

## Genetic Analysis of Fibre and Earliness Parameters in F<sub>2</sub> Progenies of Intra-hirsutum Crosses

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**Abstract.** Study of ten F<sub>2</sub> progenies of cotton along with their ten parental lines showed that the mean performance of genotypes differed significantly for the traits fibre length, seed index, lint index, micronaire value and earliness. Among F<sub>2</sub> hybrids, progeny CIM-499 x NB-111/S exhibited maximum heritability percentage for lint index and seed index, whereas progeny VH-142 x CRIS-134 expressed high genetic advances for fibre length and micronaire value. Progeny BH-147 x CIM-511 exhibited fair amount of genetic variance for earliness. The studied breeding material hence may reliably be used as a potential segregating population to improve fibre and earliness attributes in cotton.

**Keywords:** genetic analysis, fibre and earliness characters, intra-hirsutum crosses, *Gossypium hirsutum*

### Introduction

Phenotypic variations in plant populations are expressed by the joint action of both genetic and environmental factors; the proportion of genetic variation can be estimated from the available total phenotypic variations. For proper selection, the information regarding the amount of genetic variability, transferable to the progeny or heritability is important in improving any quantitative trait. The additive variance and additive genes, which pass from one generation to the next, play a significant role in selection and improving polygenic traits. A lot of work on genetic variability and heritability estimates has already been carried out, yet differences in their magnitude always exist due to difference in either material and methodology used or environment in which the material is tested (Baloch, 2004; Baloch and Bhutto, 2003; Moser and Percy, 1999; Efe and Gencer, 1998; Khadi *et al.*, 1998; Meredith, 1984).

Customarily, two types of heritability in broad and narrow sense, help plant breeders in phenotypic selection. However, when heritability for a trait is high, phenotypic selection is more effective (Baloch, 2004). The volume of genetic variations present in plant populations may also differ for quantitative traits. Hence to improve polygenic traits, segregating populations should retain more genetic variability in a smaller low sample size (Reed and Frankham, 2001).

The main objective of the present study, therefore, was to determine heritability and genetic variances so as to predict genetic responses to selection for fibre and earliness parameters in intra-hirsutum F<sub>2</sub> progenies.

### Materials and Methods

Ten parents of upland cotton were randomly crossed and ten intra-hirsutum F<sub>2</sub> hybrids were developed so as to determine genetic parameters such as genetic variance ( $\sigma^2_g$ ), heritability percentage in broad sense ( $h^2\%$ ) and genetic advance (GA) for fibre and earliness parameters in intra-hirsutum F<sub>2</sub> populations. The experiment was conducted in the Botanical Garden of the Department of Plant Breeding and Genetics at Sindh Agriculture University Tandojam, during 2005. The trial was laid-out in a Randomized Complete Block Design (RCBD) with four replications. Seeds of ten intra-hirsutum F<sub>2</sub> hybrids along with their ten parents was sown in the field through hand dibbling. Three seeds per hill were dibbled; however, after 15 days of planting, number of seedlings were thinned to one per hill. Distance between plant to plant and row to row was kept at 30 and 75 cm, respectively. The inputs like fertilizer, irrigation and insecticides were applied as and when required. For recording the data, ten plants per genotype were tagged at random from each replication and treated as index plants. The data were collected on fibre length, lint index, seed index, micronaire value and earliness. The analysis of variance was carried out according to the statistical procedures adopted by Gomez and Gomez (1984), whereas genetic parameters were calculated from variance components, according to formulae/procedures developed by Falconer (1989).

### Results and Discussion

For developing new varieties with the desirable traits, genetic variability in segregating populations and high heritability estimates for various characters are the reliable parameters. Present research was designed to estimate heritability

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percentage and genetic advance at 10% selection intensity in intra-hirsutum  $F_2$  populations. The traits studied were fibre length, lint index, seed index, micronaire value and earliness. The analysis of variance (Table 1) revealed significant differences among the genotypes for all the characters suggesting the existence of genetic variations in the mean performance of  $F_2$  progenies and their parents. The mean performance of  $F_2$  hybrids and their parental lines (Table 2) indicated that parent CIM-707 exhibited maximum fibre length (31.81 mm) while the next scoring was CIM-499 (29.68 mm). Among the  $F_2$  progenies, BH-147 x CIM-707 and CIM-499 x CIM-511 recorded maximum fibre length with mean values of 31.7 and 31.11 mm, respectively. Genetic parameters (Table 3) indicated that progenies from cross VH-142 x CRIS-134 were among the top scorers for genetic variance ( $\sigma^2g=1.12$ ) and genetic advance (1.600), yet ranked second scorer in heritability estimates (73.68%). Though, majority of the progenies expressed moderate to high heritability estimates, yet CIM-499 x CIM-511 exhibited maximum heritability (86.27%) suggesting presence of more additive variance and additive genes; thus it could be promising breeding material for selection of plants from segregating populations with longer fibres.

El-Adly *et al.* (2006), Ulloa (2006) and Baloch (2004), recorded high heritability percentage of 81.8% while other researchers like Shaheen *et al.* (2001) and Chen *et al.* (1999) reported moderate heritability sense of 38.00% for staple length.

For lint index (Table 2) mean performance demonstrated that among the parents CIM-511 and CRIS-470 produced maximum lint index of 4.67 and 4.53 g, respectively. While among the  $F_2$  hybrids, progenies VH-142 x CIM-511 (5.1 g), CIM-499 x CIM-511 (5.07 g) and BH-147 x CIM-511 (5.04 g) were the first, second and third top rankers, respectively, in producing lint index. Genetic parameters (Table 3) indicated that progenies from CIM-499 x NB-111/S with high genetic variance (0.1300) also manifested high heritability percentage (86.25%) that was associated with high genetic advance (0.60) for lint index. While some other progenies like FH-925 x NB-111/S ( $h^2=81.48$ ), BH-147 x NB-111/S ( $h^2=76.00$ ) and VH-142 x CRIS-134 ( $h^2=76.00$ ) also recorded high heritability estimates. Genetic parameters thus suggested that progenies from cross CIM-499 x NB-111/S, FH-925 x NB-111/S, BH-147 x NB-111/S and VH-142 x CRIS-134 may be the choice material to be exploited for selection in subsequent selfing generations so as to improve the lint index in cotton. Present results are in consonance with those of Shaheen *et al.* (2001) and Jagtap and Mehetre (1998) who also reported that high heritability was associated with high genetic gains for lint index.

The mean performance in respect to seed index (Table 2) indicated that parents CRIS-470 (7.75 g) and BH-147 (7.34 g)

gave maximum seed index values. Whereas among the  $F_2$  hybrids, crosses VH-142 x CIM-511 (7.73 g) and CIM-499 x CIM-511 (7.61g) exhibited maximum mean performance. The genetic parameters (Table 3) revealed that progenies from cross VH-142 x CRIS-134 though expressed high heritability percentage ( $h^2=64.28\%$ ), yet were associated with relatively low genetic variability ( $\sigma^2g=0.018$ ) and low genetic advance ( $GA=0.18$ ). Though CIM-499 x NB-111/S expressed next maximum heritability ( $h^2=60.86$ ) and genetic variance ( $\sigma^2g=0.140$ ) but was associated with high genetic advance ( $GA=0.50$ ). Moderate heritability estimates were also observed in other progenies like BH-147 x CIM-511 ( $h^2=62.74\%$ ) and NB-999 x CRIS-470 ( $h^2=50.00$ ); these progenies thus also expressed fair amount of genetic advance. Results generally suggested that progenies CIM-499 x NB-111/S, VH-142 x CRIS-134 and BH-147 x CIM-511 may be prospective breeding material for

**Table 1.** Mean squares from analysis of variance for fibre and earliness parameters in  $F_2$  progenies of intra-hirsutum crosses

Source of variation	Degree of freedom	Staple length	Lint index	Seed index	Micronaire value	Earliness
Replication	3	0.008	0.022	0.001	0.002	0.056
Genotypes	19	7.793**	0.365**	0.101**	0.092**	54.562**
Error	57	0.011	0.063	0.003	0.001	00.223

\*\* = significant at 1% probability level

**Table 2.** Mean performance of parents and  $F_2$  progenies for fibre and earliness traits in upland cotton

Parents and $F_2$ progenies	Fibre length (mm)	Lint index (g)	Seed index (g)	Micronaire value ( $\mu\text{g}/\text{inch}$ )	Earliness (%)
<b>Parents</b>					
CIM-499	29.68	4.38	6.43	4.44	10.00
NB-111/S	29.53	4.20	6.45	4.40	8.40
CIM-511	27.99	4.67	7.22	4.75	9.56
NB-999	27.93	3.33	5.87	4.45	10.08
VH-142	27.25	3.97	6.38	4.72	9.55
CRIS-134	28.31	4.31	7.24	4.70	8.49
BH-147	27.25	4.27	7.34	4.70	8.18
CRIS-470	27.34	4.53	7.75	4.66	8.63
FH-925	28.37	4.35	6.90	4.36	7.94
CIM-707	31.81	4.05	6.70	4.65	6.76
<b><math>F_2</math> Progenies</b>					
CIM-499 x NB-111/S	29.85	4.49	6.63	4.49	13.43
CIM-511 x NB-999	28.27	4.25	7.17	4.80	10.45
VH-142 x CRIS-134	28.75	4.05	6.94	4.75	13.79
BH-147 x CIM-707	31.70	4.31	7.09	4.80	18.16
BH-147 x CIM-511	28.70	5.04	7.55	4.80	19.44
BH-147 x NB-111/S	30.96	4.68	7.53	4.76	15.21
NB-999 x CRIS-470	29.65	4.56	7.52	4.81	16.26
FH-925 x NB-111/S	29.68	4.82	7.52	4.58	15.49
CIM-499 x CIM-511	31.11	5.07	7.61	4.70	11.40
VH-142 x CIM-511	28.49	5.10	7.73	4.90	13.37
LSD (5%)	0.149	0.269	0.072	0.026	0.668

selection to improve seed index in cotton. Mahmoud *et al.* (2004), Basbag and Gencer (2004) and Patel *et al.* (2005) also observed moderate to high heritability percentage ( $h^2=30$  to 93%) and genetic advance (GA=10-51) for seed index in cotton. Fibre fineness of cotton has a unique importance in textile industry for the manufacture of fine quality fabrics. The mean performance (Table 2) indicated that parent CIM-511

**Table 3.** Genetic parameters for fibre and earliness traits in  $F_2$  progenies of intra-hirsutum crosses

$F_2$ progenies and genetic parameters	Fibre length (mm)	Lint index (g)	Seed index (g)	Miconaire value ( $\mu\text{g}/\text{inch}$ )	Earliness (%)
<b>1. CIM499 x NB-111/S</b>					
Genetic variance ( $\sigma^2_g$ )	0.17	0.130	0.140	0.0068	1.44
Heritability ( $h^2$ )	38.58	86.25	60.86	52.30	14.32
Genetic advance (GA)	0.440	0.60	0.50	0.100	0.80
<b>2. CIM-511 x NB-999</b>					
Genetic variance ( $\sigma^2_g$ )	0.06	0.035	0.026	0.0022	1.19
Heritability ( $h^2$ )	36.66	62.50	45.61	44.00	16.78
Genetic advance (GA)	0.240	0.25	0.18	0.054	0.78
<b>3. VH-142 x CRIS -134</b>					
Genetic variance ( $\sigma^2_g$ )	1.12	0.019	0.018	0.0210	0.44
Heritability ( $h^2$ )	73.68	76.00	46.18	67.74	6.17
Genetic advance (GA)	1.600	0.20	0.18	0.200	0.28
<b>4. BH-147 x CIM-707</b>					
Genetic variance ( $\sigma^2_g$ )	0.02	0.001	0.011	0.0045	4.43
Heritability ( $h^2$ )	25.00	5.00	34.77	37.50	63.46
Genetic advance (GA)	0.097	0.12	0.10	0.066	2.94
<b>5. BH-147 x CIM-511</b>					
Genetic variance ( $\sigma^2_g$ )	0.04	0.022	0.032	0.0130	11.24
Heritability ( $h^2$ )	41.57	62.85	62.74	68.42	70.03
Genetic advance (GA)	0.210	0.20	0.24	0.150	4.93
<b>6. BH-147 x NB-111/S</b>					
Genetic variance ( $\sigma^2_g$ )	0.13	0.038	0.065	0.150	5.91
Heritability ( $h^2$ )	43.33	76.00	54.16	65.21	56.50
Genetic advance (GA)	0.410	0.29	0.33	0.170	3.21
<b>7. NB-999 x CRIS-470</b>					
Genetic variance ( $\sigma^2_g$ )	0.38	0.001	0.028	0.0063	5.00
Heritability ( $h^2$ )	79.16	5.55	50.0	65.62	59.55
Genetic advance (GA)	0.960	0.01	0.20	0.110	3.03
<b>8. FH-925 x NB-111/S</b>					
Genetic variance ( $\sigma^2_g$ )	0.03	0.044	0.057	0.0043	8.00
Heritability ( $h^2$ )	17.64	81.48	51.80	48.71	60.46
Genetic advance (GA)	0.120	0.33	0.30	0.780	3.85
<b>9. CIM-499 x CIM-511</b>					
Genetic variance ( $\sigma^2_g$ )	0.88	0.019	0.004	0.0088	2.66
Heritability ( $h^2$ )	86.27	45.23	42.55	46.31	35.36
Genetic advance (GA)	1.530	0.16	0.22	0.090	1.70
<b>10. VH-142 x CIM-511</b>					
Genetic variance ( $\sigma^2_g$ )	0.05	0.0007	0.004	0.0110	5.79
Heritability ( $h^2$ )	60.20	7.52	16.66	64.70	54.46
Genetic advance (GA)	0.30	0.01	0.043	0.140	3.12

(4.75 K  $\mu\text{g}/\text{inch}$ ), followed by VH-142 (4.72  $\mu\text{g}/\text{inch}$ ), CRIS-134 and BH-147 (4.70  $\mu\text{g}/\text{inch}$ ) gave higher micronaire values while among the  $F_2$  hybrid progenies, VH-142 x CIM-511 (4.9  $\mu\text{g}/\text{inch}$ ) followed by NB-999 x CRIS-470 (4.8  $\mu\text{g}/\text{inch}$ ) and BH-147 x CIM-707 (4.81  $\mu\text{g}/\text{inch}$ ) registered maximum mean values. Genetic parameters (Table 3) indicated that progenies BH-147 x CIM-511 with high heritability percentage ( $h^2=68.42$ ) was associated with fair amount of genetic advance (GA=0.150); it implied that this particular cross retains more additive genes and hence can be promising material for further improvement in micronaire value of cotton. Present results are in line with those of Yuan *et al.* (2002), Shaheen *et al.* (2001) and El-Adly *et al.* (2006) who also observed moderate to high heritability estimates. Larik *et al.* (1997) also observed high heritability percentage ( $h^2=89.75-99.74\%$ ) for micronaire value. Early maturing varieties in cotton are very desirable in that they require less fertilizer, irrigation and labour. They are also exposed for shorter period to biotic stresses, especially to insects as compared to the late maturing cotton. The mean performance presented in Table 2 indicated that among the parents, NB-999 and CIM-499 opened maximum number of bolls (10.08% and 10.00%, respectively). The genetic parameters (Table 3) revealed that progenies from cross BH-147 x CIM-511 which recorded high genetic variance ( $\sigma^2_g=11.24$ ) and maximum heritability estimates ( $h^2=70.03$ ) were associated with maximum genetic advance (GA=4.93). Earliness results by and large suggested hybrids BH-147 x CIM-511, FH-925 x NB-111/S and NB-999 x CRIS-470 may prove potential breeding material for selection of plants for early maturity in cotton in subsequent generations of selfing. Other researchers, Godoy and Palomo (1999), Ji and Zhou (1994) and Baloch (2004) also recorded moderate heritability estimates while characterizing earliness in cotton (*Gossypium hirsutum* L.).

## Conclusion

From the present research, it may be concluded that among the parental lines, CIM-707 by producing longer fibres, CIM-511 by giving maximum lint index and micronaire value and NB-999 by showing more earliness in maturity could prove best to be utilized in hybridization programme for improving respective characters. Heritability estimates being indicator of the degree of transmission of characters from one generation to the next suggested that among the  $F_2$  hybrid progenies, cross CIM-499 x NB-111/S, which expressed maximum heritability estimates and more genetic advance for seed index and lint index, may best be exploited in subsequent generations of selfing to improve both the characters. However for fibre length, progeny CIM-499 x CIM-511 and for earliness and micronaire value, progeny BH-147 x CIM-511 could serve potential segregating populations for these characters.

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