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Gene interaction and genetics for yield and its attributes in cotton (*Gossypium hirsutum* L.)

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Abstract
The present investigation was undertaken with a view to generate genetic information on gene effects for seed cotton yield and its component traits in cotton (*Gossypium hirsutum* L.). The experimental materials consisted of six generations, namely P_1, P_2, F_1, F_2, BC_1, BC_2 of four crosses of cotton *viz*., GJHV-522 × GJHV-473 (cross 1), GJHV-544 × GJHV-523 (cross 2), GJHV-497 × GJHV-511(cross 3) and G. Cot 20 × GJHV-519 (cross 4). Scaling tests such as A, B and C were significant in all crosses for all the three traits besides significance of other tests showing presence of epistasis except number of boll per plant in cross 4. The $\chi 2$ value at three degrees of freedom were significant in all the traits in four crosses supported the presence of higher order epistasis except in number of sympodia per plant in cross 2 indicated that adequacy of additive-dominance model. Scaling test and $\chi 2$ value at three degrees of freedom were significant in crosses 1 and 3 in number of sympodia per plant but all main effect and digenic effect found non significant indicated that presence of epistasis or linkage.

Keywords: Cotton (*Gossypium hirsutum* L.), gene action, gene effect, three parameter model, six parameter model

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. *Gossypium hirsutum* is predominant species cultivated in India. In India, cotton is planted in about 122.35 lakh hectares of land and it occupies second position in production with 377.00 lakh bales (each of 170 kg) among all cotton producing countries in the world i.e. next to China. Average productivity of India is 524 kg/ha which is low as compared to world average of 792 kg/ha. (Anonymous, 2017) [1]. The yield of seed cotton is a complex and polygenic character. The information on gene action for seed cotton yield 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. Hence, the present investigation was under taken to study the gene action of seed cotton yield and its component traits in cotton.

Materials and Methods
The experimental material comprised of four crosses namely, GJHV-522 × GJHV-473, GJHV-544 × GJHV-523, GJHV-497 × GJHV-511 and G. Cot 20 × GJHV-519 each having six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2). The conventional hand emasculation and pollination method develop by Dock (1934) [5] was followed. F_2 population was developed by selfing the F_1s. The experiment was laid out in compact family block design with three replication during *kharif* - 2018 at Cotton Research Station, Junagadh Agricultural University, Junagadh. All the generations of a cross were sown at 120 x 45 cm spacing. Data were recorded on randomly selected plant in each replication for seed cotton yield per plant and its contributing characters (5 plant for parents and crosses, 20 plants for F_2 generation and 10 plants for back cross generation). To decide the adequacy of three parameter model, simple scaling tests given by Hayman and Mather (1955) [8] were employed. Joint scaling test of Cavalli (1952) [3] was applied to test adequacy of three and six models. Whenever, this simple additive-dominance model failed to explain the variation in generation means, six parameter models using weighted least square method were used to estimate main, digenic effects.

Results and Discussion

The data were initially subjected to simple scaling tests A, B and C. Significant estimates of any one or more of these tests indicated the presence of digenic interactions. The results of simple scaling tests were further confirmed by joint scaling test (Cavalli, 1952) [3], 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 $\chi 2$ test at three degrees of freedom was applied to testing of three-parameter model or six-parameter model.

The failure of additive-dominance model was attributed mainly to the epistasis. Cockerham (1959) [4] 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. Mather (1949) [11], Horner *et al*. (1955) [9] and Gilbert (1958) [6] emphasized that until experimentally proved otherwise, the absence of epistasis cannot be assumed when dealing with quantitative traits. Studies have been reported in cotton which shows evidence of non-allelic interaction of economically important traits. (Haleem *et al*., 2010[7] and Nassar 2013[13]). The estimate of m, additive (d) and dominance (h) parameters calculated in additive-dominance scale for character showing epistasis interaction are biased to an unknown extent by effects not attributed to the additive and dominance actions of genes (Mather and Jinks 1980 [12]).

The results obtained for number of sympodia per plant are depicted in Table 1. Significance of scaling tests A in cross 1, B in crosses 2, 3 and 4, C in crosses 1 and 3 indicated the inadequacy of additive-dominance model. The joint scaling test for all the crosses was also significant except cross 2, indicated the presence of digenic interaction effects for this traits. In cross 1, all the gene effects were non-significant which indicates the presence of higher order epistasis and/or linkage. Gene effect 'm', additive [d], dominance [h] and dominance x dominance [l] were found significant according to Hayman six parameter model, while gene effect 'm', additive [d] and dominance were found significant according to weighted least square method in cross 2. Scaling test indicates the presence of epistatic but in weighted least square method all the gene effects were non-significant which indicates the presence of higher order epistasis and/or linkage, while additive [d] gene effect was negative and significant according to six parameter model of Hayman in cross 3. According to weighted least square method in cross 4 gene effect 'm', additive [d], additive x dominance [j] and dominance x dominance [l] were found significant, while gene effect 'm', additive x dominance [j] and dominance x dominance [l] were found significant according to six parameter model of Hayman. Opposite sign associated with dominance [h] and dominance x dominance [l] component in crosses 1, 3 and 4 suggested the duplicate type of epistasis for this trait.

The analysed results obtained for number of bolls per plant are depicted in Table 2 indicated that the scaling tests A, B and C were non-significant in cross 4 indicating the adequacy of additive-dominance model. Scaling tests B was significant in cross 1, A, B and C in cross 3 and only C in cross 2 indicating inadequacy of additive–dominance model. In cross 1 and 2 gene effect 'm', additive [d], dominance [h], additive x additive [i], dominance x dominance [l] were found significant according to weighted least square method and six parameter model of Hayman. According to weighted least square method and six parameter model of Hayman gene effect 'm', dominance [h] and dominance x dominance [l] were found significant in cross 3. In cross 4 scaling tests A, B and C were non-significant indicating the adequacy of additive-dominance model. Non-significant chi-square value of joint scaling test supported the finding of simple scaling tests that three parameter model was adequate to explain gene effect in this cross. Gene effect 'm', and dominance [h] effect were found positive and significant in cross 4. Opposite sign associated with dominance [h] and dominance x dominance [l] component in crosses 1, 2 and 3 suggested the duplicate type of epistasis for this trait.

The results obtained for seed cotton yield per plant were depicted in Table 3. Scaling tests B and C were found significant in crosses 1 and 3, scaling test A and B were found significant in cross 4, while scaling test C was significant in cross 2. In cross 1 gene effect 'm', additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant according to Hayman six parameter model, while gene effect additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant according to weighted least square method. Gene effect 'm' and dominance [h] was positive and significant according to six parameter model of Hayman, while gene effect 'm', additive [d] and dominance [h] were found significant according to weighted least square method in cross 2 and 3. In cross 4, 'm', additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] gene effect were found significant according to weighted least square method while 'm', additive x additive [i] and dominance x dominance were found significant according to six parameter model of Hayman. Opposite sign associated with dominance [h] and dominance x dominance [l] component in all the crosses suggested the duplicate type of epistasis for this trait.

The results are in the same trend with Haleem *et al*. (2010) [7], Pandit *et al*. (2014) [14] for seed cotton yield, Sawarkar *et al*. (2014) [15] for seed cotton yield and its related character, Solanki *et al*. (2015) [16] for seed cotton yield, Kannan and Saravanan (2016) [10] for seed cotton yield and majority of yield components, Balakrishna *et al*. (2017) [2] for seed cotton yield per plant and its contributing traits *viz*., number of bolls per plant, boll weight and seed index, Valu *et al*. (2018) [17] for seed cotton yield per plant and its component character.

Conclusion

In the present study seed cotton yield per plant in all the four crosses was observed to be governed by both additive and non-additive genetic effects. Similarly for most of the component traits in all the four crosses, both additive and non additive gene effects were significant. The involvement of different type of digenic interactions were noticed for all the traits in four crosses. When additive as well as non-additive effects are involved, a breeding scheme efficient in exploiting both type of gene effect should be employed. Reciprocal recurrent selection would ideal method which would facilitate exploitation of both additive and non additive gene effects simultaneously. Importance of duplicate type of gene action was observed for most of the character showing digenic interaction. Under a situation of this type, it would be difficult for the breeder to get promising segregants better than the parent involved through conventional breeding method such as making simple crosses and their exploitation through straight pedigree method. Breeding procedure involving multiple crosses, biparental crosses may be restors to get

transgressive segregants. This is especially important to develop good inbred lines having superiority in different characters. Such lines can give better hybrids. While in case of complementary type of epistasis, material can be utilized directly in breeding programme. The magnitude of epistasis interaction namely dominance x dominance [l] along with dominance [h] were found higher in few traits in respective crosses under this study. Such type of non-additive gene effects may be exploited by heterosis breeding for this crop.

Table 1: Estimation of scaling tests and gene effect for number of sympodia per plant in four crosses of cotton

Scaling tests / gene effects	GJHV-522 x GJHV-473 (cross 1)			GJHV-544 x GJHV-523 (cross 2)			GJHV-497 x GJHV-511 (cross 3)			G. Cot 20 x GJHV-519 (cross 4)		
Individual Scaling test												
A	-2.93**	±	1.07	1.93	±	1.19	1.20	±	1.29	-1.60	±	0.94
B	-1.27	±	1.27	2.80*	±	1.20	4.20**	±	1.30	-4.60**	±	1.04
C	-4.67*	±	1.79	1.60	±	1.99	5.53*	±	2.12	-2.67	±	1.90
Gene effects in different models												
Three parameters model (Cavalli, 1952)												
m	16.20**	±	0.29	15.65**	±	0.35	12.50**	±	0.25	12.76**	±	0.29
(d)	-0.67*	±	0.29	-1.14**	±	0.31	-0.38	±	0.24	-0.15	±	0.28
(h)	2.01**	±	0.50	1.85**	±	0.58	4.86**	±	0.58	4.42**	±	0.54
χ^2 (3 d.f.)	11..30**			7.00			12.57**			20.28**		
Six parameter model (Hayman, 1958)												
m	16.63**	±	0.36	16.48**	±	0.39	15.40**	±	0.37	15.10**	±	0.38
(d)	-1.36	±	0.71	-1.40*	±	0.68	-1.66*	±	0.73	0.83	±	0.53
(h)	2.73	±	2.11	4.70*	±	2.18	3.43	±	2.23	1.20	±	1.95
(i)	0.46	±	2.05	3.13	±	2.09	-0.13	±	2.10	-3.53	±	1.87
(j)	-0.83	±	0.78	-0.43	±	0.77	-1.50	±	0.77	1.50*	±	0.62
(l)	3.73	±	3.37	-7.86*	±	3.40	-5.26	±	3.61	9.73**	±	2.85
Weighted least square method (Cavalli, 1952)												
m	16.20**	±	2.07	15.65**	±	0.35	12.36**	±	2.12	16.93**	±	1.90
(d)	-0.53	±	0.32	-1.14**	±	0.31	-0.16	±	0.26	-0.66*	±	0.33
(h)	-1.00	±	5.30	1.85**	±	0.58	8.70	±	5.43	-8.53	±	4.56
(i)	0.46	±	2.05	(-	)		-0.13	±	2.10	-3.53	±	1.87
(j)	-1.66	±	1.56	(-	)		-3.00	±	1.55	3.00*	±	1.25
(l)	3.73	±	3.37	(-	)		-5.26	±	3.61	9.73**	±	2.85
Type of epistatis	D						D			D		

*, ** Significant at 5 % and 1 % levels, respective

Table 2: Estimation of scaling tests and gene effect for number of bolls per plant in four crosses of cotton

Scaling tests / gene effects	GJHV-522 x GJHV-473 (cross 1)			GJHV-544 x GJHV-523 (cross 2)			GJHV-497 x GJHV-511 (cross 3)			G. Cot 20 x GJHV-519 (cross 4)		
Individual Scaling test												
A	3.80	±	2.65	0.87	±	2.68	17.13**	±	3.33	-4.40	±	3.13
B	7.13*	±	2.69	5.33	±	2.83	22.73**	±	3.14	-2.00	±	3.47
C	-0.53	±	4.14	-11.87**	±	4.17	39.93**	±	4.62	3.80	±	5.75
Gene effects in different models												
Three parameters model (Cavalli, 1952)												
m	33.63**	±	0.67	40.18**	±	0.66	29.86**	±	0.59	37.80**	±	1.02
(d)	-3.12**	±	0.67	-2.73**	±	0.67	-2.32**	±	0.60	0.94	±	0.97
(h)	11.54**	±	1.24	5.71**	±	1.24	26.81**	±	1.18	16.32**	±	1.87
χ^2 (3 d.f.)	9.67*			17.23**			112.74**			4.36		
Six parameter model (Hayman, 1958)												
m	38.53**	±	0.81	40.45**	±	0.82	48.80**	±	0.97	(-	)	
(d)	-4.53**	±	1.57	-4.66**	±	1.64	-3.96	±	2.07	(-	)	
(h)	22.53**	±	4.71	24.16**	±	4.83	22.56**	±	5.81	(-	)	
(i)	11.46*	±	4.54	18.06**	±	4.65	0.06	±	5.67	(-	)	
(j)	-1.66	±	1.74	-2.23	±	1.80	-2.80	±	2.16	(-	)	
(l)	-22.40**	±	7.55	-24.26**	±	7.79	-39.80**	±	9.49	(-	)	
Weighted least square method (Cavalli, 1952)												
m	21.66**	±	4.60	22.30**	±	4.71	27.56**	±	5.71	(-	)	
(d)	-2.86**	±	0.75	-2.43**	±	0.74	-1.16	±	0.63	(-	)	
(h)	44.93**	±	11.76	48.43**	±	12.12	62.36**	±	14.82	(-	)	
(i)	11.46*	±	4.54	18.06**	±	4.65	-0.06	±	5.67	(-	)	
(j)	-3.33	±	3.49	-4.46	±	3.61	-5.60	±	4.33	(-	)	
(l)	-22.40**	±	7.55	-24.26**	±	7.79	-39.80**	±	9.49	(-	)	
Type of epistatis	D			D			D					

*, ** Significant at 5 % and 1 % levels, respectively

Table 3: Estimation of scaling tests and gene effect for seed cotton yield per plant in four crosses of cotton

Scaling tests / gene effects	GJHV-522 x GJHV-473 (cross 1)			GJHV-544 x GJHV-523 (cross 2)			GJHV-497 x GJHV-511 (cross 3)			G. Cot 20 x GJHV-519 (cross 4)		
Individual Scaling test												
A	3.33	±	9.38	1.53	±	11.52	12.20	±	11.71	-38.40**	±	10.62
B	43.93**	±	9.68	-12.20	±	10.42	35.33**	±	11.11	-62.07**	±	10.39
C	-35.93*	±	14.59	-49.53**	±	16.17	38.67*	±	19.00	-2.13	±	20.30
Gene effects in different models												
Three parameters model (Cavalli, 1952)												
m	92.01**	±	1.82	103.26**	±	1.71	71.12**	±	1.78	89.18**	±	2.48
(d)	-9.81**	±	1.86	-7.75**	±	1.73	4.77**	±	1.79	-7.74**	±	2.47
(h)	61.66**	±	3.03	33.59**	±	3.48	98.80**	±	4.00	55.19**	±	4.69
χ^2 (3 d.f.)	30.30**			10.27**			12.58**			46.64**		
Six parameter model (Hayman, 1958)												
m	113.28**	±	3.31	110.30**	±	3.60	126.01**	±	4.21	124.36**	±	4.45
(d)	-28.36**	±	6.24	-1.23	±	7.21	-6.53	±	7.33	1.76	±	6.30
(h)	144.66**	±	18.46	75.23**	±	20.72	101.90**	±	22.78	-36.93	±	22.35
(i)	83.20**	±	18.21	38.86	±	20.39	8.86	±	22.36	-98.33**	±	21.81
(j)	-20.30**	±	6.54	6.86	±	7.43	-11.56	±	7.56	11.83	±	6.85
(l)	-130.46**	±	28.91	-28.20	±	33.08	-56.40	±	34.97	-198.80**	±	32.36
Weighted least square method (Cavalli, 1952)												
m	8.33	±	18.31	65.63**	±	20.47	60.96**	±	22.44	192.53**	±	21.97
(d)	-8.06**	±	1.95	-8.10**	±	1.78	5.03**	±	1.85	-10.06**	±	2.68
(h)	275.13**	±	46.32	103.43*	±	58.38	158.30**	±	55.89	-235.73**	±	52.71
(i)	83.20**	±	18.21	38.86	±	20.39	8.86	±	22.36	-98.33**	±	21.81
(j)	-40.60**	±	13.08	13.73	±	14.86	-23.13	±	15.13	23.66	±	13.70
(l)	-130.46**	±	28.91	-28.20	±	33.08	-56.40	±	34.97	-198.80**	±	32.36
Type of epistatis	D			D			D			D		

*, ** Significant at 5 % and 1 % levels, respectively

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