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Full Length Research Paper

Genetics of trichomes and its association with fibre and agronomic traits in cotton

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Hairiness/trichomes act as an important insect non-preference trait. The inheritance of this trait was studied in three cross combinations involving a common pilose parent with three sparse hairy parents which showed a theoretical monohybrid ratio of 1:2:1, showing incomplete dominance in F_2. The positive correlation of number of trichomes with lint percentage and micronaire suggested that the selection for pilose hairiness would be helpful in enhancing the lint percentage and fibre fineness. The number of trichomes had no effect on the expression of the traits like number of monopodial branches, number of sympodial branches, number of bolls, boll weight and seed cotton yield which proved no chance of undesirable linkage of these traits with number of trichomes.

Key words: *Gossypium hirsutum* L., trichomes, inheritance, fibre traits, agronomic traits.

INTRODUCTION

The sustainability of cotton production worldwide has been affected due to the piercing, sucking insect pests and bollworms which are a serious threat to the cotton crop. Insect pests constitute a major factor in production in all over the cotton growing areas of the world. In recent times, insect control has been totally based on the use of chemical insecticides. During the 1970's and 1980's, the use of insecticides increased tremendously in almost all cotton producing countries of the world including Pakistan.

In Pakistan, during 2007- 2008 a total of 28 thousand tonnes of insecticides was imported which measures the foreign exchange of 74.5 million US dollars (GOP, 2007-08). Little emphasis was placed on the plant genetic resistance as a means of suppressing insect pests. Painter (1951) noted that there were no efforts made to develop genetic resistance to cotton insect pests. Genetic resistance in the form of resistant varieties is an effective means of minimizing yield losses caused by insect pests and also leads to reduction in the use of insecticides (Vaden Bosch, 1972; Van Dinther, 1972; Maxwell et al., 1972; Bhatti et al., 1976). In the present scenario, by failing to cope with all other possible means for insect control, research has been accelerated on the host plant resistance.

Hairiness/trichomes act as an important insect non-preference trait. The role of trichomes in plant defence was evaluated by Levin (1973). It is clear that trichomes play a role in plant defence, especially with regard to phytophagous insects. Hairiness has been reported to have a resistance against the sucking insect pests of cotton (Lee, 1985). The degree of hair or trichome density on the leaves of *Gossypium* species and cultivars is related to varying degrees of resistance/susceptibility to sucking pests, like whiteflies (Meagher et al., 1997), aphids and jassids (Jenkins, 1989; Watson, 1989), or the boll weevil (Thomson and Lee, 1980; Percy and Kohel, 1999). The degree of jassid resistance had definite correlation with the pilosity of the plant. The more tufted types were less prone to jassid attack (Sikka et al., 1966).

The genetics of the insect resistance traits in cotton have been reported to be governed by oligogenes (Endrizzi et al., 1984). Knight (1952) identified two genes for hairiness in cotton whereas, Niles (1980) reported that the increase in the plant hairiness is governed by two major genes and a complex of modifier genes. The major gene was designated as H_1 for sparse hairiness. A second major gene, H_2 controlled the finely dense pubescence in an upland mutant designated as 'pilose'.

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In the F_1 populations, both H_1 and H_2 showed incomplete dominance (Simpson, 1947; Niles, 1980; Rahman and Khan, 1998).

From industrial point of view, agronomic and fibre quality traits hold a special position. The effect of pilosity on agronomic traits was studied by Lee (1984) but no, significant inferences were inferred for the trichome count per cm, lint percentage and boll weight. The physical parameters required for good spinning performance of cotton fibre is a challenge for breeders. The pilose condition is associated with decreased fibre length and increased micronaire (Simpson, 1947; Lee, 1964, 1984). But Kloth (1993) discovered a pilose like plant with unexpectedly low micronaire among the homozygous pilose plants.

Breeding through conventional tools has not lost its significance even in the presence of modern tools of science. Keeping in view, the extensive use and consumption of cotton and its products, there is a need for breeding varieties by incorporating the gene for hairiness into promising cotton genotypes, which in turn will not only minimize possible insect pest attack and insecticide usage but also helps to improve yield and fibre quality attributes. The information reported herein, would be useful in determining the genetics for trichomes and its effects on agronomic and fibre traits.

MATERIALS AND METHODS

Four cotton genotypes, Acala 63-74, FH 1000, CIM 446 and HRVO-1 were selected and selfed for four generations by growing twice a year, in a glasshouse and field during 2003 to 2004. The selected parents with contrasting traits (Table 1) were planted in 300 × 300 mm earthen pots, containing a mixture of equivalent proportion of sand, soil and farmyard manure, during November, 2004 in a glasshouse. Temperature in the glasshouse was maintained at 30 ± 2°C during the day and 25 ± 2°C at night by using built in steam heaters. The plants were exposed to natural sunlight supplemented with artificial lighting, for a photoperiod of 16 h (ICAC, 2007). Three crosses were attempted to obtain F_0 seed during February to March, 2005. The selfed seed of the parents was obtained by covering their floral buds with butter paper bags. The crossing scheme is given in Table 2. The F_1 and their parents were sown during the normal crop season of 2006 in two different sets planted at two different locations. The F_1 plants of each cross were divided in three groups for developing BC_1, BC_2 and F_2 for each combination. The fresh F_0, BC_1 and BC_2 seed was developed by manual crossing, while the seed for F_2 generations was produced for each of the four combinations through manual selfing. The experimental field was fertilized with N-P-K at the rate of 100-75-00 Kg/ha. The experiment in the field was laid out in a randomized complete block design with three replications of each of the six generations of the three crosses. The length of the plot was maintained at 4.5 m, accommodating approximately 15 plants spaced 300 mm apart.

The distance between the rows was 750 mm. A single plot per replication was assigned to each of the parents and their respective F_1, while four plots per replication were assigned to each of the backcrosses and eight plots per replication were assigned to raise the F_2 population of each cross. Ten guarded plants were selected randomly in the parents and their F_1, while fifty and thirty plants in each replication were selected in F_2 and backcross generations, respectively, to record the data during 2006. At maturity, the data on various agronomic traits viz; plant height, number of monopodial branches, number of sympodial branches, number of bolls, seed cotton yield, boll weight and lint percentage were recorded. Fibre quality characteristics like fibre length, fibre strength, fibre fineness, fibre elongation percentage and fibre uniformity ratio of each plant of a generation were measured using Spin lab high volume instrument (HVI-900-A), M/S Zellweger Uster, Switzerland, available in the Department of Fibre Technology, University of Agriculture, Faisalabad, Pakistan. HVI measures fibre quality characteristics according to the international trading standard. A minimum of 10 g sample of lint from each of the guarded plants in each generation was pre-conditioned to moisture applicability for at least four to five hours prior to testing in the HVI. Fibre length was measured, on the basis of the fibrograph. The samples were prepared at fibro sampler in the form of fibre comb and the fibrograph-910 brushed the sample fibres automatically by vacuum action, and optical density of the sample was displayed on the screen. The mean fibre length was derived according to the ASTM (1977a) standard through the procedure laid down by Hunter (1991). The average fibre length was calculated in mm for further analysis. Fibre bundle strength was determined by Pressley strength tester using the flat bundle method as specified by ASTM standard (1977b). The fibre elongation was measured on HVI-900-A. When a sample was moved into an optical sensor, where the test for length and strength were performed, the percentage increase in the length before fibre breakage was measured (Anonymous, 1992a, b). For fibre uniformity ratio, the sample was moved into the optical sensor of HVI-900-A and the reading of optical density of the sample was displayed on the screen. The uniformity ratio of fibre was measured according to ASTM standard (1977a). Fibre fineness of micronaire value was measured on fibrofine-920 device of HVI-900- A. When lid of the chamber containing a sample is closed, the sample is compressed to a fix and known volume. The sample was weighed on an electric balance before placing in the test chamber. This balance transmitted the mass through the control processor. This mass was accepted if the weight was between 8.5 and 11.5 g of cotton. The measured values of mass and pressure calculated were in fineness value according to ASTM standard (1977c).

Trichome density studies

Trichomes represent the presence of small hairs on the cotton plant (Figure 1). The trichome density on leaves was estimated following the method proposed by Bourland et al. (2003). Three leaves at random, each from upper, middle and lower portion of five plants in parents and their F_1's and thirty and fifty plants were selected in BC's and F_2's in all the three replications were used to assess for the quantitative measure of trichomes on the abaxial leaf surface. Observations pertaining to the number of trichomes were recorded with the help of an index card within an area of 1 mm^2 (Figure 2) lay over the abaxial side of each leaf from three different positions and averaged. The resultant mean values for number of trichomes from three different portions of the plant were worked out as the final reading for average number of trichomes per unit area. Trichomes in the 1 mm^2 area were counted with the aid of high magnifying power microscope (Olympus Z61).

On the basis of the trichome counts made for the leaves, a rating scale was developed to categorize the trichome density on abaxial surface of leaves by using a scale of 1 for sparsely (non) hairiness, 2 for moderate number of trichomes, 3 for (pilose) hairiness (Lee, 1968; Wright et al., 1999; Bourland et al., 2003; Stiller et al., 2004; Lacape and Nguyen, 2005).

Chi-squared values and probabilities of goodness of fit of the segregation ratios of F_2 and backcross generations were tested against theoretical ratio (Harris, 1912). Phenotypic and genotypic

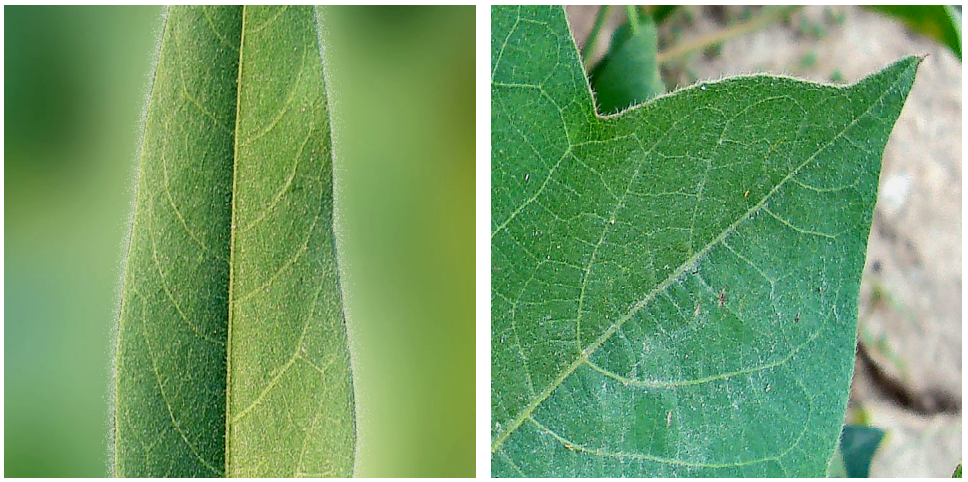
Table 1: Distinctive morphological features of the upland cotton accessions

S.No.	Variety/ Accession	Parentage	Hairiness state	Origin
1	Acala 63-74	-	Glabrous	USA.
2	CIM 446	CP 15/2 × S 12	Lightly hairy	CCRI, Multan, Pakistan.
3	FH 1000	S 12 × CIM 448	Lightly hairy	CRI, Faisalabad, Pakistan.
4	HRVO-1	B-557/2/Gambo Okra/Rajhans/3/Rajhans	Pilose hairiness	CRI, Faisalabad, Pakistan.

* CCRI = Central Cotton Research Institute, Multan. Pakistan. * CRI = Cotton Research Institute, Faisalabad. Pakistan.

Table 2: Scheme of crossing

S.No.	Cross	Trait Considered
1	HRVO-1 × FH 1000	Pilose hairiness × Lightly hairy
2	HRVO-1 × CIM 446	Pilose hairiness × Lightly hairy
3	HRVO-1 × Acala 63-74	Pilose hairiness × Glabrous



(a) Pilose hairiness (P_1)
H_2H_2

(b) Normal hairiness (P_2)
h_2h_2

(c) Intermediate class of hairiness (F_1)
H_2h_2

Figure 1. Inheritance of leaf trichome trait

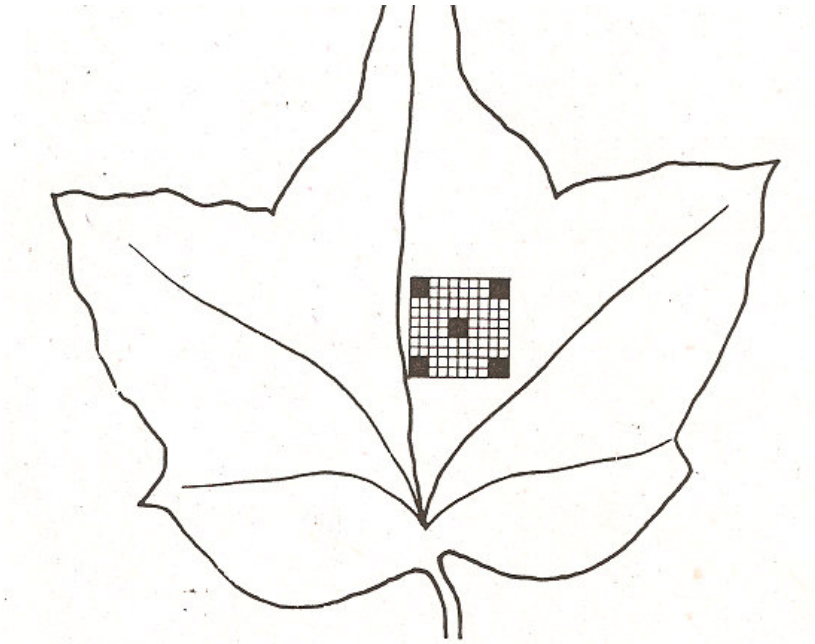


Figure 2 Trichome counts on the abaxial side of cotton leaf with an area of 1 mm2 of an index card.

correlation coefficients between trichome counts and agronomic and fibre traits were determined using the F_2 data. Phenotypic correlation coefficients were calculated following Dewey and Lu (1959) using Minitab computer programme. The genetic correlations (r_g) between two characters X and Y were calculated following Falconer (1981).

RESULTS

Genetic studies

The mean squares from the analysis of variance for agronomic/fibre and number of trichomes for six generations in three cotton crosses were tested at two different locations and are presented in Table 3. Phenotypic classes were developed as evident from Table 4, on the basis of the trichome count ratings on the abaxial leaf surface in the three crosses involving pilose hairy and normal/sparse hairy plants. The inheritance pattern for trichomes/hairiness in three different cross combinations was studied on the basis of the F_2 and test/back cross population data.

In all the three cross combinations, leaf trichomes segregated into three distinct classes (Figure 3). Non-significant chi-squared values were observed for the segregating ratios in F_2 and backcross generations of the three crosses. Observations of 1 sparse hairiness : 2 intermediate class of hairiness : 1 pilose hairiness on leaves were observed in the F_2 populations of the three crosses. In the backcrosses with parent-I, ratios of 1 pilose : 1 intermediate, leaf hairiness were obtained. Similarly, in the backcrosses with parent-II, ratios of 1 sparse : 1 intermediate, leaf hairiness were observed.

Phenotypic and genotypic correlations

In all the three crosses (Table 5), there existed positive and significant correlation of number of trichomes with lint percentage. For fibre length and fibre strength, there was highly significant and negative correlation with number of trichomes. A significant and positive correlation of number of trichomes with micronaire value meant a negative correlation of number of trichomes with fibre fineness in all of the three cross combinations. In the case of fibre uniformity ratio and fibre elongation, a negative association with number of trichomes was observed in the crosses.

The study of number of trichomes were negatively but significantly correlated with plant height in the cross HRVO-1 × CIM 446. Non-significant correlations of number of trichomes with number of monopodial branches, number of sympodial branches, number of bolls, seed cotton yield and boll weight were recorded.

DISCUSSION

Genetic studies

Highly significant differences among different generations for all characters studied (Table 3) were observed in all the three crosses. Significant differences among different generations indicated the existence of genetic variability.

Table 3. Mean squares from analysis of variance along with the calculated F-values in parenthesis for agronomic/fibre and number of trichomes for six generations in three cotton crosses tested at two different locations.

Source	D.F	HRVO-1 × FH 1000													Probability (F-value)	
		PH	NMB	NSB	NBP	BWt	SCY	L%	FL	FS	FE	U %	Mic	T	0.05	0.01
Replication	2	1.62 (1.62)	0.010 (0.47)	0.38 (1.05)	1.20 (3.37)	0.004 (0.93)	1.02 (3.39)	0.91 (3.03)	0.003 (0.16)	0.02 (0.06)	0.004 (0.45)	1.39 (1.21)	0.009 (3.0)	96.68 (1.70)	3.44	5.72
Generation	5	5.46 (5.44)	0.113 (5.33)	56.96 (156.7)	66.64 (187.3)	0.88 (190.7)	2561.12 (8485.1)	40.95 (135.6)	5.56 (357.9)	2.98 (9.84)	0.082 (9.4)	82.78 (72.25)	0.352 (140.7)	28576.09 (504.4)	2.66	3.99
Location	1	0.40 (0.40)	0.002 (0.12)	0.092 (0.25)	0.059 (0.17)	0.004 (0.82)	1.28 (4.23)	1.00 (3.33)	0.010 (0.66)	0.25 (0.82)	0.001 (0.02)	0.001 (0.00)	0.000 (0.04)	40.19 (0.71)	4.30	7.95
G × L	5	1.37 (1.37)NS	0.022 (1.06)NS	0.298 (0.82) NS	0.144 (0.40) NS	0.002 (0.47) NS	0.15 (0.49) NS	0.044 (0.15) NS	0.009 (0.58) NS	0.26 (0.87) NS	0.001 (0.09) NS	0.002 (0.001) NS	0.001 (0.25) NS	48.58 (0.85) NS	2.66	3.99
Error	22	1.00	0.021	0.364	0.356	0.005	0.302	0.302	0.016	0.30	0.009	0.146	0.003	56.65		
HRVO-1 × CIM 446																
Replication	2	1.12 (0.55)	0.00 (0.03)	0.18 (0.07)	0.235 (0.64)	0.00 (0.22)	3.29 (3.33)	0.16 (1.30)	0.24 (4.70)	0.43 (3.08)	0.035 (1.12)	0.188 (3.36)	0.00 (0.08)	4.62 (0.98)	3.44	5.72
Generation	5	62.98 (31.10)	0.023 (24.04)	17.82 (7.26)	25.95 (71.3)	0.650 (335.66)	1210.5 (1215.8)	9.74 (78.97)	12.54 (3.2)	6.30 (45.70)	0.60 (19.32)	4.64 (83.65)	0.69 (362.8)	39653.05 (8433.6)	2.66	3.99
Location	1	7.70 (3.80)	0.004 (4.20)	5.53 (2.25)	0.340 (0.93)	0.009 (4.25)	3.32 (3.36)	0.82 (6.66)	0.032 (0.42)	0.25 (1.80)	0.051 (1.61)	0.095 (1.71)	0.00 (0.18)	20.00 (4.25)	4.30	7.95
G × L	5	1.42 (0.70) NS	0.001 (0.56) NS	6.45 (6.10) NS	0.280 (0.57) NS	0.003 (1.75) NS	1.26 (1.27) NS	0.175 (1.42) NS	0.071 (0.95) NS	0.23 (0.17) NS	0.036 (1.14) NS	0.025 (0.45) NS	0.001 (0.38) NS	0.78 (0.17) NS	2.66	3.99
Error	22	2.02	0.001	2.45	0.364	0.002	0.99	0.123	0.075	0.14	0.031	0.056	0.002	4.70		
HRVO-1 × Acala 63-74																
Replication	2	4.02 (0.73)	0.09 (1.38)	0.112 (0.71)	0.34 (0.34)	0.005 (1.23)	0.55 (0.13)	0.098 (0.22)	0.006 (0.19)	0.03 (0.74)	0.02 (0.69)	0.04 (0.75)	0.001 (0.45)	158.12 (3.29)	3.44	5.72
Generation	5	71.26 (12.9)	1.87 (28.7)	33.19 (210.5)	12.93 (13.21)	1.55 (419.9)	1268.54 (301.9)	8.80 (20.10)	0.136 (4.54)	0.36 (8.48)	0.42 (14.45)	0.88 (16.35)	0.36 (181.3)	33179.38 (691.7)	2.66	3.99
Location	1	92.18 (16.79)	0.06 (0.90)	0.67 (4.24)	4.16 (4.24)	0.002 (0.63)	0.16 (0.04)	0.63 (1.43)	0.204 (6.80)	0.10 (2.40)	0.001 (0.02)	0.14 (2.63)	0.041 (20.30)	30.14 (0.62)	4.30	7.95
G × L	5	3.36 (0.61) NS	0.001 (0.02) NS	0.29 (1.85) NS	1.19 (1.22) NS	0.006 (1.57) NS	2.00 (0.47) NS	0.162 (0.37) NS	0.022 (0.74) NS	0.02 (0.51) NS	0.029 (0.98) NS	0.04 (0.78) NS	0.00 (0.21) NS	3.95 (0.08) NS	2.66	3.99
Error	22	5.49	0.065	0.16	0.97	0.004	4.20	0.44	0.030	0.04	0.029	0.05	0.002	47.96		

PH = Plant height, NMB = no. of monopodial branches/plant, NSB = no. of sympodial branches/plant, NBP = no. of bolls/plant, SCY = seed cotton yield, BWt = boll weight, L% = lint percentage, FL = fibre length, FS = fibre strength, FE = fibre elongation, U% = fibre uniformity ratio, FF = fibre fineness.

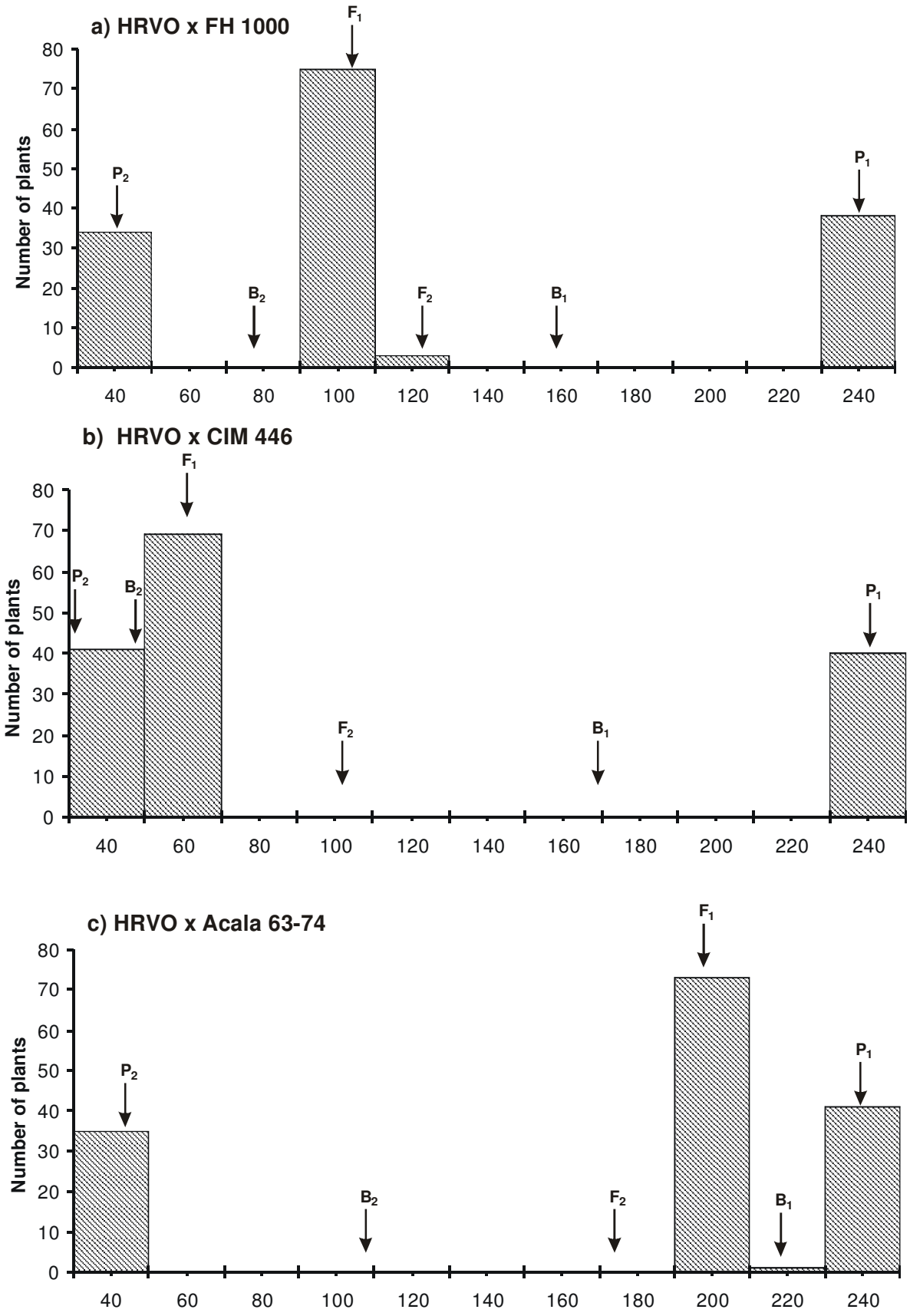


Figure 3. Frequency distributions for number of leaf trichomes in F2 generations of three crosses..

Table 4: Chi-Squared values and probabilities of goodness of fit of segregation ratios of F_2 and backcross generations in a study of inheritance of leaf trichomes trait

Cross	Gen.	Expected Ratios	Observed value			Expected value			χ^2	Prob.
			Sparse Hairy	Intermediate Hairy	Pilose Velvet	Sparse Hairy	Intermediate Hairy	Pilose Velvet		
	F_2	1: 2:1	34	79	37	37.5	75	37.5	0.55	0.90-0.75
HRVO-1 × FH 1000	BC_1	1:1	-	53	37	-	45	45	2.84	0.10-0.05
	BC_2	1:1	36	54	-	45	45	-	3.60	0.10-0.05
	F_2	1: 2:1	41	69	40	37.5	75	37.5	0.97	0.75-0.50
HRVO-1 × CIM 446	BC_1	1:1	-	37	53	-	45	45	2.84	0.10-0.05
	BC_2	1:1	48	42	-	45	45	-	0.40	0.75-0.50
	F_2	1: 2:1	35	74	41	37.5	75	37.5	0.50	0.90-0.75
HRVO-1 × Acala 63-74	BC_1	1:1	-	47	43	-	45	45	0.18	0.75-0.50
	BC_2	1:1	52	38	-	45	45	-	2.18	0.25-0.10

Table 5: Genotypic (upper value) and phenotypic (lower value) correlations along with the probability values given in parenthesis for number of trichomes and agronomic/fibre traits in three cotton crosses.

Trait	1	2	3	Trait	1	2	3
	Number of Trichomes				Number of Trichomes		
L %	0.85**	0.92**	0.90**	PH	-0.35	-0.88**	-0.12
	(0.00)	(0.00)	(0.00)		(0.064)	(0.00)	(0.20)
	0.81**	0.91**	0.88**		-0.34	-0.84**	-0.11
	(0.00)	(0.00)	(0.00)		(0.063)	(0.00)	(0.22)
FL	-0.96**	-0.95**	-0.75**		0.16	-0.07	-0.29
	(0.00)	(0.00)	(0.00)	NMB	(0.133)	(0.32)	(0.08)
	-0.71**	-0.95**	-0.72**		0.15	-0.06	-0.28
	(0.00)	(0.00)	(0.00)		(0.149)	(0.34)	(0.09)
FS	-0.98**	-0.98**	-0.90**	NSB	-0.18	0.38	-0.32
	(0.00)	(0.00)	(0.00)		(0.105)	(0.07)	(0.08)
	-0.86	-0.96**	-0.80**		-0.18	0.30	-0.29
	(0.00)	(0.00)	(0.00)		(0.105)	(0.10)	(0.061)
FE	-0.83**	-0.95**	-0.88**	NBP	-0.29	-0.34	-0.26
	(0.00)	(0.00)	(0.00)		(0.07)	(0.09)	(0.10)
	-0.71**	-0.74**	-0.72**		-0.28	-0.23	-0.21
	(0.00)	(0.00)	(0.00)		(0.068)	(0.058)	(0.07)
U%	-0.83**	-0.97**	-0.86**	SCY	0.27	0.22	-0.35
	(0.00)	(0.00)	(0.00)		(0.22)	(0.06)	(0.25)
	-0.73**	-0.92**	-0.82**		0.26	0.18	-0.32
	(0.00)	(0.001)	(0.00)		(0.18)	(0.10)	(0.19)
FF	0.69*	0.62*	0.63*	BWt	0.17	0.15	-0.22
	(0.040)	(0.042)	(0.045)		(0.12)	(0.14)	(0.072)
	0.56*	0.60*	0.60*		-0.18	0.12	-0.24
	(0.048)	(0.040)	(0.040)		(0.11)	(0.20)	(0.081)

L% = Lint percentage, **FL** = Fibre length, **FS** = Fibre strength, **FE** = Fibre elongation, **U%** = Fibre uniformity ratio,
FF = Fibre fineness**, PH** = Plant height, **NMB** = No. of monopodial branches/plant, **NSB** = No. of sympodial branches/plant,
NBP = No. of bolls/plant, **SCY** = Seed cotton yield, **BWt** = Boll weight.
1 = HRVO-1 × FH-1000, 2 = HRVO-1 × CIM-446, 3 = HRVO-1 × Acala 63-74.
***P < 0.05 = Significant, **P < 0.01 = Non-significant.**

However, the non-significant values of the generation × location interactions (G × L) in the three cross combinations further confirmed the authenticity of the results as these results were independent of the environmental

influence. The intermediate (H_2h_2) progeny in F_1 was due to incomplete dominance. The two homozygous extremes for trichomes/hairiness : pilose hairy (H_2H_2) and sparse/normal hairy (h_2h_2) were easily distinguishable (Figure 3). The F_2 data regarding number of trichomes were categorized into three main classes (Table 4): pilose hairy (H_2H_2), sparse/normal hairy (h_2h_2) and intermediate hairy (H_2h_2) (Simpson, 1947). The major gene is designated as H_1 for sparse hairing. A second major gene, H_2 controls the finely dense pubescence in an upland mutant designated as 'pilose'. In the F_1 populations, both H_1 and H_2 showed incomplete dominance (Niles, 1980; Rahman and Khan, 1998). The segregation in the backcrosses with parent-I and parent-II also fit to the theoretical ratio of 1:1 which further confirmed the incomplete dominance pattern of inheritance. The non-significant chi-square values in F_2 for trichomes in all the crosses fit well against the theoretical monohybrid ratio of 1:2:1.This ratio is in proximity to the understanding gotten from Figure 3a, suggesting that inheritance of this trait can be manipulated easily in a breeding programme. However, a very small proportion of plants fell in another interme-diately resembling hairiness category. This phenotypic expression of the intermediate hairy state in hetero-zygous condition was probably affected by the genetic background of the parents indicating, modifying gene effects (Falconer and Mackay, 1996; Rieseberg et al., 1996; Xu et al., 1997; Rahman and Khan, 1998; Schwarz-Sommer et al., 2003).

Phenotypic and genotypic correlations

Correlation in plant breeding is a useful tool of indirect selection of the secondary trait with the improvement in the primary trait. Correlation coefficient is a statistical measure which is used to find out the degree and direction of the relationship between two or more variables. A positive value gives the indication of the same direction of the two variables in question and vice-versa. Fibre quality traits hold a special position from the cotton spinning industry. It was therefore, necessary to study the effect of this insect non-preference trait (trichomes) on the fibre quality determining traits. Genotypic correlations indicated correlation between the two characters (Table 5). Similar type of magnitude was observed by Dhanda et al. (1984) and Tyagi (1987) for genetic correlations. The higher values of phenotypic correlation coefficients than the genotypic correlation coefficients where ever present, indicating that the correlation between the two characters was not only due to genes, but environment also played its role in the expression of the character. The fibre fineness is recorded in micronaire value. This means that the higher the magnitude of micronaire value, the lesser will be the fineness of the fibre and vice-versa. Significant correlation between the two characters gave dependency of the two characters, while non-significant correlation indicated the independent nature of the two characters under study as suggested by Singh and Narayanan (2000).

The positive correlation of number of trichomes with lint percentage in all of three crosses (Table 4) suggested that the selection for pilose hairiness would be helpful in enhancing the lint percentage. This result is in line with that of Lee (1984) and Kloth (1993). The negative correlation of fibre length, fibre strength, fibre uniformity ratio, fibre elongation and micronaire value (positive correlation of number of trichomes with fibre fineness) with number of trichomes in the crosses corroborated to the findings of Lee (1964, 1984). The negative correlation of hairiness/trichomes with these mentioned traits determining fibre quality gave an understanding that the presence of the genes controlling these traits might be present on the same chromosome. Reports are also available regarding the pilosity with shorter fibre (Kohel et al., 1967, Lee, 1964, 1984). Association of hairiness with short fibre length was supposed to be gene pleiotropy as it was proposed by Simpson (1947) but the later studies by Kloth (1993) proved this association to be a linkage between the genes affecting hairiness and fibre quality determining traits.

The negative correlation of trichomes with plant height in HRVO-1 × CIM 446 suggest that increase in hairiness state would decrease the plant height but otherwise, there would be no effect on other morphological traits. Yield determining traits like number of monopodial branches, number of sympodial branches, number of bolls, boll weight and seed cotton yield are components of an efficient breeding programme. Non-significant correlations of these traits with number of trichomes/ hairiness revealed that hairiness or number of trichomes had no effect on the expression of these agronomic/yield related traits. In contrast to the effect of number of trichomes on fibre related traits, a well documented proof is available but the effect of the same on yield determining traits was proved in the present manuscript as a step forward in the research on trichomes. Incorporation of the gene for hairiness into commercial cotton cultivars will not only limit the population of the sucking insects but also result in the improvement of the fibre attributes without disturbing the major traits relating to yield (number of monopodial branches, number of sympodial branches, number of bolls, boll weight and seed cotton yield).

Keeping in view, the bio-safety requirements of the emerging era and the available knowledge of the naturally conferring resistance against insects, the present studies were performed to investigate the genetics of hairiness/trichomes in relation with the agronomic and fibre related traits in cotton. The main conclusions from this work are the non-significant chi-square values in F_2 for trichomes in all the crosses which fit well against the theoretical monohybrid ratio of 1:2:1. The positive correlation of number of trichomes with lint percentage and micronaire (negative correlation of number of trichomes with fibre fineness) in all the three crosses

suggested that the selection for pilose hairiness would be helpful in enhancing the lint percentage and fibre fineness.

The present findings elaborated the novelty of the research with a confidence that incorporation of the gene for pilosity had no effect on the expression of these agronomic/yield related traits.

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