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Determination of Gene Effects and Inheritance of genes for various Generations of Soybean Crosses (*Glycine max* L. Merrill)

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ABSTRACT: Using the means of P_1, P_2, F_1, BC_1, BC_2 and F_2 generations of three crosses of soybean, estimates of gene effects were obtained using the portioning method of six parameters model that assumed the presence of epistatic gene effects. Most of the yield components had predominance of additive gene effects which would be useful in exploiting transgressive variation for those traits among the progenies. Dominant gene effects are invariably exploited in developing hybrid varieties. Duplicate type of epistatis play a significant role in expression of the majority of the characters in all crosses of soybean. Complementary type of epistatis was found to be important to be expression of pod bearing length and days to 50% flowering, protein content, which indicates the possibility of improving to those traits in RSC11-42 × PS1475 and CG Soya 11-15 × PS1475 respectively.

Keywords: Gene effects, crosses, traits, soybean, selection.

INTRODUCTION

Soybean (*Glycine max* L. Merrill) is one of the world's most important economic legume crop for important source of protein and oil. Soybean is considered as a wonder crop due to its dual qualities *viz.,* high protein (40-44%) and oil content (20%) Baraskar *et al.* (2014). It contributes about 25% to the global edible oil production, about two thirds of the world's protein concentrate for livestock feeding and is a valuable ingredient in formulated feeds for poultry and fish. It is also an important raw material for food, fodder, pharma and other industries. Its seeds contain about 35% carbohydrate, 5% ash, 40% protein and 20% oil. The soya proteins have the highest nutritional value of all the plant proteins for human food, being particularly high in lysine.

For genetic improvement of the crop, the breeding method to be adopted depends mainly on the nature of gene action involved in the expression of quantitative traits. The presence or absence of epitasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately, whether it is complementary or duplicate at the di genic level. Two genetic models *viz*; Cavalli (1952); Hayman (1958) were simultaneously used for determining the nature of gene action involved in the inheritance of yield and yield contributing characters.

The information regarding types and magnitude of gene action involved in control of inheritance for yield and yield contributing characters through generation mean analysis is of immense use to the plant breeder to decide suitable breeding strategy to improve the soybean population.

MATERIALS AND METHODS

Three crosses namely RSC11-42 × PS1475, CG Soya11-15 × MACS5171, CG Soya11-15 × PS1475 were made and evaluated in randomized block design with three replications at IGKV Raipur during *kharif* 2020. Crop was raised as per recommended package of practices.

6 elite germplasm accessions including indigenous and exotic genotypes are selected to make crosses since they have contrasting traits and wider genetic distance. F_1's and their respective parental lines were grown during *kharif* 2019-20 in order to study BC_1 and BC_2 crosses were developed in *Rabi* 2020. In *kharif* 2020 all the parents, F_1's (seeds were retained), BC_1, BC_2 and F_2 populations were grown together, in order to study the generation mean analysis.

RESULTS AND DISCUSSION

The means of P_1, P_2, F_1, BC_1, BC_2 and F_2, generations for yield and its components in all the three crosses of soybean are presented in Table 1.

The additive components of gene-effects were significant for plant height, number of seeds per plant, 100 seed weight and oil content in RCS11-42 × PS1475; for days to 50% flowering, number of primary branches per plant, number of pods per plant, pod bearing length, 100 seed weight and oil content in CG Soya 11-15 × MACS5171; days to 50% flowering, plant height, number of pods per plant, pod bearing length, number of seeds per pod, 100 seed weight, seed yield per plant and protein content in CG Soya 11-15 × PS1475. Similar findings were also reported by Rahangdale and Raut (2002); Datt *et al.* (2011) for days to 50% flowering, plant height; Adsul *et al.* (2016) for number of primary branches per plant, 100 seed weight; Shinde *et al.* (2016) for plant height, number of pods per plant, oil content; Pawale *et al.* (2020) for seed yield per plant; and Nagarajan *et al.* (2022) for oil content and seed yield per plant. Additive gene-effects would be useful in exploiting transgressive variation for these traits among the progenies.

Table 1 : Gene effects for seed yield and its components in crosses of soybean.

Parameters	Crosses	Generation mean analysis						
		m	D	h	i	j	l	Types of epistasis
Days to 50% flowering	C1	41.00±0.07**	0.07±0.49	2.80±1.08**	3.73±1.02**	-0.73±1.06	-1.87±2.11	Duplicate
	C2	42.05±0.13**	0.60±0.41*	0.68±1.05	1.68±0.98*	1.00±0.90*	-0.35±1.88	Duplicate
	C3	42.09±0.13**	0.83±0.48*	0.35±1.14	0.92±1.09	0.80±1.04	0.15±2.11	Complementary
Days to maturity	C1	93.09±0.10**	-0.57±0.52	17.89±1.21**	15.03±1.12**	-1.40±1.08	-23.36±2.31**	Duplicate
	C2	93.12±0.15**	-0.50±0.74	23.24±1.72**	17.72±1.59**	-1.10±1.54	-22.95±3.28**	Duplicate
	C3	92.94±0.07**	0.17±0.49	24.32±1.60**	17.11±1.02**	3.23±2.52*	-24.54±3.16**	Duplicate
Plant height (cm)	C1	43.49±0.72**	-5.13±1.64**	6.48±4.64	16.43±4.36**	-11.57±3.83**	-0.66±7.84	Duplicate
	C2	44.53±0.84**	-0.47±1.55	39.63±5.21**	47.36±4.56**	-4.87±3.38*	-8.42±8.66	Duplicate
	C3	53.87±1.49**	5.97±1.69**	-4.56±7.30	-2.89±6.86	-4.13±4.07*	42.56±10.33**	Duplicate
Number of primary branches per plant	C1	4.81±0.12**	-0.23±0.33	-3.17±0.87	-3.45±0.82**	-0.57±0.75**	3.62±1.52*	Duplicate
	C2	4.53±0.12**	0.33±0.30*	-2.09±0.79**	-2.51±0.76**	0.30±0.65	2.47±1.36*	Duplicate
	C3	4.53±0.13**	0.03±0.29	-1.55±0.81*	-1.80±0.78*	0.03±0.62	1.37±1.33*	Duplicate
Number of pods per plant	C1	77.48±3.21**	-7.77±5.94	1.23±18.03	11.35±17.49	0.97±12.76	-14.78±28.38	Duplicate
	C2	80.61±2.17**	9.40±5.79*	41.50±15.47**	27.98±14.47*	-0.57±12.02	-10.25±26.98	Duplicate
	C3	91.33±3.08**	8.10±5.79*	-7.36±17.84	-12.31±16.92	14.03±12.54*	44.61±28.60*	Duplicate
Pod bearing length (cm)	C1	33.77±0.56**	-2.70±1.45	25.99±3.89**	19.64±3.66**	2.70±3.26	5.86±6.74	Complementary
	C2	32.47±0.62**	-1.73±1.62*	54.03±4.91**	54.40±4.07**	-2.53±3.88	-29.00±8.84**	Duplicate
	C3	44.43±1.36**	5.17±1.53**	-4.07±6.80	-7.27±6.24*	4.13±3.65*	39.33±9.82**	Duplicate
Number of seeds per pod	C1	2.66±0.02**	-0.03±0.09	0.65±0.21**	-0.09±0.20	-0.04±0.19	0.63±0.41*	Complementary
	C2	2.58±0.02**	0.05±0.09	0.580.20**	0.23±0.19*	0.08±0.18	-0.47±0.38*	Duplicate
	C3	2.58±0.02**	0.01±0.09	0.66±0.21**	0.32±0.20*	0.03±0.19	-0.61±0.40*	Duplicate
Number of seeds per plant	C1	215.15±10.83**	-10.30±6.70*	-245.88±46.47**	-279.61±45.35**	-19.93±16.29*	314.48±54.84**	Duplicate
	C2	216.44±9.37**	-3.03±13.44	2.54±47.62	-70.23±46.12*	-51.33±29.30*	-50.04±69.68	Duplicate
	C3	200.65±8.12**	46.97±7.94**	-48.13±38.27*	-107.08±36.15**	76.30±21.40**	114.45±51.90*	Duplicate
100 seed weight (g)	C1	13.61±0.20**	0.45±0.24*	-11.63±0.95**	-11.13±0.92**	0.88±0.57*	15.32±1.32**	Duplicate
	C2	15.79±0.39**	0.81±0.24**	-19.35±1.64**	-19.09±1.63**	1.90±0.53**	23.79±1.87**	Duplicate
	C3	15.04±0.16**	0.82±0.24**	-16.18±0.83**	-16.090.80**	1.57±0.56**	20.47±1.23**	Duplicate
Seed yield per plant (g)	C1	18.53±0.84**	-0.43±0.75	-8.20±3.93*	-11.68±3.68	-0.53±2.10	23.72±5.28**	Duplicate
	C2	20.38±0.73**	1.34±1.70	7.30±4.61*	6.30±4.50*	-2.60±3.74	-26.60±7.68**	Duplicate
	C3	30.82±1.39**	6.80±1.06**	-39.70±6.17**	-46.40±5.94**	11.62±2.92**	55.01±7.74**	Duplicate
Oil content (%)	C1	14.68±0.16**	-1.01±0.27**	-2.74±0.96**	-5.23±0.85**	-0.76±0.60*	8.36±1.54**	Duplicate
	C2	15.17±0.14**	-0.37±0.21*	-1.83±0.77*	-5.05±0.70**	-0.86±0.46*	9.76±1.18**	Duplicate
	C3	14.79±0.13**	-0.15±0.21	-0.81±0.73*	-3.96±0.66**	-0.31±0.46	9.24±1.16**	Duplicate
Protein content (%)	C1	39.43±0.18**	-0.11±0.26	3.09±0.98**	4.67±0.89**	0.43±0.59	-9.05±1.52**	Duplicate
	C2	38.13±0.27**	-0.10±0.31	3.09±1.40*	5.59±1.26**	-0.60±0.70	-11.66±2.06**	Duplicate
	C3	39.31±0.18**	-1.17±0.25**	-0.27±1.06	3.01±0.87**	-1.19±0.55*	-9.66±1.72**	Complementary

** Significance at 1% level, * Significance at 5% level, m : mean, d : additive gene effects, h : dominance gene effects, i : additive × additive gene interactions, j: additive × dominance gene interactions, l : dominance × dominance gene interactions.
C1 = RSC11-42 × PS1475, C2 = CG Soya11-15 x MACS5171, C3 = CG Soya11-15 × PS1475

A dominant type of gene action was significant for days to 50% flowering, days to maturity, pod bearing length, number of seeds per pod, number of seeds per plant, 100 seed weight, seed yield per plant, oil content and protein content in RSC11-42 × PS1475; for days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod bearing length, number of seeds per pod, 100 seed weight, seed yield per plant, oil content, protein content in CG Soya 11-15 × MACS5171; for days to maturity, number of primary branches per plant, number of seeds per pod, number of seed per plant, 100 seed weight, seed yield per plant and oil content in CG Soya 11-15 × PS1475. Dominant gene effects are invariably exploited in developing hybrid varieties. Similar findings were also reported by Rahangdale and Raut (2002); Datt *et al.* (2011); Bhor *et al.* (2014); Patil *et al.* (2016); Thakre *et al.* (2011); Abou Sen (2020) for seed yield per plant; and Nagarajan *et al.* (2022) for oil content and seed yield per plant; Patil *et al.* (2016); Shinde *et al.* (2016); Thakare *et al.* (2017) for 100 seed weight.

Among the epistatic interactions, additive × additive were found to be significant for all the traits except number of pods per pod and seed yield per plant in RSC11-42 × PS1475; for all traits in CG Soya 11-15 × MACS5171; for all traits except days to 50% flowering, plant height and number of pods per plant in cross CG Soya 11-15 × PS1475. Additive × dominance gene interaction were significant for plant height, number of primary branches per plant, number of seeds per plant, 100 seed weight and oil content in RSC11-42 × PS1475; for days to 50% flowering, plant height, number of seeds per plant, 100 seed weight and oil content in CG Soya 11-15 × MACS5171; and for all traits except days to 50% flowering, number of primary branches per plant, number of seeds per pod and oil content in RSC11-15 × PS1475.

Dominance × dominance type of gene interaction were significant for all the traits except days to 50% flowering, plant height, number of pods per plant and pod bearing length in RSC11-42 × PS1475 and CG Soya 11-15 × MACS5171; for all traits except days to 50% flowering in RSC11-15 × PS1475.

Duplicate type of epistasis were exhibited for the traits like days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant and oil content in all three crosses. Similar findings were also reported by Bhor *et al.* (2014) for seed yield per plant and Adsul *et al.* (2016) for all most all the traits under study. Hence, biparental mating or few recurrent cycle selection followed by pedigree method of selection is suggested for the improvement of seed yield in soybean.

The cross RSC11-42 × PS1475 exhibited complementary type of epistasis for pod bearing length and CG Soya 11-15 × PS1475 for days to 50% flowering and protein content indicated considerable amount of heterosis. Similar findings was reported by Patil *et al.* (2016); Pawale *et al*. (2020) for days to 50% flowering.

CONCLUSIONS

An improvement of seed yield in these crosses can be achieved by following the procedure of recurrent selection for specific combining ability in order to exploit dominance and epistasis gene action. Most of the yield components had predominance of additive gene effects which would be useful in exploiting transgressive variation for those traits among the progenies. Duplicate type of epistatis play a significant role in expression of the majority of the characters in all crosses of soybean. Complementary type of epistatis was found to be important to be expression of pod bearing length and days to 50% flowering, protein content, which indicates the possibility of improving to those traits in RSC11-42 × PS1475 and CG Soya 11-15 × PS1475 respectively.

FUTURE SCOPE

Genetic analysis experiment should be repeated over the seasons and locations in order to estimate the contribution of season and location interaction effects towards the estimation of gene effects. Generated material may be subjected to the study on the effectiveness of various selection schemes in exploiting additive gene action in the segregating population.

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Conflict of Interest. None.

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