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EXPRESSIVITY OF H_2 GENE OF HAIRINESS AND L_o GENE OF LEAF SHAPE OF COTTON UNDER DIFFERENT GENETIC BACKGROUNDS

HAFEEZ-UR-RAHMAN AND WAHEED SULTAN KHAN

Cotton Research Institute, Faisalabad, Pakistan.

Abstract

The expressivity of H_2 gene of hairiness (pilose) and L_o gene of leaf shape in cotton (*Gossypium hirsutum* L.) was studied in F_1 and F_2 generations of four crosses involving a female Okra Pilose strain (HR-Velvet Okra) and four broad leafed and semi/sparsely hairy varieties/strains of cotton. Both pilose and okra leaf shape of cotton plant were partially dominant in F_1 generation. The F_2 generations of all the four crosses segregated into four classes of hairiness as well as that of leaf shape. The summation of the two intermediate classes of leaf hairiness and shape helped to fit the segregating classes of three crosses to the theoretical 1:2:1 ratio of partial dominance. The two homozygous extreme classes of both the characters were easily distinguishable however, the heterozygous condition for hairiness was highly influenced by the genetic background i.e., modifying gene effect. It was perceptible from the study that hairiness and leaf shape in cotton though monogenically inherited, their phenotypic expressions especially in heterozygous conditions were affected by a complex of modifier genes (genetic back ground) especially that for pubescence. Hairiness, as compared to leaf shape was more influenced by the minor (modifier) gene effect. Homozygous condition for both H_2 and L_o genes, however, imparts pilose hairiness and narrow okra leaf shape, respectively, without the aid of modifier genes. A significant level of genetic association (linkage) existed between H_2 and L_o genes in two crosses; HRVO x S-12 and HRVO x S-14, which was indicative of the higher number of velvet okra combination in the advance segregating generations of these crosses.

Introduction

The study of plant pubescence is of significant importance in cotton especially in country like Pakistan where insect pests are growing into a very serious menace. The soaring costs of chemical control and growing ineffectiveness of these pesticides against insects have necessitated an effective alternative. In built resistance (non preference and antibiosis) against insect pests like plant pubescence and modified leaf shape provides a dependable umbrella against several insect pests of cotton (Agarwal *et al.*, 1978, Wilson & Wilson, 1975, 1977, Jones *et al.*, 1976, Wilson, 1994).

Increased plant pubescence above the degree normally found in the pubescent cultivated varieties are governed by two major genes and a complex of modifiers (Niles, 1980), H_1 gene derived from a Genome (Knight, 1954, 1955) is found in *hirsutum, barbadense, herbaceum* and *arboreum* cotton. A stronger gene, H_2 gene, identified and derived from Hawaiian wild tetraploid cotton, *Gossypium tomentosum* (Knight, 1952) and homologous to a mutant gene in T611 (Knight & Sadd, 1953) confer finely dense (pilose) pubescence. Saunders (1964) reported the presence of H_2 gene in the B-genome of wild diploid *G. anomalum* but Gerstel & Phillips (1958) located it in A-genome. A later study of cotton monosomics confirmed the presence of H_2 gene in A-genome

(Endrizzi, 1963).

Modified leaf shape in cotton is conditioned by L_o (okra) and L_o (super okra) genes which are partially dominant to normal broad (palmate) leaf shape (Niles, 1980) HR-Velvet okra, developed at Cotton Research Institute, Faisalabad and homozygous for both H_2 and L_o genes (Rahman, 1996) was used in crosses to see the expressivity of these two genes in different genetic back grounds and their apparent linkage strength to help transfer of these characters into otherwise desirable varieties.

Materials and Methods

The study was a part of the Cotton Breeding Programme for Insect Resistance at Cotton Research Institute, Faisalabad. The data were observed during 1995 and 1966 crop seasons. HR-Velvet Okra (HR-VO) homozygous for both H_2 and L_o genes was crossed as female to four strains/varieties viz., FDR-9, AUS-A, S-12, and S-14. The information regarding gene (s) controlling hairiness in the four male varieties/strains was not known. Cotton varieties S-12 and S-14 are semi hairy whereas FDR-9 and AUS-A are sparsely hairy strains. Hairiness and leaf shape was studied in F_1 and F_2 generations of the four crosses and plants based on their expressivity, were categorized in descending order into velvet (pilose) hairiness (grade 1), highly hairy (grade II), hairy (grade III) and sparsely (non) hairy (grade IV) categories. Similarly leaf shape was categorized into: narrow okra (grade I), broad okra (grade II), semi okra (grade III) and broad normal leaf (grade IV). The segregating ratios were tested for their fitness to theoretical mono hybrid, di-hybrid or epistatic ratios through chi-square test. Yates correction was used to nullify the possible bias due to fewer (less than 5) number of classes. Strength of genetic linkage between H_2 and L_o genes in each cross was also estimated using percentage of homozygous recessive plants in F_2 generation. Chi-square test was used to see the significance of correlation indicating linkage between the H_2 and L_o genes.

Results and Discussion

In F_1 generation, 25 plants in each cross were studied. Expressivity of H_2 gene was intermediate in all the four crosses. All the 25 plants of the crosses HRVO x S-12 and HRVO x S-14 were highly hairy (category II). All the plants of the cross HRVO x AUS-A were hairy (category III) whereas 80% plants of the cross HRVO x FDR-9 were hairy and 20% highly hairy in F_1 generation (Table 1).

Expression of okra leaf shape (L_o gene) was also intermediate in F_1 generation and all the plants in all the four crosses produced broad okra leaves. In F_2 generation, expressivity of H_2 gene was highly variable. Plants in F_2 generation of all the crosses could be categorized into four categories (Table 1). In the cross HRVO x FDR-9, about 36% plants were velvet hairy (pilose) 21% hairy, 19% semi hairy and 24% plants were sparsely (non) hairy. Regarding leaf shape, 22% plants produced narrow okra leaves, 37% produced broad okra, 10% semi okra and remaining about 30% plants produced broad normal leaves.

In the cross HRVO x AUS-A, 28% plants were velvet hairy (pilose), 14% highly

Table 1a. Status of the four crosses in F_1 and F_2 generations.

Particulars	HRVO x FDR-9		HRVO x AUS-A		HRVO x S-12		HRVO x S-14	
Generation	F1	F2	F1	F2	F1	F2	F1	F2
Total # of plants	25	134	25	194	25	194	25	158
Pubescence:								
I Velvet (Pilose)	-	48	-	56	-	54	-	20
II Highly hairy	5	-	-	28	25	44	25	14
III Hairy	20	28	25	-	-	40	-	54
IV Semi hairy	-	26	-	32	-	-	-	-
V Sparse hairy	-	32	-	78	-	58	-	70
Leaf Shape								
I Narrow Okra	-	30	-	42	-	34	-	42
II Broad Okra	25	50	20	36	25	96	25	72
III Semi Okra	-	14	5	84	-	2	-	6
IV Broad (normal)	-	40	-	32	-	62	-	38

hairy, 16% semi hairy and 40% were sparsely or non hairy. Regarding leaf shape, about 21% plants had narrow okra leaf shape, 18% broad okra, 43% semi okra and about 16% had broad leaves. Similarly in F_2 generation of the cross HRVO x S-12, about 28% plants were velvet hairy (pilose), 23% highly hairy, 20% hairy and 30% were sparsely or non hairy. Regarding leaf shape, in this cross, 17% plants had narrow okra leaves, 49% had braod okra, 1% had semi okra leaves and 32% had broad shape of leaves.

Cross HRVO x S-14 in F_2 generation produced about 13% plants with velvet (pilose) hairiness, 9% plants were highly hairy, 34% hairy and remaining, 44% plants were sparsely (non) hairy. Regarding leaf shape 26% plants produced narrow okra leaf shape, 45% broad okra, 4% semi okra, and 24% plants produced broad (normal) leaf shape.

The segregation ratio in F_2 generation of all the four crosses, as such, did not match to monohybrid or dihybrid or non-allelic interactive segregating ratios. In order to reach some understanding, the two intermediate classes of both hairiness and leaf shape were added and then tested against the theoretical 1:2:1 monohybrid ratio of incomplete dominance. The modified classification is given in Table 1b.

Regarding leaf pubescence, Chi-square value was non-significant in all the F_2 populations except for that of cross HRVO x AUS-A (Table-1b) indicating that segrega-

Table 1b. Extension of TAble 1 resulting from summation of intermediate classes of F_2 generation.

		Leaf Pubescence					Leaf Shape			
Crosses	H_2H_2	H_2h_2	h_2h_2	Chi Sq.	Probability	L°L°	L°I°	I°I°	Chi Sq	Probability
HRVO x FDR9	48	54	32	03.149	0.25-0.1*	30	64	40	01.436	0.5-0.25*
HRVO x AUS-A	56	60	78	32.085	0.005	42	120	32	11.239	0.005
HRVO x S-12	52	84	58	03.466	0.25-0.1*	34	98	62	07.528	0.025
HRVO x S-14	20	68	70	03.421	0.25-0.1*	42	78	38	01.138	0.50*

* Data fit to theoretical ratio

tion in F_2 population of these crosses, except that of HRVO x AUS-A, was according to 1:2:1 ratio of mono genic partial dominance. Regarding leaf shape, segregating ratio in F_2 populations of the crosses; HRVO x FDR-9 and HRVO x S-14, fit well against the theoretical 1:2:1 ratio.

It was perceptible from the study that the behavior of H_2 and L_0 genes in F_1 generation was partially dominant to their counterparts. The results were predictable from the early findings of Knight (1952) for H_2 gene and the report of Niles (1980) for leaf shape. It could further be confirmed from the analyses of F_2 generations wherein after combining the intermediate classes, the segregating ratio fit well against 1:2:1 theoretical mono hybrid ratio in three of the four crosses for hairiness as well as for leaf shape. Kloth (1995) observed glaborous, normally pubescent and densely pubescent plants in a ratio of 3:3:10 resulting from the gene interaction of two dominant, non allelic loci affecting plant pubescence in cotton. In the present study the extreme homozygous classes i.e., pilose hairy (H_2H_2) and sparsely hairy (h_2h_2) for hairiness and narrow okra (L_0L_0) and broad leaves (l^0l^0) for leaf shape were easily distinguishable. The intermediate classes in both the characters were different expressions of the heterozygous condition under the influence of differential modifying genes that the intermediate classes received during segregation. It was then obvious that hairiness and leaf shape in cotton (material in hand), was though monogenically inherited, their phenotypic expressions especially in heterozygous conditions were affected by a complex of modifier genes (genetic back ground) especially that for pubescence. Hairiness, as compared to leaf shape was more influenced by the minor (modifier) gene effect. Homozygous condition for both H_2 and L_0 genes, however, imparts pilose hairiness and narrow okra leaf shape respectively, without the aid of modifier genes.

Variety S-12 seemed to be carrying maximum favourable modifying genes for the expression of hairiness since all the F_1 plants of its cross were highly hairy (grade II) and in F_2 generation it not only yielded high number of velvet (pilose) plants but also yielded maximum percentage of highly hairy (grade II) plants in heterozygous condition. All the plants of the cross of S-14 were also highly hairy but in F_2 generation, only 21 % of the heterozygotes were highly hairy and the tendency of the heterozygotes was towards less hairiness.

In all the crosses, heterozygotes carried hair through out their plant body, however, the homozygous recessive (h_2h_2) in all the crosses except that of S-12 carried sparse hair density on the leaves while plant body was devoid of them. From this fact though it

Table 2. Estimates of Linkage strength between H_2 and L_0 genes in F_2 generations of the four crosses.

Crosses	Double recessive %	Linkage strength	Chi-square value	Probability
HRVO x FDR-9	04.478	0.423	09.836	0.500-0.250
HRVO x AUS-A	06.186	0.497	14.644	0.010
HRVO x S-12	10.309	0.642	62.068	< 0.005
HRVO x S-14	10.127	0.636	32.563	< 0.005

could not be concluded that the semi hairy S-12 carried H_1 gene of hairiness but it was obvious that S-12 did carry favorable modifiers that Saunders (1965) has described to be required for the development of hairiness.

The estimates of genetic linkage based on the percentage of double recessive in F_2 populations were high (more than 10 %) in crosses of HRVO with S-12 and S-14 (Table-2). Chi-saqure test, used to assess the significance of the level of association (linkage) between H_2 and L_0 genes, was also significant for these two crosses, indicating that the two genes i.e., H_2 and L_0, were lying closer to each other enhancing their tendency to go together at segregation. It further connotes that the crosses of HRVO with S-12 and S-14 were likely to yield, comparatively, more number of velvet okra combinations in the advance segregating generation.

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