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Combining ability studies for yield and related traits in soybean (*Glycine max*)

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ABSTRACT

The present investigation was undertaken in F_1 population of 36 crosses, obtained by crossing 18 inbred lines of soybean with two diverse testers in line × tester mating design during *kharif* 2012. All the parental lines and their F_1 hybrids were evaluated in randomized complete block design at the Experimental Farm of Department of Crop Improvement, CSK HPKV, Palampur (HP) during *kharif* 2013. The aim of this study was to identify suitable parents and hybrids for yield and its contributing traits. Experimental results revealed significant differences for lines, testers and line × tester for majority of the traits studied. Lines Bragg, Shivalik and P9-2-2 were found to be good general combiners for most of the traits. The cross combinations, Bragg × Hara Soya, DS-1213 × Hara Soya, H-330 × Hara Soya, PK-472 × Him Soya and H-330 × Him soya showed high *per se* performance and SCA effects for seed yield per plant and were rated as potential crosses for further improvement. Further, non-additive gene action (σD^2) played a major role in the manifestation of almost all the traits which suggested the use of breeding approaches such as single seed descent method, reciprocal recurrent selection with one or two intermatings and diallel selective mating for the improvement of seed yield and related traits. Selection of parents based on their combining ability is an effective approach in hybrid breeding programme.

Key words: Combining ability, Line × Tester, Soybean, Yield

Soybean [*Glycine max* (L.) Merrill] is considered as a golden bean. It is the cheapest source of vegetable oil, having an ideal combination of high quality protein (40%) and oil (20%) than the other grain legumes. Soybean cultivation is speedily increasing due to its high dietary value for both humans and livestock and as an important industrial crop. Amongst grain legumes, this is potential crop for combating protein calorie malnutrition. In any hybridization program, recognition of the best combination of two (or more) parental genotypes to maximize variance within related breeding populations, and as a result the chance of recognizing better transgressive segregants in the segregating populations, are the most important challenge to plant breeders. The combining ability is an important tool for the selection of desirable parents together with the information regarding nature and magnitude of genetic variances controlling quantitative traits of economic importance. It is important to plant breeders for choosing the desirable parents for hybridization programme and to frame well-organized breeding plan leading to rapid improvement and further development.

Studies on the combining ability of autogamous species consider the ratio of the mean square values of GCA and SCA as indicators of the predominant type of gene action in the trait expression. It is also expressed that GCA is mainly the result of additive gene effects and additive × additive interactions, while SCA is consequences of dominance, epistatic deviation and genotype × environmental interactions. For selection of parents in early generations, combining ability analysis is an efficient approach. In a breeding program, information on the combining ability is needed for selection of both parents and crossing partners, as well as identification of offspring for developing high-yielding varieties (Susanto 2018). The present study had the objectives of determining the general and specific combining ability of traits of agronomic interest in soybean and to provide base material for the soybean improvement programme.

MATERIALS AND METHODS

The experimental materials consisted of 18 fixed lines, viz. SL-682, P6-1, SL-679, P9-2-2, DS-1213, PK-472, Hardee, Bragg, SL-795, Shivalik, PS-1466, P2-2, H-330, PS-1469, VLS-59, JS-335, P169-3 and P13-4 and crossed with two contrasting testers, viz. Him Soya (T_1) and Hara Soya (T_2) resulting in a total of 36 crosses. The materials were grown in a completely randomized block design with three replications at the Experimental Farm of Department

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of Crop Improvement, CSK HPKV, Palampur (HP) during *kharif* 2013. Geographically, the farm is situated at an elevation of about 1290 m amsl with 36°6 N latitude and 76°3'E longitude representing the mid-hill zone (Zone-2) of Himachal Pradesh and is characterized by humid sub-temperate climate with high rainfall (2,500 mm per annum). The soil is acidic in nature with pH ranging from 5.0 to 5.6. The experimental plot of each treatment consisted of one row of 2 m length. Row to row and plant to plant distances were maintained at 50 and 20 cm, respectively. The observations were recorded on randomly taken five competitive plants from each entry in each replication for the characters such as days to 50% flowering, days to 75% maturity, reproductive phase, plant height (cm), branches per plant, nodes on main stem, internode length (cm), petiole length (cm), pods per plant, pod length (cm), seeds per pod, biological yield per plant (g), seed yield per plant (g), harvest index (%) and 100-seed weight (g). Data were subjected to line × tester analysis as per the method given by Kempthorne (1957).

RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance for combining ability indicated significant differences among hybrids (crosses) for all the traits except petiole length and harvest index (Table 1). The mean squares due to crosses were partitioned into three components, viz. lines, testers and lines × testers interaction. Mean squares due to lines were significant for all the traits except days to 75% maturity, branches per plant, petiole length, pod length and harvest index. Mean squares due to testers were non-significant for all the traits except petiole length. Mean squares due to lines × testers interactions were significant for all the traits except plant height, internode length, petiole length, seeds per pod and harvest index suggesting that the experimental material possessed considerable variability and that both GCA and SCA were involved in the genetic expression of these factors thereby indicating that they are suitable for combining ability studies. The significant difference between line × tester interactions indicated that specific combining ability attributed heavily in the expression of these traits and provide the importance of non-additive variance for all the traits. The significant mean squares due to lines and testers also revealed the prevalence of additive variance for the traits studied.

The estimates of additive and dominance variances are also presented in Table 1. The relative magnitudes of additive and dominance variance components showed that non-additive variance was predominant for all the traits except plant height where preponderance of additive variance was observed. Occurrence of both additive and non-additive variance for yield and related component traits in soybean have also been reported in earlier studies by El-Sayad *et al.* (2005) and Agrawal *et al.* (2005).

The major role of non-additive gene effects in the manifestation of almost all the traits except plant height

Table 1 Analysis of variance for combining ability and estimates of genetic parameters

Source of variation	Replica-tions	Crosses	Lines	Testers	Lines × Testers	Error	Estimates of genetic parameters				
Traits df	2	35	17	1	17	70	σA^2	σD^2	$(H/D)^{1/2}$	h^2	GA (5%)
Days to 50% flowering	12.890	33.980*	50.640*	14.080	18.490*	5.260	0.380	4.620	3.460	5.890	0.310
Days to 75% maturity	46.230*	8.090*	10.930	15.560	4.820*	2.640	0.080	0.390	2.190	4.840	0.130
Reproductive phase	0.003*	0.003*	0.004*	0.0007	0.001*	0.0008	0.000	0.0002	2.150	6.880	0.003
Plant height (cm)	281.840*	98.620*	164.490*	2.770	38.390	33.720	1.500	1.330	0.940	10.500	0.820
Branches/plant	0.560	2.280*	2.870	6.210	1.470*	0.510	0.020	0.330	4.010	3.980	0.060
Internode length (cm)	1.840*	0.770*	1.350*	0.010	0.250	0.270	0.010	-	-	13.480	0.080
Nodes/main stem	1.730	3.760*	5.560*	0.007	2.190*	1.008	0.040	0.430	3.280	5.110	0.090
Petiole length (cm)	4.590*	1.090	0.660	10.890*	0.940	1.400	0.004	-	-	1.190	0.020
Pods/plant	110.130	1209.040*	2091.690*	648.760	359.340*	142.820	21.180	81.660	1.960	15.030	3.670
Seeds/pod	0.810*	0.040*	0.070*	0.008	0.020	0.030	0.0007	-	-	11.770	0.020
Pod length (cm)	0.010	0.070*	0.060	0.010	0.090*	0.009	-	0.030	-	-	-
Biological yield/ plant (g)	49.640	240.160*	412.580*	9.540	81.310*	36.710	3.960	16.450	2.040	12.750	1.460
Seed yield/plant (g)	8.000	75.370*	140.280*	10.760	14.260*	7.710	1.520	2.860	1.370	24.270	1.250
Harvest index (%)	0.004	0.007	0.008	0.0003	0.005	0.005	0.000	0.0002	2.370	2.200	0.002
100 seed weight (g)	1.870	23.640*	44.210*	0.090	4.450*	1.660	0.480	1.060	1.480	24.390	0.700

* Significant at $P \leq 0.05$ $(H/D)^{1/2}$ = Degree of dominance, σA^2 = Additive variance, h^2 = Narrow sense heritability, σD^2 = Dominance variance, GA (5%) = Genetic advance at 5%, - = Not calculated (because of negative value)

Table 2 Estimates of GCA effects of lines (females) and testers (males) for different traits

Lines	Days to 50% flowering	Days to 75% maturity	Reproductive phase	Plant height (cm)	Branches/ plant	Internode length (cm)	Nodes / main stem	Petiole length (cm)	Pods/ plant	Seeds/ pod	Pod length (cm)	Biological yield/ plant (g)	Seed yield/ plant (g)	Harvest index (%)	100-seed weight (g)
P6-1	-2.45*	-2.28*	-0.02	- 9.22*	-0.36	-0.56 *	-0.92*	0.39	0.21	-0.06	-0.06	-4.07	-3.11*	-0.02	-1.44*
SL-682	-0.28	0.05	-0.003	-0.75	-0.32	-0.32	0.53	-0.34	11.22*	-0.005	-0.02	3.96	2.09*	0.01	-0.86
SL-679	1.71	-1.12	0.03*	3.31	0.65*	0.58 *	-0.53	0.23	23.82*	0.05	-0.11*	2.16	2.17*	0.03	-1.53*
P9-2-2	3.38*	0.05	0.05*	4.14	0.73*	0.09	0.69	-0.04	47.72*	0.11	-0.12*	20.47*	13.45*	0.07*	-0.61
DS-1213	-0.12	-0.78	-0.03*	-0.22	-0.56	0.04	-0.20	0.16	-3.67	0.07	-0.16*	-3.49	-1.59	0.003	0.06
PK-472	-1.95*	-0.45	-0.01	2.68	0.47	-0.20	1.03*	0.43	0.35	0.06	0.04	2.32	-0.36	-0.04	-0.44
Hardee	0.71	1.38	0.008	6.83*	1.13*	0.32	0.63	-0.11	3.91	-0.04	-0.006	7.19*	1.84	-0.04	0.06
Bragg	2.71*	1.55	-0.02	11.2*	1.67*	0.18	1.82*	0.49	18.89*	0.21*	0.06	14.24*	5.84*	-0.02	-0.27
SL-795	-1.95*	0.21	-0.01	-2.34	-0.58*	-0.08	-0.35	0.53	-0.36	-0.07	-0.12*	-4.65*	-2.39*	-0.005	-3.36*
P2-2	-3.95*	0.88	-0.04 *	-0.77	-0.16	-0.25	0.36	-0.26	-6.46	-0.11	0.04	-0.31	-0.61	-0.02	-0.36
Shivalik	6.54*	3.38*	0.05 *	6.16*	-0.36	1.03*	-0.78*	-0.44	-28.33*	0.14*	0.19*	2.410	3.81*	0.08*	9.72*
PS-1466	-0.62	-0.62	0.02	-4.52	-0.89*	0.91*	-2.45*	-0.02	-35.66*	-0.13*	-0.12*	-13.17*	-7.14*	-0.04	2.89*
H-330	-2.12*	-2.12*	-0.008	-9.42*	-0.25	-0.55*	-0.93*	-0.14	-9.84*	-0.21*	0.04	-8.95*	-6.07*	-0.06*	-0.27
PS-1469	-1.62	-0.45	-0.007	-3.90	-0.86*	-0.55*	0.43	-0.31	-10.71*	-0.15*	0.11*	-8.31*	-3.64*	0.008	-0.69
VLS-59	5.21*	1.05	0.04*	0.19	-0.06	0.13	-0.28	-0.41	-9.69*	0.02	0.03	-6.96*	-3.37*	0.01	-1.63*
JS-335	-0.78	0.21	-0.01	-0.60	0.23	-0.50*	1.02*	-0.21	-7.36	0.04	-0.006	-5.56*	-3.84*	-0.01	-0.94*
P169-3	-0.78	0.05	-0.01	-1.32	-0.06	-0.16	-0.001	0.36	9.16*	0.02	0.04	3.26	3.07*	0.04	-0.86
P13-4	-3.62*	-0.95	-0.03*	-1.45	-0.38	-0.11	-0.07	-0.32	-3.19	0.002	0.16*	-0.56	-0.16	0.00	0.56
SE(gi) ±	0.88	0.78	0.01	2.39	0.28	0.22	0.39	0.49	4.36	0.06	0.04	2.31	0.97	0.03	0.46
SE(gi-gj) ±	1.24	1.10	0.02	3.38	0.40	0.32	0.55	0.69	6.17	0.09	0.05	3.26	1.37	0.04	0.65
Testers															
Him Soya	-0.36	-0.38	-0.003	-0.16	-0.24*	-0.01	0.008	-0.32	2.45	-0.009	-0.01	-0.29	-0.32	-0.002	0.03
Hara Soya	0.36	0.38	0.003	0.16	0.24*	0.01	-0.008	0.32	-2.45	0.009	0.01	0.29	0.32	0.002	-0.03
SE (gi) ±	0.29	0.26	0.004	0.79	0.09	0.07	0.13	0.16	1.45	0.02	0.01	0.77	0.32	0.009	0.15
SE (gi-gk) ±	0.41	0.37	0.006	1.12	0.13	0.11	0.18	0.23	2.06	0.03	0.02	1.08	0.46	0.01	0.22

* Significant at $P \leq 0.05$

Table 3 Estimates of SCA effects of different cross combinations for different traits

Crosses	Days to 50% flowering	Days to 75% maturity	Reproductive phase	Plant height (cm)	Branches/ plant	Internode length (cm)	Nodes/ stem	Petiole length (cm)	Pods/ plant	Seeds/ pod	Pod length (cm)	Biological yield/ plant (g)	Seed yield/ plant (g)	Harvest index (%)	100 seed weight (g)
P9-2-2 x Him Soya	0.69	-1.12	0.003	-3.69	0.41	-0.17	-0.47	0.08	-8.82	0.02	-0.04	-2.25	-0.57	0.02	-0.36
P9-2-2 x Hara Soya	-0.69	1.12	-0.003	3.69	-0.41	0.17	0.47	-0.08	8.82	-0.02	0.04	2.25	0.57	-0.02	0.36
PS1466 x Him Soya	-0.47	-0.78	0.01	1.87	-0.11	-0.21	0.94	0.42	6.46	0.02	-0.006	2.51	0.83	-0.002	-0.11
PS1466 x Hara Soya	0.47	0.78	-0.01	-1.87	0.11	0.21	-0.94	-0.42	-6.46	-0.02	0.006	-2.51	-0.83	0.002	0.11
P6-1 × Him Soya	0.53	-0.62	-0.003	2.34	0.65	0.02	0.41	0.35	1.96	-0.01	-0.19*	0.38	-1.18	-0.04	-1.28
P6-1 × Hara Soya	-0.53	0.62	0.003	-2.34	-0.65	-0.02	-0.41	-0.35	-1.96	0.01	0.19*	-0.38	1.18	0.04	1.28
PK-472 × Him Soya	-1.47	0.21	-0.007	1.41	0.17	0.42	-0.59	-0.02	19.66*	0.02	-0.006	3.39	-0.03	-0.03	0.14
PK-472 × Hara Soya	1.47	-0.21	0.007	-1.41	-0.17	-0.42	0.59	0.02	-19.66*	-0.02	0.006	-3.39	0.03	0.03	-0.14
VLS-59 × Him Soya	1.03	-0.62	0.01	0.21	-0.39	0.17	-0.32	-0.35	0.19	0.04	-0.04	2.03	0.98	-0.002	0.97
VLS-59 × Hara Soya	-1.03	0.62	-0.01	-0.21	0.39	-0.17	0.32	0.35	-0.19	-0.04	0.04	-2.03	-0.98	0.002	-0.97
P13-4 × Him Soya	1.52	0.71	0.009	-5.42	-0.43	-0.27	-0.56	0.12	-7.57	-0.03	-0.04	-3.72	-1.28	0.005	-0.69
P13-4 × Hara Soya	-1.52	-0.71	-0.009	5.42	0.43	0.27	0.56	-0.12	7.57	0.03	0.04	3.72	1.28	-0.005	0.69
PS1469 × Him Soya	0.19	-0.12	0.007	-2.24	-1.23*	-0.15	-0.26	0.25	-8.78	-0.01	0.01	-4.55	-2.52*	-0.01	-0.53
PS1469 × Hara Soya	-0.19	0.12	-0.007	2.24	1.23*	0.15	0.26	-0.25	8.78	0.01	-0.01	4.55	2.52*	0.01	0.53
DS1213 × Him Soya	-4.14*	0.71	-0.02	-1.69	-0.29	0.18	-0.81	-0.02	2.69	-0.04	0.18*	-3.30	-1.42	0.00	0.14
DS1213 × Hara Soya	4.14*	-0.71	0.02	1.69	0.29	-0.18	0.81	0.02	-2.69	0.04	-0.18*	3.30	1.42	0.00	-0.14
SL-679 × Him Soya	-0.80	0.05	0.006	0.33	0.62	0.01	-0.008	0.55	1.15	-0.04	0.13*	0.76	1.25	0.03	0.38
SL-679 × Hara Soya	0.80	-0.05	-0.006	-0.33	-0.62	-0.01	0.008	-0.55	-1.15	0.04	-0.13*	-0.76	-1.25	-0.03	-0.38
SL-682 × Him Soya	1.19	-2.28*	-0.006	-0.21	-0.09	0.08	-0.23	0.13	-9.82	0.03	0.26*	-4.68	-2.30*	-0.005	-0.28
SL-682 × Hara Soya	-1.19	2.28*	0.006	0.21	0.09	-0.08	0.23	-0.13	9.82	-0.03	-0.26*	4.68	2.30*	0.005	0.28
H-330 × Him Soya	1.36	0.55	0.01	-0.57	0.47	-0.16	0.19	-0.08	3.52	-0.04	0.11*	7.19*	2.32*	-0.04	-1.19
H-330 × Hara Soya	-1.36	-0.55	-0.01	0.57	-0.47	0.16	-0.19	0.08	-3.52	0.04	-0.11*	-7.19*	-2.32*	0.04	1.19
P169-3 × Him Soya	0.53	1.21	0.01	-0.52	0.34	0.17	-0.34	-0.33	-4.75	0.002	0.13*	-0.72	-0.30	0.002	2.14*
P169-3 × Hara Soya	-0.53	-1.21	-0.01	0.52	-0.34	-0.17	0.34	0.33	4.75	-0.002	-0.13*	0.72	0.30	-0.002	-2.14*
P2-2 × Him Soya	0.69	0.38	0.001	3.61	0.29	0.34	0.07	-0.78	5.16	0.04	-0.04	5.63*	1.99	-0.02	1.14
P2-2 × Hara Soya	-0.69	-0.38	-0.001	-3.61	-0.29	-0.34	-0.07	0.78	-5.16	-0.04	0.04	-5.63*	-1.99	0.02	-1.14
Shivalik × Him Soya	0.19	0.71	-0.01	4.09	0.61	-0.21	1.54*	0.18	10.76*	0.10	-0.006	3.28	3.09*	0.04	0.05

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Table 3 (*Concluded*)

Crosses	Days to 50% flowering	Days to 75% maturity	Reproductive phase	Plant height (cm)	Branches/ plant	Internode length (cm)	Nodes/ stem	Petiole length (cm)	Pods/ plant	Seeds/ pod	Pod length (cm)	Biological yield/ plant (g)	Seed yield/ plant (g)	Harvest index (%)	100 seed weight (g)
Shivalik × Hara Soya	-0.19	-0.71	0.01	-4.09	-0.61	0.21	-1.54*	-0.18	-10.76*	-0.10	0.006	-3.28	-3.09*	-0.04	-0.05
Hardee × Him Soya	-4.31*	-0.78	-0.05*	-3.27	-0.56	-0.14	-0.44	0.35	-9.25	-0.09	-0.26*	-6.24*	-0.87	0.07	-0.34
Hardee × Hara Soya	4.31*	0.78	0.05*	3.27	0.56	0.14	0.44	-0.35	9.25	0.09	0.26*	6.24*	0.87	-0.07	0.34
JS-335 × Him Soya	0.69	0.38	0.02	0.53	-0.26	0.005	0.06	-0.92	-4.12	0.03	-0.09	-0.64	-0.40	-0.01	0.47
JS-335 × Hara Soya	-0.69	-0.38	-0.02	-0.53	0.26	-0.005	-0.06	0.92	4.12	-0.03	0.09	0.64	0.40	0.01	-0.47
SL-795 × Him Soya	0.36	1.21	-0.004	1.37	-0.16	0.12	0.008	0.25	-0.70	0.04	-0.04	-0.12	-0.05	-0.002	0.38
SL-795 × Hara Soya	-0.36	-1.21	0.004	-1.37	0.16	-0.12	-0.008	-0.25	0.70	-0.04	0.04	0.12	0.05	0.002	-0.38
Bragg × Him Soya	2.19	0.21	0.01	1.84	-0.04	-0.21	0.81	-0.19	2.72	0.02	-0.06	1.03	0.45	-0.005	-1.03
Bragg × Hara Soya	-2.19	-0.21	-0.01	-1.84	0.04	0.21	-0.81	0.19	-2.72	-0.02	0.06	-1.03	-0.45	0.005	1.03
SE (Sij) ±	1.24	1.10	0.02	3.38	0.40	0.32	0.55	0.69	6.17	0.09	0.05	3.26	1.37	0.04	0.65
SE (Sij-Skl) ±	1.76	1.56	0.02	4.78	0.57	0.45	0.78	0.98	8.73	0.13	0.07	4.61	1.95	0.06	0.92

* Significant at $P \leq 0.05$

was observed by higher value of σ^2D than σ^2A and degree of dominance $[(H/D)^{1/2}]$ being greater than one, i.e. over dominance. The role of non-additive gene action in the inheritance of different traits by following line × tester mating design has also been reported by Gadag *et al.* (1999) for grain yield per plant and days to 75% maturity and Agrawal *et al.* (2005) for indeterminate growth habit. In this situation, population improvement programme like reciprocal recurrent selection which may allow to accumulate the fixable gene effect as well as to maintain considerable variability and heterozygosity for exploiting non-fixable gene effect may prove to be the most effective method. However, soybean being a self pollinated crop, produces few seeds per pollination, thus, selection procedure is not practically economical. So, possible choice is the use of biparental progenies among selected crosses or use of selection procedure such as diallel selective mating to exploit both additive and non additive genetic components.

Estimates of GCA effects: The estimates of GCA effects were worked out for all the traits and are presented in Table 2. The significant negative GCA effects were observed for six lines for days to flowering, two lines for days to 75% maturity and three lines for reproductive phase. In case of days to 50% flowering, genotype P2-2 was observed to be the best general combiner as it showed the highest significant negative GCA effect. The line P13-4 was also good general combiner for earliness followed by P6-1, H-330, PK-472 and SL-795. Female parent Shivalik was found to be the poorest general combiner exhibiting maximum positive GCA effect for the trait. In case of days to 75% maturity, genotype P6-1 was the best general combiner as it showed the highest negative GCA effects. The female H-330 was also observed to be a good general combiner for earliness in maturity. Reproductive phase was studied to evaluate the parents and crosses for synchronous flowering. For this trait, negative effects were considered to be favourable. For this trait, P9-2-2 and Shivalik were found to be good general combiners for longer reproductive phase and P2-2, DS-1213 and P13-4 were found to be good general combiner for shorter reproductive phase.

Estimates of SCA effects: The estimates of SCA effects (Table 3) revealed that all the cross combinations were average combiners for different traits. In case of days to flowering, cross combination Hardee × Him Soya showed the highest significantly negative SCA effects followed by DS-1213 × Him Soya. For days to 75% maturity, SL-682 × Him Soya showed the highest significantly negative SCA effect and was the best combination for early maturity. For reproductive phase, the highest significant positive SCA effects was obtained from the cross Hardee × Hara Soya. For shorter reproductive phase, the best specific combination was Hardee × Him Soya. Rest of the cross combinations were either having negative or positive non-significant SCA effects. For pods per plant, two cross combinations showed significant positive SCA effects. The highest significant SCA effects were observed for PK-472 × Him Soya followed by Shivalik × Him Soya. The other cross combinations which also exhibited highly significant positive SCA effects for the trait were SL-682 × Him Soya, P6-1 × Hara Soya, DS-1213 × Him Soya, SL-679 × Him Soya, P169-3 × Him Soya and H-330 × Him Soya. For biological yield per plant, the highest positive SCA effect was obtained for the cross combination H-330 × Him Soya. For seed yield per plant, the highest positive SCA effects were obtained for Shivalik×Him Soya, PS-1469 × Hara Soya, H-330 × Him Soya and SL-682 × Hara Soya. For 100-seed weight, only one combination (P169-3 × Him Soya) showed significant positive SCA effect. For protein content, only three cross combinations, viz. P9-2-2 × Him Soya, PK-472 × Hara Soya and DS-1213 × Him Soya exhibited positive significant SCA effects. For oil content, the highest positive SCA effect was obtained for the cross combination P169-3 × Hara Soya. It was observed that no single cross could reveal significant SCA effects for all the traits. Three cross combinations, viz. PS-1469 × Hara Soya, Shivalik × Him Soya and H-330 × Him Soya were found to be good specific combiners for seed yield per plant. Earlier workers have also reported significant SCA effects for different traits, viz. seed weight by Cho and Scott (2000) and number of pods per plant and seed yield per plant by El-Sayad *et al.* (2005).

The cross combinations involving one good and other poor or average combiner may give desirable transgressive segregants. The specific interaction effects of poor × poor crosses may perform better than good × good and good × poor combinations because of the prevalence of high magnitude of non-additive component for the superiority of the pertinent cross combination. Singh *et al.* (1985) observed that the best crosses involving atleast one parent with good combining ability may produce transgressive segregants which are also possible in many of the crosses of the present study. Singh *et al.* (2006) gave examples to suggest that when SCA effects are predominant in self-pollinated crops, the major portion of the variability is due to additive × additive effects. Therefore, selection should be delayed to later generations. Further, it was observed that the per cent contribution of lines was higher than the corresponding testers and their interaction for all the traits. Therefore, it can be concluded that lines played a significant role in the expression of different characters in various cross combinations.

The most outstanding parental lines such as Bragg, Shivalik and P9-2-2 were found to be good general combiners for most of the traits. Cross combinations like Shivalik × Him Soya, H-330 × Him Soya, DS-1213 × Him Soya, SL-682 × Him Soya, PS-1469 × Hara Soya, P169-3 × Him Soya and SL-679 × Him Soya were the best specific combiners which may give desirable transgressive segregates if the additive effect of one parent and complementary epistatic effect act in the same direction and maximize desirable plant characters.

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