ESTIMATION OF GENE ACTION FOR SEED COTTON YIELD AND ITS QUALITY TRAITS IN COTTON (*Gossypium hirsutum* L.)

***VALU, M. G.; POLARA, A. M.; PATEL, J. A.; MADARIYA, R. B. AND VARIYA, M. V.**

COTTON RESEARCH STATION
JUNAGADH AGRICULTURAL UNIVERSITY
JUNAGADH-362 001 (GUJARAT), INDIA

****Email: mgvalu@jau.in***

ABSTRACT

The experimental materials consisted of twelve generations, namely P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s of two crosses of cotton viz., G.Cot-12 x GTHV-95/145 (cross-1) and 76IH20 x GJHV-460 (cross-2) with a view to generate genetic information on gene effects for seed cotton yield and its quality traits in cotton (Gossypium hirsutum L.). Special scaling tests such as X and Y were significant either in cross-1 or cross-2 for all the four traits besides significance of other tests showing presence of epistasis. The $X^2_{(2)}$ value at six degrees of freedom were significant in all the traits in both the crosses supported the presence of higher order epistasis. The $X^2_{(3)}$ value at two degrees of freedom was non-significant for ginning percentage, seed index and lint index in cross-1 and for seed index and lint index in cross-2 proving the ten parameter model as the best fit model. The $X^2_{(3)}$ value at two degrees of freedom was significant for seed cotton yield per plant in cross-1 and seed cotton yield per plant and ginning percentage in cross-2 indicating the presence of higher order epistasis and/or linkage.

KEY WORDS: Cotton, Digenic, Gene Effects, Trigenic

INTRODUCTION

Cotton (*Gossypium spp.*) popularly known as “King of fibre” and “White Gold”, is one of the most important commercial cash crops and plays a key role in economic, political and social affairs of the world. Cotton enjoys a pre-eminent status among all the cash crops in the country, being the principal material for flourishing textile industries. India is the only country where all the four cultivated species of cotton are grown on commercial scale and covers cultivated area about 105 lakh ha. It occupies second position in production with 351 lakh bales among all cotton producing countries, next to China. Average productivity of India is 568 kg/ha which is much lower as compared to the world average productivity of 766 kg/ha. Gujarat is the second largest cotton growing state with acreage of 24 lakh ha and the largest cotton producing state of India with production of 95 lakh bales. The average productivity of cotton in the state is 673 kg/ha which is higher than national productivity (Anonymous, 2016). The yield of seed cotton is a complex and polygenic character. The information on gene action for seed cotton yield and quality traits is very essential for deciding the effective selection method in segregating generations. The additive and dominance gene effects may have great value on the improvement of seed cotton yield. The information on epistatic gene effect is also important for the yield improvement in cotton with quality traits. Hence, the present investigation was under taken to study the gene action of seed cotton yield and its quality traits in cotton.

MATERIALS AND METHODS

The experimental materials consisted of twelve generations, namely P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s of two crosses of cotton *viz*., G.Cot-12 x GTHV-95/145 (cross-1) and 76IH20 x GJHV-460 (cross-2). Experiment was laid-out in Compact Family Block Design with three replications during *Kharif* 2013 at Cotton Research Station, Junagadh Agricultural University, Junagadh. Each replication was divided into two compact blocks each consists of single cross and blocks were consisted of twelve plots comprised of twelve basic generations of each cross. The crosses were assigned to each block and twelve generations of a cross were randomly allotted to individual plot within the block. The plots of various generations contained different number of rows *i.e*., parents and F_1 in single row; B_1 and B_2 in two rows and F_2, B_{1S}, B_{11}, B_{12}, B_{2S}, B_{21} and B_{22} in three rows. Each row was of 6.3 m in length with 120 cm and 45 cm inter and intra row spacing, respectively. All the recommended agronomical practices and necessary plant protection measures were followed timely to raise good crop of cotton. The observations were recorded on seed cotton yield per plant, ginning percentage, seed index and lint index on five randomly selected plants in each replication for P_1, P_2 and F_1; ten plants for B_1 and B_2 and twenty plants for F_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s. To decide the adequacy of three, six and ten parameter model, simple scaling tests given by Hayman and Mather (1955), Hill (1966) and Van Der Veen (1959) were employed. Joint scaling test of Cavalli (1952) was applied to test adequacy of three, six and ten-parameter models. Whenever, this simple additive-dominance model failed to explain the variation in generation means, six and ten-parameter models using weighted least square method were used to estimate main, digenic and trigenic effects.

RESULTS AND DISCUSSION

The data were initially subjected to simple scaling tests A, B, C and D. Significant estimates of any one or more of these tests indicate the presence of digenic interactions. Further, simple scaling tests B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s given by Hill (1966) and X and Y given by Van Der Veen (1959) were also computed. The significant estimate of the test(s) given by Hill (1966) showed the contribution of particular generation to higher order epistasis which indirectly indicating the presence of epistasis. If any of the Van Der Veen's tests deviate significantly from zero indicates the presence of trigenic or higher order epistasis. The results of simple scaling tests were further confirmed by joint scaling test (Cavalli, 1952), which effectively combines the whole set of simple scaling tests. Thus, it offers a more general, convenient, adoptable and informative approach for estimating gene effects and also for testing adequacy of additive-dominance model. The $\chi2_{(1)}$ test at nine degrees of freedom; $\chi^2_{(2)}$ at six degrees of freedom and $\chi^2_{(3)}$ at two degrees of freedom were applied to test the fitness of three-parameter model, six-parameter model and ten-parameter model, respectively. The ten-parameter model was used to estimate higher order epistasis (Hill, 1966). To draw inference on adequacy of ten-parameter model, chi-square test $\chi^2_{(3)}$ at two degrees of freedom was applied. The degree of freedom for χ^2 was computed by subtracting number of parameters considered under the respective model from the number of generations. The results are presented in Table 1 and 2.

Out of all the scaling tests only A, B_{12}, B_{21}, B_{22}, X and Y in cross-1 and B, D, B_{11}, B_{12}, B_{1S} and special scaling test Y in cross-2 were significant showing presence of epistasis for seed cotton yield per plant, while all the scaling tests except D, X and Y in cross-1 and scaling tests B, D, B_{12}, X and Y in cross-2 were significant showing presence of digenic and trigenic gene action for ginning percentage. For seed index, the scaling tests A, B, C, B_{11}, B_{22}, B_{2s}, X and Y in cross-1 and all the scaling tests except D, B_{21} and X in cross-2 were significant showing presence of epistasis. On the other hand, all the scaling tests except D in cross-1 and B, C, B_{11}, B_{22}, B_{1S}, B_{2s}, X and Y in cross-2 were significant showing presence of digenic and trigenic gene interaction for lint index. All the three parameters i.e. 'm', additive [d] and dominance [h] of three parameter model were significant in cross-1 and cross-2 for all the characters under study. The $X^2_{(1)}$ values with nine degrees of freedom of joint scaling test was significant in all the characters indicating the failure of additive-dominance model which indirectly pointed out the presence of epistasis. Cockerham (1959) postulated that the epistatic gene action is common in the inheritance of quantitative traits and there is no sound biological reason why this type of gene action should be less common for these traits.

When the simple additive-dominance model failed to explain the variation among generation means, a six parameter model involving three digenic interactions ([i], [j] and [l]) based on weighted least square technique proposed by Hill (1966) was tested which had provision of testing the adequacy of model with six degrees of freedom besides being utilizing means of all the twelve generations. Hence, the present study was planned to execute with means of twelve generations and model of Hill (1966) was tested in which six degrees of freedom left for testing the adequacy of six parameter model of Hill (1966). According to the six parameter model of Hill, the parameters 'm', [d] and digenic [j] in cross-1 and all the parameters in cross-2 were significant for seed cotton yield per plant, while all the parameters except [d] and digenic [i] in cross-1 and all the parameters except [h] in cross-2 were significant for ginning percentage. Likewise, for seed index, the estimate of 'm', [d], [h] and [l] in cross-1 and 'm', [d] and digenic [i] in cross-2 were significant, while all the estimate of gene effects except [i] in cross-1 and 'm', [d] and digenic [i] in cross-2 were significant for lint index. The $X^2_{(2)}$ value at six degrees of freedom were significant in all four traits in two crosses indicating the presence of higher order epistasis.

In ten parameter model, all the parameters were significant for seed cotton yield per plant in cross-1 and 'm' and dominance x dominance x dominance [z] in cross-2. For ginning percentage, the gene effects 'm', additive [d] and additive x additive x dominance [w] in cross-1 and 'm', dominance [h], additive x additive [i], dominance x dominance [l], additive x additive x dominance [x], additive x dominance x dominance [y] and dominance x dominance x dominance [z] in cross-2 were significant. The gene effects 'm', dominance [h], dominance x dominance [l], additive x dominance x dominance [y] and dominance x dominance x dominance [z] were found significant in cross-1 and 'm', additive x additive [i] and additive x additive x dominance [x] in cross-2 were significant for seed index. For lint index, the gene effects 'm', dominance [h] and dominance x dominance [l], were significant in cross-1, while 'm', dominance x dominance [l], additive x dominance x dominance [y] and dominance x dominance x dominance [z] were significant in cross-2. The $X^2_{(3)}$ value at two degrees of freedom was non-significant in both the crosses for seed index and lint index and in cross-1 for ginning percentage depicting that the ten parameter model as the best fit model. The $X^2_{(3)}$ value at two degrees of freedom was significant in both crosses for seed cotton yield per plant and for ginning percentage in cross-2 indicating the presence of higher order epistasis and/or linkage.

These findings were further confirmed from the investigations done by several researchers who worked on different kind of gene effects mostly up to digenic interactions and there is no report on trigenic interactions in cotton so far. However, few reports are available in different crops *viz*., Bhapkar and D'cruz (1967) and Singh (2012) in castor and Sharma *et al*. (2002) in wheat. The opposite signs of either two or all the three gene effects *viz*., dominance [h], dominance x dominance [l] and dominance x dominance x dominance [z] suggested the presence of duplicate type of epistasis. In present study, duplicate epistasis was observed in both the crosses for all the four traits under investigation. Duplicate type of epistasis also reported by Thombre *et al.* (1987) for seed cotton yield; by Mehetre (2003) for seed cotton yield per plant and ginning percentage; by Haleem *et al.* (2010) for seed cotton yield and seed index and by Kannan *et al.* (2013) for seed index, lint index, ginning out turn and single plant yield.

CONCLUSION

From the foregoing discussions it could be concluded that seed cotton yield per plant and its quality traits recorded in two crosses were governed by additive, dominance and digenic and/or trigenic epistasis gene effects along with duplicate type of gene action. When additive as well as non-additive gene effects are involved, a breeding scheme efficient in exploiting both types of gene effects should be employed. Bi-parental mating could be followed which would facilitate exploitation of both additive and non-additive gene effects simultaneously for genetic improvement of seed cotton yield and its quality traits in cotton.

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Table 1: Scaling tests and estimation of gene effects for seed cotton yield per plant and ginning percentage in two crosses of cotton

Scaling Tests /Gene Effects	Seed Cotton Yield Per Plant		Ginning Percentage	
	G.Cot-12 x GTHV-95/145 (cross 1)	76IH20 x GJHV-460 (cross 2)	G.Cot-12 x GTHV-95/145 (cross 1)	76IH20 x GJHV-460 (cross 2)
A	-23.87* ± 9.01	-8.20 ± 8.59	3.87** ± 0.71	0.60 ± 0.42
B	3.93 ± 11.32	-34.47** ± 7.22	6.38** ± 0.66	-1.79** ± 0.41
C	19.27 ± 18.27	3.40 ± 18.92	8.67** ± 1.38	0.85 ± 0.87
D	19.60 ± 10.92	23.03* ± 10.21	-0.79 ± 0.745	1.02* ± 0.46
B_{11}	27.13 ± 20.60	-32.07* ± 13.35	-5.98** ± 1.28	-0.26 ± 1.08
B_{12}	123.73** ± 16.16	72.40** ± 17.90	-6.69** ± 1.45	9.75** ± 1.08
B_{21}	58.13** ± 20.21	8.47 ± 16.66	-4.65** ± 1.24	1.21 ± 1.03
B_{22}	-36.00* ± 15.90	-26.93 ± 18.12	-9.84** ± 1.20	-0.83 ± 1.08
B_{1S}	19.60 ± 37.22	-85.13** ± 28.47	-10.85** ± 2.40	0.07 ± 2.26
B_{2S}	42.27 ± 28.03	-49.13 ± 34.04	-26.74** ± 2.48	1.16 ± 2.25
X	32.18** ± 8.41	14.70 ± 7.45	0.46 ± 0.53	2.28** ± 0.48
Y	47.68** ± 8.85	34.97** ± 7.99	1.12 ± 0.60	3.01** ± 0.51
Three Parameter Model				
m	111.15** ± 1.37	105.82** ± 1.24	35.54** ± 0.12	33.66** ± 0.09
(d)	13.68** ± 1.38	-13.12** ± 1.23	-0.25* ± 0.12	-1.16** ± 0.09
(h)	25.52** ± 2.76	32.65** ± 2.68	2.84** ± 0.25	3.10** ± 0.17
$\chi^2_{(1)}$ (9 df)	82.28**	62.57**	203.27**	108.72**
Six Parameter Model				
m	130.56** ± 9.41	140.46** ± 8.69	35.45** ± 0.65	35.06** ± 0.56
(d)	13.97** ± 1.57	-16.06** ± 1.42	0.20 ± 0.15	-1.51** ± 0.11
(h)	-39.19 ± 25.40	-54.70* ± 22.51	9.69** ± 1.76	-0.85 ± 1.39
(i)	-18.19 ± 9.46	-35.32** ± 8.74	-1.07 ± 0.66	-1.36* ± 0.56
(j)	1.15 ± 8.65	30.52** ± 7.40	-2.66** ± 0.62	2.62** ± 0.46
(l)	49.54** ± 17.67	55.12** ± 15.55	-8.80** ± 1.29	2.74** ± 0.92
$\chi^2_{(2)}$ (6 df)	73.76**	28.03**	20.63**	66.98**
Ten Parameter Model				
m	90.05** ± 27.75	101.89** ± 26.94	37.05** ± 1.89	27.87** ± 1.61
(d)	63.52** ± 20.51	-10.19 ± 18.88	-3.84** ± 1.37	-0.51 ± 1.32
(h)	693.76** ± 145.08	174.87 ± 142.33	1.86 ± 9.91	38.32** ± 7.94
(i)	111.41** ± 27.77	1.99 ± 26.95	-2.77 ± 1.89	5.73** ± 1.61
(j)	-190.63** ± 57.59	-17.79 ± 50.99	5.01 ± 3.71	-5.34 ± 3.46
(l)	-1154.72** ± 222.72	-384.28 ± 217.24	-0.55 ± 15.16	-62.12** ± 12.02
(w)	-48.65* ± 20.48	-5.65 ± 18.85	4.16** ± 1.36	-0.88 ± 1.32
(x)	-352.78** ± 82.23	-61.17 ± 82.87	7.38 ± 5.74	-17.09** ± 4.25
(y)	222.92** ± 56.71	75.50 ± 50.01	-2.05 ± 3.55	12.97** ± 3.31
(z)	607.45** ± 106.75	252.89* ± 103.15	-1.81 ± 7.28	33.11** ± 5.77
$\chi^2_{(3)}$ (2 df)	6.86*	6.29*	1.50	6.77*
Type of Epistasis	Duplicate	Duplicate	Duplicate	Duplicate

, ** Significant at 5 and 1 per cent levels, respectively

Table 2: Scaling tests and estimation of gene effects for seed index and lint index in two crosses of cotton

Scaling Tests /gene Effects	**Seed Index (g)**		**Lint Index (g)**	
	G.Cot-12 x GTHV-95/145 (cross 1)	**76IH20 x GJHV-460 (cross 2)**	**G.Cot-12 x GTHV-95/145 (cross 1)**	**76IH20 x GJHV-460 (cross 2)**
A	0.65** ± 0.23	0.43** ± 0.14	1.13** ± 0.19	0.16 ± 0.11
B	1.26** ± 0.26	0.78** ± 0.19	1.89** ± 0.21	0.49** ± 0.14
C	1.69** ± 0.48	1.30** ± 0.39	2.57** ± 0.35	1.09** ± 0.25
D	-0.11 ± 0.28	0.04 ± 0.21	-0.22 ± 0.20	0.22 ± 0.13
B_{11}	-1.28* ± 0.49	-3.31** ± 0.53	-1.81** ± 0.33	-1.24** ± 0.33
B_{12}	0.69 ± 0.54	-1.51** ± 0.51	-0.82* ± 0.39	0.47 ± 0.34
B_{21}	-0.83 ± 0.54	-0.97 ± 0.52	-1.42** ± 0.46	-0.15 ± 0.33
B_{22}	-2.68** ± 0.52	-2.66** ± 0.57	-3.16** ± 0.34	-2.83** ± 0.39
B_{1S}	-1.95 ± 1.08	-6.41** ± 0.99	-3.19** ± 0.82	-2.86** ± 0.65
B_{2S}	-3.30** ± 1.06	-6.91** ± 0.96	-6.53** ± 0.73	-5.43** ± 0.72
X	0.73** ± 0.24	-0.29 ± 0.25	0.49** ± 0.17	0.55** ± 0.16
Y	0.95** ± 0.25	0.87** ± 0.26	0.68** ± 0.19	1.10** ± 0.17
Three Parameter Model				
m	7.25** ± 0.03	7.22** ± 0.04	3.97** ± 0.03	3.62** ± 0.03
(d)	0.49** ± 0.03	0.35** ± 0.04	0.26** ± 0.03	0.16** ± 0.03
(h)	0.77** ± 0.07	0.74** ± 0.07	1.07** ± 0.07	1.01** ± 0.05
$\chi^2_{(1)}$ (9 df)	75.55**	134.70**	236.15**	129.77**
Six Parameter Model				
m	7.17** ± 0.30	8.08** ± 0.25	3.94** ± 0.21	4.26** ± 0.17
(d)	0.51** ± 0.04	0.41** ± 0.04	0.31** ± 0.03	0.22** ± 0.03
(h)	2.33** ± 0.76	-0.04 ± 0.61	3.18** ± 0.55	0.19 ± 0.43
(i)	-0.02 ± 0.30	-1.06** ± 0.25	-0.18 ± 0.21	-0.78** ± 0.17
(j)	-0.27 ± 0.24	-0.31 ± 0.19	-0.52** ± 0.18	-0.25 ± 0.14
(l)	-1.76** ± 0.50	-0.39 ± 0.40	-2.75** ± 0.38	0.05 ± 0.28
$\chi^2_{(2)}$ (6 df)	25.83**	49.03**	34.70**	64.01**
Ten Parameter Model				
m	5.71** ± 0.84	9.37** ± 0.75	3.48** ± 0.58	3.74** ± 0.49
(d)	0.98 ± 0.66	0.16 ± 0.59	-0.13 ± 0.46	0.09 ± 0.41
(h)	10.68* ± 4.21	-5.70 ± 3.76	6.06* ± 2.89	3.99 ± 2.44
(i)	1.42 ± 0.84	-2.38** ± 0.75	0.26 ± 0.58	-0.33 ± 0.49
(j)	-3.12 ± 1.75	0.95 ± 1.66	-0.81 ± 1.19	-1.42 ± 1.12
(l)	-16.59** ± 6.39	5.08 ± 5.78	-8.86* ± 4.42	-8.73* ± 3.72
(w)	-0.45 ± 0.66	0.25 ± 0.59	0.47 ± 0.46	0.18 ± 0.41
(x)	-2.98 ± 2.33	5.39** ± 1.97	-0.35 ± 1.60	0.18 ± 1.26
(y)	4.33** ± 1.67	-1.84 ± 1.68	2.13 ± 1.13	2.68* ± 1.10
(z)	8.03** ± 3.06	-1.01 ± 2.81	3.82 ± 2.14	5.56** ± 1.81
$\chi^2_{(3)}$ (2 df)	3.18	3.82	5.49	5.27
Type of Epistasis	Duplicate	Duplicate	Duplicate	Duplicate

, ** Significant at 5 and 1 per cent levels, respectively

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