Genetic Analysis of Morphological Characteristics and Seed Oil Content of Cotton (*Gossypium hirsutum L.*)

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Abstract: Inheritance pattern of sympodia per plant, plant height, bolls per plant, seed cotton yield and seed oil content of cotton was assessed using diallel crossing model in which six genotypes B-557, Culture 728-4, MNH156, B-1850 (in), Culture-604-4 and MNH147 were crossed in all possible combinations. The results from scaling tests for the adequacy of additive-dominance model indicated that sympodia per plant, plant height, bolls per plant, seed cotton yield and seed oil content were partially adequate for further genetic analysis. Sympodia per plant, plant height, bolls per plant and seed cotton yield and were controlled by additive genes, whereas over-dominance was prevalent in seed oil content characteristics. Narrow sense heritability for plant height, bolls per plant and seed cotton yield suggested that these parameters could effectively be improved through selection in the early segregating generations.

Key words: Gene action, additive, over-dominance, heritability, cotton

Introduction

Thorough knowledge and complete understanding of inheritance pattern of economic 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 morpho-genetic characters and to predict the performance of the progenies in the latter segregating generations.

Sanyasi (1991) reported additive and dominant effects of genes for seed cotton yield of and number of boll per plant. Additive type of gene action with partial dominance for plant height, number of bolls per plant, seed cotton yield per plant have been investigated by Shah et al. (1992). The findings of Tariq et al. (1992) revealed over dominance for seed cotton yield and low narrow sense heritability for the same character. Both additive and non-additive gene actions were found equally important in the expression of boll number with high heritability whereas seed cotton yield showed non-additive gene action (Tiwari et al., 1992). Ikram et al. (1993) found non-additive type of genetic behavior for yield and plant height while boll number and sympodial branches were predominantly controlled by additive gene action. Azhar and Rana (1993) reported genetic effects to be predominantly non-additive for seed cotton and number of bolls per plant. Additive effects for sympodial branches have been given by Azhar et al. (1994). Khan et al. (1999) computed additive with partial dominance for plant height and over dominance was found to be
operative for bolls per plant and seed cotton yield. Estimates of narrow sense heritability were low to moderate. The results of gene action in intra specific hybrids of \textit{G. hirsutum L} by Saeed \textit{et al.} (1996) showed that plant height, number of bolls per plant, seed cotton yield were controlled by additive type of gene action. Ahmad \textit{et al.} (1996) found additive gene action for bolls per plant. Paxasla \textit{et al.} (1998) calculated additive gene action for number of sympodia per plant and plant height. In another study, Yingxin and Xiangming (1998) found that bolls per plant and seed cotton yield were controlled by additive and non-additive gene actions respectively. Broad sense heritability was high and narrow sense heritability was medium for these traits. Jagtap and Mehtari (1998) reported high heritability for sympodia per plant. Kaiwar and Babar (1999) indicated the non-additive type of gene action for sympodia per plant bolls per plant seed cotton yield per plant. Hussain \textit{et al.} (1999) analyzed gene action in upland cotton for seed cotton yield and reported additive type of gene action with partial dominance. From the study of quantitative inheritance in cotton for oil percentage, Hussain \textit{et al.} (1999) found additive with partial dominance type of gene action. Non-additive type of gene action for plant height sympodia per plant, bolls per plant and seed cotton yield per plant have been found by Puntha \textit{et al.} (1999). In gene action study of height of the main stem and bolls per plant in cotton (\textit{G. hirsutum L}) both characters were controlled by additive type of gene action with partial dominance (Khan \textit{et al.}, 1999). Esmali \textit{et al.} (1999) reported additive dominance gene action for boll number and seed cotton yield. Both broad and narrow sense heritability estimates were high. Rady \textit{et al.} (1999) computed both additive and non additive genetic effects for seed cotton yield and number of bolls per plant. The findings of Kumareshan (2000) indicated additive dominant gene action for seed cotton yield and bolls per plant in cotton (\textit{G. hirsutum L}) high estimates of broad sense heritability for these traits. Hassan \textit{et al.} (1999) estimated non-additive genetic effects for boll number, seed cotton yield and plant height. Predominance of additive effects in inheritance of seed cotton yield has been reported by Baloch \textit{et al.} (2000). Similarly Subhan \textit{et al.} (2001) observed additive type of gene influence for number of bolls per plant and over-dominance for seed cotton yield per plant. The present studies were aimed to investigate the genetic basis for some economic cotton traits, e.g. monopodia per plant, sympodia per plant, plant height, bolls per plant, seed cotton yield per plant and seed oil content to lay basis for the development of high yielding with high oil content of cotton varieties.

\textbf{Materials and Methods}

Six parental genotypes of cotton i.e. B-557, MNH-147, MNN-156 (local) Culture-728-4, B-1580 (ne) Culture 604-4 (exotic) were used to produce F1 seed.

The parental material was grown in normal soil under natural field conditions during the month of June, 2000. At flowering, during August-September, the parental lines were crossed in a complete diallel fashion (6x6 diallel) to generate 30 F1 crosses. At maturity, crossed bolls were picked and seed cotton was ginned with roller ginning machine. Six parents and their F1 hybrids were grown in four replications at Cotton Research Station, Multan with plant to plant distance of 1.25 ft. and row to row distance of 2.5 ft. At maturity, data were recorded for monopodia per plant, sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield.
Diallel technique (Mather and Jinks, 1982) was applied for determination of gene action of different traits.

Assumptions of diallel analysis and tests for the adequacy

The validity of information from a group of genotypes obtained from the diallel cross method is based on the following assumptions (Crumpacker and Allard, 1962).

(i) Diploid segregation of chromosomes
(ii) Homozygosity of parents
(iii) Absence of reciprocal effects
(iv) Absence of epistasis
(v) No multiple allelism
(vi) Independent distribution of genes among the parents

To fulfill the assumptions of absence of epistasis, no multiple allelism and independent gene distribution, data were subjected to three scaling tests. The first test was $t^2$ test. The second was the joint regression analysis of $W$ and $V$. According to Mather and Jinks (1982) the regression co-efficient is expected to be significantly different from zero and not from unity. Failure of this test means the presence of epistasis or the genes are not independent. If dominance or certain types of non-allelic interaction is present, $W+V$, must change from array to array. Similarly, if there exists epistasis, $W-V$, will vary between arrays. Failure of these three tests completely invalidates the additive-dominance model. However, if one fulfills the assumptions, the additive-dominance model is considered to be partially adequate. Genetic components of variation were obtained using the procedures described by Hayman (1954) and adopted by Singh and Chaudhry (1985).

Genetic components of variation

Genetic components of variation were obtained using the procedures described by Hayman (1954a) and Mather and Jinks (1982) and adopted by Singh and Chaudhry (1985). Formulae for genetic components are given as under:

1. Additive variation ($D$).
2. Variation due dominant effect of genes ($H_1$).
3. Variation due to dominant effect of genes correlated for gene distribution ($H_2$). Relative frequency of dominant and recessive alleles ($F$). If $F$ was positive dominant alleles are more than the recessive and if $F$ is negative vice-versa is true.
4. Overall dominance of heterozygous loci ($h^2$).
6. Environmental variance ($E$)
7. Average degree of dominance ($H_1/D_1$).
8. Proportion of genes with positive and negative effects in the parents i.e. $u\nu$ over all loci where $u$=frequency of increasing alleles and $v=1-u$ = Frequency of decreasing alleles. This ratio is equal to $0.25$. When $u=v$ at all loci (Singh and Chaudhary, 1985) $H_2/4H_1$.
9. Proportion of dominant and recessive genes in the parents $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$
Results

Number of sympodia per plant

Diallel analysis was carried out after obtaining highly significant genotypic differences (Table 1). When the scaling tests were applied to determine the adequacy of additive dominance model, the data were found partially adequate (Table 2).

Estimates of genetic components of variation (Table 3) depicted the additive and dominant gene effects. Gene distribution \((H_1+H_2)\) was observed to be asymmetrical which confirmed by the value of \(H_2/4H_1\) (0.168). Lesser value for D than H indicated over-dominance which was also supported by the value (1.140) of \((H_1/D)^{1/2}\). Frequency of dominant alleles for the trait under consideration was higher which was also indicated by \((4DH_1)^{1/2}+F/(4DH_1)^{1/2}+F = (1.975)\). Environment played an important role for the expression of character. Narrow sense (NS) heritability 0.528, was medium that indicated the importance of both additive and non-additive genetic variation. Similar results were found by Yingxi and Xiangming (1998) in cotton for sympodial branches, however Shanti and Raveendran (1999) reported high heritability estimates for the same trait. The Intercept \(W/V\) (Fig. 1) on positive side indicated partial dominance.

Plant height

Highly significant genotypic differences (Table 1) paved way for diallel analysis. The data were found partially fit (Table 2). Table 3 showed presence of both additive and dominant effects of genes. Unequal values of H1 and H2 revealed asymmetrical gene distribution and this was supported by the value of \(H_2/4H_1=0.209\). Pre-dominance of recessive alleles governing the expression of trait was shown by negative value of F. Proportion of dominant and recessive genes in the parents (0.476) also strengthened the results shown by the value of \(-F\). Value of \((H_1/D)^{1/2}\), 0.682, reflected incomplete or partial dominance. Narrow-sense heritability estimate (0.837) suggested that improvement could be made through individual plant selection in the latter generations. Similar results were reported by Shanti and Raveendran (1999) in cotton for plant height.

\(W/V\) graph (Fig. 2) showed additive type of gene action. These results were in accordance with the previous studies of Saeed et al. (1996), Paxasia et al. (1998) and Khan et al. (1999). However non-additive gene action was observed for plant height by Puntha et al. (1999).
Number of bolls per plant

Analysis of variance (Table 1) showed highly significant (P=0.01) genotypic differences. Three scaling tests for the validity of additive-dominance model (Table 2) indicated partial adequacy of data that allowed for the computation of genetic components of variation (Table 3). The significance of D indicated the presence of additive effects among the parents, whereas H₁ and H₂ pointed out the absence of dominance effects of genes and symmetrical distribution of positive and negative alleles among the parents. It was supported by the value of H₂/H₁ (0.248), which suggested equal proportion of genes with positive and negative effects. The higher value
of D than H1 reflected the partial or incomplete dominance. The negative value of $h^2$ showed that direction of dominance was negative and the mean degree of dominance (0.825) revealed partial or Incomplete dominance. The proportion of dominant and recessive genes in the parents (0.813) suggested that recessive genes are more frequent than dominant genes. These results were also confirmed by the value of $F$ (6.571). The environment played a significant role for the expression of trait under consideration. Narrow sense heritability (0.65) suggested that selection based on individual plants, in the latter generations, would give rapid progress. Similar findings were observed for number of bolls per plant by Ahmad et al. (1996), Esmail et al. (1999) and Kumaresan et al. (2000). The regression line (Fig. 3) expressed additive gene action. Saeed et al. (1996) and Kumaresan et al. (2000) also found similar observations. This is in contrast to the findings of Kalwar and Babar (1999) and Puntha et al. (1999) who reported non-additive gene action for this trait.

Seed Oil Content

The data were found partially adequate as it did not qualify all the three scaling tests. The genetic components showed (Table 3) that both additive and dominant effects were significant. Almost equal values of $H_1$ and $H_2$ indicated symmetrical gene distribution that was supported by $H_2/4H_1$ (0.251). Degree of dominance $(H_1/D)^{1/2} = 1.455$ indicated over-dominance genes effects. $F$ value (0.371) expressed dominance genes. Significant value (0.937) of $h^2$ reflected that overall dominance was due to heterozygous loci. Higher values of $H_1$ and $H_2$ than $h^2$ indicated presence of directional dominance. The effect of environment was significant. The narrow-sense heritability (0.267) was low suggesting slow progress for individual plant selection in segregating population for the character under study. Low to high heritability estimates were found in cotton for the trait by Kohel (1987) and Dani (1989).

$W/V$ graph (Fig. 4) reflected over-dominance as the regression line passed towards negative side. In contrast to these results, Kohel (1987) and Dani (1989) observed additive genetic effects.
Table 1: Mean squares from analysis of variance for monopodia per plant, sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield per plant of F₁ of cotton

<table>
<thead>
<tr>
<th>Items</th>
<th>Monopodia/plant</th>
<th>Symodia/plant</th>
<th>Plant height</th>
<th>Bolls per plant</th>
<th>Seed oil content</th>
<th>Seed cotton yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>0.037</td>
<td>2.71</td>
<td>468.72</td>
<td>24.98</td>
<td>0.57</td>
<td>482.92</td>
</tr>
<tr>
<td>Genotype</td>
<td>1.799**</td>
<td>88.622**</td>
<td>2065.02**</td>
<td>129.244**</td>
<td>3.37**</td>
<td>1378.1**</td>
</tr>
<tr>
<td>Error</td>
<td>0.540</td>
<td>9.538</td>
<td>121.96</td>
<td>22.32</td>
<td>0.74</td>
<td>274.98</td>
</tr>
</tbody>
</table>

*,** = Significant at 0.05 and 0.01 levels, respectively.

Table 2: Tests of adequacy of additive-dominance model for 6×6 diallel of cotton

<table>
<thead>
<tr>
<th>Characters</th>
<th>Joint regression</th>
<th>Test for b=0</th>
<th>Test for b=1</th>
<th>W=Vr</th>
<th>W-R</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Monopodia per plant</td>
<td>b=-0.048±0.061</td>
<td>1.648*</td>
<td>-0.299**</td>
<td>6.491*</td>
<td>0.429**</td>
<td>3.406* Inadequacy of additive-dominance model</td>
</tr>
<tr>
<td>Symodia per plant</td>
<td>b=0.509±0.562</td>
<td>0.216*</td>
<td>0.906**</td>
<td>0.873**</td>
<td>2.184**</td>
<td>2.567* Partial adequacy of additive-dominance model</td>
</tr>
<tr>
<td>Plant height</td>
<td>b=0.974±0.176</td>
<td>0.043**</td>
<td>5.536**</td>
<td>0.146**</td>
<td>11.335**</td>
<td>11.905* Full adequacy of additive-dominance model</td>
</tr>
<tr>
<td>Bolls per plant</td>
<td>b=0.860±0.084</td>
<td>1.354*</td>
<td>10.406**</td>
<td>1.148**</td>
<td>4.734**</td>
<td>2.901* Full adequacy of additive-dominance model</td>
</tr>
<tr>
<td>Seed oil content</td>
<td>b=0.649±0.309</td>
<td>0.102*</td>
<td>2.103**</td>
<td>1.136**</td>
<td>7.124**</td>
<td>2.201** Partial adequacy of additive-dominance model</td>
</tr>
<tr>
<td>Seed cotton yield</td>
<td>b=0.774±0.052</td>
<td>14.324**</td>
<td>14.994**</td>
<td>1.121**</td>
<td>5.475**</td>
<td>2.681** Partial adequacy of additive-dominance model</td>
</tr>
</tbody>
</table>

Partial adequacy of additive-dominance model*, ** = Significant at 0.05 and 0.01 levels, respectively = Non-significant
Table 3: Components of genetic variation for sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield per plant of F₁ of cotton when grown in normal soil

<table>
<thead>
<tr>
<th>Components</th>
<th>Sympodia per plant</th>
<th>Plant height</th>
<th>Bolls per plant</th>
<th>Seed oil content</th>
<th>Seed cotton yield/plant</th>
</tr>
</thead>
<tbody>
<tr>
<td>D</td>
<td>28.53 ±4.416**</td>
<td>609.07 ±42.46**</td>
<td>38.66 ±2.928**</td>
<td>0.839 ±0.228**</td>
<td>297.84 ±40.23**</td>
</tr>
<tr>
<td>H₁</td>
<td>37.09 ±11.209**</td>
<td>283.75 ±107.79**</td>
<td>26.29 ±7.432**</td>
<td>1.776 ±0.570**</td>
<td>322.26 ±102.11**</td>
</tr>
<tr>
<td>H₂</td>
<td>25.02 ±10.013**</td>
<td>237.28 ±96.28**</td>
<td>26.11 ±6.538**</td>
<td>1.785 ±0.517**</td>
<td>310.98 ±91.21**</td>
</tr>
<tr>
<td>h²</td>
<td>12.19 ±6.714**</td>
<td>756.26 ±64.83**</td>
<td>-2.66 ±4.47ns</td>
<td>0.937 ±0.348**</td>
<td>-34.68 ±61.41ns</td>
</tr>
<tr>
<td>F</td>
<td>21.32 ±10.784**</td>
<td>-295.43 ±103.69ns</td>
<td>-6.57 ±7.15ns</td>
<td>0.371 ±0.557ns</td>
<td>-166.95 ±98.24ns</td>
</tr>
<tr>
<td>E</td>
<td>2.33 ±1.685ns</td>
<td>32.89 ±16.21**</td>
<td>5.59 ±1.12*</td>
<td>0.183 ±0.087ns</td>
<td>70.18 ±15.35**</td>
</tr>
</tbody>
</table>

(H₁/D)²/4H₁ 1.140 0.682 0.825 1.455 1.04
H₁/4H₁ 0.168 0.209 0.248 0.251 0.241
([4DH₁]²+F)/
([4DH₁]²-F) 1.975 0.476 0.813 1.359 0.575
h²/H₁ 0.487 3.187 -0.102 0.525 -0.111
h² (NS) 0.764 0.837 0.652 0.267 0.617
h² (BS) 0.911 0.942 0.973 0.786 0.818

Table 4: 10 outstanding combinations of F₁ of cotton.

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Sympodia/plant</th>
<th>Plant height</th>
<th>Bolls per plant</th>
<th>Seed oil contents</th>
<th>Seed cotton yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>B557XC728-4</td>
<td>30.90</td>
<td>133.87</td>
<td>28.75</td>
<td>22.37</td>
<td>81.67</td>
</tr>
<tr>
<td>B557XWNH156</td>
<td>26.27</td>
<td>120.25</td>
<td>29.60</td>
<td>22.15</td>
<td>88.95</td>
</tr>
<tr>
<td>C728-4X8557</td>
<td>23.55</td>
<td>107.32</td>
<td>22.05</td>
<td>20.80</td>
<td>77.12</td>
</tr>
<tr>
<td>C728-4XC604-4</td>
<td>23.05</td>
<td>112.00</td>
<td>22.55</td>
<td>21.55</td>
<td>75.95</td>
</tr>
<tr>
<td>C728-4XWNH156</td>
<td>24.30</td>
<td>104.67</td>
<td>27.45</td>
<td>22.15</td>
<td>97.67</td>
</tr>
<tr>
<td>MNH156X8557</td>
<td>22.90</td>
<td>124.25</td>
<td>30.57</td>
<td>23.47</td>
<td>96.57</td>
</tr>
<tr>
<td>MNH156XC728-4</td>
<td>26.00</td>
<td>123.37</td>
<td>28.77</td>
<td>22.65</td>
<td>94.85</td>
</tr>
<tr>
<td>MNH156XC604-4</td>
<td>17.67</td>
<td>123.00</td>
<td>21.32</td>
<td>21.57</td>
<td>61.42</td>
</tr>
<tr>
<td>MNH156XWNH147</td>
<td>17.00</td>
<td>123.42</td>
<td>22.67</td>
<td>21.12</td>
<td>70.50</td>
</tr>
<tr>
<td>MNH147XC728-4</td>
<td>21.47</td>
<td>115.52</td>
<td>22.35</td>
<td>20.00</td>
<td>66.45</td>
</tr>
</tbody>
</table>
The cultivar MNH147 and Culture-728 had maximum recessive genes and C604-possessed both dominant and recessive genes while MNH156 and B-557 had more dominant genes than the recessive.

**Seed Cotton Yield**

Analysis of variance (Table 1) showed highly significant (P<0.01) genotypic differences. Tests for the validity of the additive-dominance model (Table 2) showed partial adequacy of data. The estimates for genetic components of variation for seed cotton yield are given in Table 3. The positive and significant values of D and H suggested control of both the additive and dominant gene effects, which corresponds to the findings of Sanyasi (1991). The lesser value of D than H1 indicated over dominance. Unequal values of H1 and H2 signified asymmetrical distribution of positive and negative alleles. The negative value of F showed excess of recessive genes for the expression of the character under study. The greater values of H1 and H2 over h2 suggested the absence of directional dominance non-significance of h2 showed absence of overall dominance effect due to heterozygous loci. The environmental influence was significant. The positive intercept of W/V, regression line (Fig. 5) reflected additive gene action. Similar results have been obtained by Saeed *et al.* (1996), Esmall *et al.* (1999), Shanti and Raveendran (1999) and Kumaresan *et al.* (2000). Narrow sense heritability (0.617) suggested that selection based on individual plant will give better progress for the character under study. Yingxin and Xiangming (1998), Esmall *et al.* (1999) and Kumaresan *et al.* (2000) also reported high heritability for seed cotton yield.

**References**


