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Inheritance studies for earliness, yield and fibre traits using simplified triple test cross in *G. hirsutum*

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Abstract

The simplified triple test cross analysis provides a precise test for epistasis along with unambiguous estimates of additive and dominance genetic variance. Different generations of simplified triple test cross analysis grown in a randomized complete block design with three replications were evaluated for major quantitative characters of earliness, yield and fibre quality. The analysis of variance for epistasis revealed the presence of epistasis for most of the characters studied. The analysis of variance for sums indicated the presence of additive genetic component in the inheritance of most of the characters except for number of monopods and sympods per plant, plant height, bolls at first sympod, bolls at sympod at 50 per cent plant height, boll weight, fibre strength and fibre quality index. Whereas the analysis of variance for differences indicated the involvement of dominance component in the inheritance of length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn, 2.5% span length, fibre fineness and fibre maturity. Both additive and dominance components of genetic variation were observed to be involved in the inheritance of length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn and 2.5% span length. Out of these, length of first sympod, days to maturity, number of bolls per plant, ginning outturn and 2.5% span length showed higher magnitude of dominance genetic component indicating degree of dominance to be in the range of over dominance. The appropriate breeding methods for the improvement of different characters have been discussed.

Key words: Simplified triple test cross, epistasis, additive genetic component, dominance genetic component, *G. hirsutum*

Introduction

Cotton is the most important commercial fibre crop playing key role in economic, political and social development of the world. In India, cotton was cultivated on 9.3 million hectares with the production and productivity of 290 lakh bales and 526 kg lint per hectare, respectively during 2008-09 [1]. In northern India, cotton is mainly grown under cotton-wheat cropping system so the success of any variety of cotton depends mainly upon three complex characters viz, maturity period, yield and fibre quality. The main breeding effort is being directed to develop early maturing and high yielding types having long, fine and strong fibres with better spinability. Plant frame and relative number and position of vegetative and fruiting branches govern the duration and time of maturity in cotton. Such an earliness complex related to crop maturity can be evaluated for genetic variation for number of monopods and sympods, their position in relation to total height of the plant, length of sympods, their fruiting pattern and days to final maturity of the crop. The yield of seed cotton is strongly influenced by number and size of bolls, seed index and lint index through which ginning outturn ultimately determines the yield of lint. Similarly, the quality of fibre depends upon its length, fineness, strength and maturity.

Genetic improvement in the crop plants depends upon the knowledge of the genetics of the particular character and its component characters based on which the breeding strategies are followed. The simplified triple test cross analysis [2] provides not only a precise test for epistatic variation but also gives unambiguous estimates of additive and dominance components of genetic variance together with dominance directional element ‘F’ with less requirement of (2n) crosses and seasons as compared to diallel set (n^2) crosses and

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generation mean analysis (F_2 and backcrosses) etc. The present investigation was, therefore, undertaken to study the nature and magnitude of genetic variation for earliness, yield and fibre quality traits using simplified triple test cross analysis [2].

Materials and methods

The present investigation was carried out in the cotton experimental area of Department of Plant Breeding and Genetics located at Punjab Agricultural University, Ludhiana. The experimental material consisted of crossing of seventeen genetically diverse genotypes viz. CNH 1012, CNH 123, RS 992, RS 2013, RS 2059, RS 2060, LH 1990, LH 1991, LH 1992, LH 1993, Senegal, LRA 5166, LRK 516, RS 875, G Cot 16, LH 1972 and LH 1980 with two testers. The testers namely LH 900 (L_1) and LH 1832 (L_2) with divergent maturity, boll weight and fibre quality traits were crossed with each of the seventeen lines and resulting 34 F_2's were grown during *kharif* 2001 with two rows each of the parental lines and four rows of F_2 populations in a randomized complete block design with three replications. Recommended cultural practices were followed to raise a good crop. The data was recorded for characters related to earliness, seed cotton yield and fibre quality. The information on genetic control of the traits under investigation was obtained using simplified triple test cross analysis of Jinks *et al.* [2] which is specifically applicable to inbred lines consisting of crossing each 'n' inbred line to two inbred testers L_1 and L_2 to yield 2n progenies. The analysis was conducted by taking F_2's of L_{1i} and L_{2i} of 2n = 17 lines and two testers i.e. LH 900 (L_1) and LH 1832 (L_2). The comparison ($L_{1i}+L_{2i}-P_i$) was used for detecting the presence of epistasis. The additive and dominance components were estimated from the analysis of sums ($L_{1i}+L_{2i}$) and differences ($L_{1i}-L_{2i}$). The expectations of components of variance for sums and variance for differences were modified for application to F_2 generation of L_{1i} and L_{2i} families. The expectation of variance for sums remains same but that of variance for differences estimates 1/16H as compared to 1/4H given by Jinks *et al.* [2]. Therefore, the expectations are as follows:

Variance for sums = 1/4D (additive effects of genes)

Variance for differences =1/16H (dominance effects of genes)

The degree of dominance was estimated by using the formula as $(H/D)^{1/2}$.

Results and discussion

The test of epistasis ($L_{1i}+L_{2i}-P_i$) of simplified triple test cross analysis indicated the involvement of non-allelic interactions in the inheritance of all studied characters of maturity, yield and fibre quality (Tables 1 and 2) except for number of monopods, number of sympods, plant height, bolls at first sympod, number of bolls on sympod at 50 per cent plant height, boll weight, fibre strength and fibre quality index. Overall, the tests for epistasis revealed the presence of allelic and non-allelic interactions for characters of maturity, yield and fibre quality. Epistasis for seed cotton yield and yield contributing characters [3, 4] and various fibre quality characters [5] has also been reported by many workers.

The tests and estimates of components of genetic variation are expected to be unbiased only if epistasis is absent. But in the present study irrespective of presence or absence of epistasis, additive genetic component, D and dominance genetic component, H, were estimated in order to have an over all idea of the magnitude of additive and dominance components and their relative contribution towards genetic variation in the population. Significant mean squares for sums were observed for node number of first monopod, node number of first sympod, length of first sympod, length of sympod at 50 per cent plant height, days to maturity, seed cotton yield per plant, number of bolls per plant, seed index, lint yield, ginning outturn, lint index, 2.5% span length and fibre uniformity ratio which showed that additive gene action was present for these characters (Tables 1 and 2). Significant mean squares for differences was observed for length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn, 2.5% span length, fibre fineness and fibre maturity indicating the involvement of dominance gene action in the inheritance of these characters (Tables 1 and 2). Both additive and dominance components of genetic variation were observed to be involved in the inheritance of length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn and 2.5% span length. The involvement of both additive and dominance components of variation in the inheritance of most of the plant and fibre characters has also been reported in earlier studies [6]. Out of these, length of first sympod, days to maturity, number of bolls per plant, ginning outturn and 2.5% span length showed higher magnitude of dominance genetic component, thereby indicating degree of dominance to be in the range of over dominance (Table 3). However, the value of degree

Table 1. Analysis of variance for epistasis, sums and differences for earliness complex in cotton

Source	df	No. of monopods	No. of sympods	Node no. of first monopod	Node no. of first sympod	Plant height (cm)	Length of first sympod (cm)	Bolls at first sympod	Length of sympod at 50% plant height (cm)	Bolls at sympod at 50% plant height	Days to maturity
Analysis of variance for epistasis											
Epistasis	16	0.5928	11.8692	1.5797*	1.1018*	42.8048	15.3460**	0.1525	12.9763*	0.8613	39.8167**
Error	32	0.6100	11.1246	0.6130	0.4839	26.5855	3.3086	0.2388	6.1843	0.5913	0.1378
Analysis of variance for sums											
Sums	16	0.4649	12.9003	2.3405**	1.3812*	73.8001	15.5249*	0.3067	22.7980*	1.3242	42.9609**
Error	32	0.8831	10.7685	0.5919	0.5735	53.8619	5.9734	0.2511	9.9276	1.0610	0.2079
Analysis of variance for differences											
Differences	16	0.6812	5.5331	1.5229	1.2588	57.1763	20.8428*	0.2516	25.1743	1.2096	47.5153**
Error	32	0.6178	8.4278	1.3614	0.6563	43.8943	8.5860	0.1683	15.3420	1.4196	0.2956

*,** significance at 5% and 1% level of significance respectively

Table 2. Analysis of variance seed cotton yield/plant for epistasis, sums and differences for yield and fibre quality traits in cotton

Source	df	Seed cotton yield/ plant (g)	Number of bolls per plant	Boll weight (g)	Seed index (g)	Lint yiled/ plant	Ginning outturn (%)	Lint index (g)	2.5% span length (mm)	Fibre fineness (Mic)	Fibre strength (g/tex)	Fibre uniformity ratio	Fibre maturity	Fibre quality index
Analysis of variance for epistasis														
Epistasis	16	25.895**	13.715*	0.245	0.297*	3.912**	1.472**	0.0728**	1.261**	0.1186*	1.3328	13.085**	0.00010*	610.201
Error	32	5.738	5.845	0.429	0.138	0.801	0.101	0.0193	0.029	0.0532	1.4180	4.863	0.00004	600.646
Analysis of variance for sums														
Sums	16	62.364**	27.097*	0.291	0.558**	8.812**	4.282**	0.1554**	1.635**	0.0675	1.4354	9.939*	0.00005	774.375
Error	32	9.273	10.322	0.595	0.167	1.311	0.169	0.0293	0.042	0.0585	1.3997	4.037	0.00006	579.151
Analysis of variance for differences														
Differences	16	16.816*	22.186*	0.441	0.126	2.784**	1.823**	0.0396	1.786**	0.0868*	1.6614	8.407	0.00007*	539.006
Error	32	4.972	6.300	0.377	0.127	0.611	0.308	0.0236	0.039	0.0399	1.4151	5.980	0.00003	350.938

*,** significance at 5% and 1% level of significance respectively

of dominance for seed cotton yield and lint yield were close to unity indicating an equal importance of additive and dominance type of gene action in the inheritance of these two characters. The presence of significant additive genetic variation for node number of first monopod and sympod suggested that the position of these branches on the main stem can be reduced which would result in early maturing genotypes even without reducing plant height.

The analysis of the most important components of yield showed the presence of epistasis, additive and dominance genetic variance in the inheritance of number of bolls per plant only but all these three components of genetic variation were found to be absent for number of bolls at first sympod, number of bolls at sympod at 50 per cent plant height and boll weight. But the boll weight was reported to be under the control of both additive and non additive gene effects [7], while some workers [8, 9] revealed the involvement of dominance component only in the inheritance of this trait. As the dominance component was more than that of additive component, so the number of bolls per plant was observed to be influenced by over dominance (Table 3). The manipulation of number of bolls per plant would thus be the main source to improve yield potential of such type of set of lines. The inheritance of this trait was reported to be controlled by dominance component [9, 10], and both by additive and dominance components [6, 7] of variation. Both seed cotton yield and lint yield were observed to be influenced by epistasis, additive and dominance components of variation, and both the additive and dominance genetic components played an equal role in the inheritance of these characters as the value of degree of dominance is very close to unity which are in corroborative with the earlier results [3, 11], but contradicts the findings [12] where it has been reported

Table 3. Estimates of additive, dominance and degree of dominance for different characters in upland cotton

S.No.	Character	D	H	$(H/D)^{1/2}$
1	Number of monopods	1.6728	0.5078	-
2	Number of sympods	4.2636	23.1573	-
3	Node number of first monopod	3.4971**	1.2920	-
4	Node number of first sympod	1.6154*	4.8193	-
5	Plant height (cm)	39.8765	106.2558	-
6	Length of first sympod (cm)	19.1030*	98.0543*	2.2656
7	Bolls at first sympod	0.2224	0.6666	-
8	Length of sympod at 50% plant height (cm)	25.7408*	78.6588	-
9	Bolls on sympod at 50% plant height	0.5264	1.6797	-
10	Days to maturity	85.5059**	377.7574**	2.1018
11	Seed cotton yield per plant (g)	106.1818**	94.7535*	0.9446
12	Number of bolls per plant	33.5514*	127.0887*	1.9462
13	Boll weight (g)	0.6085	0.5153	-
14	Seed index (g)	0.7831**	0.0076	-
15	Lint yield per plant (g)	15.0025**	17.3904**	1.0766
16	Ginning outturn (%)	8.2244**	12.1204**	1.2139
17	Lint index (g)	0.2523**	0.1277	-
18	2.5% span length (mm)	3.1853**	13.9765**	2.0947
19	Fibre fineness (Mic value)	0.0181	3.7551*	-
20	Fibre strength (g/tex)	0.0714	1.9703	-
21	Fibre uniformity ratio	11.8036*	19.4118	-
22	Fibre maturity	0.00001	0.00034*	-
23	Fibre quality index	390.4480	1504.5472	-

D and H are additive and dominance gene effects, respectively.
*,** significance at 5% and 1% level of significance, respectively

the role of over dominance in the inheritance of seed cotton yield and lint yield. The epistasis, additive and dominance effects were non significant for number of monopods and sympods per plant, plant height, number of bolls at first sympod, number of bolls at sympod at 50 per cent plant height and boll weight indicating that there are no differences among genotypes for these characters. Alternately, the testers may not be widely divergent for these characters except for boll weight.

Among the fibre quality traits, only 2.5% span length showed significant epistatic component and, highly significant additive and dominance genetic variation which is in accordance with other similar reports [5, 6, and 13]. The predominance of dominance genetic component over additive genetic component as observed from greater value of degree of dominance indicated over dominance. But the fibre strength and fibre quality index did not record significance for epistasis, additive and dominance effects indicated that there are no differences among genotypes for these characters. The parental lines were known to be variable for plant height, fibre strength and fibre quality index but lack of all components of genetic variation indicated inadequacy of the testers, which in fact were quite similar for height. In such a case, epistasis and dominance components of gene action are expected to be detected only for those loci for which testers are different.

It has been concluded that only additive and epistatic gene action was involved in the inheritance of node number of first monopod, node number of first sympod, length of sympod at 50 per cent plant height, seed index and lint index which suggested that specific breeding strategy like simple recurrent selection has to be adopted to get improvement in different characters of economic importance. For length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn and 2.5% span length both additive and dominance components were found significant with greater magnitude of dominance gene effects for their respective component traits, thereby indicating that superior recombinants with early maturity, high yield performance and better fibre length can be identified and isolated by further recurrent selection. But for characters like node number of first monopod and seed index with highly significant additive gene effects, the pure lines can be developed.

References

1. **Anonymous.** 2009. All India Coordinated Cotton Improvement Project Annual Report (2008-09). Central Institute of Cotton Research, Regional Station, Coimbatore, pp. 3-4.
2. **Jinks J. L., Perkins J. M. and Breese E. L.** 1969. A general method of detecting additive, dominance and epistatic variation for metrical traits II. Application to inbred lines. Heredity, **24**: 45-57.
3. **Bhatti M. A., Azhar F. A., Alvi A. W. and Ayub M.** 2006. Triple test cross analysis of seed cotton (*Gossypium hirsutum* L.) yield and its components grown in salinized conditions. Int. J. Agri. Biol., **8**: 820-823.
4. **Singh Paramjit, Chahal G. S., Mittal V. P. and Brar K. S.** 2008. Genetic analysis of yield components and fibre quality characters in upland cotton (*Gossypium hirsutum* L.). Indian J. Genet., **68**: 33-37.
5. **Phogat D. S. and Singh D. P.** 2000. Genetic analysis of gossypol and fibre characters in American cotton (*G. hirsutum* L.). J. Cotton Res. Dev., **14**: 23-36.
6. **Singh Paramjit, Chahal G. S. and Sohu R. S.** 2005. Estimation of components of variation in upland cotton (*Gossypium hirsutum* L.) using single tester analysis. Crop Improv*.,* **32:** 147-152.
7. **Ahmed M. A. and Mehra R. B.** 2000. Genetic characterization of a *Gossypium hirsutum* cross 45-3-6 x Pusa 19-27. Indian J. Genet., **60**: 503-510.
8. **Tang B., Jenkins J. N., Watson C. E., McCarty J. C. and Creech R. G.** 1996. Evaluation of genetic variances, heritabilities and correlations for yield and fibre traits among cotton F_2 hybrid populations. Euphytica, **91**: 315-322.
9. **Ahuja S. L., Tuteja O. P. and Singh A. K.** 1999. Genetic nature of some quantitative characters in upland cotton (*Gossypium hirsutum* L.). J. Cotton Res. Dev., **13**: 157-159.
10. **Tyagi A. P.** 1988. Genetic architecture of yield and its components in upland cotton (*G. hirsutum* L.). Indian J. Agric. Res., **22**: 75-80.
11. **Singh Paramjit and Chahal G. S.** 2004. Simultaneous improvement of yield and fibre quality in upland cotton (*G. hirsutum* L.). Indian J. Agric. Sci., **74**: 643-648.
12. **Chandio M. A., Kalwar M. S. and Baloch G. M.** 2003. Gene action for some quantitative characters in upland cotton (*Gossypium hirsutum* L.). Pak. J. Sci. Ind. Res., **46**: 295-299.
13. **Patel U. G., Patel J. C., Patel P. G., Vodadaria K. V. and Sutaria C. M.** 1997. Combining ability analysis for seed cotton yield and mean fibre length in upland cotton (*G. hirsutum* L.). Indian J. Genet., **57**: 315-318.