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Genetic Analysis of Fiber Quality Parameter under Water Stress in Upland Cotton (Gossypium hirsutum L.)

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Abstract

The present study was carried out to determine the genetic mechanism controlling variation in staple length, fiber strength and fiber fineness in diverse varieties of upland cotton (*Gossypium hirsutum*) under water stress and non-stressed condition in the fields. The joint regression analysis of F₁ data revealed that the additive-dominance model was fond adequate for characters studied. The unit slope of regression lines for fiber length ($b = 1.00 \pm 0.15$), fiber strength ($b = 0.99 \pm 0.19$) and ($b = 0.79 \pm 0.17$) fiber fineness suggested the absence of epistatic component in the inheritance of the characters studied. Degree of dominance for $\sqrt{H_1/D}$ for fiber length was almost complete, whilst it was less than partial for fiber strength and fineness. The results revealed that both additive and non-additive gene affected variation for water stressed tolerance, but the additive gene influence was more prominent. Consequently estimation of h²_{ns} for fiber length (0.61), fiber strength (0.65) and fiber fineness (0.72) were encouraging. The mode of gene action and moderate to high narrow-sense heritability for the fiber characteristics suggested that it is possible to improve water stress tolerance in *Gossypium hirsutum* by single plant selection in later segregating generation.

Keywords: Gene action, fiber length, fiber strength, fiber fineness, water stress

1. Introduction

Cotton is an essential commodity among the agricultural crops. It is the main source of natural fibers and vegetable oil in the world. In Pakistan cotton is grown on an area of about 2689 thousand hectare with production of 11.5 million bales (Anonymous, 2010). Different biotic and abiotic stresses influence the yield of cotton in many region of the world including Pakistan (Ritchie, 1980; Malik & Wright, 1998; Ahmed *et al.*, 2000; Basal *et al.*, 2005). Scarcity of water and high temperature is a complex phenomenon that badly influences the growth of cotton plant (Basal *et al.*, 2005; Malik *et al.*, 2006). Water stress tolerance is genetically controlled with many morphological and physiological features of crop plant.

However, breeding for high yield in stressed environmental condition is naturally occurring stress scenarios in the world (Levi *et al.*, 2009,). A substantial interaction of genotype to environment causes complexity in fiber quality yield of cotton (Song & Zhang, 2009). Thus, to fulfil the emerging needs of fine cotton in the market, cotton breeders mainly focused on better improvement of fiber traits that perform well under drought stress conditions.

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Imran et al.

High yield can be obtained by genetic potential of genotype and avoiding the crop from drought stress conditions (Cattivelliet *al.*, 2009). Therefore, selection of fiber quality trait for high yield under drought stress condition increases the efficiency of breeding programs, suggested by cotton breeders (Malik & Wright, 1998, Misraetal., 1994; Muniret *al.*, 2007)

In order to bring successful breeding programme in fiber quality parameter, genotypic responses to water stress and the mode of inheritance of variation must be significantly variable and genetically controlled. Otherwise, choice of breeding method will be useless for better improvement (Munir*et al.*, 2007). Therefore, studies of these two components is most important for breeding material (Mitra, 2001). The present study was planned to examine the genetic basis of water stress tolerance of 25 entries using indices of water stress tolerance. The relative data were analyzed following simple genetic model (Hayman, 1954 a, b and Jinks, 1954). Information reported in the script may be useful for continuing work on drought stress in *Gossypium hirsutum*.

2. Research Methods

The present investigations were carried out on the genetic basis water stress tolerance in upland cotton in the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. The detail of the experimentation is described in the following paragraphs. The parents were sown in controlled conditions. Five varieties of upland cotton i.e. MNH-512, Arizona-6218, CIM-482, MS-39, and NIAB-78, were grown in glass house with controlled temperature and light condition during December 2010and were crossed in all possible combinations. The five parents were also selfed. The seeds of 20 hybrids and their parents were planted in two sets in water stressed and non-stressed conditions in the field during June 2010. The climatic data were obtained from Agromet Bullet in Agriculture Meteorology Cell, Department of Crop Physiology, University of Agriculture, and Faisalabad, Pakistan. A graph of the climatic conditions during the cotton-growing period is shown in Fig.1.

In each set, seeds were sown in lines having 9 plants spaced 30 cm within row and 75 cm between the rows. After emergence, the sufficient number of desired plants was adjusted by removing the extra plants. The 25 genotypes in one treatment were given normal irrigation, and in the other treatment, 25 genotypes were grown without watering till maturity. Both experiments were planted using triplicate randomized complete block design. No irrigation was applied throughout the growth period of entries tested under drought conditions. The experiment was monitored daily for growth and attack of insect pests and sprayed, if required. Each entry was planted in a 290 cm long row having 10 hills spaced 30 cm apart. Rows were kept 75 cm apart. Two seeds of each entry was dibbled 5-6 cm deep per hill, and later thinned to one seedling. Lint samples of the two sets were tested using High Volume Instrument (HVI) and the data stressed conditions were compared with that of non-stressed conditions water stressed and non-stressed. Relative water stress tolerance (Index of Tolerance) was calculated using the following formula under water stressed and non-stressed conditions.

Stressed Relative water stress tolerance = ------ × 100 Control

Biometrical Analysis. Partitioned analysis of variance (Steel *et al.*, 1997) was performed on the data for all the characters in order to see whether the genotypic differences are significant or non-significant. Only significant genotypic differences allow the genetic analysis of the data.

3. Results

3.1 Adequacy of additive-dominance model to the F₁ data sets.

In order to assess how accurate the indices of water stress tolerance based upon various plant characters of *Gassypium hirsutum* L. Following the additive dominance model, it is necessary to test the adequacy of simple genetic model to the present data sets. Adequacy of the additive-dominance model and validity of some of the assumptions underlying the genetic model are usually tested by joint regression analysis (b), of the data.

The results of the test are presented in Table 1. The regression coefficients (b) of all the characters, described above, deviated significantly from zero but not from unity. This property of the regression line indicated the presence of intra-allelic interaction (dominance), and independent distribution of the genes among the parents for the traits, and the genes were independent in action.

Further unit slope of regression lines (b) for all the characters suggested that all the assumptions underlying the additive-dominance model were met as suggested by Hayman, (1954a)

3.2 Estimation of components of variation in various plant characters measured under water stressed conditions.

The estimation of components of variation in the three components was made in the table 1. The results showed that D was positive (P ≤ 0.05) for the three fiber quality parameters. Similarly H1 and H2 were non-significant (P > 0.05) for fiber length, fiber strength and fiber fineness. The extent of D was greater than those of H1 and H2 suggesting that additive gene affect appeared to be important for controlling fiber length, strength, and fineness. The degree of dominance $\sqrt{H_1/D}$ was less than unity, thus showing partial dominance of genes and this was verified by the slope of regression line for fiber strength and fineness. While for fiber length, it was almost equal to one thus showed complete dominance. The genes were unequally distributed for fiber length, strength and fineness as their magnitude H₂ was greater than H₁ with low ratio of H₂/4H₁ (0.18) for fiber length, H₁ was greater than H₂, with ratio of H₂/4H₁ (0.11) for fiber strength, and H₁ was not equal to H₂, with the ratio of H₂/4H₁ (-0.073) for fiber length, strength and fineness, respectively. The negative value of F supported by low ratio of $[\sqrt{4DH_1+F}] / [\sqrt{4DH_1-F}]$ for fiber length, strength, strength and fineness was 0.63, 0.59 and 0.46 respectively which indicated the presence of recessive genes in the parents controlling the characters. Due to the presence of additive gene in the genetic control the estimate of narrow sense heritability for fiber length, strength and fineness were 0.61, 0.65, and 0.72, respectively Table 1.

The pattern of variety distribution showed maximum variation in the parents for fiber length. From the Fig. 2 it is clearly seen that variety NIAB-78 being closer to the point of origin possessed maximum number of dominant genes, and by contrast Arizona-6218 contained maximum recessive genes for fiber length, whilst varieties MNH-512, CIM-482 and MS-39 got intermediate position. The scatter of array points along the regression line in the Fig. 3 showed that MS-39 contained the greatest number of dominant genes, whilst Arizona-6218 carried the greatest number of recessive genes for fiber strength. Varieties CIM-482, NIAB-78 and MNH-512 carried both dominant and recessive genes for the character. The wider scatter of varieties in Fig. 4 revealed that parents differed widely from each other with respect to the presence of dominant and recessive genes. Variety CIM-482 contained more number of dominant genes and MS-39 carried the more number of recessive genes, whilst remaining varieties contained both genes for fiber fineness.

4. Discussion

Simple additive-dominance model appeared to be adequate for analysis of the data F1 on fiber length, strength, and fineness and in all these cases genes acted additively with varying degree of dominance. The unit slopes of regression line provided no evidence of the involvement of epitasis in the inheritance of these characters, consequently the water stress tolerance. This indicated that plant selection is straight forward and easy to identify the desired plants from segregating populations. Estimate of h_{ns}^2 varied from 34% to 89% in all the characters assessed under stressed conditions, and these estimates seem to be encouraging for plant breeder for the development of drought tolerance in the plant material examined in the present study. It has been suggested elsewhere that estimates of h_{ns}^2 are subjected to environmental influences, and therefore may be used with great care and caution (Falconer and Mackey, 1997).

It is noted that trend of dominance in case of fiber length and fiber strength were towards the parents with decreasing the characters, whilst the negative sign of 'h' fiber fineness is good indication of the potential of plant material and provided hope for bringing further improvement under water stress conditions. Availability of variation in cotton germplasm for moisture stress condition and its genetic basis is of principal importance for breeding cotton material with enhanced water stress tolerance following conventional breeding methods. When a lot of germplasm is available for screening against any stress condition, a rapid and efficient technique should be used for the identification of variation present in the material.

Imran et al.

In the present study, the relative values of 20 F₁ hybrids and their five parents grown under water stressed and controlled conditions in the field were examined for fiber characters. This method distinguished tolerant and susceptible genotypes. Previously, scientists had studied growth of cotton to moisture stress (Radin and Ackerson, 1981; Loffroy *et al.*, 1983 and Ball *et al.*, 1994).

In the present study, both additive and dominance properties of the genes appeared to be important for the variations in the characters related to water stress tolerance, the genes acting additively showed the predominance influence on the genetic control of all these traits. It was also studied that water stress tolerance cannot be credited to a single genotype due to its dominance for a single trait; therefore different parameters were required for evaluation (AI-Hamdani and Barger, 2003). The present results revealed that fiber characteristics were reduced due to adverse affects of water stress, genotypes responded differently and some of the families like NIAB-78 × NIAB-78, CIM-482 × CIM-482, NIAB-78 × Arizona-6218, CIM-482 × Arizona-6218 and NIAB-78 × MS-39 showed have fewer indexes for water stress tolerance while all the other families have greater values. It was also found that all the characters measured under water stress and controlled conditions, thereby meaning water stress tolerance, were largely influenced by additive genes.

5. Conclusion

In conclusion, the above studies revealed that water stress has drastic effect on fiber quality traits and were found to be genetically controlled. It was further confirmed that water stress tolerance was polygenic complex trait and governed by additive gene action. Additionally, in case of fiber length and strength trend of dominance was towards the decreasing characters. Negative sign of 'h' for fiber fineness gave an indication of potential of plant material for further improvement. Narrow sense heritability for all the characters studied was very high suggesting single plant selection in later segregating generation. Assessment of genotypic responses to water stress in upland cotton by using data on fiber quality traits in water stressed environment is helpful to the breeders for comparing the potential of varieties/lines of cotton to drought tolerance. The information derived from these studies may be used to develop drought tolerant cotton material that could give economic yield in water stress.

6. References

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Table1: Components of variation in fiber length, strength, and fineness in Gossypium hirsutum

Components	Fiber	Fiber	Fiber
-	length	strength	fineness
D = additive Variance	3.023±0.16	2.34 ± 0.15	4.47±0.14
H ₁ = dominance Variance	-2.8±0.48	-0.38±0.40	-0.35 ± 0.40
H_2 = proportion of positive and negative genes in the parents	-2.09±0.39	-0.17±0.37	0.1±0.36
F = relative frequency of dominant and recessive alleles in the parents	-1.37±0.40	-0.48±0.37	92±0.37
E = environmental variance	1.72 ± 6.5	0.72±3.91	0.91±6.1
$\sqrt{H_1/D}$ = degree of dominance	0.94	0.40	0.28
H_2 / $4H_1$ = proportion of genes with positive and negative effects in	0.18	0.11	-0.73
parents			
$[\sqrt{4}DH_1 + F] / [\sqrt{4}DH_1 - F] =$ proportion of dominant and recessive genes	0.63	0.59	0.46
in theparents			
Heritability (ns)	0.61	0.65	0.72







Fig. 2: Wr-Vr graph for Fiber length



MNH 512 CIM 482

Fig. 4: Wr-Vr graph for fiber fineness

