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MODE OF GENE ACTION CONTROLLING SEED COTTON YIELD AND VARIOUS COMPONENTS IN *Gossypium hirsutum* L.

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The gene action controlling the inheritance of yield of seed cotton and some related traits was studied in a 4 x 4 diallel cross experiment in cotton. Additive type of gene action with partial dominance was observed for number of boils per plant, number of seeds per boil, boil weight and yield of seed cotton. No epistatic effects were observed in the inheritance of these characters.

Key words: mode of gene action, seed cotton yield

INTRODUCTION

Biometrical techniques, dealing with the genetic analysis of varietal differences in different field crops have led to the development of specific procedures which have helped the plant breeders to synthesize superior genotypes of various crop plants and thus increasing the production on a unit area basis. Hayman' s (1954) diallel technique for genetic analysis of different genotypes which has also been frequently advocated by various plant breeders and geneticists like Goudar et al. (1996), Hussain et al. (1999) and Ahmad et al. (2000) for its efficiency and usefulness, was applied in a 4 x 4 diallel cross experiment on cotton to study gene action involved in the phenotypic manifestation of various plant characters.

MATERIALS AND METHODS

Parental Populations: Four varieties of cotton *(Gossypium hirsutum* L.) including one local NIAB-78 and three exotic i.e. B-8890, BAMBO-SA-49 and BARE-8 were crossed in all possible combinations during the months of February-March, in the greenhouse. The F_1 seeds of all the crosses including reciprocals thus obtained along with selfs were sown in the field in June.

Experimental Design: The layout of the experiment was according to randomized complete block design with three replications. Sowing was done by dibbling three seeds per hole to ensure uniform stand, later thinned to only one plant per hill. Of ten, middle six plants of each family were treated as experimental. . The distance between and within the plants was 75 cm and 30 cm respectively. The data in respect of yield of seed cotton per plant and its contributing traits such as number of boils per plant, number of seeds per boil and boil weight were collected according to the standard techniques used in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, where the study was carried out.

Statistical and Genetic Analyses: The data were analysed for their variance following Steel and Torrie (1984). Joint regression analysis was applied to test the adequacy of the data for the application of Hayman's additive-dominance model (1954) to evaluate the gene action involved in the inheritance of these characters.

RESUL TS AND DISCUSSION

Analysis of variance indicated significant differences among parents and their F_1 progenies for all the characters (Table I). The joint regression analysis revealed the fitness of the data for Hayman's additive-dominance model for genetic analysis (Table 2). The variance (Vr) and covariance (Wr) graphs for the characters are depicted in Fig. I to 4. Further results of the study are discussed as under:

I. Yield of Seed Cotton per Plant: The mean values of parents and crosses for yield of seed cotton per plant are given in Table 3 and *Vr/Wr* graph in fig. I. A study of Fig. I revealed that the regression line with a unit slope intercepted the Wr-axis above the origin hence signifying additive type of gene action with partial dominance controlling the inheritance pattern of this character. . Position of array points on the regression line indicated that B-8890 and BARE-8 possessed maximum dominant and recessive genes due to their closest and farthest position from the origin respectively.

2. Number of Boils per Plant: For genetic analysis the mean values are given in Table 3 and *Vr/Wr* graph is shown in Fig. 2. The regression line with a unit slope passed through the Wr-axis above the origin indicating thereby additive type of gene action involved in the inheritance of this character. From the position of array points along the regression line, B-8890 seemed to have maximum dominant genes while BARE-8 possessed the recessive ones.

Table I. Mean squares from the analysis of variance for yield of seed cotton per plant, number of boils per plant, number of seeds per boil and boil weight in a 4 x 4 diallel cross of *Gossypium hirsutum* L.

Source of variation	d.f	Yield of seed cotton per plant	Number of boils per plant	Number of seeds per boil	Boil weight
Replication	2	1964.2	100.5	23.9	1.90
Genotypes	15	161.7**	24.9**	7.2**	0.22**
Error	30	43.0	8.0	1.3	0.06

** = Highly significant. .

Table 2. Joint regression analysis for yield traits of cotton

Characters	Regression coefficient (b)	Conclusion
Yield of seed cotton per plant	0.92 ± 0.18 deviated significantly from zero but not from unity	The data were fit for additive dominance model
Number of bolls per plant	0.97 ± 0.09 deviated significantly from zero but not from unity	The data were fit for additive dominance model
Boll weight	0.97 ± 0.09 deviated significantly from zero but not from unity	The data were fit for additive dominance model

Table 3. Mean performance of parents and hybrids for some yield components in cotton

Parents and crosses	Number of seed cotton per plant	Number of boils per plant	Number of seeds per boil	8011 weight
B-8890	33.30	12.30	26.30	2.80
Bambo-SA-49	37.80	13.00	25.00	3.00
BARE-8	53.80	20.70	24.00	2.60
NIAB-78	43.20	12.70	30.00	3.40
B-8890 x Bambo-SA-49	28.30	10.20	25.15	2.75
B-8890 x BARE-8	32.65	12.65	24.70	2.60
B-8890 x NIAB-78	36.80	11.50	25.85	2.95
Bambo-SA-49 x BARE-8	38.75	14.70	24.80	2.75
Bambo-SA-49 x NIAB-78	40.25	13.35	26.00	3.10
BARE-8 x NIAB-78	43.35	14.70	26.20	2.95

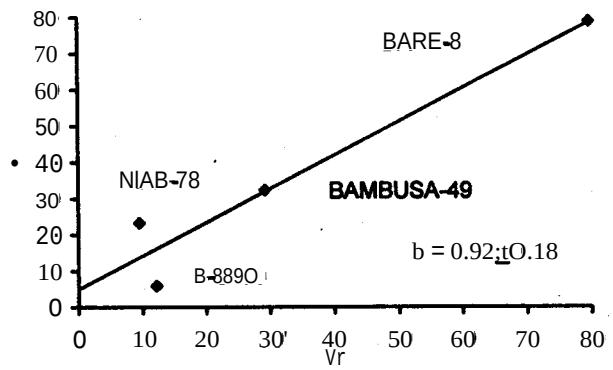

Fig.1. VrfWr graph for yield of seed cotton/plant.

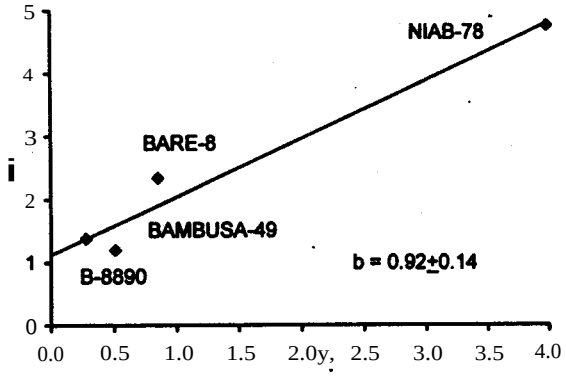

Fig.3. VrfWr graph for nwnber of~1I

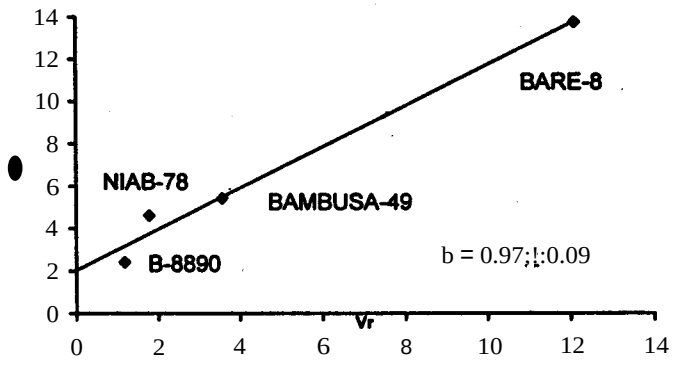

Fig.2. Vr/wr graph for nwnber of 0011 per plant

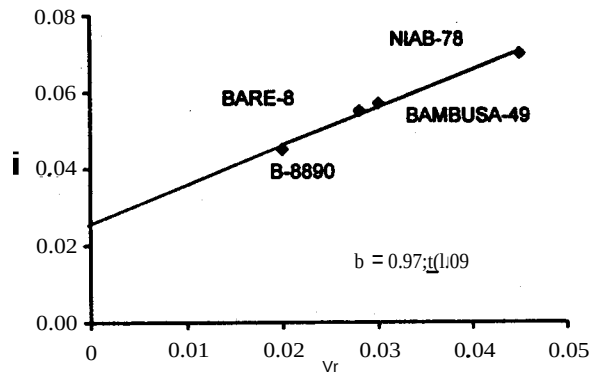

Fig.4. VrfWr ppjh for boll"weight

3. Number of Seeds per Boil: The mean values for genetic analysis are presented in Table. 3, and Vr/Wr graph is depicted in Fig. 3. The study of the graph indicated additive type of gene action controlling the inheritance of this trait as the regression line with a unit slope intercepted the Wr-axis above the origin. From the distribution of dominance and recessive genes point of view, B-8890 got the maximum dominant genes while NIAB-78 the recessive ones, being the closest and the farthest from origin respectively.

4. Boil Weight: For genetic analysis, the mean values are given in Table 3, and Vr/Wr in Fig. 4. A study of the graph revealed additive type of gene action with partial dominance as the regression line with a unit slope intercepted the Wr-axis above the origin. The position of array points on the regression line showed that B-8890 possessed the maximum dominant genes while NIAB-78 the recessive ones.

Additive type of gene action without epistatic effects is an ideal situation for a plant breeder because populations can be improved for the characters under study through simple selection procedures. The above mentioned results are supported by the findings of Sandhu and Mittal (1988), Khan et al. (\ 990), Hussain et al. (1999), Ahmad et al. (2000), while Ma et al. (1983) reported overdominance type of gene action for number of bolls per plant, number of seeds per boll, boll weight and yield of seed cotton.

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