

## Genetic architecture of seed yield and yield components in soybean (*Glycine max* (L.) Merrill.).

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**Abstract :** Generation mean analysis was carried out involving four parents for yield and yield components in soybean (*Glycine max* (L.) Merrill.). The study has brought out the influence of additive gene action for seed yield and dry matter production. Number of pods and 100 seed weight were found to govern by both additive and non-additive gene action. Protein content was found to be controlled by additive and non-additive gene action with preponderance of non-additive component.

**Key words :** Soybean, Generation mean analysis, Additive, Nonadditive, Interaction.

### Introduction

The choice of the parents in hybridisation programme is of immense importance for getting segregants in crop like soybean where hybridisation followed by pedigree method is most commonly used. The information on additive, dominance and interaction effects associated with yield and yield components in soybean is scanty. Keeping in view the importance of soybean crop as a rich source of vegetable oil and protein, it was felt that a thorough insight into the types of genetic effects such as additivity, dominance and three kind of epistasis will be helpful by adopting generation mean analysis for a better understanding of the genetic architecture of the crop.

### Materials and Methods

Four genotypes with diverse origin viz. Co 1, Bragg, EC 4296 and Co 2 were crossed among themselves and six population viz.  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$  were obtained from six crosses viz. Co 1 x Bragg, Co 1 x EC 4296, Co 1 x Co 2, Bragg x EC 4296, Bragg x Co 2 and EC 4296 x Co 2. These populations were raised in a randomised block design replicated three times adopting an uniform spacing of 45 cm x 10 cm. Data were recorded on five quantitative traits from the population of 20 in  $P_1$ ,  $P_2$  and  $F_1$ , 40 in  $B_1$  and  $B_2$  and 90 in  $F_2$  per replication. The mean values were computed for each generation over all the replications in each cross. The adequacy of the data for a simple additive dominance model was tested utilising the scaling test for scales A, B and C after Mather and Jinks (1971). To confirm the scaling tests, the procedure suggested by Cavalli (1952) was adopted. The three parameters viz. mid parental value m,

additive (d) and dominance (h) were estimated by weighted least square method (Mather and Jinks, 1982). The adequacy of simple, additive dominance observed mean values with the means was estimated from the above three parameters for three degrees of freedom. Extension of the analysis of simple additive dominance model to digenic interaction was required due to the inadequacy of the data to fit well with the additive dominance model. Using the generation means, the estimates of additive x additive (i), additive x dominance (j) and dominance x dominance (l) interactions were obtained in addition to m, (d) and (h) by a perfect fit method by the equations formulated by Mather and Jinks (1971).

### Results and Discussion

The estimates of the parameters m, (d), (h), (i), (j), (l) and chi square values are given for six cross combinations for all the five characters from Table 1 to 5.

A simple additive dominance model was found to be adequate for determining the gene action for number of pods, dry matter production and seed yield in Bragg x Co 2 and EC4296 x Co 2, 100 seed weight, drymatter production and seed yield in Co 1 x EC 4296, dry matter production and seed yield in Co 1 x Co 2 and 100 seed weight in Co 1 x Bragg. Among these characters, number of pods in EC 4296 x Co 2, dry matter production and seed yield in Co 1 x EC 4296, Co 1 x Co 2, Bragg x Co 2 and EC 4296 x Co 2 were governed by additivity.

Among the five characters under study applying the digenic model, seed yield was found to be governed by additive gene action in Co 1 x Bragg and Bragg x EC 4296. None of the crosses showed dominance gene action for seed

**Table 1.** Joint scaling test and genetic effects - Number of pods in soybean

	Crosses					
	Co 1 x Bragg	Co 1 x EC4296	Co 1 x Co 2	Bragg x EC4296	Bragg x Co 2	EC4296 x Co 2
$\chi^2$ value	8.19*	7.63 *	25.45**	28.03**	5.44	2.03
n	63.68**±13.01	86.43**±18.99	125.12**±14.98	53.94**±15.89	68.25**±15.4	73.82**±12.99
d)	17.13**±1.68	7.58**±1.93	16.22**±1.59	9.55**±1.59	0.92±1.15	8.64**±1.50
a)	-15.60±31.12	-25.41±4.91	-128.02**±33.15	17.07±41.05	-50.67-EC35.69	36.77±32.54
i)	4.52±12.91	-8.68±20.77	-56.00**±14.89	6.68±15.81	-	-
o)	11.88±8.04	5.76±8.47	8.37±6.77	-62.70**±11.87	-	-
o)	0.68±19.45	35.78±24.23	93.17**±19.45	-14.58±26.17	-	-

**Table 2.** Joint scaling test and genetic effects - 100 seed weight in soybean

	Crosses					
	Co 1 x Bragg	Co 1 x EC4296	Co 1 x Co 2	Bragg x EC4296	Bragg x Co 2	EC4296 x Co 2
$\chi^2$ value	1.82	0.49	48.53*	9.17*	32.76**	668.69**
n	13.23**±0.59	12.45**±0.57	11.95**±0.80	12.80**±0.35	10.86**±1.13	14.50**±0.44
d)	0.01±0.06	0.21** 0.06	0.89**±0.06	0.20**±0.03	0.90**±0.05	1.10**±0.05
a)	-1.67±1.41	-0.34±1.41	4.68**±2.05	-0.91±0.93	4.10±3.34	-2.87±1.14
i)	-	-	1.42±0.80	-0.54±0.35	2.50*±1.13	-1.34**±0.43
o)	-	-	-3.92**±0.58	-0.34±0.28	-2.54*±1.10	4.74**±0.34
o)	-	-	-3.40**±1.27	0.42±0.60	-2.68±2.23	1.78*±0.73

**Table 3.** Joint scaling test and genetic effects - protein content in soybean

	Crosses					
	Co 1 x Bragg	Co 1 x EC4296	Co 1 x Co 2	Bragg x EC4296	Bragg x Co 2	EC4296 x Co 2
$\chi^2$ value	75.02**	50.37**	93.82**	217.59**	273.61**	9.71*
M	45.26**±0.97	41.06**±0.91	38.47**±0.98	40.56**±0.65	41.09**±0.72	36.99**±1.16
d)	0.54**±0.19	0.51*±0.20	0.96**±0.22	1.04**±0.14	1.49**±0.16	0.45**±0.18
h)	-16.98**±2.21	-8.19**±2.33	-0.83±2.46	-3.64*±1.84	-6.322**±1.67	6.62*±2.64
o)	-7.22**±0.95	-1.98*±0.89	1.06±0.95	-2.02**±0.63	-2.10**±0.10	3.04**±1.14
o)	0.83±0.57	-2.71**±0.73	-4.33**±0.76	-6.10**±0.63	-5.72**±0.48	-1.14±0.65
o)	11.25**±4.02	6.51**±1.51	2.83±1.56	1.40±1.24	5.44±0.99	-3.4*±1.53

yield. Dry matter production was governed by additive gene effects in Co 1 x EC 4296, Bragg x Co 2 and EC 4296 x Co 2. In the other two cross combinations for which digenic model applied, only additive and additive x dominance epistatic effects were significant.

Number of pods is an important character determining the seed yield. This character was found to be governed by additive gene action in all crosses except Bragg x Co 2, while it

was governed by dominance in addition to additivity in Co 1 x Co 2. The character 100 seed weight was found to be governed by additive gene action in five out of six crosses. All the three types of epistasis were significant in EC 4296 x Co 2, while additive x dominance was predominant in Co 1 x Co 2 also. The action of duplicate dominant epistasis governing the protein content was inferred.

This study has revealed that seed yield and dry matter production in soybean was governed

Table 4. Joint scaling test and genetic effects - Dry matter production in soybean

	Crosses					
	Co 1 x Bragg	Co 1 x EC4296	Co 1 x Co 2	Bragg x EC4296	Bragg x Co 2	EC4296 x Co 2
X <sup>2</sup> value	25.91**	7.10	7.19	12.57**	4.37	5.98
M	33.99**±5.17	44.59**±8.21	55.58**±7.28	34.91**±8.65	42.45*±7.91	50.87**±8.46
(d)	10.60**±0.86	6.62**±0.81	13.22**±0.73	3.98**±0.87	2.63**±0.81	6.61**±0.75
(h)	-4.61±14.09	-2.40±19.92	-40.91*±17.96	-4.32±20.52	-29.25±18.85	-34.87±20.81
(i)	6.06±5.09	-	-	-1.48±8.60	-	-
(j)	17.37**±4.49	-	-	-18.20**±5.13	-	-
(l)	1.63±9.44	-	-	1.96±12.45	-	-

by additive gene action. Since none of the crosses showed significant dominance effect, all the crosses are expected to respond selection in pedigree breeding. The crosses viz. Co 1 x EC 4296, Co 1 x Co 2 and EC 4296 x Co 2 were found to be promising in getting high yielding segregants.

Presence of additive gene action for seed yield and drymatter production in soybean was reported by Paschal and Wilcox (1975) and for seed yield by Brim and Cokerham (1961) and Verma (1970).

In the present study, number of pods and 100 seed weight were controlled by both additive and dominance gene action. One or more of the epistasis effects were found to be significant in most of the cross combinations bringing out the interplay of additive and non additive genetic effects in determining these characters. Additive and nonadditive gene action for these characters, was reported by Singh *et al.* (1974), Kaw and Menon (1980) and Harer and Deshmukh (1993). Protein content was controlled by additive, dominance and interaction effects. However, among the epistatic effects, dominance x dominance interaction effect was predominant in most of the crosses. Non-additive gene action for this character was reported by Sharma and Phul (1994). The opposite signs of (h) and (l) in all the crosses for the traits such as number of pods, 100 seed weight and protein content indicated that they are governed by non-fixable effects and selection in the early segregating generations adopting simple selection procedure may not yield results and hence selection should be postponed to later generations when the epistatic gene effects gradually disappear. Intermating of segregants and

effecting selection in the progenies of such intermated segregating populations may result in improvement of seed yield in soybean.

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