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GENETIC ARCHITECTURE OF *GOSSYPIUM ARBOREUM*

B. S. SANDHU, M. S. GILL AND V. P. MITTAL

Department of Plant Breeding, Punjab Agricultural University, Ludhiana 141004

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ABSTRACT

A set of nine generations, viz. P_1, P_2, F_1, F_2, BC_1, BC_2, $F_2 \times P_1$, $F_2 \times P_2$, and $F_2 \times F_1$, derived from the cross G27 x H436 of *G. arboreum* L. was used to estimate the type of gene effects for seed-cotton yield, fibre and other traits. The analysis of components of means indicated prevalence of dominance gene effects for seed-cotton yield, boll number per plant, and plant height. Both additive and dominance gene effects were significant for boll weight, ginning outturn, seed index and halo length, whereas for lint index, additive component was significant. For ginning outturn and seed index, the balancing of gene effects led to predominance of additive gene effects. In addition, one or more of the digenic interaction components were involved in the inheritance of all these characters except seed-cotton yield. Interactions were mostly of duplicate type.

Key words: Genetic architecture, generation means analysis, *Gossypium arboreum*, gene action.

The efficiency of selection for the improvement of quantitative traits depends upon the nature and magnitude of gene effects involved in the inheritance of a particular character. In *Gossypium arboreum*, the importance of additive as well as nonadditive gene effects has been reported [1–5] for yield and fibre traits. The relative magnitude and importance of additive and nonadditive gene effects varied with the materials involved. The present study aims to estimate gene effects for yield, fibre and other traits using a set of nine generations derived from the cross G 27 x H 436.

MATERIALS AND METHODS

Nine generations, viz. P_1, P_2, F_1, F_2, BC_1, BC_2, $F_2 \times P_1$, $F_2 \times P_2$, $F_2 \times F_1$, derived from the cross G 27 x H 436, were sown in a single plant randomization fashion at the Punjab Agricultural University Farm, Ludhiana at row-to-row and plant-to-plant spacing 60 and 30 cm, respectively. Observations on seed-cotton yield (g), bolls/plant, boll weight (g), ginning percentage, seed index, lint index, halo length (mm), and plant height (cm) were recorded on 20 plants each in P_1, P_2 and F_1, on 115 plants in F_2 and on 75 plants each in the remaining five generations.

The generation means were analysed following the weighted least squares method [6] based on F_∞ metric [7]. The three-parameter model was fitted for m (a constant), (d) (pooled additive effects) and (h) (pooled dominance effects), and tested for goodness of fit. Where this model was inadequate to explain the variation among the generation means different models were fitted by including digenic nonallelic interaction components, viz. (i)—pooled additive x additive effects, (j)—pooled additive x dominance effects, and (l)—pooled dominance x dominance effects, in all possible combinations and the model which showed minimum value of χ^2 and maximum number of significant parameters was considered as the best fit model.

RESULTS AND DISCUSSION

The estimates of genetic components based on the best fit model are given in Table 1. The additive component (d) was significant for boll weight, ginning outturn, seed index, lint index and halo length. In these traits either dominance (h) or at least one of the nonallelic interaction effects was also significant. Several earlier reports [1–3] also suggested the importance of both additive and nonadditive gene effects for these traits. Dominance (h) component was significant for all the characters studied, except lint index. The sign of (h) was negative for seed index, halo length and plant height which indicated that decreasing alleles were dominant for these characters. For seed-cotton yield, only the dominance (h) gene effects were significant which are in agreement with earlier reports [2, 4, 5]. With regard to epistasis, one or more kinds of digenic nonallelic interaction effects were involved in the genetic control of all the characters studied, except seed-cotton yield. Additive x additive (i) type of interactions were significant for boll number per plant, boll weight, ginning outturn, halo length and plant height. This component, being positive, would increase the expression of characters in successive generations by throwing transgressive segregates. Additive x dominance (j) component was important for boll number per plant, ginning outturn and lint index, whereas dominance x dominance (l) gene effects were significant for boll weight, ginning outturn, seed index, and plant height. The negative sign of (j) for ginning outturn and lint index implied that sum of the interaction effects from dispersed pairs of genes was more than the remaining interaction effects from associated pairs of genes. For ginning outturn and seed index, the balancing of effects between (h) and (i), (j) and (l) would enhance the importance of additive gene effects relative to nonadditive effects as in these characters the sum of additive and additive x additive gene effects was more in magnitude than nonadditive gene effects. In all the cases where both (h) and (l) were significant, the signs of these effects were opposite in direction, indicating duplicate type of gene action which would hinder progress through selection.

The importance of additive as well as dominance gene effects for boll weight, ginning outturn, seed index, and halo length suggested that selection for desirable segregates will

Table 1. Components of generation means for different characters based on best-fit model in the cross G27 x H436 in cotton

Character	Parameters						d.f.	χ^2
	m	(d)	(h)	(i)	(j)	(l)		
Seed-cotton yield per plant	31.61 ± 0.81**	1.32 ± 0.80	16.18 ± 1.18**	—	—	—	6	8.58
Bolls/plant	14.77 ± 1.93**	0.82 ± 0.58	13.19 ± 2.62**	5.41 ± 1.20**	7.38 ± 1.31**	—	4	11.89*
Boll weight	1.40 ± 0.10**	0.06 ± 0.01**	1.11 ± 0.24**	0.21 ± 0.09*	0.11 ± 0.06	–0.82 ± 0.14**	3	20.19**
Ginning outturn	32.69 ± 0.82**	2.97 ± 0.18**	7.75 ± 1.95**	1.75 ± 0.80*	–3.62 ± 0.56**	–6.29 ± 1.21**	3	56.75**
Seed index	4.79 ± 0.02**	0.17 ± 0.02**	–0.95 ± 0.12**	—	—	1.01 ± 0.13**	5	11.79**
Lint index	2.53 ± 0.01**	0.24 ± 0.02**	–0.02 ± 0.02	—	–0.38 ± 0.07**	—	5	27.54**
Halo length	19.32 ± 0.27**	1.32 ± 0.12**	–1.09 ± 0.39**	1.38 ± 0.31**	—	—	5	35.47**
Plant height	177.31 ± 9.53**	1.97 ± 1.02	–72.34 ± 23.67**	24.84 ± 9.48**	12.44 ± 6.49	43.92 ± 14.63**	3	16.63**

*,**Significant at P = 0.05 and P = 0.01, respectively.

be more effective in advanced generations when dominance gene effects would have minimised. The importance of dominance component for seed-cotton yield suggested the feasibility of hybrid breeding programme. In spite of closer mean values of P_1 and P_2 for bolls/plant and plant height, considerable genetic variation was observed which probably could be an indication of genic dispersion for these characters. The χ^2 values were significant, though marginally, for most of the characters even with the best-fit model. This could be due to the presence of higher order interactions or linkages, or large sampling error.

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