



Identification of Best General and Specific Combiners for Soybean Improvement

B. L. Meena^{a++}, N. R. Koli^{a#} and R K. Meena^{b++}

^a Department of Genetics and Plant Breeding, Agricultural Research Station, Kota, Rajasthan, India.

^b Department of Agronomy, College of Agriculture, Kota, Rajasthan, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present study on general combining ability effects and specific combining ability effects involves 15 parents viz., lines RKS 18, RKS 113, AUKS 199, AUKS 200, AUKS 212, RVSM 2011-35, JS 20-98, AUKS 202, AUKS 208, AUKS 218, JS 21-72, NRC 165 and tester JS 20-34, NRC 138, SL 958 with their 36 F₁ hybrid through Line x Tester mating system. The present investigation was undertaken using Randomized Block Design with three replications. The combining ability effects were estimated for thirteen characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-Seed weight, seed yield per plant, biological yield per plant, harvest index, protein content and oil content. The result showed that gca effects of parents and sca effects of hybrids were

⁺⁺ Assistant Professor;

[#] Associate Professor;

*Corresponding author: E-mail: blmeena.ubi45@gmail.com;

significant differed. Among the parents, AUKS 212 was found to be good general combiner based on the *per se* performance and gca effects for seed yield and other contributing traits and four hybrids AUKS 113 x SL 958, RVSM 2011-35 x NRC 138, AUKS 199 x JS 20-34 and NRC 165 x JS 20-34 were superior high sca effects for seed yield and yield contributing traits. These crosses can be utilized in future breeding programmes and exploitation of better segregants through pedigree method or single seed descent method in advance generations for improvement of yield and yield attributes coupled with quality traits sound soybean genotypes.

Keywords: Soybean; best general and specific combiners.

1. INTRODUCTION

“Soybean [*Glycine max* (L.) Merrill] is one of most important oil seed crop. It is rank first in oil seed production and it is also contributed 38% among the oil seed crops of India” [1]. “It is commonly known as *bhat* and *Kalitur* etc. Because of its multi uses, the soybean crop is called as “Golden Bean” or “Miracle crop of the world. It contain 18-20% oil and 38 to 42 percent protein, which has biological value as meat and fish protein. Soybean is predominantly self-pollinated crop due to cleistogamous nature and it is belong to the family fabaceae and sub family papilionace with $2n=40$ chromosome and is believed to have originated in North Eastern China” [2,3]. Soybean oil contain 85% poly-unsaturated fatty acid with two essential fatty acids (linoleic and linolenic acid) and good quality protein, which has biological value as meat and fish protein. Globally, the crop contributes about 25% to the total edible oil production. Five countries viz., United State of America, Brazil, Argentina, China and India account for 90% of total world production. Surpassing China, India ranks fourth in term of area but in term of production it ranks fifth after China. In India, Madhya Pradesh is the single largest producer in the country followed by Maharashtra, Rajasthan, accounting for about 45%, 39% and 8% of total production. respectively. Even after being a leading oilseed crop, the yield level is well below the potential and almost stagnated at around 10-11 qt/ha in the country from the variation through recombination followed by selection.

“Combining ability analysis is a powerful tool to identify the parents having good potential to transmit desirable characteristics to their offspring and also to help in sorting out promising crosses for seed yield and other yield contributing traits in soybean” [4]. “The knowledge of combining ability is useful to assess the nicking ability of parents and at the same time elucidating the nature and magnitude of

different types of gene action involved. This can also be immense help to exploit hybrid vigor in the heterosis breeding, which indicates the ability of parents to combine well in hybrid combinations. One of the most important factors which determine the success of hybrid production is the nature and magnitude of heterotic over the better parent and the check. Latter a commercially exploitable heterosis exhibits by the cross commercial exploitation of heterosis has not become a reality in soybean mainly due to the self-pollinated nature of crop and it's not feasible to produce sufficient quantity of F_1 hybrid seed” [5]. This information can be utilized for adoption of appropriate breeding methods for improving the crop.

2. MATERIALS AND METHODS

Thirty six F_1 hybrids and fifteen parental lines along with one check JS 95-60 were grown in a randomized block design with three replication at Research field of Agricultural Research Station, Ummedganj, Agriculture University, Kota during *Kharif*, 2021. Each parent was sown in two rows along with a single row of F_1 hybrids of three-meter in length by adopting the spacing 45×10 cm. The recommended package and practices were followed to raise healthy crops during the crop period. Five representative plants from each parental line and all F_1 s were selected from each replication and tagged. The data for plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed yield per plant (g), biological yield per plant (g) and harvest index (%) were recorded on these selected plants. Whereas, observations for days to 50% flowering and days to maturity were recorded on whole plot basis and hundred seed weight (g), oil content (%) and protein content (%) were calculated from composite seeds of selected plants. The average values for these characters were calculated and used for statistical analysis. The technique of Line x tester analysis [5]. However, there are few reports to utilize line x tester analysis for

combining ability analysis in self-pollinating crops such as soybean [6-8]. tends itself to detailed genetic analysis, identification of superior parents and cross combination on the basis of combining ability besides providing information pertaining to the nature and magnitude of gene action.

3. RESULTS AND DISCUSSION

The general and specific combining ability are the main criteria rapid genetic assaying of the tested genotypes under line x tester design. The good general and specific combiners for thirteen characters of soybean have been presented in Table 1 and 2. The negative GCA effect are desirable in days to 50 % flowering, days to maturity and plant height. The parents, AUKS 199, AUKS 202, AUKS 208, NRC 165 among lines and JS 20-34 and NRC 138 among testers were good general combiner for days to 50 % flowering, day to maturity and plant height. Therefore, these parents could be utilized in future breeding programme to exploit better segregants for earliness and dwarfness.

In terms of seed production per plant, number of branches per plant, number of pods per plant, number of seeds per pod, length of pod, 100-seed weight, biological yield per plant, harvest index, protein content, and oil content, the line AUKS 212 was a good general combiner. RVSM 2011-35 was demonstrated to be a good general combiner in terms of seed production per plant, number of pods per plant, pod length, 100-seed weight, biological yield per plant, harvest index protein content, and oil content. The line RKS 18 was determined to be a capable general combiner in terms of seed production per plant, days to maturity, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, and protein content. In terms of seed yield per plant, number of branches per plant, number of pods per plant, pod length, and harvest index, the tester SL 958 was found to be an excellent general combiner.

On the basis of general combining ability revealed that lines AUKS 212, RVSM 2011-35, RKS 18 and tester SL 958 were observed as good general combiner with high *per se* performance for seed yield and most of the its contributing traits. The findings as observed in present study is accordance with Tadesse et al. [9], Indu et al. [10], Painkra [11], Nag et.al. [12] in

soybean. The gca effect is confined to additive gene action which is fixable in nature therefore, direct selection of these parents might be useful for recombination breeding programme as parents for yield improvement in soybean.

Based on the specific combining ability estimates the cross RKS 113 x SL 958 had the greatest performance for seed yield per plant, Plant height (cm), Number of branches per plant, number of pods per plant, Number of seeds per pod, biological yield per plant (g), harvest index (%), protein content (%) and oil content (%). from out of twelve characters which shows this cross was the best specific combiner for those characters, while the cross RVSM 2011-35 x NRC 138 was the best performed cross for seed yield per plant, Days to 50% flowering, days to maturity, pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant (g), Harvest index (%) and oil content (%) and protein content (%). The cross AUKS 199 x JS 20-34 was found to be the good specific combiner for seed yield per plant, number of seeds per pod, number of seeds per pod, pod length (cm), biological yield per plant (g) and oil content. The cross NRC 165 x JS 20-34 was found to be the good specific combiner for seed yield per plant, number of pods per plant, Number of seeds per pod, Pod length, 100-Seed weight, biological yield per plant, protein content and oil content. These results are in agreement with the earlier results reported by Felahi et al [13], Samant et. al. [14], Wahyu et al. [15], Tadesse et al. [9], and Painkra et. al. [11].

The result showed that gca effects of parents and sca effects of hybrids were significant differed. Among the parents, AUKS 212 was found to be good general combiner based on the *per se* performance and gca effects for seed yield and other contributing traits. Among the 36 F₁ hybrids, crosses AUKS 212 x SL 958, RKS 113 x SL 958, RVSM 2011-35 x NRC 138, AUKS 212 x NRC 138, AUKS 212 x JS 20-34 and RVSM 2011-35 x JS 20-34 were superior on the basis of *per se* performance and sca effects for seed yield and yield contributing traits [16]. These crosses can be utilized in future breeding programmes and exploitation of better segregants through pedigree method or single seed descent method in advance generations for improvement of yield and yield attributes coupled with quality traits sound soybean genotypes.

Table 1. Promising parents (lines and testers) based on gca effects for seed yield and its contributing traits in soybean

Sr. No.	Genotypes	GCA effects	Desirable gca effects for yield and its contributing traits
1.	AUKS 212	7.27**	Plant height, Primary branches per plant, pods per plant, number of seeds per pod, pod length, 100-seed weight, biological yield per plant, harvest index, protein content and oil content
2	RVSM 2011-35	5.34**	Number of pods per plant, Number of seed per pod, pod length, 100-seed weight, biological yield, harvest index, protein content and oil content.
3	RKS 18	3.82**	Days to maturity, Plant height, Number of pods per plant, Number of seed per pod, biological yield, harvest index and protein content.
4	SL 958	0.53*	Number of branches per plant, Number of pods per plant, pod length, and Harvest index.

*, ** Significant at 5 % and 1 % levels of significance, respectively

Table 2. Promising hybrids based on SCA effects of seed yield and its contributing traits in Soybean

Sr.No	Hybrids	SCA effects	Component traits showing SCA effects in desired direction
1	RKS 113 x SL 958	7.57**	Plant height, Number of branches per plant, number of pods per plant, Number of seeds per pod, biological yield per plant, harvest index, protein content and oil content.
2	RVSM 2011-35 x NRC 138	2.13**	Days to flowering, days to maturity, pods per plant, number of seeds per pod, 100-seed weight and biological yield per plant, Harvest index and oil content.
3	AUKS 199 x JS 20-34	1.81*	number of seeds per pod, Number of seeds per pod, pod length, biological yield per plant and oil content.
4	NRC 165 x JS 20-34	1.54*	number of pods per plant, Number of seeds per pod, Pod length, 100-Seed weight, biological yield per plant, protein content and oil content.

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

The cross combinations RKS 113 x SL 958 and RVSM 2011-35 x NRC 138 were the best particular combinations, whereas the parental genotypes AUKS 212, RVSM 2011-35, and RKS Line x tester were the greatest general combiners. Although heterosis breeding may benefit greatly from certain cross combinations, it is not widely used in crops such as soybeans [17]. In order to improve yield and yield attributes in conjunction with quality traits in sound soybean genotypes, these potential genotypes can be used in future breeding programs and to exploit better segregants using the pedigree technique or single seed descent method in advance generations.

4. CONCLUSION

Line x Tester analysis is used in estimating the effects of the general combining ability of parents and specific combining ability of crosses. Over all present study on gca and sca effects, the line AUKS 212, RVSM 2011-35, and RKS 18 were found good general combiner and four hybrids RKS 113 x SL 958, RVSM 2011-35 x NRC 138, AUKS 199 x JS 20-34 and NRC 165 x JS 20-34 were found good specific combiners for yield and yield contributing traits. These crosses can be utilized in future breeding programmes and exploitation of better segregants through pedigree method or single seed descent method in advance generations for improvement of yield and yield attributes coupled with quality traits sound soybean genotypes.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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