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Short Communication

Combining ability for oil and protein content in soybean [*Glycine max* (L.) Merrill]

S. R. Maloo and S. C. Sharma

Deptt. of Plant Breeding and Genetics, RCA, Maharana Pratap University of Agril. and Technol., Udaipur 313 001

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Soybean is the world's most important source of edible oil. It accounts for nearly 60 per cent of global oil seed production. The protein content of soybean is rich in limiting amino acid lysine. Any strategy to break the yield and quality barriers need measures which can address to the problem of narrow genetic base of cultivated varieties of soybean. Combining ability studies were under taken in F_1, F_2 and F_3 generations for oil and protein content of soybean.

Experimental material comprised 15 F_1, F_2 and F_3 generations of 5 soybean lines crossed with 3 testers in line × tester mating design. The parents were selected on the basis of diverse pedigree, growth habit and adaptation. The material was planted in randomized block design with three replications under rainfed conditions at the Instructional Farm, Rajasthan College of Agriculture, Udaipur during *kharif*, 2002. One row of parents and F_1s, while three rows of F_2 and F_3 generations were sown in 3 m long rows. Seeds were dibbled with spacing of 45 cm × 10 cm row to row and plant to plant. Bulk seeds of ten randomly selected competitive plant of parents and F_1s, where as twenty plants in F_2 and F_3 generations in each replication were used for analysis of oil and protein content. Analysis of line × tester data for combining ability was done according to Kempthorne [1] and estimation of gene effects was done according to Hayman [2].

Analysis of variance revealed highly significant differences among the genotypes (Parents + F_1s + F_2s + F_3s), indicating sufficient variation present in the material for both oil and protein content. Parents NRC 12, MACS 58 and PK 327 for seed protein while Pusa 22 and PK 472 for seed oil content were found superior. Over the three generations the highest protein content was observed in Pusa 22 × MACS 58 involving at least one high protein containing parent. Seed oil content showed highly variable mean values for three generations. Among the F_1s Pusa 22 × PK 472 showed maximum oil content. However, in F_2 and F_3 generations, MACS 13 × PK 472 and Pusa 22 × NRC 12 showed the highest oil per cent.

Analysis of variance for combining ability indicated that variance due to crosses, lines and tester were significant for both protein and oil contents in F_2 generation while for protein content in F_1 only. In F_3 generation mean squares due to crosses were significant for both protein and oil content while due to lines for oil content and due to testers for protein content. Further, variance due to line x tester was significant for seed oil content in F_2 and F_3 generations. Predominance of estimated component of *sca* variance over *gca* indicated importance of non-additive genetic effects for both the quality characters. Contribution of lines and their interaction with testers were more than 65 per cent for protein content and more than 75 per cent for oil content in all the three generations.

For seed protein content lines JS 335 and Pusa 22 and tester MACS 58 recorded positive but insignificant *gca* effects in all the three generations. Similarly, positive *gca* effects for oil content were recorded by Pusa 22 in all the three generations while by MACS 58 and MACS 13 in F_2 generation (Table 1a). *sca* effects revealed that for oil content among the 15 crosses, 7 in F_2 generation and 3 in F_3 generation were positive and significant. On the contrary, no specific cross combination exhibited significant *sca* effects for seed protein content. However, Pusa 22 × MACS 58 and MACS 13 × NRC 12 were spotted as promising. Crosses PK 327 × PK 427 (in F_1s and F_2s), Pusa 22 × NRC 12 and MACS 13 × PK 472 (in F_2s) while MACS 13

Table 1a. General combining ability effects for quality characters in soybean

S. No.	Genotypes	Seed protein content			Seed oil content		
		F_1	F_2	F_3	F_1	F_2	F_3
1.	PK 472	–0.27	0.15	0.11	0.40	0.04	–0.25
2.	MACS 58	0.85	0.63	0.68	–0.21	0.44**	0.05
3.	NRC 12	–0.58	–0.79	–0.80	–0.19	–0.48**	0.19
4.	JS 335	0.90	0.82	0.42	0.17	–0.11	–0.60*
5.	Punjab 1	–1.36*	–0.43	–0.10	–0.33	–0.30*	–0.05
6.	MACS 13	0.77	0.03	–0.61	–0.06	0.43**	–0.26
7.	PK 327	–0.83	–0.96	–0.44	–0.10	–0.69**	0.00
8.	Pusa 22	0.52	0.53	0.72	0.32	0.67**	0.91**
	GCA$_{Ti}$	0.44	0.38	0.40	0.28	0.11	0.18
	GCA$_{Lj}$	0.54	0.47	0.49	0.35	0.13	0.22
	GCA$_{Ti\text{-}j}$	0.54	0.47	0.49	0.35	0.13	0.22
	GCA$_{Li\text{-}j}$	0.70	0.61	0.63	0.45	0.17	0.28
	GCA$_{Ti\text{-}Lj}$	0.62	0.54	0.56	0.40	0.15	0.25

*,**Significant at 5 and 1% level, respectively

Table 1b. Specific combining ability effects for quality characters in soybean

S. No.	Genotypes/ cross	Seed protein content			Seed oil content		
		F_1	F_2	F_3	F_1	F_2	F_3
1.	JS 335 × PK 472	–0.86	–0.74	–0.31	–1.08	–2.08**	–0.91*
2.	Punjab 1 × PK 472	–0.30	–0.59	–0.75	0.19	0.55*	0.05
3.	MACS 13 × PK 472	–0.43	–0.55	–0.88	0.22	1.28**	–0.04
4.	PK 327 × PK 472	1.27	1.34	1.55	0.52	1.20**	0.96*
5.	Pusa 22 × PK 472	0.32	0.55	0.39	0.14	–0.95**	–0.05
6.	JS 335 × MACS 58	0.12	0.23	–0.28	0.60	0.73*	1.09*
7.	Punjab 1 × MACS 58	–0.32	0.45	0.24	0.56	1.05**	0.58
8.	MACS 13 × MACS 58	–0.55	0.07	0.05	–0.50	–1.31**	–1.24**
9.	PK 327 × MACS 58	0.05	–0.82	–0.02	–0.60	0.01	–0.01
10.	Pusa 22 × MACS 58	0.70	0.07	0.02	–0.06	–0.48	–0.42
11.	JS 335 × NRC 12	0.75	0.52	0.60	0.48	1.34**	–0.18
12.	Punjab 1 × NRC 12	0.62	0.15	0.52	–0.76	–1.60**	–0.63
13.	MACS 13 × NRC 12	0.98	0.47	0.83	0.28	0.03	1.28**
14.	PK 327 × NRC 12	–1.32	–0.52	–1.54	0.08	–1.21**	–0.95*
15.	Pusa 22 × NRC 12	–1.03	–0.61	–0.40	–0.08	1.43**	0.47
	SCA$_{ij}$	1.08	0.94	0.97	0.69	0.27	0.44
	SCA$_{Ti\text{-}Tj}$	1.33	1.15	1.19	0.85	0.33	0.54
	SCA$_{iL\text{-}jL}$	1.40	1.22	1.25	0.89	0.34	0.57
	SCA$_{ij\text{-}kl}$	1.50	1.30	1.34	0.96	0.37	0.61

*,**Significant at 5 and 1% level, respectively

× NRC 12 (in F_3s) which also had high *per se* performance involving good general combiner could be used in quality improvement programme (Table 1b).

In generation mean study for seed protein content crosses PK 327 × MACS 58, Punjab 1 × NRC 12, PK 327 × NRC 12 and Pusa 22 × NRC 12 recorded significant C scale while rest of the crosses showed adequacy of additive dominance model (Table 2). However, D scale was adequate in all the crosses for protein content. Additive (d) and additive x additive (i) type interaction were significant in MACS 13 × MACS 58. While (d) was significant in MACS 13 × PK 472 and MACS 13 × NRC 12 suggesting predominant role of additive component for seed protein content. Further, additive × additive (i) interactions were significant in JS 335 × NRC 12, PK 327 × NRC 12 and Pusa 22 × NRC 12 for protein content [3, 4].

For seed oil content adequacy of both C and D scale was found for 3 crosses indicating that higher order interactions were present for most of the crosses. All the 5 parameters were significant in crosses MACS 13 × PK 472 and Pusa 22 × PK 472 indicating dominance and epistasis gene effects were operating in the inheritance of seed oil content. Crosses Punjab 1 × PK 472, Punjab 1 × MACS 58 and Pusa 22 × NRC 12 showed insignificant (d), (h), (i) and (l), indicating importance of fixable additive gene effects for oil content. Both dominance (h) and dominance × dominance (l) type interactions were significant in PK 327 × MACS 58, Punjab 1 × NRC 12 and PK 327 × NRC 12. Additive × additive (i) type interactions were also significant in total 5 crosses (Table 2). Hence, seed oil content appeared to be largely under the control of both additive and non-additive gene effects for most of the crosses [5]. Frequency of duplicate type of epistasis was higher in most of the crosses of seed oil content while for protein content complementary epistasis is also equally important.

Based on various estimates *viz.*, mean performance, combining ability and gene effects results of present study suggested that crosses PK 327 × PK 472 and JS 335 × MACS 58 involved as least one parent with high *per se* performance and high *gca* effects revealing that all the favourable genes got accumulated in these crosses and appeared promising for further improvement for seed oil content in soybean. Both the crosses showed duplicate type epistasis for oil and protein content so that reciprocal recurrent selection could be effectively utilized for exploiting both additive and non-additive gene effects simultaneously [6].

Table 2. Scaling test and gene effects for protein and oil content in soybean

Crosses		Scale		Genetic component					Non-allelic interaction
		C	D	m	(d)	(h)	(i)	(l)	
Protein content									
1.	JS 335 × PK 472	–2.90	–3.10	38.10*	–0.05	0.33	1.48	–0.27	Duplicate
2.	Punjab 1 × PK 472	–2.60	–3.44	37.00*	0.60	–0.44	3.06	–1.12	Complementary
3.	MACS 13 × PK 472	–2.60	–5.00	37.50*	1.60*	3.60	6.10	–3.20	Duplicate
4.	PK 327 × PK 472	–3.50	–0.70	38.40*	–0.55	–1.47	–1.22	3.73	Duplicate
5.	Pusa 22 × PK 472	0.00	–0.60	39.10*	0.20	0.20	0.80	–0.80	Duplicate
6.	JS 335 × MACS 58	–2.40	–4.70	39.55*	0.50	3.03	3.73	–3.07	Duplicate
7.	Punjab 1 × MACS 58	0.18	–1.34	38.52*	1.15	–0.83	3.22	–2.03	Complementary
8.	MACS 13 × MACS 58	–1.30	–2.30	38.60*	2.15*	2.47	5.62*	–1.33	Duplicate
9.	PK 327 × MACS 58	–11.12*	–2.44	36.72*	0.00	–2.23	–0.23	11.57	Duplicate
10.	Pusa 22 × MACS 58	–4.10	–0.90	39.10*	0.75	0.67	1.42	4.27	Complementary
11.	JS 335 × NRC 12	–5.62	–5.14	38.42*	0.65	1.84	3.79*	0.64	Complementary
12.	Punjab 1 × NRC 12	–6.02*	–3.00	36.80*	1.30	–1.39	3.60	4.03	Duplicate
13.	MACS 13 × NRC 12	–5.88	–3.36	37.58*	2.30*	2.36	5.86	3.36	Complementary
14.	PK 327 × NRC 12	–10.30*	–12.50*	35.60*	0.15	1.67	6.92*	–2.93	Duplicate
15.	Pusa 22 × NRC 12	–6.48*	–4.60	37.00*	0.90	–0.57	3.79*	2.51	Duplicate
Oil content									
1.	JS 335 × PK 472	–8.53*	–1.27	16.07*	1.23*	–0.24	1.89*	9.69*	Duplicate
2.	Punjab 1 × PK 472	–2.53*	–2.33	18.50*	0.13	1.13	1.40	0.27	Complementary
3.	MACS 13 × PK 472	4.10*	–5.10*	19.97*	0.82*	5.07*	5.72*	–12.27*	Duplicate
4.	PK 327 × PK 472	2.03*	1.57*	18.77*	0.42*	–0.53	–0.55	4.80*	Duplicate
5.	Pusa 22 × PK 472	–7.17*	0.90	17.97*	–0.52*	–1.84*	–2.83*	10.76*	Duplicate
6.	JS 335 × MACS 58	2.27	1.67	19.27*	1.17*	0.73	1.60	–0.80	Duplicate
7.	Punjab 1 × MACS 58	1.67	–0.67	19.40*	0.07	0.56	0.86	–3.11	Duplicate
8.	MACS 13 × MACS 58	–1.90*	–4.17*	17.77*	0.75*	2.18*	3.96*	–3.02	Duplicate
9.	PK 327 × MACS 58	–1.63*	0.63	17.97*	0.35*	–1.51*	0.00	3.02*	Duplicate
10.	Pusa 22 × MACS 58	–1.97	–0.97	18.83*	–0.58*	–0.47	–0.85	1.33	Duplicate
11.	JS 335 × NRC 12	0.13	–3.40*	18.97*	1.73*	3.09*	5.76*	–4.71	Duplicate
12.	Punjab 1 × NRC 12	–11.13*	1.07	15.83*	0.63	–4.60*	–1.30	16.27*	Duplicate
13.	MACS 13 × NRC 12	–2.90	4.50	18.20*	1.32*	–3.53	–0.85	9.87	Duplicate
14.	PK 327 × NRC 12	–12.70*	0.57	15.83*	0.92*	–3.18*	–0.66	17.69*	Duplicate
15.	Pusa 22 × NRC 12	0.90	0.03	19.83*	–0.02	–1.22	0.09	–1.16	Complementary

*Significant at 5% level of significance

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