SHORT COMMUNICATION

Combining Ability Analysis for Yield and Other Quantitative Traits in Soybean (*Glycine max* L. Merril)

Shiv Datt[1,2]*, PR Sharma[1], KN Singh[1] and Mukul Kumar[1]
[1]*Directorate of Research, Central Agricultural University, Imphal-795 004, Manipur*
[2]*IP&TM Unit, Krishi Anusandhan Bhavan-I, Indian Council of Agricultural Research, Pusa, New Delhi-110 012*

(Received: 3 April 2010; Revised: 5 April 2011; Accepted: 2 May 2011)

Genetic analysis was carried out using 5x5 diallel set of soybean crosses along with the parents for estimation of combining ability. The analysis revealed that the parents and crosses differ significantly for general combining ability and specific combining ability effects. The *gca* and *sca* components suggested predominance of additive gene effects for days to 50% flowering, days to maturity and plant height and non-additive gene effects for all the traits. Parents JS 335 and RAUS 5 were the good combiners for grain yield/plant whereas parent Bragg was best combiner for days to 50% flowering and days to maturity. The crosses JS 93-05 x PS 562, RAUS 5 x Bragg and PS 562 x RAUS 5 were found to be the best specific combiners for grain yield/plant while cross PS 562 x RAUS 5 for days to 50% flowering, days to maturity and plant height.

Key Words: Combining ability, Quantitative traits, Soybean, Yield components

Soybean [*Glycine max* (L.) Merril] is world's most important oil seed crop and is recognized as miracle bean due to its high nutritive value and numerous uses. It is rich in oil (18-22 %) and protein (38-42%). In India area under soybean cultivation is about 8.87 mha and production is about 9.46 mt whereas, its contribution to total production of oil seeds and total oil availability from 9 major oilseeds would be about 37% and 25%, respectively (Anonymous, 2008).

The productivity of soybean is very low in India (1.0 ton/ha) as compared to world's average yield of 2.24 tones/ha. So the present strategies and investigations for development of early maturing and high yielding soybean genotypes need further strengthening that requires adequate genetic information about this crop. Genetic information about the combining ability of parents and nature of gene effects helps in proper understanding of inheritance of characters, selection of suitable parents for hybridization and in isolating the promising early generation hybrids for further exploitation in breeding programmes. Such information is quite limited to soybean. In the present investigation efforts have been made to generate information on these aspects for different quantitative characters in soybean to help breeders in designing suitable breeding strategy to enhance the production potential of this crop.

Five genetically diverse genotypes originating from various agro-climatic zones of the country, namely JS 93-05, PS 562, JS 335, RAUS 5 and Bragg were included in investigation. These lines were crossed in diallel fashion in all possible combinations excluding reciprocals. Thus, the experimental material consisted of 15 entries (5 parents and 10 F_1's) and were grown during *kharif* 2007-08 in Randomized Block Design with three replications at Agricultural Research Farm, Andro, under Central Agricultural University, Imphal. The row-to-row and plant-to-plant distance were 45 and 10 cm, respectively. Observations were recorded on five randomly selected plants from each entry in each replication in respect of nine important characters namely days to 50% flowering, days to maturity, branches/plant, plant height (cm), number of pods/ plant, number of nodules/plant, grain yield/plant (g), 100-seed weight (g) and oil content (%). The combining ability analysis was carried out following method 2, model I (Griffing, 1956).

The knowledge on the mechanisms that control the main quantitative traits of agronomic interest of soybean is fundamental for genetic improvement and can be acquired through methodologies of diallel crosses. The values associated to the general combining ability (*gca*) of each parent and to the specific combining ability (*sca*) of each cross are estimated. The significant mean squares due to *gca* and highly significant mean squares due to *sca* for all the traits except number of branches/plant (Table 1)

**Author for Correspondence: E-mail:* shivdatts1@gmail.com, ssharma@icar.org.in

suggested that both additive and non-additive gene effects were important for the characters under investigation. Estimates of variances due to *gca* and *sca* suggested preponderance of additive gene effects for days to 50% flowering, days to maturity and plant height whereas non-additive gene effects for all the traits *viz*., days to 50% flowering, days to maturity, plant height (cm), number of pods/plant, number of nodules/plant, grain yield/plant, 100-seed weight and oil content (%).

Estimates of *gca* effects (Table 2) revealed that parent, Bragg was best combiner for days to 50% flowering and days to maturity. For grain yield/plant JS 335 and RAUS 5 exhibited positive and significant *gca* effects whereas, parent PS 562 was good combiner for number of nodules/plant. Significant positive *gca* effect for plant height was expressed by RAUS 5. The genotype JS 93-05 was best general combiner for days to maturity. Agrawal *et al*., (2006) reported the preponderance of non-additive gene effects for these traits in soybean. Sharma *et al*. (1997) also reported the preponderance of non-additive gene effects for days to maturity, plant height while non-additive effect for other traits. Singh *et al*. (1974); Gadag *et al*. (1999) have emphasized the importance of both additive and non-additive type of gene action for days to 50% flowering, days to maturity, plant height, 100-seed weight and grain yield/plant. Dominance of non-additive gene effects were also reported for pods/plant, seeds/plant and grain yield (Tawar *et al*., 1989; Li *et al*., 1991).

The crosses with high *sca* effects for different characters are presented in Table 3. Crosses JS 93-05 x PS 562, RAUS 5 x Bragg and PS 562 x RAUS 5 were high specific combiners for grain yield/plant. Amongst these, the cross PS 562 x RAUS 5 for days to 50% flowering, days to maturity and plant height had high specific combiner for these characters in addition to its being best combiner for grain yield/plant. The crosses JS 93-05 x Bragg and PS 562 x JS 335 showed maximum *sca* effects for 100-seed weight and best cross combiners for days to 50% flowering and number of pods/plant, respectively. The cross combination PS 562 x RAUS 5 exhibited best combiner for days to 50% flowering, days to maturity and plant height.

In the present study (Table 3), the parents involved in the crosses exhibited as general combiners as high x low or/ low x high and low x low in which the former combinations were more frequent. In crosses involving the parents in the combination of high x low and low x low performance, the genetic interactions might be of

Table 1. Analysis of variance for combining ability for nine traits in 5x5 diallel crosses of soybean

Source of variance	d.f.	Days to 50% flowering	Days to maturity	Number of branches/ plant	Plant height (cm)	No. of pods/ plant	No. of nodules/ plant	Grain yield/ plant	100-seed weight	Oil content (%)
gca	4	8.021 **	20.503 **	0.114	12.584 **	30.052	20.932 *	4.594 *	0.787 *	0.150
sca	10	4.535 **	19.574 **	0.266	14.510 **	41.212 **	85.224 **	4.655 **	1.466 **	1.181 **
Error	28	0.374	0.798	0.131	2.960	13.195	7.472	1.212	0.234	0.223
σ^2g		1.092	2.815	-0.002	1.375	2.408	1.923	0.483	0.079	-0.010
σ^2s		4.161	18.776	0.135	11.550	28.017	77.752	3.443	1.231	0.958
σ^2g / σ^2s		0.263	0.150	-0.018	0.119	0.086	0.025	0.140	0.064	-0.011

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

Table 2. Estimates of gca effects of the parents for different characters in 5x5 diallel cross of soybean

S.No.	Parents	Days to 50% flowering	Days to maturity	Number of branches/ plant	Plant height (cm)	No. of pods/ plant	No. of nodules/ plant	Grain yield/ plant	100-seed weight	Oil content (%)
1.	JS 93-05	-0.495 *	1.467 **	0.171	-0.352	-0.790	1.276	-0.521	0.174	-0.033
2.	PS 562	-0.829 **	-1.343 **	-0.019	-2.162 **	0.686	2.276 *	-0.240	0.327	0.229
3.	JS 335	-0.781 **	-1.057 **	-0.033	0.695	1.352	-1.581	0.841 *	-0.420 *	-0.033
4.	RAUS 5	0.410	-1.295 **	-0.176	1.267 *	1.971	-0.390	0.850 *	0.217	0.01
5.	Bragg	1.695 **	2.229 **	0.057	0.552	-3.219 *	-1.581	-0.930 *	-0.298	-0.176
	S.E. (gi)	0.206	0.301	0.122	0.581	1.227	0.924	0.372	0.163	0.159
	S.E. (gi-gj)	0.326	0.477	0.193	0.909	1.941	1.461	0.588	0.258	0.252

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

Table 3. Estimates of sca effects of the parents for different characters in 5x5 diallel cross of soybean

Crosses	Days to 50% flowering	Days to maturity	Branches/ plant	Plant height (cm)	No. of pods/ plant	No. of nodules/ plant	Grain yield/ plant (g)	100-seed weight (g)	Oil content (%)
JS 93-05xPS 562	0.63	0.69	-0.39	-2.39	-12.65 **(LxL)	-1.17	3.99 **(LxL)	-1.78	-1.04
JS 93-05xJS 335	-0.41	-5.58 **(HxL)	0.68 *	0.08	0.68	-4.98	0.02	-0.76	1.55
JS 93-05xRAUS 5	-0.60	-0.01	-0.34	-4.82 **(LxH)	1.06	-4.58	0.45	0.19	0.17
JS 93-05xBragg	1.11 *(LxH)	1.12 *(HxH)	0.09	-1.77	-0.74	-5.65	-0.77	1.21 *(LxL)	0.53
PS 562xJS 335	-0.41	-1.11	0.04	-3.11	4.20 *(LxL)	-0.98 1.01	1.48 *(LxH)	-1.37	
PS 562xRAUS5	3.06 **(LxL)	7.46 **(LxL)	-0.64 *	3.31 *(LxH)	-5.08 **(LxL)	-7.50 **(HxL)	1.87 *(LxH)	-1.89 *(LxL)	-0.58
PS 562x Bragg	-2.55 *(LxH)	-5.39 **(LxH)	0.28	0.69	2.44	14.01 **(HxL)	0.54	-0.41	-0.39
JS 335x RAUS 5	-1.65 *LxL)	-1.82 *(LxL)	0.19	-5.54 **(LxH)	2.92	8.68 **(LxL)	1.25	0.19	-0.82
JS 335x Bragg	-3.27 **(LxH)	-3.34 **(LxH)	0.29	2.50	6.44 **(LxH)	13.54 **(LxL)	1.19	0.23	-0.13
RAUS 5x Bragg	0.87	0.88	-0.55 *	-2.06	-4.84 *	-6.31 *(LxL)	2.64 *(HxL)	-0.26	-0.68
S.E. (Sij)	0.53	0.77	0.31	1.50	3.17	2.38	0.96	0.42	0.41
S.E. (Sij-Sik)	0.80	1.16	0.47	2.25	3.36	3.57	1.44	0.63	0.62

*, ** significant at 5% and 1% level, respectively; L: Low *gca* of parents, H: High *gca* of parents

additive x dominance and dominance x dominance type, respectively.

The category of combination for high x low *gca* effect play an important role in the expression of positive and significant *sca* effects. The cross combinations PS 562 x RAUS 5 and RAUS 5 x Bragg which involved one parent with desirable and significant *gca* effect for grain yield and other with poor or even negative *gca* effects. Such crosses showing high *sca* effects with at least one general combiner could produce desirable transgressive segregants in subsequent generations. Langhan, (1961) also suggested that high x low crosses might produce better transressive segregants in later generations.

In the present study, cross JS 93-05 x PS 562 was found to be in category of low x low *gca* effects. Such cross could be utilized in production of homozygous high yielding lines (Cho and Roy, 2000). It is evident that the crosses exhibited desirable *sca* effects involved parents with good, average or poor *gca* effects, indicating thereby influence of non-additive interactions in these crosses. Further, *gca* and *sca* of the parents and crosses, respectively, for grain yield largely depend on their respective combining abilities for one or more yield components. Parents JS 335, RAUS 5 and Bragg having been isolated as good general combiners for different traits may be suitably used in breeding programme.

Acknowledgement

The authors acknowledge the financial support rendered by All India Co-ordinated Research Project on Soybean for conducting the study.

References

Agrawal AP, PM Salimath and SA Patil (2005) Gene action ans combining ability analysis in soybean {*Glycine max* (L.) Merril}. *Legume Res.* **28:** 7-11.

Anonymous (2008) Directors Report and Summary Tables of Experiment. National Research Centre for Soybean, ICAR p 3.

Cho Y and AS Roy (2000) Combining ability of seed vigor and seed yield in soybean. *Euphytica* **112:** 145-150.

Gadag RN, HD Upadhyaya and JV Goud (1999) Genetic analysis of yield, protein, oil and other related traits in soybean. *Indian J. Genet.* **59:** 487-492.

Griffing B (1956) Concept of general and specific combining ability in relation to diallel cross system. *Aus. J. Biol. Sci.* **9:** 463-493.

Langham DC (1961) The high-low method of improvement. *Crop Sci.* **1**: 376-378.

Li XH, WM Chen and ZL Li (1991) Analysis of gene effects for some important agronomic characters in summer soybean. *Acta Agron. Sinica*. **17:** 453-460.

Sharma SR, PS Phul, RK Raheja and KL Ahuja (1997) Nature of gene effects for fatty acids in soybean. *Crop Imp.* **24:** 273-274.

Singh TP, KB Singh and JS Brar (1974) Diallel analysis in soybean. *Indian J. Genet.* **34:** 427-432.

Tawar ML, AK Mishra and SK Rao (1989) Gene action in soybean. *Indian J. Hered.* **21:** 10-16.