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Genetic analysis of some seed quality characters in upland cotton (*Gossypium hirsutum* L.)*

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Summary. A set of diallel crosses involving ten parents was evaluated over two locations to determine the genetic control of protein per cent, oil per cent, seed index, percentage of mature seeds and number of seeds per boll. The analysis of pooled data showed that percentage of mature seeds was controlled by additive (D) and non-additive (H_1 and H_2) genetic effects. Over-dominance was noticed. For seed index the D component measuring additive, and the H_2 component measuring dominance, variation were significant. Protein content and oil content were primarily under the control of non-additive (H_1 and H_2) genetic effects, while for number of seeds per boll the variability was accounted for by dominance (H_1) effects only. The development of pure lines through appropriate methods is suggested.

Key words: Cotton – Diallel analysis – Additive and non-additive effects – G × L interactions

Introduction

Although upland cotton (*G. hirsutum* L.) is grown primarily for its fibre to be used in the textile industry, approximately 65–67% of its total economic impact is contributed by its seed which is a rich source of oil and protein. The cotton seed contains about 20% oil and 24% protein. Among the world oil seed crops, cotton seed protein production is second only to soybean protein. In the USA cotton seed flour products are now marketed and in Latin America cotton seed flour is blended with other flours to combat malnutrition (Spadaro and Homes 1979). These blends have special significance for less developed countries like India where the ever increasing population poses a serious problem of malnutrition. The present article reports the results of a study conducted to obtain information about the genetic control of some seed quality characters which could be used to improve these characters through appropriate breeding procedures.

Material and methods

Ten diverse lines of upland cotton, namely F-414, LH 372, IAN 4903, H 655C, KH 33/1146, A 318, J 127, II/16-5-5(g1), Hopicala and 6939 were crossed in all possible combinations (expect reciprocals). The resulting 45 F1 crosses along with their 10 parents were planted during Kharif, 1978 at two location in the Punjab State: Ludhiana (which lies between 30°.56′ North latitude and 75°.52′ East longitude and Muktsar (which lies between 30°.31′ North latitude and 74°.31 East longitude). At each location all 55 entries were represented by a single row of 10 plants in each of the three completely randomized blocks. At maturity, seed cotton was picked from five random plants for each entry in each replication. The data were recorded in the laboratory on seed index, percentage of mature seeds, number of seeds per boll, protein content (%) and oil content (%). For estimating protein content, first nitrogen percent on whole seed and moisture free basis was estimated by the usual Microjeldahl method; the value obtained was subsequently multiplied by a factor of 6.25. Oil content was estimated by an NMR instrument (Newport Analyser, MK III A).

For estimating the components of genetic variance, the methods of Hayman (1954) and Jinks (1954) were followed using pooled data.

Results and discussion

The choice of breeding method and the selection procedure for the genetic improvement of cotton, like any other crop, is mainly dependent upon the type and relative amount of

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genetic variance in the base population. The genetic interpretation of the data is meaningful only when the breeding materials satisfy the assumptions of a theoretical model, since failure of some of these assumptions is likely to give baised estimates which have little predictive value for practical plant improvement.

In the present study, significant mean squares due to genotypes were observed for all the characters which implied that there were genetic differences for these characters and that further analysis could be conducted (Table 1). The mean squares due to location and genotype×location interaction were significant for seed index, protein content and oil content which indicated that the locations were widely divergent and that different genotypes responded differently to the varying locations. The environmental influences associated with a location contributed far more than the genotype and G×L to the total variability in these characters. The number of seeds per boll was not influenced by the sampled locations. A significant G×L interaction was observed for percentage of mature seeds. Turner et al. (1976) also reported environmental influences on the level of oil and seed maturity of four cotton cultivars. They observed that cultivars had as much influence on protein content as environmental conditions, but no interaction was detected. Gridley and Smithson (1977) reported that a relatively small interaction occurred between cultivars and environments for oil content, but differences between sites accounted for a large proportion of variation in oil content of cotton seed.

The component analysis revealed that the D component was significant for seed index and percentage of mature seeds, and non-significant for the remaining characters (Table 2). Though genotypic differences among the parents were detected for protein content, oil content and the number of seeds per boll, the D component, which measures the additive variation, was non-significant due to the large standard error associated with it.

Table 1. Analysis of variance for the design of experiment for seed quality characters in upland cotton

Source of variation	d.f.	Mean squares				
		Seed index	Mature seeds	Protein content (%)	Oil content (%)	Seeds/ boll
Location (L)	1	101.45**	0.98	183.98**	76.04**	35.02**
Genotypes (G)	54	2.98**	92.75**	5.60**	7.51**	27.31**
Parents (P)	9	4.45**	110.09**	2.25**	4.35**	26.84**
Hybrids (H)	44	2.23**	90.10**	5.73**	7.57**	25.44**
P vs. H	1	22.80**	226.86**	3.03*	24.36**	113.93**
G×L	54	1.64**	76.16**	6.77**	3.99**	11.10
P×L	9	2.24**	117.54**	2.80**	1.44	7.94
H×L	44	1.18**	61.61**	6.03**	3.67**	11.40
P vs. H×L	1	16.19**	3.31	58.81**	40.70**	26.17
Error	216	0.56	7.84	0.69	1.59	0.58

*, ** Significant at $P=0.05$ and $P=0.01$ probability levels, respectively

Table 2. Components of genetic variance, genetic ratios and t^2 values in the crosses of upland cotton

Components/ratio	Seed index	Mature seeds	Protein content	Oil content	Seeds/ball
D	0.73±0.11**	15.58± 4.97*	0.13±0.28	0.36±0.22	1.71±1.31
H_1	0.47±0.24	42.56± 1.06**	1.90±0.39*	1.37±0.47*	5.69±2.39*
H_2	0.46±0.19*	35.48± 8.99**	1.54±0.58*	1.05±0.38*	4.46±2.46
E	0.19±0.03**	2.61± 1.50	0.23±0.08*	0.53±0.06**	2.86±0.41**
F	0.03±0.25	12.36±11.45	0.55±0.64	1.21±0.48*	0.08±3.14
h^2	0.40±0.13*	3.55± 6.01	2.35±0.34**	1.66±0.25**	8.09±1.65**
$(H^1/D)½$	–	1.65	–	–	–
$H_2/4H_1$	–	0.21	0.20	0.19	–
h^2/H_2	0.87	–	1.53	1.58	–
'r' yr (Wr+Vr)	0.10	0.04	0.19	–0.55	0.66*
t^2	0.11	2.12	58.27**	0.02	0.17

*,** Significant at $P=0.05$ and $P=0.01$ probability levels, respectively

The H_1 and H_2 components of genetic variance were significantly different from zero for protein content, oil content and percentage of mature seeds, implying that non-additive genetic effects are important in the inheritance of these quality characters. The ratio $(H_1/D)^{1/2}$ was greater than unity which was taken as an indication of overdominance for the latter character. In Egyptian cotton, Abdel-Bary et al. (1975) reported that additive genetic variance accounted for a major portion of phenotypic variance for protein content, oil content and seed index.

A significant F value for oil content only suggested the prevalence of more dominant genes, whereas dominant and recessive genes were equally distributed among the parental lines for the remaining characters. The allelic frequencies at the gene loci showing dominance for protein content, oil content and percentage of mature seeds were not in equal proportion since $H_2/4\ H_1$ was less than the maximum value of 0.25.

This study reveals the presence of only the dominance components H_1 and H_2 of genetic variance for protein content, oil content and the number of seeds per boll, which indicates that these characters are primarily under the control of non-additive genetic effects. The possibility of attaining improvement in these, as well as percentage of mature seeds, would be through the use of a breeding programme utilizing F1 hybrids. A low magnitude of heterobeltiosis recorded for the characters limit the usefulness of such hybrids. Seed index was predominantly under the control of genes acting additively and this character could be easily manipulated through selection for the production of pure line varieties. Gururajarao et al. (1977) also reported a high proportion of additive genetic component for seed index.

H^2/H_2 estimates the number of effective factors operating for a trait. Its value is expected to be underestimated unless the dominance effects of all the genes are equal in sign and magnitude, and the distribution of genes is uncorrelated (Jinks 1954; Mather 1949). Estimates from h^2/H_2 indicate that at least one gene group showing dominance is operative for seed index and two each for protein content and oil content, whereas the number is very low for other characters. The low number did not, however, overrule the contribution of dominance for the characters in question. In the present situation, the lack of unidirectional dominance might be responsible for such low values.

A meaningful estimate of the direction of dominance is provided by correlation between parental means, yr, and the parental order of dominance, W_r+V_r. Only one coefficient (number of seeds per boll) was significantly different from zero at the 0.05 probability level. Because parents with a preponderance of recessive alleles have higher array values, the positive coefficient indicates that recessive alleles are positive in direction, i.e. operating in the direction of more number of seeds per boll. The correlation coefficients were non-significant for rest of the characters suggesting ambidirectional dominance.

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