

Inheritance Pattern of Seed Cotton Yield and its Components under Nitrogen Stress Condition

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ABSTRACT

The genetic basis of variation in eight varieties/lines of *Gossypium hirsutum* L., due to nitrogen stress was examined using simple additive dominance model of genetic analysis. The parents were crossed in all possible combinations. The response of 56 F₁ hybrids and the parents to nitrogen stressed growing conditions was studied till maturity. The plants were given nitrogen @ 27 kg/acre only at the time of planting. At maturity data on number of bolls, boll weight and seed cotton yield were recorded. Analysis of variance of the means of 64 families showed highly significant differences for the three characters. The two scaling tests i.e. joint regression analysis and analysis of (W_r + V_r) and (W_r-V_r) suggested that the genetic model was partially adequate for number of bolls, and fully adequate for boll weight and seed cotton yield. The components of variation estimated revealed that affects of the genes showing dominance properties were more pronounced than those of additive genes. Estimates of narrow sense heritability of the three plant characters were very low, suggesting that selection of desirable plants should be delayed till later generations.

Key Word: Upland cotton; Nitrogen stress; Variation; Additive; Dominance; Diallel cross

INTRODUCTION

Cotton being the major exporting commodity of Pakistan fetches about 65% of foreign exchange earnings annually. In addition to providing lint, cotton seed contains considerable amount of edible oil and thus contributes 70% of total edible oil obtained from oil and non oil crops (Anonymous, 2000). The breeders had made tremendous efforts in order to make the cotton plant more profitable, and they had developed numerous varieties having greater yield of seed cotton with improved fibre characteristics.

The breeding and selection work for the development of existing commercial cotton varieties was done under favorable environments e.g. supplying increasing doses of nutrients (nitrogen and phosphorus), adequate moisture supply and ideal plant protection measures. Thus the existing varieties have to potential of giving maximum yields in the fields which are supplied optimum amount of inputs recommended in "Cotton Production Technology". It had been reported that nitrogenous fertilizer determine the wide range of variables e.g. plant stage, fruiting density, boll retention, boll size, number of bolls and ultimately affects plant performance (Gerik *et al.*, 1989). According to the studies of Pettigrew *et al.* (1996) and Baver *et al.* (2000) higher application of nitrogenous fertilizer decrease yield up to 3% and lint percentage 1%.

Keeping in view the present scenario of WTO the production of organic cotton has become more important these days, and this may be achieved studying the response of cotton plant to biotic and abiotic stresses. The development of cotton varieties having adaptability to soil having low content of nitrogen and other nutrients is one of them. In order to make this programme a good success, the evaluation of the genetic material with respect to its response to low inputs of

nitrogenous fertilizer is essential. Therefore a genetic experiment involving 56 F₁ families originated from crosses involving eight parents of *Gossypium hirsutum* L. was conducted in the department. The information reported here in may be helpful for developing a well conceived breeding programme to achieve the objective.

MATERIALS AND METHODS

The plant materials used in the present genetic studies was developed by crossing eight parental lines of *Gossypium hirsutum* L. namely MS-84, NIAB-78, MNH-93 and AC-134 (all four indigenous lines) and Coker-201, Coker-3113, Har-M-32-7-4 and HG-HN-134 (all four exotics). The parents were crossed according to diallel mating design. The seed of 56 F₁ hybrids along with the parents were planted in the field following randomized complete block design with three replications. The 64 families were sown in single row plot keeping 12 plants spaced 75 cm between rows and 30 cm within the row. Nitrogen was applied @ 27 kg/acre at the time of planting, and after that no nitrogen was supplied to the growing plants, against the recommended dose of 139 kg/acre by the Department of Agriculture.

The dose of phosphatic fertilizer was that recommended by Agricultural Department for cotton crop. Appropriate plant protection measures and agronomic practices were followed to obtain healthy plant population.

At maturity of plants total number of bolls and seed cotton of ten guarded plants were counted separately. Average boll weight was calculated dividing seed cotton yield of each plant by respective number of bolls.

Statistical procedure. Before subjecting the data to diallel analysis technique, these were subjected to ordinary analysis of

variance in order to see whether the genotypic differences among F₁ hybrids and their parents are significant. Further genetic analysis of data is valid only where such genotypic differences are significant.

To determine the adequacy of the additive dominance model to account for data, and to assess the validity of some of the assumptions underlying the model, preliminary analysis of the data were done following Hayman (1954a,b). From the data set, variance of components of each array (V_r), the covariance of the parents with their offspring in each array (W_r), and the variance of parental means (V₀L₀ = V_p) were calculated. Other statistics include the computation of the means of array variance (V₁L₁), the variance of means of arrays variance (V₀L₁), and the mean of array covariance (W₀L₀). All these statistics were used to calculate the genetic components of variation in characters. The components under the simple additive-dominance model are: D, the component of variation due to additive effects of the genes; H₁, the component of variation due to dominance effects of the genes; H₂ = h₁² [1 - (U₁-V₁)²]². Where U is the proportion of positive genes in the parents, and V is the proportion of negative gene in parents, h is the dominance effects; F, provides an estimate of the relative frequency of dominant to recessive alleles in the parents, and variation in dominance over the loci. These estimates were obtained by removing the environmental component. E, which in the present study was halved, since reciprocal F₁ families were assumed to have identical expectations and therefore, are averaged (Mather & Jinks, 1982). Estimates of narrow sense heritability of seed cotton yield, number of bolls and boll weight were calculated from the genetic components according to the formula given by Verhalen *et al.* (1971).

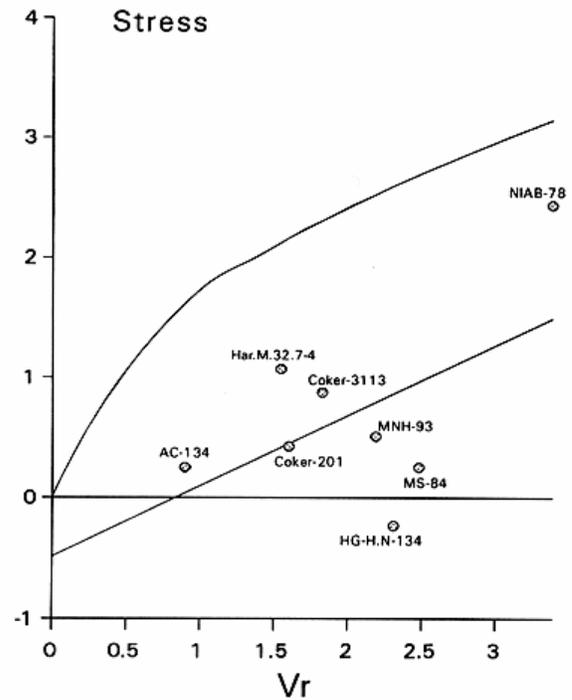
RESULTS

Assessment of the data for genetic analysis. The analysis of variance of means of parents and 56 F₁ families revealed highly significant differences (P ≤ 0.01) for number of bolls/plant, average boll weight and seed cotton yield (Table I). These significant differences validated the use of simple additive dominance model for genetic analysis of the diallel data. To test the suitability of the present data for genetic analysis and validity of the major assumptions underlying the genetic model two scaling tests i.e. joint regression analysis and analysis of variance of (W_r + V_r) and (W_r - V_r) were carried out. Regression coefficient (b) is expected to be significantly different from zero but not from unity if all the assumption are met (Hayman, 1954). The unite slope of regression line for

Table I. Estimates of analysis of variance for number of bolls, boll weight and yield of seed cotton under normal and nitrogen stress condition

Source of variation	D.F	No. of Bolls	Boll Weight	Yield
Replication	2	1.938	0.007	3.563
Genotype	63	15.69*	0.197*	7.486*
Error	126	3.615	0.029	2.00

Fig. 1. W_r / V_r graph for number of bolls



number of bolls (b = .998 ± 0.397, Fig. 1a), boll weight (b = 1.232 ± 0.390 Fig. 2) and seed cotton yield (b = 0.490 ± 0.156, Fig. 3), and significance of differences of (W_r+V_r) and (W_r-V_r) of the three characters (Fig. 1 to 3) revealed that additive dominance model was partially adequate for number of bolls and fully adequate for data set on boll weight and seed cotton yield. The scaling test provided further evidence of the presence of non allelic interaction in the inheritance of number of bolls.

The estimates of genetic variation in number of bolls, boll weight and seed cotton yield are given in Table II. Although D, H₁ and H₂ items were positive and significant for number of bolls, the greater magnitude of H₁ and H₂ than that of D revealed that genes with non additive effects were important. As the magnitude of H₁ is greater than H₂ therefore distribution of negative and positive alleles were unequally distributed in the parents and further proof of this unequal distribution of alleles over loci is provided by the ratio H₂/4H₁ (0.233) which is lesser than its maximum value 0.25 (Table II). Positive value of F (1.089) suggested that dominant alleles were more abundant than the recessive alleles in the parents, and this claim was supported by the ratio of (4DH₁)^{0.5}+F/(4DH₁)^{0.5}-F. Negative value of h in F₁ indicated the trend of dominance towards lesser number of bolls/plant. The ratio of √H₁/D is greater than 1, and therefore presence of over dominance in the genes was revealed. The ratio of 1/2 F√[D(H₁-H₂)] was used to determine whether the dominance level varies from one locus to another. In the present case the estimate was 0.836 which is almost near to 1, suggesting that dominance existed at all the loci in the parents. Narrow sense heritability of number of bolls

Table II. Components of variation in *Gossypium hirsutum* L. characters measured in nitrogen stress conditions

Components	Number of bolls	Boll weight	Seed cotton yield
E	1.175 ± 0.155	0.010 ± 0.004	7.58 ± 0.228
D	1.463 ± 0.464	0.087 ± 0.011	3.167 ± 0.683
H ₁	4.285 ± 1.066	-0.154 ± 0.026	9.604 ± 1.540
H ₂	3.995 ± 0.928	0.093 ± 0.023	6.201 ± 1.366
F	1.089 ± 1.096	0.126 ± 0.027	6.394 ± 1.614
H	-0.617 ± 0.622	-0.259 ± 0.015	8.236 ± 0.916
$\sqrt{H_1/D}$	1.711	1.332	1.742
H ₂ /4H ₁	0.233	0.151	0.161
$\sqrt{4DH_1 + F/\sqrt{4H_1} - F}$	1.556	3.387	3.758
$1/2F/\sqrt{[D(H_1 - H_2)]}$	0.836	0.863	0.974
h ² _{ns}	0.132	0.252	0.037

is very low (0.132). The study of Wr Vr graph in Fig. 1 shows that AC-134 had maximum number of dominant genes and NIAB-78 being away from origin carried maximum number of recessive genes for number of bolls.

Genetic components of variation in boll weight measured in limited nitrogen stress condition are given in Table II. The greater magnitude of H₁ than that of D suggest that genes acting non additively were important controlling boll weight. The ratio of (H₁/D)^{0.5} is greater than 1 which suggest that over-dominance was present in the inheritance of boll weight. The slope of Wr/Vr line also revealed the presence of over-dominance (Fig.2). As the magnitude of H₁ is greater than H₂ therefore distribution of unequal gene frequencies among the parents was suggested. The ratio H₂/4H₁, and positive values of F revealed that there were more dominant genes in the parents than the recessive genes. Negative values of h indicated that trend of dominance was towards decreased boll weight. The estimate of (4DH₁)^{0.5} + F/(4DH₁)^{0.5} - F is more than 1, which indicated that there were more number of dominant genes in the parents. The higher magnitude of ratio of 1/2 F/[D(H₁-

H₂)^{0.5}], i.e. 0.86 showed that dominance existed at all the loci in F₁ generation. The distribution of array points in Fig. 2 showed that Coker-201 and Coker 3113 being closer to the point of origin had maximum number of dominant genes, whilst Har-M-32-8-4 being away from origin carried maximum number of recessive genes for boll weight.

The components of variation in seed cotton yield in F₁ generation under limited nitrogen stress condition are given in Table II. As item D < H₁ and H₂, the genes acting non-additively, were present in the parents. The positive value of F indicates that dominant genes were more frequent in the parents than recessive genes. Since the sign h was negative therefore the trend of dominance in the parents was toward decreasing the yield of seed-cotton. As ratio (H₁/D)^{0.5} is more than 1, therefore genes showed over-dominance. Ratio H₂/4H₁ is lower than 0.25, therefore distribution of genes in the parent was unequal, and this information was confirmed by the value of H₁ > H₂. The ratio of (4DH₁)^{0.5} + F/(4DH₁)^{0.5} - F is more than 1, and it is indicated that dominant genes were more

Fig. 2. W_r / V_r graph for boll weight

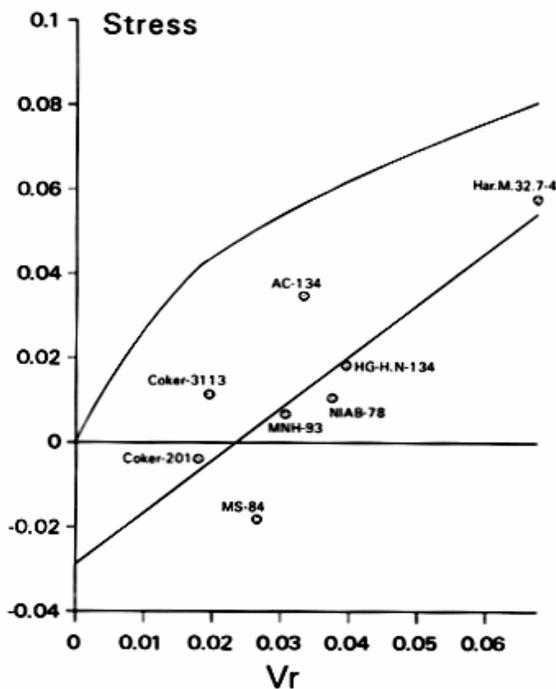
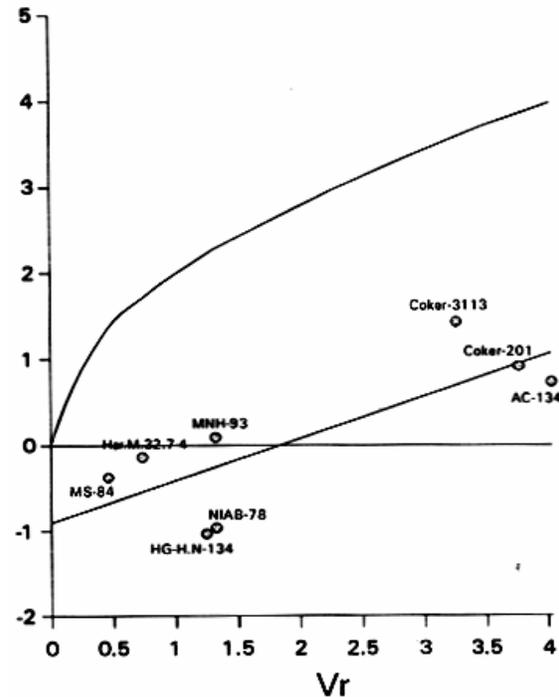


Fig. 3. W_r / V_r graph for yield of seed cotton



frequent in the parents. The estimates of $\frac{1}{2} F/[D(H_1-H_2)]^{0.5}$ is nearly 1 suggesting that dominance existed at all the loci in the parents for seed cotton yield under limited nitrogen stress.

Distribution of array points along the regression line (Fig. 3) indicated that MS-84 and Har-M.32-7-4 being closer to the origin contained maximum number of dominant genes, and Coker-3113, Coker-201 and AC-134 due to occupying farther position from the origin carried maximum number of recessive genes for plant yield under nitrogen stress.

DISCUSSION

In order to bring an evolutionary change, through selection, in adaptation of cotton plant to stress conditions due to nitrogen, the availability of genetically based variation in breeding population is essential. In the present studies application of limited nitrogen to plants had adverse effect on number of bolls, average boll weight and seed cotton yield and the statistical analysis of the data showed that the genotypes differed significantly from each other for these three characters measured under limited nitrogen conditions (Table I). The phenotypic variation in the characters studied may have arisen due to the diverse germplasm used in the hybridization programme as suggested by Panchal *et al.* (1994), Gururajan and Henery (1995) and Pandey *et al.* (1995). According to Mather and Jinks (1977), the significant amount of phenotypic variation observed in the three characters may involve an additive component.

When such a potential plant material is available to a research worker, the use of an appropriate biometrical methods which could provide dependable information on the genetic basis of variation in the plant characters would be helpful. Amongst the biometrical techniques available now-a-days, diallel cross method developed by Hayman (1954 a,b) and Jinks (1954) provides authentic information on patterns of inheritance in early generations like F_1 . The diallel cross technique had been used frequently for analysing quantitative characters in cotton (Carvalho *et al.* 1995; Tomer & Singh, 1996), sorghum (Azhar & McNeilly, 1988; Kasuga & Inoue, 2001), wheat (Wagoire *et al.*, 1998) and rice (Singh *et al.*, 1997, Gu *et al.*, 1998) and therefore the same method was followed here.

The simple Hayman-Jinks genetic model was found to be fully adequate for analysing data on boll weight and seed cotton yield (Fig. 1 to 3), however, it showed partial adequacy to the data on number of bolls per plant (Fig. 1). The partial adequacy of the additive dominance model to account for number of bolls may be due to the presence of non-allelic interaction involved in the inheritance of the character or due to non-independent distribution of genes in the parents as suggested by Mather and Jinks (1982). The data thus showed partial failure to meet the assumptions underlying the simple additive-dominance model. There are numerous workers who found similar inadequacy of the genetic model to the diallel cross data, yet they made analysis e.g. in *Sorghum bicolor*

(Azhar & McNeilly, 1988), *Hordeum vulgare* (Johnson & Aksel, 1964), *Gossypium hirsutum* L. (Azhar *et al.*, 1994). Therefore, the data on number of bolls were also analysed here to derive genetic inferences.

Plant yield and its components in cotton, like in many other crops, are polygenic characters and thus influenced by environments. In the present plant material assessed under nitrogen stress the presence of genes having both additive and dominance properties were revealed for number of bolls, boll weight and seed cotton yield, but greater magnitude of H_1 than D showed that genes with non additive influence were more pronounced. The previous studies conducted on this aspect of cotton plant do not exist in the literature. However there is ample evidence which show that seed cotton yield and its components were controlled by the genes acting non additively under normal growing conditions (Pandey *et al.*, 1995; Tomer & Singh, 1996; Green & Culp, 1990; Singh *et al.*, 1990; Carvalho *et al.* 1995).

Due to the overwhelming effects of non additive gene effects the estimates of narrow sense heritability of number of bolls (0.132) boll weight (0.252) and seed cotton yield (0.037) are very low. These results suggest that improvement in the responses of *Gossypium hirsutum* L. to nitrogen stress using present genetic material does not seem easy. According to suggestion of Marwan *et al.* (1981), the breeding material may be amenable to selection in later generations like F_4 and F_5 . The present studies revealed the occurrence of over dominance in the three characters which is an indication of the manifestation of significant amount of heterobeltiosis as suggested by Paul *et al.* (1987), and this phenomenon had been reported to occur in stress conditions (Blum, 1977; Ekanayake *et al.*, 1985).

This information suggests that development of hybrids may be advantageous for having yield from soils with poor nitrogen supply. However it is suggested that further experiments may be conducted in order to substantiate the present results.

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