



Full Length Article

Genetic Analysis of Fiber Traits in Cotton

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ABSTRACT

Thirty four genotypes were grown in the field to select contrasting genotypes for staple length, fiber fineness and fiber strength. Two genotypes contrasting for these traits were identified and crossed. The F₁, F₂ and backcross populations were developed and studied along with the parents. In generation means analysis a simple model with additive or additive and dominance parameters were found fit to explain inheritance of the fiber quality traits. The variance analysis revealed that only additive and environmental variance was involved for the traits. High heritability (>0.78) also indicated that most of the genetic variance was additive for the traits.

Key Words: Cotton; Fiber traits; Heritability; Generation means analysis

INTRODUCTION

Cotton fiber has global importance. Although its dominant position has been systematically displaced by synthetic fibers, people still prefer cotton due to its natural qualities, such as comfort, softness, durability and versatility. Cotton is processed into an array of materials and goods, which are being used daily in one or the other form. Cotton plays a pivotal role in the agriculture based economy of Pakistan. The statistics indicate that in the years of low cotton production, GDP growth rate goes down drastically and vice versa. Cotton crop in Pakistan feeds 943 ginning factories, 443 spinning mills, 8.45 million spindles, 2585 oil expelling units and over 5 million labor engaged in cotton and cotton related business.

In cotton breeding, only improvement of lint yield is not the objective rather quality characters like staple length, fiber strength, and fineness and maturity etc., are very important to textile industry. Improvements in textile processing, particularly advances in spinning technology, have led to increased emphasis on breeding cotton for improved fiber properties. Good staple length, fiber strength and high tensile strength of the fiber are needed for good spinning, especially with fast modern spinning machines. Fiber fineness determines the texture of cotton fiber. Cotton fiber may be classified as soft and silky or coarse and harsh. A successful cotton breeding programme depends on the genetic information of the traits need to be improved.

The knowledge about the nature and magnitude of genetic effects prevailing in the breeding material is necessary to decide about the kind of breeding procedure to be chosen. Traits related to quality of cotton are

quantitatively inherited. Although gene action of these traits is reported by many workers but the genetics of a particular trait may vary with variation in plant material and environment. So it is necessary to study gene action of quantitative traits before starting any breeding programme. Diallel and generation means analyses are commonly used in inheritance studies of quantitatively inherited traits (Innes *et al.*, 1975; Malik *et al.*, 1999).

Pathak (1975) used six populations (P₁, P₂, F₁, F₂, BC₁ & BC₂) of five upland cotton (*Gossypium hirsutum* L.) crosses to evaluate genetic effects for fiber traits in cotton. Iqbal (2003) used six populations to estimate genetic effects for yield of seed cotton and number of sympodial branches per plant through generation means analysis. The objective of the present work was to study the genetics/heritability of the fiber quality traits.

MATERIALS AND METHODS

The research work was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. Thirty four genotypes were grown under field conditions to identify contrasting parents for crossing. The F₁ crosses were made during the year 2003 under field conditions. Two genotypes HRVO1 with lower fiber traits (fiber fineness, fiber strength, staple length) and B1580-94 with higher fiber traits were selected. During the first week of December 2003, half of the F₁ seed harvested from the hybrid plants along with the parents was planted in pots for making backcrosses and to produce seed of F₂ population in glasshouse.

Then parental, F₁, F₂ and backcross (BC₁ & BC₂)

generations were raised in field during the year 2004. Experiment was laid out in randomized complete block design with three replications. A single row for parental and F₁, eight rows for each of the backcrosses and 15 for the F₂ generation were planted in a replication. The length of each row was four meter. Row to row and plant to plant distance was 75 and 30 cm, respectively. Normal agronomic practices were followed for growing the crop. At maturity, five guarded plants per replication for F₁ and each parent, 50 for each of the backcrosses and 100 for the F₂ generation were selected to harvest seed cotton on individual plant basis. After ginning of seed cotton the samples were tested for staple length, fiber strength and fiber fineness by using Spinlab HVI-900 in the Department of fiber Technology, University of Agriculture Faisalabad.

Standard analysis of variance technique, described by Steel *et al.* (1996) was applied to test the significance of differences among the generations used in the experiment. A generation means analysis was performed following the method described by Mather and Jinks (1982) using a computer program. Means and variances of each population (parents, backcrosses, F₁ & F₂) used in the analysis were calculated from individual plants pooled over replications. The coefficients of the genetic components of generation means are shown in the Table I. A weighted least square analysis was performed on the generation means commencing with the simplest model using parameter *m* only. Further models of increasing complexity (*md*, *mdh*, etc.) were fitted if the chi-squared value was significant. The best model was chosen as the one which had significant estimates of all parameters along with non-significant chi-squared value. For each trait the higher value parent was always taken as P₁ in the model fitting.

A weighted least squares analysis of variance based on the method as described by Mather and Jinks (1982) was performed on the data of the experiment containing six generations (Parents, F₁, F₂, BC₁ & BC₂). The coefficients of additive (D), dominance (H), cross product of dominant and additive effects (F) and environmental variation (E) are shown in Table II. Model fitting was started using the E parameter only; D, H and F parameters were successively included until a satisfactory fit was obtained. The best fit model was chosen as the one with all significant parameters and non-significant chi-squared value.

Heritability in narrow sense (h^2_{ns}) was calculated (Mather & Jinks, 1982) using the components of variance from the best fit model of weighted least squares analysis.

RESULTS AND DISCUSSION

Significant differences (P<0.05) were found among generation means in all the traits. The mean performance of the populations in different crosses is given in Table III. In quantitatively inherited traits, gene action is described as additive, dominance and epistatic effects. Additive effect is defined as the average effect of genes; dominance as the

Table I. Coefficients of the mean (*m*), additive (*d*), dominance (*h*), additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) parameters for the weighted least squares analysis of generation means (Mather & Jinks, 1982)

| Generations | Components of genetic effects | | | | | |
|-----------------|-------------------------------|--------------|--------------|--------------|--------------|--------------|
| | <i>m</i> | [<i>d</i>] | [<i>h</i>] | [<i>i</i>] | [<i>j</i>] | [<i>l</i>] |
| P ₁ | 1 | 1.0 | 0.0 | 1.00 | 0.00 | 0.00 |
| P ₂ | 1 | -1.0 | 0.0 | 1.00 | 0.00 | 0.00 |
| F ₁ | 1 | 0.0 | 1.0 | 0.00 | 0.00 | 1.00 |
| F ₂ | 1 | 0.0 | 0.5 | 0.00 | 0.00 | 0.25 |
| BC ₁ | 1 | 0.5 | 0.5 | 0.25 | 0.25 | 0.25 |
| BC ₂ | 1 | -0.5 | 0.5 | 0.25 | -0.25 | 0.25 |

Table II. Coefficients of the D, H, F and E effects for the weighted least squares analysis of generation variances (Mather & Jinks, 1982)

| Generation | Components of variation | | | |
|-----------------|-------------------------|------|-------|---|
| | D | H | F | E |
| P ₁ | 0.00 | 0.00 | 0.00 | 1 |
| P ₂ | 0.00 | 0.00 | 0.00 | 1 |
| F ₁ | 0.00 | 0.00 | 0.00 | 1 |
| F ₂ | 0.50 | 0.25 | 0.00 | 1 |
| BC ₁ | 0.25 | 0.25 | -0.50 | 1 |
| BC ₂ | 0.25 | 0.25 | 0.50 | 1 |

Table III. Generation means of fiber fineness (FF, micronaire), fiber strength (FS, g tex⁻¹), staple length (SL, mm) in cross HRV01×B1580-94 of cotton

| Trait | Generation | | | | | | Pop. effects | LSD (0.05) |
|-------|----------------|----------------|----------------|----------------|-----------------|-----------------|--------------|------------|
| | P ₁ | P ₂ | F ₁ | F ₂ | BC ₁ | BC ₂ | | |
| FF | 4.61 | 3.53 | 4.37 | 4.39 | 4.42 | 4.14 | ** | 0.27 |
| FS | 9.84 | 18.01 | 15.17 | 15.04 | 13.26 | 11.76 | ** | 1.58 |
| SL | 25.44 | 26.93 | 28.96 | 27.14 | 25.94 | 27.17 | ** | 0.78 |

*, P < (0.05); **, P < (0.01).

Table IV. Estimates of the best fit model for generation means parameters (±, standard error) by weighted least squares analysis in respect of fiber fineness (FF), fiber strength (FS), Staple length (SL) in cross HRV01x B1580-94 (1) of cotton

| Trait | Genetic Effects | | | | | χ^2 (df) |
|-------|-----------------|--------------|--------------|--------------|--------------|---------------|
| | <i>m</i> | [<i>d</i>] | [<i>h</i>] | [<i>i</i>] | [<i>j</i>] | |
| FF | 4.12±0.10 | 0.42±0.08 | 0.39±0.20 | - | - | 4.96(3) |
| FS | 13.96±0.25 | 3.92±0.25 | 1.41±0.60 | - | - | 4.50(3) |
| SL | 26.16±0.22 | 0.90±0.22 | 0.78±0.39 | - | - | 1.04(3) |

interaction of allelic genes and epistasis as the interaction of non-allelic genes that influence a particular trait. Gene action has been estimated using diallel crosses following the methods described by Hayman (1954) and Jinks (1954) or by using generation means and variance of different populations (generally segregating & backcross populations) by the method described by Mather and Jinks (1982). Generation means and variance analyses have been used for studying gene action in cotton (Pathak, 1975; Iqbal, 2003) and in other crops (Malik *et al.*, 1999).

In generation means analysis, a simple model with additive [*d*] and dominance [*h*] parameters were suitable to

Table V. Variance components D (additive), H (Dominance), F (Additive × Dominance) and E (Environmental) following weighted analysis of components of variance, and heritability (ns, narrow sense and F_∞ generation) for fiber fineness (FF), fiber strength (FS), staple length (SL), in cross HRV01xB1580-94 of cotton

| Trait | Variance Components | | | | χ^2 (df) | Heritability | |
|-------|---------------------|---|---|-------------|---------------|--------------|----------------|
| | D | H | F | E | | ns | F _∞ |
| FF | 0.83 ± 0.14 | - | - | 0.09 ± 0.03 | 0.43(4) | 0.82 | 0.90 |
| FS | 25.11 ± 3.96 | - | - | 2.45 ± 0.66 | 4.07(4) | 0.84 | 0.91 |
| SL | 4.02 ± 1.09 | - | - | 1.16 ± 0.30 | 1.40(4) | 0.63 | 0.78 |

explain inheritance of staple length, fiber fineness and its strength (Table IV). In variance analysis simple model with D and E parameter explained the variance of the traits. The absence of epistatic interactions shows that the inheritance is simple so, selection of plants for improved fiber quality can be started in early segregating generations.

Pathak (1975), Rehman *et al.* (1993), Babar and Khan (1999) and Mukhtar *et al.* (2000) also reported additive and dominance genetic effects for fiber fineness. While Innes *et al.* (1975) and Pavasias *et al.* (1999) reported that the trait was mainly controlled by additive gene action. Similarly Ahmad *et al.* (2003) concluded that fiber fineness and strength were controlled by additive genes whereas over-dominance was prevalent in the control of staple length. Results of Murtaza *et al.* (2004) support the present study as they have observed that fiber strength was governed by additive and dominance effects. Pathak (1975) and Hendawy *et al.* (1999) reported additive and dominance effects as well as additive × additive interactions for the trait. Kohel *et al.* (2001) identified four QTLs showing additive effects, which influenced fiber strength. In case of staple length three parameter model (m, [d] & [h]) provided a good fit to the data (Table IV). The presence of additive and dominant type of gene action for staple length was also reported by Nistor and Nistor (1999) and Babar and Khan (1999). On the other hand, Singh and Yadavendra (2002) reported additive, dominance as well as additive × additive and additive × dominance genetic effects for staple length. Pathak (1975) indicated the presence of dominance and dominance × dominance type of genetic effects for the control of staple length. Murtaza *et al.* (2004) also reported epistatic effects in the control of staple length. Different types of gene actions for the trait in different studies may be due to difference of genetic backgrounds of the parents involved and environment × genotype interactions. As under salt stress gene action for the traits, fiber fineness, fiber strength and staple length in cotton was found to be under the control of epistatic interactions (Bhatti *et al.*, 2006). They observed that ‘j’ (additive × dominance) and ‘l’ (dominance × dominance) type epistasis was highly significant in the inheritance of fiber strength under two salt stress levels whereas, for staple length and fiber fineness j+l type epistasis was significant in 10 dSm⁻¹, whilst it was highly significant in 20 dSm⁻¹ stress. This shows the

influence of environment on the type of gene action.

The traits had high narrow sense heritability estimates (0.78 to 0.90). Infinity generation heritability was consistently higher than the narrow sense heritability for all the traits (Table V). High heritability estimates for the traits show that a large proportion of the genetic variance was composed of additive genetic component.

Ulloa (2006) reported high heritability for fiber fineness, staple length and fiber strength (0.95, 0.78, 0.89, 0.80, respectively). Vyahalkar *et al.* (1984), found medium to high estimates of narrow sense heritability for fiber strength, staple length and fiber fineness in cotton.

The absence of epistatic interactions shows that inheritance of the traits, fiber fineness, strength and staple length is simple so, selection of plants for improved fineness, strength and staple length can be started in early segregating generations. The presence of interaction in some earlier reports shows that some alleles showing interactions are present in some populations so, during breeding for fiber strength selection of plants in early generations would not be effective as they would not reproduce progeny with the same magnitude of the trait due to recombinations. Selection in later generations would be more feasible.

High heritability estimates observed in present studies for all the three traits show that a large proportion of the genetic variance was composed of additive genetic component, which was also revealed by the generation means analysis. High heritability estimates suggested that these traits could effectively be improved through selection in the early segregating generations.

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