Genetic Analysis for Seed Cotton Yield and Fibre Quality Traits in Cotton (*Gossypium hirsutum* L.)

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Adoption of modern rotor spinning system by textile industry has increased demand for high fibre strength cottons. Most of the presently developed *G. hirsutum* cultivars have low fibre strength. Thus, there is an urgent need to develop improved cultivars having high yield and superior fibre quality, especially high fibre strength to meet the requirements of modern textile industry. Strain P 56-4 identified for high fibre strength was crossed with low fibre strength variety RS 2013 during 2005-06. Crosses were made during 2006 to obtain 6 generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) which were evaluated at IARI, New Delhi during 2007-08. Additive, dominance and epistatic gene effects were important for seed cotton yield, boll number, boll weight, ginning outturn, seed index and plant height. Dominance gene effects and epistasis were important for 2.5% span length and fibre elongation, and epistatic effects were important for monopodial branches, uniformity ratio and fibre strength. Heterosis breeding approach may be followed to exploit dominance and epistatic gene effects for high yield and superior fibre quality.

Key Words: Cotton, Fibre quality, Heterosis, Seed cotton yield

Introduction

Cotton is an important commercial crop in India and plays a key role in the national economy. The total cotton production of the country has shown tremendous improvement since 2003-04 and recorded an all time high production of 315 lakh bales from an area of 9.55 m hectares during 2007-08 with an average lint yield of 560 kg/ha. The productivity of cotton in India was still one of the lowest among the major cotton growing countries of the world and was also significantly lower than the world average of 794 kg/ha during 2007-08. It is, therefore, important to use the genetic variability available for different traits effectively and efficiently to increase production and productivity. Modernization of textile industry has increased the demand for high fibre strength cottons as the high speed rotor spinning reduces yarn strength by about 20-25%. Besides genetic improvement of seed cotton yield, the genetic improvement of fibre quality traits has also become essential in order to meet the requirements of the modern textile industry. Proper understanding of nature of gene action for yield and fibre quality parameters is therefore important to exploit the available genetic variability. The estimates of components of variance also have a strong bearing on the choice of breeding methods to be followed to achieve the objectives of a breeding programme. High additive gene effects are useful in the development of pure lines. On the other hand dominance and epistatic gene effects are useful to exploit hybrid vigour. The present investigation was therefore taken up at Indian Agricultural Research Institute (IARI), New Delhi, during 2005-08 to estimate gene effects for yield and fibre quality traits by generation mean analysis.

Materials and Methods

Contrasting parents (‘P 56-4’ and ‘RS 2013’) for fibre quality traits, especially for fibre strength and fibre length, were used in this investigation. The mean fibre strength of ‘P 56-4’ was 27.8 g/tex as compared to 19.3 g/tex of ‘RS 2013’. Its mean 2.5% span length was 28.2 mm and micronaire value was 3.9. In contrast, ‘RS 2013’ showed mean fibre length of 25.4 mm and micronaire value of 4.4. Crosses were made between ‘P 56-4’ and ‘RS 2013’ during 2005 to obtain F_1. During 2006-07, the F_1 (P 56-4 x RS 2013) was advanced to F_2 generation through selfing and crosses were also made to obtain BC_1 and BC_2 generations, besides making ‘P56-4’ x ‘RS 2013’ crosses to obtain F_1. The 6 generations P_1, P_2, F_1, F_2, BC_1 and BC_2 were evaluated in a field trial during 2007-08 at the research farm of IARI, New Delhi. The parents P 56-4 (P_1), RS 2013 (P_2) and F_1 were planted in 2 row plots; BC_1 and BC_2 in 4 row plots and F_2 in 8 row plots with 3 replications. The row

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length was 4.2 m accommodating 15 plants, spaced 30 cm apart. The row-to-row spacing was 75 cm. All the recommended agronomic and plant protection practices were followed to raise a good crop. Data were recorded on randomly selected 10 plants each in 2 parents and F_1, 20 plants each in back cross generations (BC_1, BC_2) and 40 plants in F_2 generation in each replication. Observations were recorded on important traits like seed cotton yield/ plant, ginning percent, boll number, boll weight, seed index, number of monopodial and sympodial branches, plant height and fibre quality traits namely 2.5% span length, uniformity ratio, fibre strength, micronaire value and fibre elongation. The generation means were calculated by taking the average over all the replications for each generation. To test the adequacy of the additive-dominance model, the individual scaling tests given by Mather (1949) as well as joint scaling test by Cavalli (1952) were used. First simple additive-dominance model consisting of mean 'm', additive component [d] and dominance component [h] was tried and adequacy of the model was tested by the chi-square test. When this model failed to explain variation among generation means, successively non-allelic parameters, *i.e.*, additive × additive [i], additive × dominance [j] and dominance × dominance [l] were included in the model. Thus all possible models with different combinations of epistatic parameters were tried to identify the best fit model with minimum non-significant value of the chi-square and maximum number of significant parameters as suggested by Mather and Jinks (1982).

Results and Discussion

The scaling tests, joint scaling test and best fit model for yield and yield components are given in Table 1 and for fibre quality traits in Table 2. The scaling test detected the presence of epistasis for all the characters included in this study as the values for at least one or more scales 'A', 'B', 'C' and/or 'D' were significant. After the scaling test failed, the joint scaling test was applied, in which Chi-square values were also found significant for all characters except for micronaire value. This suggested the presence of epistasis for all characters except for the micronaire value. The three parameter model thus identified both additive [d] and non additive [h] components of variance as important for fibre fineness. Significance of different components detected by three parameter model for seed cotton yield, ginning outturn, boll number, boll weight, seed index, number of monopodia and sympodia, plant height, and fibre quality traits 2.5% span length, uniformity ratio, fibre strength and fibre elongation is of little value due to inadequacy of the model. The model involving m, [d], [h], [i], [j] and [l] with all parameters significant was adequate for seed cotton yield, boll number and boll weight, and opposite signs for [h] and [l] components suggested the presence of duplicate type of epistssis for these characters. Components [d], [h] and [i] were significant for ginning outturn, [d], [h], [i] and [l] for

Table 1. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for yield and yield components in the cross P 56-4 × RS 2013

Parameter	Seed cotton yield	Ginning out-turn	Boll number	Boll weight	Seed index	No. of monopodia	No. of sympodia	Plant height (cm)
Scaling test								
A	-82.42**±9.42	0.31±0.61	-15.47**±3.69	-0.84**±0.10	-0.13±0.24	0.20±0.23	-2.83*±1.32	22.75**±4.87
B	-238.48**±19.92	1.18*±0.49	-57.37**±4.92	0.14±0.10	-0.40*±0.18	-1.57**±0.24	3.07**±1.04	31.70**±4.72
C	-6.89±15.25	3.90**±0.74	-2.63±6.30	0.71**±0.23	1.29**±0.40	-0.90*±0.45	-1.93±2.05	36.70**±7.91
D	-157.00**±12.49	-1.21*±0.47	-35.10**±3.82	-0.70**±0.12	-0.91**±0.23	-0.23±0.22	1.08±1.01	8.87±4.69
Joint scaling test								
m	80.00**±2.26	32.67**±0.12	34.22**±0.76	3.00**±0.02	7.87**±0.04	3.22**±0.07	16.19**±0.34	146.59**±0.77
[d]	-6.13**±2.35	1.23**±0.12	2.01**±0.76	-0.61**±0.02	-1.48**±0.04	-0.40**±0.07	-0.87**±0.32	-22.54**± 0.78
[h]	3.63±3.68	0.90**±0.20	3.96*±1.59	0.61**±0.04	0.35**±0.07	-0.78**±0.13	-0.96±0.63	-9.62**±1.67
X^2	**217.06****	**30.22****	**149.77****	**89.73****	**17.29****	**47.48****	**19.18****	**69.43****
Best fit model								
m	75.05**±3.34	32.45**±0.16	33.24**±1.32	3.09**±0.05	7.73**±0.09	2.87**±0.09	16.23**±0.39	137.01**±1.76
[d]	-75.46**±10.56	-0.76*±0.35	-22.15**±2.77	1.02**±0.06	1.37**±0.14	-0.23±0.13	2.98**±0.64	26.54**±3.09
[h]	316.64**±25.25	3.43**±0.96	69.90**±7.83	2.02**±0.25	2.14**±0.47	-0.42±0.46	-2.93±2.13	-22.12*±9.55
[i]	314.01**±24.98	2.42*±0.94	70.20**±7.64	1.40**±0.24	1.81**±0.47	0.47±0.44	-2.17±2.03	-17.75±9.38
[j]	-156.06**±21.70	0.87±0.75	-41.90**±5.76	0.99**±0.12	-0.27±0.29	-1.77**±0.30	5.90**±1.49	8.95±6.39
[l]	-634.91**±44.90	-0.93±1.59	-143.03**±12.73	-2.10**±0.33	-2.34**±0.69	-1.83**±0.68	2.40±3.29	72.22**±14.68

*, **Pdd0.05 and 0.01, respectively

Table 2. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for fibre quality parameters in the cross P 56-4 × RS 2013

Parameter	2.5% Span length (mm)	Uniformity ratio (%)	Fibre strength (g/tex)	Micronaire value	Fibree longation
Scaling test					
A	1.85**±0.43	-1.50*±0.58	3.02**±0.55	-0.01±0.11	0.08±0.04
B	-2.01**±0.49	-1.82**±0.58	-3.84**±0.49	0.28*±0.14	-0.25**±0.05
C	1.36±0.70	-2.15±1.36	0.73±0.82	0.19±0.20	0.05±0.09
D	-0.76*±0.34	-0.59±0.59	-0.77±0.43	0.04±0.11	-0.06±0.04
Joint scaling test					
m	26.28**±0.10	53.21**±0.18	24.96**±0.10	**4.11**±0.03**	6.21**±0.02
[d]	-1.75**±0.10	-0.59**±0.15	-3.35**±0.10	**0.28**±0.03**	-0.06**±0.02
[h]	0.34±0.22	1.23**±0.37	0.28±0.22	**0.28**±0.06**	0.12**±0.03
÷2	54.38**	12.02**	120.88**	4.58	27.67**
Best fit model					
m	26.26**±0.11	53.77**±0.27	24.87**±0.15	4.23**±0.04	6.26**±0.01
[d]	0.10±0.25	0.38±0.25	0.26±0.31	-0.16*±0.07	0.03±0.02
[h]	2.20**±0.73	1.77±1.26	1.60±0.91	0.22±0.22	0.26**±0.09
[i]	1.53*±0.68	1.17±1.19	1.55±0.87	-0.07±0.21	0.12±0.08
[j]	-3.86**±0.55	-0.32±0.65	-6.86**±0.64	0.29±0.16	-0.34**±0.07
[l]	-1.69±1.23	-4.50**±1.69	-2.36±1.47	0.34±0.35	-0.29*±0.14

*, **Pd”0.05 and 0.01, respectively

seed index, [d], [h] and [l] for plant height, [d] and [j] for number of sympodia, and [j] and [l] for number of monopodia indicating the importance of additive and/or dominance gene effects and epistasis for different traits. Dominance gene effects and epistasis were found significant for fibre quality traits, such as components [h] and [j] for 2.5% span length, [h], [j] and [l] for fibre elongation. Epistatic effects like components [l] for uniformity ratio and [j] for fibre strength were significant. Duplicate type of epistasis was also indicated for ginning outturn, seed index, number of monopodia, 2.5% span length, uniformity ratio, fibre strength and elongation. In the present study additive, non additive and epistatic gene effects were important for seed cotton yield and yield components, *i.e.*, boll number, boll weight, ginning outturn, seed index and plant height. Additive and epistatic effects were important for number of sympodial branches. Non-additive gene effects and epistasis be involved in the inheritance of 2.5% span length and fibre elongation and epistatic effects were important for monopodial branches, uniformity ratio and fibre strength. The involvement of additive, non additive and/or epistatic effects in different yield components and fibre quality characters has also been reported by other workers (Ahuja *et al.*, 1999; Singh and Singh, 2001; Patel *et al.*, 2007). Singh *et al.*, 2008 have also reported that additive as well as non additive gene effects were important in the inheritance of seed cotton yield, boll number, boll weight, ginning outturn and 2.5% span length. These findings are similar to the work reported in this study. They also reported different magnitude of gene effects in different crosses. It is, therefore, important to select a specific breeding strategy for a particular cross to achieve improvement in desired characters. It is also clear from the present study that besides the additive and non additive gene effects there is involvement of epistatic effects in most of the traits. It is thus important to take into consideration gene interactions in addition to additive or non additive gene effects to formulate the right breeding strategies for genetic improvement of seed cotton yield and fibre quality traits.

The study suggests heterosis breeding approach to exploit dominance and epistatic gene effects to obtain high yield and superior fibre quality.

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