Indian J. Genet., **52** (3): 245–251 (1992)

GENETIC ANALYSIS OF CERTAIN FIBRE CHARACTERS IN *GOSSYPIUM HIRSUTUM* L.

N. NADARAJAN* AND S. R. SREE RANGASAMY

School of Genetics, Tamil Nadu Agricultural University, Coimbatore 641003

(Received: September 15, 1990; accepted: November 29, 1991)

ABSTRACT

An investigation was undertaken to assess the gene action underlying the inheritance of fibre traits, viz., 2.5% span length, fibre uniformity, fineness and maturity coefficient, and to suggest breeding methodologies for improvement of these characters. Mean data of six generations of five crosses were partitioned into their components. In general, all the traits were governed by additive, dominance, and digenic nonallelic interaction effects. However, nonadditive gene action predominated the additive gene action. Hence, one or two cycles of recurrent selection techniques followed by pedigree method of handling the segregates could be successfully adopted for improvement of the traits studied.

Key words: Genetic analysis, fibre traits, cotton.

The unique features of fibre quality in cotton has to be taken into account in its breeding programmes. Tai [1] stated that the success of any plant breeding programme depends to a greater extent on the knowledge of the genetic constitution of the population handled by the breeder. Hence information on the genetic architecture of fibre yield and other quality traits is essential. An attempt has been made in the present study to understand the nature of gene action governing the inheritance of different fibre quality traits and to suggest breeding methodologies for improvement of these traits.

MATERIALS AND METHODS

Five genotypes, viz., MCU 5, a high yielding extralong staple variety from Tamil Nadu; MCU 7, an early maturing medium staple variety from Tamil Nadu; Express Sindh (W), a short staple accession from Pakistan; Piedmont Cleveland, a long staple accession from U.S.A.; and Sindis Wild, a medium staple type from Pakistan were used as seed parents. Using a fuzzless–lintless type, maintained in the germplasm collections of the Cotton

---

*Present address: Department of Agricultural Botany, Agricultural College, Madurai 625104.

Breeding Station, Coimbatore, as common pollen parent, five F_1s were obtained. These combinations will be hereafter referred to as Cross 1, Cross 2, Cross 3, Cross 4 and Cross 5, respectively. Six generations, i.e. P_1, P_2, F_1, F_2, BC_1 and BC_2 of each cross were raised in randomised block design with three replications. The number of rows assigned to P_1, P_2, F_1, F_2, BC_1 and BC_2 generations in each replication were 1, 1, 1, 8, 4 and 4, respectively. A spacing of 75 x 30 cm was adopted with 20 plants per row. The crosses were first randomised within each replication, while the six families within each cross were randomized individually. The total number of plants studied in each of the crosses were: 60 in P_1, P_2 and F_1; 480 in F_2; and 240 in BC_1 and BC_2.

The means and variance of means for 2.5% span length, uniformity ratio, fibre fineness, and maturity coefficient were computed for each generation. The mean of P_2 was '0' since the second parent was a lintless type. The variance of mean of P_2 was set as equal to that of average of P_1 and F_1. The '0' values observed in certain plants in F_2 and BC_2 generations were excluded (based on personal communication from Prof. Jinks and Dr. H. S. Pooni, University of Birmingham, England). The gene effects were estimated using the models suggested by Mather and Jinks [2] and Jinks and Jones [3].

RESULTS AND DISCUSSION

The mean values of different generations, significance of scaling tests A, B and C and the estimates of genetic parameters m, (d), (h), (i), (j) and (l) for different characters were estimated (Tables 1–4).

2.5% SPAN LENGTH

All the three scales, i.e., A, B and C were significant for the crosses 1, 2, 4 and 5, while for cross 3, only the scales B and C were significant. Hence, a simple additive–dominance model was inadequate for all the crosses and a digenic nonallelic interaction model was assumed for inheritance of this trait. Estimates of additive (d) and dominance (h) effects were significantly positive for all the crosses. In all the cases, the dominance effect was predominant over the additive effect. The additive x additive interaction effect (i) was significantly negative for cross 3 and significant and positive for crosses 1 and 4. The additive x dominance effects (j) and dominance x dominance interaction effects (l) were significantly negative for all the crosses (Table 1). Although the estimate of (h) was larger in magnitude than (d), sum of (j) and (l) with negative gene effects was larger than (h). Thus, these gene effects reduce 2.5% span length. A duplicate type of digenic nonallelic interaction was involved in the inheritance of this trait, as can be seen from the opposite signs of (h) and (l). Importance of both additive and dominance effects was reported by several workers [4–6]. On the other hand, Gill and Kalsy [7] and Dhillon and Singh [8] observed digenic nonallelic interaction effects to be more important in the inheritance of this character.

Table 1. Mean values (mm), scaling tests and estimates of genetic parameters for 2.5% span length (mm) in cotton

Parameter	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5
Mean:					
P_1	32.8 ± 0.09	26.2 ± 0.08	25.2 ± 0.08	30.4 ± 0.13	25.7 ± 0.13
P_2	0.0 ± 0.12	0.0 ± 0.10	0.0 ± 0.10	0.0 ± 0.13	0.0 ± 0.11
F_1	29.8 ± 0.14	24.5 ± 0.12	26.3 ± 0.12	28.3 ± 0.12	25.0 ± 0.09
F_2	27.6 ± 0.08	25.5 ± 0.08	26.1 ± 0.12	27.9 ± 0.11	25.1 ± 0.14
BC_1	30.6 ± 0.10	26.0 ± 0.10	25.7 ± 0.09	30.2 ± 0.09	25.1 ± 0.10
BC_2	25.3 ± 0.10	25.5 ± 0.11	24.2 ± 0.10	26.8 ± 0.12	25.4 ± 0.10
Scales:					
A	–1.3* ± 0.27	1.4* ± 0.24	–0.1 ± 0.22	1.8* ± 0.25	–0.6* ± 0.26
B	20.7* ± 0.27	26.4* ± 0.26	22.1* ± 0.25	25.4* ± 0.31	25.8* ± 0.25
C	18.1* ± 0.47	27.0* ± 0.41	26.6* ± 0.54	24.7* ± 0.53	24.6* ± 0.61
Genetic parameters:					
m	15.1* ± 0.45	12.3* ± 0.42	17.2* ± 0.54	12.7* ± 0.53	12.1* ± 0.63
(d)	16.4* ± 0.07	13.1* ± 0.06	12.6* ± 0.07	15.2* ± 0.09	12.9* ± 0.09
(h)	35.3* ± 1.11	40.8* ± 1.08	26.6* ± 1.23	45.3* ± 1.29	38.9* ± 1.43
(i)	1.3* ± 0.44	0.8 ± 0.42	–4.6* ± 0.53	2.5* ± 0.53	0.7 ± 0.63
(j)	–22.0* ± 0.32	–25.0* ± 0.32	–22.2* ± 0.28	–23.6* ± 0.35	–26.4* ± 0.34
(l)	–20.6* ± 0.74	–28.6* ± 0.71	–17.5* ± 0.75	–29.7* ± 0.08	–26.0* ± 0.84

*Significant at 5% level.

UNIFORMITY RATIO

In the crosses 1, 3, 4 and 5, all the three scaling tests were significant. However, in cross 2, only two scales namely B and C were significant. Digenic nonallelic interaction was responsible for inheritance of this trait in all crosses. It was seen that both additive (d) and dominance (h) effects were significantly positive. Estimate of dominance effects was larger in magnitude than additive effects. The interaction effect (i) was significantly negative in crosses 1 and 4 but positive in cross 3. Other interaction effects (j) and (l) were significantly negative in all the crosses (Table 2). The nonadditive nonallelic interaction effects (j) and (l) balanced the (h) effects which were positive. Further, the (h) and (l) effects exhibited opposite signs indicating duplicate gene interaction. Predominance of additive gene action for uniformity ratio was reported earlier [9, 10] in contrast to the present study.

FIBRE FINENESS

The three scaling tests were significant in all the crosses, indicating inadequacy of a

Table 2. Mean values (%), scaling tests and estimates of genetic parameters for uniformity ratio

Parameter	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5
Mean:					
P_1	46.6 ± 0.21	51.0 ± 0.23	48.1 ± 0.14	47.2 ± 0.13	48.1 ± 0.15
P_2	0.0 ± 0.22	0.0 ± 0.19	0.0 ± 0.16	0.0 ± 0.13	0.0 ± 0.16
F_1	49.2 ± 0.23	51.1 ± 0.16	48.4 ± 0.18	49.4 ± 0.12	48.2 ± 0.18
F_2	50.2 ± 0.09	50.7 ± 0.09	47.8 ± 0.13	48.3 ± 0.13	46.4 ± 0.19
BC_1	49.3 ± 0.15	50.9 ± 0.12	48.6 ± 0.14	47.2 ± 0.14	46.9 ± 0.13
BC_2	49.6 ± 0.13	50.2 ± 0.14	48.3 ± 0.13	48.6 ± 0.11	46.6 ± 0.14
Scales:					
A	2.8* ± 0.44	–0.2 ± 0.37	0.7* ± 0.35	–2.2* ± 0.33	–2.5* ± 0.35
B	50.1* ± 0.41	49.2* ± 0.38	48.2* ± 0.36	47.8* ± 0.29	45.0* ± 0.36
C	55.7* ± 0.67	49.7* ± 0.57	46.6* ± 0.66	47.1* ± 0.59	41.2* ± 0.86
Genetic parameters:					
m	26.1* ± 0.57	26.3* ± 0.55	21.6* ± 0.65	25.1* ± 0.62	22.7* ± 0.85
(d)	23.3* ± 0.15	25.5* ± 0.15	24.1* ± 0.11	23.6* ± 0.09	24.0* ± 0.11
(h)	73.2* ± 1.51	73.0* ± 1.43	78.1* ± 1.58	68.5* ± 1.50	69.4* ± 1.93
(i)	–2.8* ± 0.55	–0.80 ± 0.52	2.4* ± 0.64	–1.5* ± 0.62	1.4 ± 0.85
(j)	–47.2* ± 0.50	–49.4* ± 0.48	–47.5* ± 0.44	–50.0* ± 0.40	–47.4* ± 0.44
(l)	–50.1* ± 1.04	–48.2* ± 0.95	–51.4* ± 1.01	–44.1* ± 0.93	–43.9* ± 1.15

*Significant at 5% level.

simple additive–dominance model. In all the crosses, the additive and dominance effects were positive and significant. However, the magnitude of (h) was many times larger than (d). The additive x additive interaction effect (i) was significantly negative in cross 2 and positive in cross 5. The additive x dominance (j) and dominance x dominance (l) effects were significantly negative in all the crosses (Table 3). Though the estimate of (h) was many times larger than (d), the sum of negative (j) and (l) gene effects balanced the positive influence of (h). The opposite signs of (h) and (l) indicated the predominance of duplicate type of interaction. While the presence of additive gene action for fineness was emphasised by Tabrah [11], importance of dominance gene action was also reported [10, 12].

MATURITY COEFFICIENT

All the scaling tests deviated significantly from zero in all the five crosses. The additive (d) and dominance (h) effects were significantly positive in all the crosses. The magnitude of (h) was greater than (d) in all the crosses. The (i) effect was significant and positive in the crosses 1 and 5, but significantly negative in crosses 2 and 3. The (j) and (l) effects were

Table 3. Mean values (millitex), scaling tests and estimates of genetic parameters for fibre fineness in cotton

Parameter	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5
Mean:					
P_1	141.1 ± 1.10	141.8 ± 1.57	146.1 ± 0.86	168.3 ± 0.88	140.0 ± 0.77
P_2	0.0 ± 1.11	0.0 ± 1.64	0.0 ± 0.87	0.0 ± 0.98	0.0 ± 0.75
F_1	154.3 ± 1.12	169.9 ± 1.74	151.0 ± 0.89	181.6 ± 1.04	141.6 ± 0.75
F_2	165.4 ± 1.30	175.8 ± 1.51	159.0 ± 1.33	173.6 ± 1.46	137.2 ± 1.29
BC_1	156.1 ± 1.13	149.6 ± 1.52	142.4 ± 1.78	155.4 ± 1.30	129.4 ± 1.12
BC_2	180.3 ± 2.47	182.2 ± 2.14	176.2 ± 1.89	191.0 ± 1.68	155.2 ± 1.92
Scales:					
A	16.8* ± 2.76	−12.4* ± 3.84	−12.2* ± 3.77	−39.1* ± 2.93	−22.8* ± 2.49
B	206.2* ± 5.18	194.5* ± 4.90	201.5* ± 3.99	200.4* ± 3.65	168.8* ± 3.99
C	211.9* ± 5.87	221.4* ± 7.33	187.9* ± 5.75	163.1* ± 6.33	125.6* ± 5.49
Genetic parameters:					
m	59.5* ± 7.56	110.2* ± 8.08	71.6* ± 7.47	85.8* ± 7.23	49.6* ± 6.85
(d)	70.6* ± 0.78	70.9* ± 1.14	73.0* ± 0.61	84.1* ± 0.66	70.0* ± 0.54
(h)	328.9* ± 19.51	202.6* ± 20.21	270.2* ± 19.00	255.4* ± 17.39	258.3* ± 17.00
(i)	11.1 ± 7.52	−39.3* ± 8.00	1.5 ± 7.44	−1.7 ± 7.20	20.4* ± 6.83
(j)	−189.4* ± 5.63	−207.0* ± 5.72	−213.7* ± 5.34	−239.5* ± 4.44	−191.6* ± 4.58
(l)	−234.0* ± 12.35	−142.8* ± 12.80	−190.8* ± 11.88	−159.7* ± 10.58	−166.4* ± 10.47

*Significant at 5% level.

significant and negative in all the five crosses. The sum of (j) and (l) with negative effects exceeded (h) with positive effects in all the crosses. The duplicate type of interaction predominated the other type of digenic interactions as indicated by the opposite signs of (h) and (l) in all the crosses (Table 4). Tabrah [11] and Meredith et al. [13] concluded that additive effect was the major type of gene action involved in fibre maturity. However, Singh et al. [14] reported both additive and nonadditive genetic effects for this trait.

As a whole, additive, dominance and digenic nonallelic interaction effects appear to govern all the fibre properties studied. However, predominance of nonadditive gene action, particularly j and l types, was observed for all the fibre characters. The nonfixable combined gene effects (h), (j) and (l) exceeded many times the magnitude of fixable effects (d) and (i). Therefore, improvement of these fibre traits appears to be difficult as simple pedigree breeding will not be able to fix the superior lines in the early generations. However, one or two cycles of recurrent selection, followed by pedigree breeding, will be effective and useful [15, 16] for improvement of fibre traits in cotton.

Table 4. Mean values, scaling tests and estimates of genetic parameters for maturity coefficient in cotton

Parameter	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5
Mean:					
P_1	71.4 ± 0.23	74.8 ± 0.39	76.4 ± 0.19	76.4 ± 0.20	73.8 ± 0.20
P_2	0.0 ± 0.26	0.0 ± 0.31	0.0 ± 0.21	0.0 ± 0.17	0.0 ± 0.24
F_1	75.0 ± 0.29	77.7 ± 0.21	78.9 ± 0.24	78.6 ± 0.12	74.9 ± 0.28
F_2	74.9 ± 0.08	77.4 ± 0.16	76.8 ± 0.22	77.4 ± 0.16	72.4 ± 0.33
BC_1	74.0 ± 0.19	75.0 ± 0.32	72.6 ± 0.30	76.0 ± 0.22	71.1 ± 0.36
BC_2	76.7 ± 0.19	78.2 ± 0.13	77.3 ± 0.15	78.8 ± 0.10	76.0 ± 0.21
Scales:					
A	$1.6^{*} \pm 0.53$	$-2.6^{*} \pm 0.77$	$-10.1^{*} \pm 0.67$	$-3.1^{*} \pm 0.49$	$-6.5^{*} \pm 0.80$
B	$78.4^{*} \pm 0.55$	$78.7^{*} \pm 0.46$	$75.7^{*} \pm 0.43$	$79.0^{*} \pm 0.28$	$77.1^{*} \pm 0.55$
C	$78.2^{*} \pm 0.99$	$79.4^{*} \pm 0.90$	$72.9^{*} \pm 1.02$	$75.8^{*} \pm 0.72$	$66.0^{*} \pm 1.48$
Genetic parameters:					
m	$33.9^{*} \pm 0.92$	$40.6^{*} \pm 0.96$	$45.6^{*} \pm 1.10$	$38.0^{*} \pm 0.80$	$32.2^{*} \pm 1.58$
(d)	$35.7^{*} \pm 0.17$	$37.4^{*} \pm 0.25$	$38.2^{*} \pm 0.14$	$38.2^{*} \pm 0.13$	$36.9^{*} \pm 0.16$
(h)	$123.0^{*} \pm 2.25$	$110.1^{*} \pm 2.52$	$91.5^{*} \pm 2.67$	$116.7^{*} \pm 1.94$	$118.0^{*} \pm 3.68$
(i)	$1.8^{*} \pm 0.90$	$-3.2^{*} \pm 0.93$	$-7.4^{*} \pm 1.09$	0.2 ± 0.79	$4.7^{*} \pm 1.57$
(j)	$-76.7^{*} \pm 0.64$	$-81.3^{*} \pm 0.84$	$-85.8^{*} \pm 0.72$	$-82.1^{*} \pm 0.54$	$-83.6^{*} \pm 0.88$
(l)	$-81.9^{*} \pm 1.47$	$-73.0^{*} \pm 1.64$	$-58.2^{*} \pm 1.67$	$-76.1^{*} \pm 1.19$	$-75.3^{*} \pm 2.22$

REFERENCES

1. G. C. C. Tai. 1979. An internal estimation of expected response to selection. Theor. Appl. Genet., **54**: 273–275.

2. K. Mather and J. L. Jinks. 1971. Biometrical Genetics. Chapman and Hall Ltd. London.

3. J. L. Jinks and R. M. Jones. 1958. Estimation of the components of heterosis. Genetics, **43**: 223–234.

4. A. Marani. 1968. Inheritance of lint quality characteristics in intraspecific crosses among varieties of *G. hirsutum* L. and *G. barbadense* L. Crop Sci., **8**: 36–38.

5. W. R. Meredith Jr. and R. R. Bridge. 1972. Heterosis and gene action in cotton, *G. hirsutum* L. Crop Sci., **12**: 304–310.

6. R. A. Patil and P. R. Chopde. 1983. Genetics of yield, its components and halo length in *G. hirsutum* L. and *G. barbadense* L. Cottons. ISCI Journal, 8(1): 28–32.

7. M. S. Gill and H. S. Kalsy. 1981. Genetic analysis in four crosses of upland cotton. Crop Improv., 8(2): 95–99.

8. S. S. Dhillon and T. H. Singh. 1982. Estimates of epistasis in upland cotton. Indian J. Genet., **42**: 389–392.

9. J. A. Lee, P. A. Miller and J. O. Rawlings. 1967. Interaction of combining ability effects and environments in diallel crosses of upland cotton. Crop Sci., **7**: 477–481.

10. F. C. Ma, Y. Y. Zhou, R. T. Wang and C. G. Lin. 1983. Genetic analysis of characters in the progeny of an intervarietal hybrid of upland cotton. Acta Agriculture Universitatis Pakinensis, 9(4): 27–34. Cotton Trop. Fibre Crop Abstr., 9(5): 210.

11. T. A. Tabrah. 1970. Estimating Genetic Parameters in Cotton (*G. hirsutum* L.) Using Comstock and Robinson's Design III. Ph. D. Thesis. Oklahoma State Univ., U. S. A.

12. L. M. Verhalen and J. C. Murray. 1967. A diallel analysis of several fibre property traits in upland cotton. Crop Sci., **7**: 501–504.

13. W. R. Meredith, Jr., R. R. Bridge and J. F. Chism. 1970. Relative performance of F_1 and F_2 hybrids from doubled haploids and their parent varieties in upland cotton. Crop Sci., **10**: 295–298.

14. R. B. Singh, R. P. Dahiya and D. K. Jain. 1972. Genetics of ginning and fibre characters in upland cotton. Indian J. Genet., **32**: 125–137.

15. R. S. Pathak. 1975. Gene effects for fibre properties in upland cotton. Theor. Appl. Genet., **46**: 129–133.

16. R. Rajagopalan. 1985. Study of Gene Action and Recombination Potential in Intervarietal Crosses in *Gossypium hirsutum* L. Utilising Generation Means, BIPs and NC III Backcrosses. Ph. D. Thesis. T.N.A.U., Coimbatore.