

Genetics Mechanism Controlling *Gossypium hirsutum* L. Character Measurement under Nitrogen Condition

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ABSTRACT

In order to study the genetic mechanism controlling variation in number of bolls, boll weight, and seed cotton yield measurement in F_2 generation grown under nitrogen stress condition. The diallel cross data were analysed following graphic approach of Hayman (1954a, b) and Jinks (1954). The 56 F_2 families were derived from F_1 hybrids developed by crossing 8 parents (four local and four exotic) of *Gossypium hirsutum* L. Adequacy of the genetic model is the data sets was tested using the two scaling i.e. regression analysis and analysis of variance of W_r+V_r and W_r-V_r tests, and it was found to be adequate for analysing number of bolls and boll weight. Genetic analysis of the data revealed that the two characters were effected by the genes showing additive and dominance properties, but the role of non-additive genes was more predominant in controlling variation in number of bolls and boll weight. The genes showed the presence of over dominance. Due to the low estimates of narrow sense heritability organs selection for the plants showing good response to nitrogen stress conditions is suggested

Key Word: Diallel; Generation; F_2 ; Inheritance; Additive effects

INTRODUCTION

Keeping in view the role of cotton plant in the economy of Pakistan, the cotton breeders have studied it extensively in order to exploit its potential under conducive environments. Although a great deal of progress has been made in the domain of cotton breeding, the charging concomitance around necessitate the research workers for bringing genetic modifications to make the plant adaptable to stress condition. The people in European countries are becoming more aware about their health and are looking for cotton lint produced without using pesticides and artificial fertilizers. Clearly development of cotton material adaptable to stress environments would be more economical. Therefore the present studies were carried out in the Department of Plant Breeding and Genetics, with the view to study the response of *Gossypium hirsutum* L. varieties/lines to nutritional stress particularly nitrogen, which is being luxuriously by the farmers, and chances of making selection of such plants, which may be, grow successfully with limited nitrogen supply.

Previous studies on the genetics of responses of upland cotton nutritional stress conditions have not been reported in the literature. However, some earlier agronomic and physiological studies revealed the adverse effects of nitrogen on the growth and development of cotton plant (Scott *et al.*, 1973; Nuttle *et al.*, 1989; Boquet *et al.*, 1993) claimed that excessive use of nitrogenous fertilizer cause luxurious growth which becomes attractive to insect pest, complex, cause late maturity and ultimately low yield is obtained.

This paper is explains the genetic basis of variation in the plant material of upland cotton to limited nitrogen supply, and the information may be helpful to the researchers for continued genetic improvement in the plant.

MATERIALS AND METHODS

For present studies the plant material was developed by crossing eight lines MS-84, NIAB-78, MNH-93, AC-134, Coker-201, Coker-3113, Har-M-32-7-4 and HG-HN-134 in all possible combinations in greenhouse, during 1997. During 1998-99 the F_1 generation was grown to obtained F_2 seed, and the following cropping season, F_2 seed was grown under nitrogen stress condition (nitrogen was applied only at time of planting) other production practices i.e. agronomic and plant protection measures were similar as recommended by Agricultural Department. At maturity data for number of bolls and seed cotton yield were recorded and boll weight data was calculated by dividing seed cotton yield from 120 guarded plants by their 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 F_1 hybrids and their parents. Analysis of data following diallel technique 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 (1954). 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 ($V_0L_0 = V_p$) were calculated. Other statistics include the computation of the means of array variance (V_1L_1), the variance of means of arrays variance (V_0L_1), and the mean of array covariance (W_0L_0). All these statistics were used to calculate the genetic components of variation in the 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 = h²_i [1 - (U₁-V₁)²]². where U is the proportion of positive genes in the parents, and is the proportion of negative genes in parents, h² 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 calculated from the genetic components according to the formula given by Mather and Jinks (1982).

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 data. To test the suitability of the data for genetic analysis and validity of the

Table I. Mean squares obtained from simple analysis of variance of different yield components in F₂ population grown under normal and limited nitrogen stress

SOV	DF	No. of bolls	Boll weight	Seed cotton yield
Replications	2	0.146	0.003 ^{NS}	25.964 [*]
Genotypes	63	23.172 ^{**}	0.267 ^{**}	25.967 ^{**}
Error	126	2.543	0.023	6.860

*,**and NS show significant, highly significant and non-significant differences respectively

Table II. Components of variation in number of bolls, boll weight in *Gossypium hirsutum* L. in F₂ under nitrogen stress conditions

Components	Estimates			
E	0.967 ± 0.270	0.835 ± 0.457	0.005 ± 0.001	0.012 ± 0.135
D	5.129 ± 0.810	9.235 ± 1.370	0.027 ± 0.003	0.309 ± 0.406
H ₁	44.788 ± 7.452	37.889 ± 12.597	0.104 ± 0.026	4.651 ± 3.734
H ₂	40.188 ± 6.484	33.878 ± 10.959	0.069 ± 0.022	3.581 ± 3.249
F	5.818 ± 3.821	2.566 ± 6.459	0.055 ± 0.013	1.024 ± 1.915
h	-12.993 ± 4.348	-9.112 ± 7.350	-0.052 ± 0.015	-0.151 ± 2.179
$\sqrt{H_1/D}$	2.955	2.026	1.954	3.880
H ₂ /4H ₁	0.224	0.224	0.166	0.192
$\sqrt{4DH_1 + F/\sqrt{4H_1 - F}}$	1.475	1.147	3.187	2.491
$1/2F/\sqrt{D(H_1 - H_2)}$	0.599	0.211	0.901	0.890
h ² _{ns}	0.297	0.445	0.622	0.307

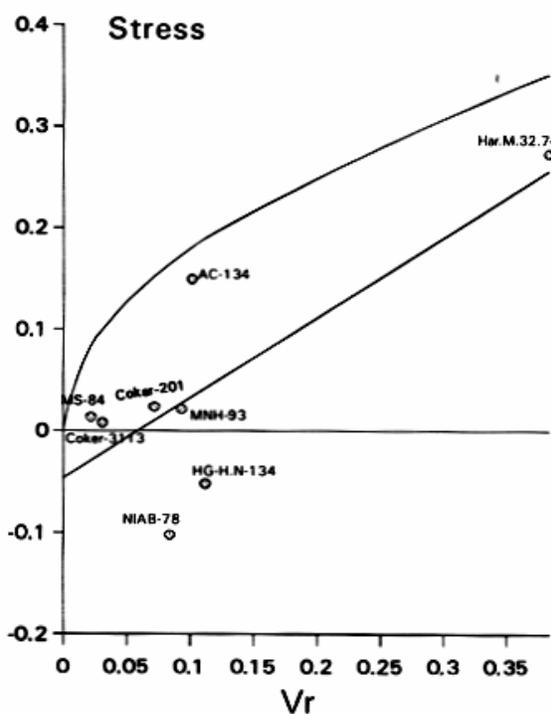
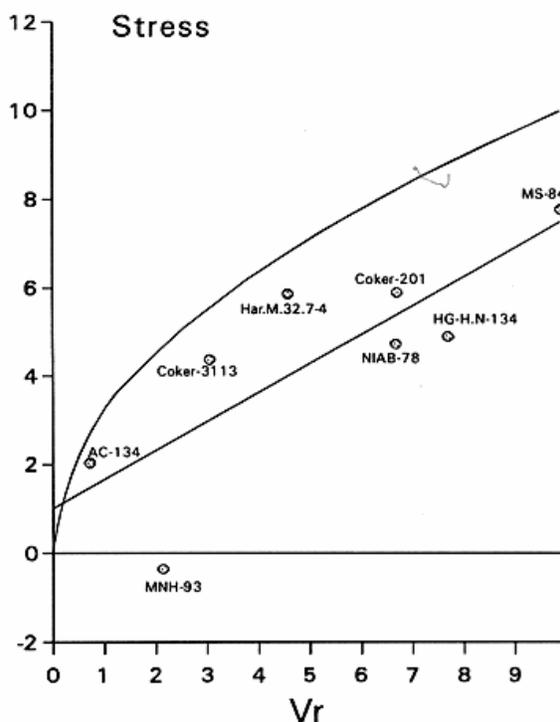
E= Environmental components of variation ;H₂= Dominance effects of genes corrected for gene distribution; D= Additive effects of gene; F= Frequency of dominant alleles; H₁= Dominance effects of gene; h = Overall dominance effects of heterozygous

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 assumptions are met (Hayman, 1954). The unite slope of regression line for number of bolls (b = .655 ± .195), boll weight (b =.790 ± .270 Fig. 1b) and significance differences between the array (W_r+V_r) and within the arrays (W_r-V_r) (given in Fig. 1) revealed that additive dominance model was partially adequate for number of bolls, and boll weight for data set, but yield of seed cotton failed to qualify the null hypothesis for further analysis of data. The scaling tests provided evidence of the presence of non allelic interaction in the inheritance of number of bolls.

Estimates of genetic components of variation in number of bolls measured in F₁ and F₂ generation under limited nitrogen supply are given in Table II. Although estimates of D, H₁ and H₂ are positive the greater magnitude of H₁ and H₂ than that of D revealed the pronounced effect of genes with non-additive properties. As the magnitude of H₁ > H₂ therefore distribution of unequal gene frequencies in the parents was indicated, which was verified by the ratio of H₂/4H₁ which is lesser than 0.25. Positive value of F indicated 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/(4DH₂)^{0.5} - F. Negative value of h indicated the trend of dominance towards decrease number of bolls. The degree of dominance was indicated by the ratio (H₁/D)^{0.5} which is greater than 1, thus indicated the presence of over-dominance in F₂ generation. The ratio of ½ F/ [D(H₁-H₂)]^{0.5} is low estimate, 0.211 indicated that dominance existed at only few loci under nitrogen stress conditions.

In case of F₂, comparison of the array points showed that AC-134 and MNH-93 possessed maximum number of dominant genes, and MS-84 being away from the origin contained maximum number of recessive genes for number of bolls under nitrogen stress condition.

Fig. 1. W_r / V_r graph for (a) number of bolls and (b) boll weight



Genetic components of variation in boll weight measured

in limited nitrogen stress condition are given in Table II. Since the magnitude of H_1 is greater than that of D , therefore the genes with dominance influence were shown to affect variation in boll weight in F_2 generations. The ratio of $(H_1/D)^{0.5}$ is greater than 1 which suggesting the presence of over-dominance in the inheritance of boll weight. The slope of W_r/V_r line also revealed the presence of over-dominance (Fig.1b). As the magnitude of H_1 is greater than H_2 therefore distribution of unequal gene frequencies among the parents was suggested. The ratio of $H_2/4H_1$, 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 in boll weight was towards lower side. The estimate of $(4DH_1)^{0.5} + F/(4DH_1)^{0.5} - F$ is more than 1, which indicated that there were more number of dominant genes in the parents. The higher magnitude of ratio of $\frac{1}{2} F / [D(H_1-H_2)]^{0.5}$, i.e. (0.89) showed that dominance existed at all the loci.

In case of F_2 , MS-84 and Coker-3113 being close to the origin carried maximum number of dominant genes, as compared to Har-M-32-7-4 which carried maximum number of recessive genes for boll weight.

DISCUSSION

The development of a plant character through selection becomes easier if a breeding population contains sufficient amount of variability in the character to be improved. The analysis of the plant material that significant amount of variation was present in (a) number of bolls, boll weight and seed cotton (b) yield suggesting that F_2 population is amenable to selection. Selection of the plants bearing maximum number of bolls with good boll weight under nitrogen stress condition may contribute towards greater plant productivity. Selection of such desirable plant will be effective if a working knowledge about the pattern of inheritance about these characters is available. The two scaling tests i.e. joint regression analysis and analysis of variance between the arrays (W_r+V_r) and within the arrays (W_r-V_r) suggested that the simple additive dominance model of Hayman (1954ab) and Jinks (1954) revealed that the model was fully adequate to account for the data on number of bolls and boll weight. Whereas the data seed cotton yield was unfit for genetic analysis.

The components of variation in number of bolls and boll weight (Table II) suggested that although both additive and non-additive gene effects were shown to control variation in two characters. In previous literature genetic aspect in relation to are not available, however, some suitability studied cotton plant for different stress in cotton (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) same method was adopted for study of diallel crosses. The effects on genes with dominance properties appeared to be more important (Table II). The estimates of heritability for number of bolls in moderate (0.445) and low for

boll weight (0.307). Table II suggested that selection of plants having larger number of bolls acceptable boll weight is possible under nitrogen stress condition. Non-the-less these magnitude of estimates seems to be encouraging when the plant material is grown under stress environment i.e. deficiency of nitrogen supply.

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