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GENETIC ANALYSIS OF PINK BOLLWORM RESISTANCE AND OTHER QUANTIATIVE CHARACTERS IN COTTON

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ABSTRACT

Generation mean analysis was done by using six parameter model in an interspecific cross between a pink bollworm resistant local variety of *Gossypium hirsutum* and the highly susceptible variety P.S.H.-1 of *G. barbadense* by using P_1, P_2, F_1, F_2, BC_1 and BC_2. Mean values of F_1 were intermediate between two parents for pink bollworm damage, locules/boll, seeds/boll and fibre length while for seed-cotton yield/plant, bolls/plant and lint index they exceeded the better parent. The F_2 means were significantly lower than F_1 for pink bollworm damage, seed-cotton yield/plant, bolls/plant, and fibre length. Backcross means were intermediate between F_1 and their respective recurrent parent. Scale tests and joint scaling test revealed presence of epistatic interactions for all the characters except for locules/boll. Additive gene effects predominated in the inheritance of most characters followed by dominance gene effects. Additive, dominance and additive x additive gene effects were involved in the inheritance of pink bollworm resistance. For seed-cotton yield/plant, bolls/plant and fibre length epistasis was of complementary type. Duplicate epistasis for pink bollworm damage is suggested to be desirable. Reciprocal recurrent selection method of breeding is suggested for further improvement in resistance and other agronomic characters.

Key words: *Pectinophora gossypiella*, generation mean analysis, epistasis, host plant resistance.

Among several insect pests pink bollworm (*Pectinophora gossypiella* Saund.) is a very serious pest of cotton which causes losses to the tune of 55% (around 6525 tonnes of seed-cotton per year). Information on genetics of pink bollworm resistance in cotton is very limited [1, 2]. An attempt has been made to study gene effects governing pink bollworm resistance and other quantitative characters in cotton.

MATERIALS AND METHODS

Twentyeight diverse tetraploid cotton varieties belonging to *Gossypium hirsutum* and *G. barbadense* were screened for genetic resistance to pink bollworm. At least six varieties recorded significantly low seed-cotton damage due to pink bollworm. Among these a local variety of *G. hirsutum* with high resistance to pink bollworm, high yield, and better agronomic characters was used as female parent. The other parent in the cross was a highly susceptible *G. barbadense* variety, P.S.H.-1. Hybridizations were carried out and sufficient quantity of F_1, F_2, BC_1 (F_1 x P_1) and BC_2 (F_1 x P_2) seed was obtained.

The experiment was laid out in randomized block design with four replications. The parents, F_1, BC_1 and BC_2 generations were represented by two rows/replication whereas F_2 by five rows/replication. Each row had 12 plants with 75 and 45 cm distance between and within rows, respectively. The border rows and border plants of each row were of the susceptible var. P.S.H.-1 so as to ensure uniform inoculum of pink bollworm. The data were recorded on pink bollworm damage and other quantitative characters, and analysed by the standard procedures. Epistatic gene interactions were detected by scale tests of Hayman and Mather [3] and joint scaling test of Rowe and Alexander [4]. Gene effects were estimated as per the Hayman's six-parameter model [5].

RESULTS AND DISCUSSION

GENERATION MEANS

ANOVA of generation means for different characters (Table 1) indicated highly significant differences among generation means. Mean pink bollworm damage in F_1 was intermediate between the parents. Similar results were also reported earlier [1, 2], although

Table 1. Generation means for pink bollworm damage and other agronomic characters in cotton

Character	Local Variety-2	P.S.H.-1	F_1	F_2	BC_1	BC_2	CD (%)
Locule damage (%)	40.91	72.57	60.33	47.39	47.46	61.63	6.57
Seed-cotton damage (%)	19.57	39.75	30.06	25.48	24.11	33.55	3.58
Seed-cotton yield/plant (g)	22.80	9.61	40.94	20.15	23.45	15.43	12.55
Bolls/plant	19.97	12.06	36.85	18.16	22.80	16.12	8.67
Boll weight (g)	1.91	1.66	2.01	1.90	1.77	1.72	0.22
Locules/boll	4.12	3.16	3.65	3.68	3.85	3.35	0.11
Seeds/boll	18.85	12.87	15.06	15.74	14.54	12.93	1.68
Plant height (cm)	99.83	69.59	104.55	86.01	91.18	81.83	17.67
Seed index (g)	6.48	8.24	8.00	7.28	6.84	7.61	0.71
Lint index (mg/seed)	4.39	4.26	6.09	5.72	5.28	6.05	14.03
Ginning percentage	39.08	32.52	39.77	41.10	41.83	38.24	2.60
Fibre length (mm)	18.64	27.33	25.83	22.53	20.96	24.47	1.29

with higher mean values in F_2 than in F_1. The significantly low F_2 means obtained in the present study indicate the possibility of improvement for bollworm resistance in advanced generations.

Seed-cotton yield/plant, bolls/plant and lint index recorded significantly higher values of F_1 than the better parent (BP) indicating significant BP heterosis. In general, backcross means were intermediate between F_1 and their respective recurrent parents. The F_2 means were significantly lower than F_1 for seed- cotton yield/plant, bolls/plant, plant height, seed index, and fibre length. In case of lint index, in spite of closer mean values of the parents, F_1 showed significantly high mean value, which indicates genic dispersion in parents for this character. Gill and Kalsy [6] have reported similar observations for seed- cotton yield, boll number, and ginning outturn in some of the intervarietal crosses of *G. hirsutum*. In such cases, they have predicted chances of obtaining transgressive segregates for these characters.

DETECTION OF EPISTASIS

The estimates of scale tests and joint scaling test (Table 2) indicated presence of epistasis for all the characters except locules/boll. Scale tests are generally indicative of presence of epistasis in the inheritance of a character. However, in many cases, although epistasis is

Table 2. Estimates of scale tests and joint scaling test for different characters in cotton

Character	Estimates of scale tests				Estimates of joint scaling test			
	A	B	C	D	m	d	h	χ^2
Locule damage	-9.64	-6.92^{**}	-44.58^{**}	-14.01^{**}	55.3^{**}	-15.26^{**}	0.27	38.3^{**}
Seed-cotton damage	-2.71	-1.71	-17.82^{**}	-6.70^{*}	28.8^{**}	-9.44^{**}	-0.18	9.9^{**}
Seed-cotton yield/plant	-6.40	-19.26^{**}	-14.70	5.48	15.4^{**}	6.62^{**}	13.41^{**}	29.0^{**}
Bolls/plant	-11.22^{**}	-16.67^{**}	-33.09^{**}	-2.60	15.3^{**}	4.30^{**}	10.70^{**}	26.2^{**}
Boll weight	-0.38^{**}	-0.23^{*}	0.01	0.31^{**}	1.8^{**}	0.11^{**}	0.20^{**}	15.5^{**}
Locules/boll	-0.07	-0.11	0.14	0.16^{*}	3.6^{**}	0.48^{**}	0.01	4.2
Seeds/boll	-4.83^{**}	-2.06^{*}	1.12	4.01^{**}	15.5^{**}	2.67^{**}	-1.10^{*}	24.9^{**}
Plant height	-22.02^{**}	-10.48	-34.48^{**}	-0.49	80.9^{**}	12.97^{**}	18.13^{**}	16.5^{**}
Seed index	-1.02^{*}	-0.80^{*}	-1.60^{*}	-0.11	7.2^{**}	0.83^{**}	0.55^{**}	11.4^{**}
Lint index	-0.72	17.53^{**}	20.57^{*}	1.16	44.0^{**}	0.14	18.69^{**}	11.4^{**}
Ginning percentage	4.81^{**}	4.19^{*}	13.26^{**}	2.13	36.5^{**}	3.33^{**}	4.63^{**}	25.7^{**}
Fibre length	-4.22^{**}	-2.55^{**}	-7.51^{**}	-0.37	22.6^{**}	-4.27^{**}	1.75^{**}	57.9^{**}

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

detected by scaling test, either none or only one or two of the inheritance components are significant. According to Gill and Kalsy [6], this is due to sampling error. Joint scaling test also confirmed presence of epistasis for all the characters (significant χ^2), except for locules/boll. Only additive gene effects were important for locules/boll.

GENE EFFECTS

Estimates of gene effects for different characters (Table 3) gave significant additive gene effects for all the characters except boll weight. Pink bollworm damage, seed-cotton yield/plant, bolls/plant, seeds/boll, and fibre length also recorded significant dominance effects. Among epistatic gene interactions, additive x additive (i) component was significant for pink bollworm damage, boll weight, and seeds/boll, whereas dominance x dominance (l) interaction was important for seed-cotton yield/plant, bolls/plant, boll weight, seeds/boll, and fibre length. Complementary interaction (j) was significant for seeds/boll and lint index. In general, the magnitudes of epistatic gene effects were in the order of l > i > j.

Table 3. Estimates of gene effects following six-parameter model for eleven characters in cotton

Character	m	d	h	i	j	l	Type of epistasis
Locules damage	47.39**	– 14.47**	31.61**	28.02**	1.36	– 11.46	Duplicate
Seed-cotton damage	25.48**	– 9.44**	13.65*	13.40*	0.50	– 8.98	Duplicate
Seed-cotton yield/plant	20.15**	8.02**	21.89*	– 2.84	1.42	39.37**	Complementary
Bolls/plant	18.16**	6.68**	26.04**	5.20	2.72	22.69*	Complementary
Boll weight	1.90*	0.05*	– 0.39	– 0.62**	– 0.07	1.23**	Duplicate
Seeds/boll	15.74**	1.61*	– 8.82**	– 8.02**	– 1.38*	14.92**	Duplicate
Plant height	86.01**	9.35*	21.82	1.98	– 5.77	30.52	Complementary
Seed index	7.28**	– 0.77*	0.42	– 0.22	0.11	2.04	Duplicate
Lint index	5.72**	– 0.78*	1.53	– 0.23	– 0.84*	– 1.59	Complementary
Ginning percentage	41.10**	3.59**	– 0.29	– 4.26	0.31	– 4.74	Complementary
Fibre length	22.53**	– 3.51**	3.58*	0.74	0.83	6.03**	Complementary

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

Singh et al. [1] mainly reported additive gene effects with some dominance and complementary interaction for pink bollworm damage. Wilson and George [2] reported only additive and additive x additive gene effects to be significant. These reports corroborate with the present studies except that, in addition, dominance gene effects are also found to be important. Epistasis for seed-cotton yield/plant, bolls/plant, and fibre length was of complementary type. However, seeds/boll recorded duplicate type of epistasis which causes hindrance in the progress of procedure through which additive component is amenable [7]. Duplicate epistasis observed for pink bollworm damage could be helpful in resistance breeding.

A perusal of gene effects for different characters indicates that both main gene effects (i.e. additive and dominance) and epistatic gene effects are important for most of the characters. Under such conditions improvement in these characters might be expected through standard selection procedures which may first exploit the additive component. Simultaneously, care should be taken that dominance variances are not dissipated; rather they should be concentrated. Under such circumstances, the reciprocal recurrent selection seems to be the best available method.

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