GENE EFFECTS FOR MAJOR QUANTITATIVE TRAITS IN SOYBEAN [*Glycine max* (L.) Merrill]

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Abstract

Breeding methods are dictated by the gene action, interaction, and linkage relationship of genes conditioning continuous phenotypic variation of various metric traits. Thus both additive and non-additive components of genetic variance, along their allied parameters are of immense use for plant breeders under different situations. An estimate of additive variance and non-additive variance provides a measure of how likely particular traits can be selected for or against and that of whether hybridization or a population improvement programme. The present investigation was carried out at Crop Research Center, Pantnagar during the *Kharif* season of 2008-2009. Five generations *viz.* P_1, P_2, F_1, F_2, and F_3 were evaluated in an experiment under a compact family block design to estimate gene effects for major agronomic traits in three soybean single crosses (PS 1347 x *G. soja*, JS 335 x UPSM 534 and PS 1347 x JS 335). The results showed additive gene effects determined the inheritance of agronomic characters *viz.* days to 50 per cent flowering, days to maturity, plant height, and harvest index. Dominance gene action was critical in determining the yield. Duplicate epistasis was significantly important in inheritance of most traits studied. On the basis of results obtained from the present investigation, it is suggested that these major quantitative traits in the desirable genotypes play a major role in the improvement of high yielding varieties of soybean through exploitation of additive and non-additive variances.

Key words: Soybean, quantitative traits, gene effects, additive, non-additive.

Introduction

The objectives of the present investigation were to study the nature and magnitude of gene effects governing the yield and its components. Most of the earlier studies conducted on nature and magnitude of genetic variation in soybean are based on diallel, partial diallel set, and gca/sca analysis with the assumption that the epistasis is negligible or absent. The results of the studies indicated that epistasis plays a significant role in the inheritance of yield and its component characters in soybean. Thus, the assumption of absence of epistasis may not hold

true suggests some breeding methods may not be appropriate for the genetic improvement of these characters. Hence, in the present investigation, an effort has been made to find out the inheritance of yield and its attributes for their further utilization in the breeding program.

Materials and methods

Five generations, namely P_1, P_2, F_1, F_2, and F_3 of each of three crosses *viz.,* JS 335 x UPSM 534, PS 1347 x *G. soja*, and PS 1347 x JS 335 were evaluated in a compact family block design with three replications during the *Kharif* season of 2008-09. Each plot had three rows of 3 m length, spaced at 60 cm apart, with a plant to plant distance maintained at 5 to 7 cm by appropriate thinning of plants. The standard agronomic practices were followed to raise a healthy soybean crop. Ten competitive plants from generations namely, P_1, P_2, and F_1, 30 in F_2, and 50 in F_3 were randomly selected from each replication in each plot to record observations on major quantitative characters *viz.,* plant height, days to 50 per cent flowering, days to maturity, number of pods per plant, seed yield per plant, dry matter weight per plant, harvest index, and oil and protein content. Data were subjected to individual scaling tests *viz.,* C and D to detect the presence of epitasis following **Mather (1949).** The gene effects were estimated by the five parameter model as proposed by **Haymen (1958).**

Results and discussion

Importance of epistatic variation in the inheritance of various quantitative traits was observed from significant estimates of gene effects for different crosses. Presence of significant and highly significant estimates of either one or two scaling tests were found for all traits studied except oil and protein per cent in interspecific cross (PS 1347 x *G. soja*), C scale for days to 50 per cent flowering and D scale for most of the traits was found significant in PS 1347 x JS 335. In the case of JS 335 x UPSM 534, D scale was found significant for number of traits *viz.,* plant height, days to 50 per cent flowering, days to full maturity, seed yield per plant, and harvest index. These results (Table 1) indicated the presence of epistatic variation in the inheritance of various quantitative traits studied. **Maloo and Nayer (2005)** also found significant at least one or two scales for days to 50 per cent flowering, days to full maturity, yield per plant, harvest index, number of pods per plant, and plant height.

The estimates of mean (m) were highly significant for all the traits studied in all crosses. Highly significant value of 'm' from generation mean analysis in all the crosses showed that the five generations differed from each other significantly. Additive (d) component was predominant in the inheritance of all the traits in the interspecific cross PS

1347 x *G. soja:* whereas, in the case of intervarietal crosses, PS 1347 x JS 335 and JS 335 x UPSM 534), it was predominant for some characters *viz.,* plant height, days to 50 per cent flowering, days to full maturity, number of pods per plant, dry matter weight per plant, and oil content, revealed that selection in early segregating generations would be effective for obtaining genetic gain of these characters.

The dominance gene effect (h) was significant and greater in magnitude than the additive effect (d) for days to 50 per cent flowering and harvest index, in PS 1347 x JS 335 and days to 50 per cent flowering, harvest index and seed yield per plant in JS 335 x UPSM 534, indicating a predominant role of dominance gene action in controlling these traits in soybean.

Among the digenic interactions effects, additive x additive was significant for all the traits in PS 1347 x *G. soja*, and days to maturity, number of pods per plant in PS 1347 x JS 335, and number of pods per plant, dry matter weight per plant, harvest index, and oil per cent in JS 335 x UPSM 534. Standard hybridization and selection for these traits in early segregating generations may be suggested.

Dominance x dominance type of interaction also showed greater effects in the present study. It was found significant for plant height, in JS 335 x UPSM 534, days to 50 per cent flowering along with oil per cent in PS 1347 x JS 335, and days to 50 per cent flowering in PS 1347 x *G. soja*.

Complementary epistasis was observed for number of pods per plant, dry matter weight per plant, harvest index, and oil per cent in JS 335, x UPSM 534 and plant height and oil per cent in PS 1347 x JS 335 and days to full maturity, dry matter weight per plant and protein content in cross PS 1347 x *G. soja*, which appeared to be desirable and would be helpful in further improvement of these traits. Opposite and significant signs of 'h' and 'l' components indicated the importance of duplicate epitasis in almost all the crosses for various quantitative characters. Hence there is a hindrance in selection as well as complex nature of inheritance for improvement of these traits. In this situation reciprocal recurrent selection is likely to be useful for effective utilization of both types of additive and nonadditive gene effects simultaneously.

Considering overall results, it is apparent that most of the characters in either of the crosses were found to be under the control of additive and non-additive gene effects coupled with duplicate type of epitasis. This indicated that heterosis breeding and recurrent selection would be more fruitful for the improvement of most of the characters. The duplicate epitasis for most characters showed their complex nature of inheritance. Therefore, breeding

strategies should be designed accordingly to get desired results. Use of recurrent selection has been suggested to improve the characters when both additive and non-additive gene effects are involved in expression of the traits.

Acknowledgements

References

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Table 1 : Scaling tests and gene effects for different quantitative traits in soybean crosses

Sl. No.	Characters	Scales		Genetic components					Non allelic
		C	D	m	d	h	i	l	interaction
				PS-1347 x *G. soja*					
1.	**Days to 50 % Flowering**	-19.16*	-14.74**	45.23**	-11.65**	-3.88**	-16.66**	5.9*	Duplicate
2.	**Days to full maturity**	-6.58*	-8.37**	121.04**	4.25**	0.23	-4.01*	2.38	Complementary
3.	**Plant height (cm)**	79.40*	20.03	187.76**	-92.08**	20.07	-184.29**	-79.15	Duplicate
4.	**Number of Pods/plant**	76.21*	55.06**	179.94**	-58.11**	22.8	-140.24**	-28.19	Duplicate
5.	**Dry matter weight/plant (g)**	-8.52*	-5.47**	8.64**	7.34**	-3.4*	16.92**	4.05	Duplicate
6.	**Harvest index (%)**	-5.87	-11.26**	26.23**	8.66**	-5.34**	23.85**	-7.19	Complementary
7.	**Seed yield/plant (g)**	-0.177*	-0.007	0.32**	0.12**	-2.89**	0.21**	0.22	Duplicate
8.	**Oil %**	-1.831	-0.441	10.85**	4.53**	-0.95	-9.06**	1.85	Duplicate
9.	**Protein %**	-5.774	-1.064	47.73**	-6.23**	0.77	-12.73**	6.27	Complementary
				PS-1347 x JS 335					
1.	**Days to 50 % Flowering**	9.43*	-1.43	46.83**	-0.98**	3.91**	0.56	-14.50**	Duplicate
2.	**Days to full maturity**	-2.00	-2.82	121.0**	-0.26	1.97	0.97	-0.74	Duplicate
3.	**Plant height (cm)**	-5.20	-3.52	63.47**	-0.17	1.19	1.14	2.23	Complementary
4.	**Number of Pods/plant**	1.866	5.733*	75.0**	5.96**	-2.92	8.41**	5.17	Duplicate
5.	**Dry matter weight/plant (g)**	-0.017	-0.184**	0.50**	-58.33**	0.14**	0.12**	-0.24**	Duplicate
6.	**Harvest index (%)**	-0.495	28.536**	41.61**	0.30	-18.74**	-18.5**	38.71**	Duplicate
7.	**Seed yield/plant (g)**	-0.758	1.657*	21.01**	-0.12	-0.57	-1.36*	3.23	Duplicate
8.	**Oil %**	-1.738	0.654	16.18**	0.23	0.21	-0.24	3.19*	Complementary
9.	**Protein %**	-0.081	1.082	41.90**	0.20	-1.49**	-0.31	1.55	Duplicate
				JS-335 x UPSM 534					
1.	**Days to 50 % Flowering**	4.055	-3.931**	45.22**	0.85**	3.88**	4.99**	-10.64**	Duplicate
2.	**Days to full maturity**	-7.67	3.042	120.65**	-0.98*	-2.52	-5.27**	14.29**	Duplicate
3.	**Plant height (cm)**	9.456	26.50**	62.11**	6.82**	-1.07	-2.442	22.72**	Duplicate
4.	**Number of Pods/plant**	1.02	6.368	67.48**	7.06**	6.99**	10.05**	7.12	Complementary
5.	**Dry matter weight/plant (g)**	-0.461	-0.354**	20.38**	-0.25	3.96**	3.31**	-5.43**	Duplicate
6.	**Harvest index (%)**	39.97	27.488**	47.94**	-0.45	-15.97**	-12.58**	-16.64	Complementary
7.	**Seed yield/plant (g)**	-1.710	-5.786**	0.44**	-0.008	0.23**	0.15**	0.14	Complementary
8.	**Oil %**	-0.264	-0.410	16.50**	-0.65**	-0.19	-1.07*	-0.19	Complementary
9.	**Protein %**	-0.312	-0.110	41.78**	-0.09	-0.06	-0.17	0.26	Duplicate

** Significant at 1% level of probability, * Significant at 5% level of probability