H ₁ -H ₂) ^{1/2}	-0.635	0.534	-0.584	-1.032	-0.071
[(4DH ₁) ^{1/2} +F]/[(4DH ₁) ^{1/2} -F]	0.634	0.666	0.546	0.654	0.960
H _{N.S}	0.866	0.782	0.877	0.864	0.768
H _{B.S}	0.988	0.938	0.976	0.967	0.995

* Significant at 0.05 level.

fiber length was controlled mainly by additive genes (Haq and Azhar, 2004; Ali et al., 2009). However, D was higher than H₁ and H₂ for all the traits under study which revealed that genetics of these characters was primarily handled by additive effects. Preponderance of additive effects for these parameters suggested less inbreeding depression in F₂ generation which indicated that these parents can be utilized to develop such hybrids where F₂ inbreeding depression will be low than expected. It also indicated that hybrid vigor in F₂ will be sufficient to be exploited commercially (Iqbal et al., 2008).

The negative value for F component for the studied parameters suggested the presence of additive genes in the parental material. The significance for the component h² in boll weight, seed cotton yield, lint percentage and fiber length confirmed that dominance was unidirectional. The ratio (H₁/D)^{1/2} measured the overall degree of dominance which was in the range of partial dominance for all the quantitative parameters under study. The ratio H₂/4H₁, estimated the frequency of negative versus positive alleles at loci showing dominance. As it was less than 0.25 which showed that additive component did not contain all the dominance effects in all the traits except lint percentage which is very close to 0.25 (Table 3). The estimates for the ratio of dominance to recessive genes in the parents [(4DH₁)^{1/2}+F]/[(4DH₁)^{1/2}-F] for all the characters were less than 1, indicating the presence of an excess of recessive genes for these traits in the parents. The traits under study are controlled by additive

gene action, exhibited higher estimates (Basal and Turgut, 2005; Ali and Khan, 2007) of narrow sense heritability (Table 3). Hayman (1957) also suggested that non allelic interaction can decrease or increase degree of dominance which affects heritability estimates.

Higher estimates of heritability in narrow sense represented flexible additive, heritable variation which indicated that response to selection should be rapid for the traits under study. It also offered a scope for improving these characters through single plant selection.

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