Line x Tester Analysis of Combing Ability for Seed Yield and Its Contributing Traits in Soybean [*Glycine max* (L.) Merrill]

ABSTRACT

Hybridization in Line x Tester mating design was conducted with seven lines and three diverse testers in soybean to understand the nature of gene action, combining ability of the parents (*gca*) and to assess the potential for the exploitation of heterosis (*sca*) in hybrids. Data on eleven quantitative characters *viz.*, days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g), seed yield per plant (g), biological yield per plant and harvest index were collected on 21 hybrids and their 10 parents. The ratio of SCA variance to GCA variance is less than unity indicated that non additive genetic effects were predominant for control of most of the seed yield and its attributing characters. Among the lines, AUKS 238, RKS 18, RVS 2011-10 were found high *gca* effects which are use as general combiner parents for enhancing yield potential by assembling the favourable genes and crosses with *sca* effects such as AUKS 224 x JS 20-98 and RVS 2011-10 x NRC 150 were found to be superior for seed yield and yield components. These crosses may be utilized for heterosis breeding as well as for isolating the superior recombinants in advance generation for seed yield

Keywords : Seed Yield, Line x Tester Analysis, , Combing Ability , Soybean

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is one of most important oil seed crops in the world as well as in India. Soybean is first rank in our country in oil seed production followed by rapeseed-mustard, groundnut and sunflower among oil seed crops of India and it is also contributes about 38% in oil seed production Joshi *et. al.* [1]. Soybean is self-pollinated, diploid (2n=40) crop and originated from North Eastern China, Vavilov [2] and Leppik [3]). It is cheapest source of vegetable protein (38-42%) and oil content in seed (18-21%), which makes it participate in many industries such as the production of poultry & animal feed and some human foods like baby milk and soy sauce. Soybean crop is called as “Golden Bean” or Miracle crop due to its high nutritive value and numerous uses. It is also help to improve the soil fertility by fixing atmospheric nitrogen with the help of symbiotic bacteria, Rhizobium present in root nodules.

Recombination breeding has been extensively used to create the variability reservoir for exploitation in a breeding program. In a systematic breeding program, it is essential to identify the elite parents for hybridization and superior crosses to expand the variability reservoirs for the selection of superior genotypes. Combining ability essentially tell us how well a parent performs when crossed with different partners. This help breeder identify parent which consistently produce high performing progeny. Whereas, gene action delves deeps, revealing the underlying mechanism by which gene influence traits like yield and its related traits. Therefore, evaluating breeding materials both GCA and SCA along with heterosis for seed yield and its contributing traits, becomes the foundation for any successful breeding programme. Its unlocking these genetic secret for full potential of their crops. The current studies focus to analysed the capacity and genetic makeup of seed yield and its related traits in soybean through using the Line x Tester mating design.

MATERIALS AND METHODS

The experiment material was consist ten parents of soybean, consisting seven lines *viz*., AUKS 224, RKS 18, AUKS 207, AUKS 234, AUKS 238, RVS 2011-10, JS 20-116 and three testers *viz.*, NRC 130, NRC 150, JS 20-98 were crossed in all possible combinations in Line x Tester mating design during *Kharif*-2022 and all genotypes including 21 F_1 hybrids and 10 parents were evaluated in Randomized Block design with three replications during *Kharif*, 2023 at Research field on Agricultural Research Station, Agriculture University, Kota (Rajasthan). Each parent was sown in two rows along with a single row of F_1hybrids of three meter in length by adopting the spacing 45 x 10 cm. Recommended agronomic & plant protection package of practice were followed to raise healthy crop. Observation were recorded on randomly selected five tagged plants and other yield contributing traits viz., Days to 50% flowering, Days to maturity, Plant height (cm), Number of branches per plant, Number of pods per plants, Pod length (cm), Number of seeds per pod, 100-seed weight (g), Seed yield per plant (g), biological yield per plant (g) and harvest index (%). Line x tester analysis was carried out for determining the effects due to general combining ability and specific combining ability as describe by Kempthorne [4] and adapted by Singh and Chaudhary [5].

RESULT AND DISCUSSION

The ANOVA exhibited mean square due to genotypes, parents, crosses, lines, testers (except for pod length and harvest index) and line x tester (except for pod length) were highly significant differences for all the traits namely days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100- seed weight (g), seed yield per plant (g), biological yield per plant and harvest index (%)indicating the existence of wider genetic diversity among the lines, testers and crosses under study (Table-1). The ratio of variance of GCA to SCA was less than unity

Table-1. Analysis of variance for combining ability in Line x Tester analysis for seed yield and its related traits in soybean

Source of variation	D f	Days to flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Seed yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
Replications	2	0.70	0.51	24.14	0.08	105.21	0.04	0.01	0.11	0.33	10.88	1.36
Genotypes	31	117.94**	186.95**	277.28**	4.56**	265.72**	0.16**	0.15**	1.38**	49.90**	144.65**	45.60**
Parents	9	116.58**	266.24**	305.38**	4.79**	99.10*	0.17**	0.10**	1.45**	8.99**	44.67**	24.50**
Lines	6	113.96**	119.81**	187.13**	4.29**	272.72**	0.28**	0.54**	3.92**	131.44**	185.95**	140.33**
Testers	2	722.11**	1074.11**	1833.32**	4.86**	215.95*	0.08*	0.02	0.81**	11.45**	63.02**	8.99
Crosses	20	121.72**	164.01**	283.69**	3.58**	210.38**	0.16**	0.18**	1.40**	60.21**	112.05**	58.94**
P vc C	1	5.85*	1.57	17.10	26.63**	201.15*	0.10*	0.10	0.29*	122.24**	602.95**	12.77
Lines x Testers	12	25.54**	34.43**	73.70**	3.01**	178.28**	0.11**	0.03	0.24**	32.73**	83.26**	26.52**
Error	62	1.29	1.61	23.58	0.11	44.58	0.02	0.03	0.07	1.13	4.73	4.16
GCA Variance		10.338	11.883	15.300	-0.026	-10.297	-0.009	-0.007	-0.026	-3.217	-6.264	-2.541
SCA variance		14.346	22.982	35.125	1.169	72.039	0.067	0.060	0.437	26.392	50.676	23.141
GCA/SCA		0.721	0.517	0.436	0.022	-0.143	-0.134	-0.117	-0.059	-0.122	-0.124	-0.109

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

for all traits, indicating preponderance of non-additive gene action governing the traits. Similar result were reported by Nag *et.al*. [6], Indu *et.al*. [7] and Sen *et. al*. [8].

The success of any breeding programmes extensively depends on choice of parents used in the hybridization. Gilbert [9] suggested that the parents with good *per se* performance would result in better hybrids. Genotypes with high *per se* performance and high *gca* effects could be useful in developing desirable segregants in the breeding programme. The *gca* effects is due to additive gene action is fixable, Sprague and Tatum [10]. The general and specific combining ability are the main criteria of rapid genetic assaying of tested genotypes under line x tester design. The effects of general Combining ability of parents (lines and Testers) are useful tools for selecting the cross parents. The general combining ability effects of parents for different traits are presented in Table -2. Among the genotypes studies, no entry had manifested good general combining ability for all the quantitative traits. However, good combiners identified for high seed yield per plant are AUKS 238 (5.50) followed by RVS 2011-10 (3.57) and AUKS 224 (2.06). Earliness is an important breeding objective. Negative GCA effects are desirable for days to 50% flowering and days to maturity. The lines AUKS 207 (-4.62), AUKS 234 (-2.29), AUKS 224(-1.95) and tester NRC 130 (-4.21), NRC 150 (-2.49) for days to 50% flowering and lines, AUKS 207 (-5.00), AUKS 224 (-2.67), AUKS 234 (-2.00) and tester NRC 130 (-4.78) and NRC 150 (-3.44) for days to maturity were exhibited significant GCA effects respectively, which are identified to be good general combiners to achieve earliness. Two lines AUKS 234 (-5.85) and AUKS 207 (-4.86) were found to be best general combiner for short plant stature. The lines RKS 18 (0.61), AUKS 238 (0.59), AUKS 207 (0.55). RVS 2011-10 (0.27) and tester JS 20-98 (0.52) were found good general combiner for number of branches per plant. For the trait, number of pods per plant, lines AUKS 238 (8.03) and tester JS 20-98 (3.48) were identified to be good general combiners. The lines AUKS 238 (0.22), AUKS 224 (0.18), RVS 2011-10 (0.13) were found good general combiners for number of seeds per pod. The lines, RVS 2011-10 (0.37), and AUKS 238 (0.24) were found best general combiners for pod length. For the trait, 100-Seed weight, lines AUKS 234 (0.81), RVS 2011-10 (0.62), AUKS 238 (0.42) and tester NRC 130 90.17) were identified best combiners. The lines AUKS 238 (6.16), AUKS 224 (4.02), RVS 2011-10 (2.46) and tester NRC 150 (1.91) were found good general combiners for biological yield per plant. The line, AUKS 238 (5.42), RVS 2011-10 (4.52) and AUKS 224 (1.78) were identified to be good general combiners for harvest index, thus it was observed from this studies that parents AUKS 238, RVS 2011-10 and AUKS 234 have recorded high *per se* performance and high *gca* effects. Hence, improvement

Table-2: General combing ability (*gca*) effects in the parental genotypes for seed yield and its related traits in soybean.

S. No.	**Parents**	**Days to 50% Flowering**	**DaystoMaturity**	**Plant height (cm)**	**Number of branches/ plant**	**Number of pods/per plant**	**Number of seeds/ pod**	**Pod length**	**100-seed weight**	**Seed yield per plant**	**Biological yield per plant**	**Harvest index (%)**
	LINES											
1	AUKS 224	-1.95**	-2.67**	-0.49	-0.47**	4.14	0.18**	-0.12*	-0.88**	2.06**	4.02**	1.78*
2	RKS 18	2.83**	4.67**	5.20**	0.61**	-3.04	-0.07	0.01	-0.07	-1.60**	-0.61	-2.54**
3	AUKS 207	-4.62**	-5.00**	-4.86**	0.55**	-0.85	-0.15**	-0.36**	-0.14	-3.16**	-2.75**	-3.51**
4	AUKS 234	-2.29**	-2.00**	-5.85**	-1.19**	-4.00	-0.10	0.00	0.81**	-1.24**	-2.12**	-0.64
5	AUKS 238	0.71	1.56**	-2.28	0.59**	8.03**	0.22**	0.24**	0.42**	5.50**	6.16**	5.42**
6	RVS2011-10	-0.73	-0.89	4.43*	0.27*	3.57	0.13**	0.37**	0.62**	3.57**	2.46**	4.52**
7	JS 20-116	6.05**	4.33**	3.84*	-0.36**	-7.85**	-0.22**	-0.14*	-0.77**	-5.13**	-7.16**	-4.74**
	SE	0.40	0.45	1.73	0.12	2.38	0.05	0.06	0.09	0.38	0.78	0.73
	gi-gj	0.54	0.60	2.29	0.16	3.15	0.06	0.08	0.12	0.50	1.03	0.96
	TESTER											
1	NRC 130	-4.21**	-4.78**	-5.75**	-0.09	-2.84	0.01	-0.04	0.17*	-0.85**	-1.46**	-0.50
2	NRC 150	-2.49**	-3.44**	-5.03**	-0.43**	-0.63	0.06	0.02	0.05	0.46	1.91**	-0.24
3	JS 20-98	6.70**	8.22**	10.78**	0.52**	3.48*	-0.07*	0.01	-0.22	0.39	-0.46	0.74
	SE	0.29	0.32	1.22	0.09	1.68	0.03	0.04	0.07	0.27	0.55	0.51
	gi-gj	0.35	0.39	1.50	0.10	2.06	0.04	0.05	0.08	0.33	0.67	0.63

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

Table-3: Specific combining ability effects (*sca*) of Line x Tester hybrids for seed yield and its related train in soybean.

Crosses	**Days to 50% Flowering**	**DaystoMaturity**	**Plant height (cm)**	**Numberof branches /plant**	**Number of pods/plant**	**Number of seeds/ pod**	**Pod length**	**100-seed weight**	**Seed yield per plant**	**Biological yield per plant**	**Harvest index (%)**
AUKS 224 x NRC 130	1.10	2.00*	0.20	-0.09	-1.00	0.06	-0.02	-0.17	-0.62	1.43	-1.68
RKS 18 x NRC 130	-2.68**	-5.33**	1.39	-0.87**	-1.99	-0.29**	-0.05	0.16	-2.53**	-3.40*	-2.20
AUKS 207 x NRC 130	3.43**	3.00**	-5.38	-1.42**	7.73	0.19	0.08	-0.11	1.84*	3.85*	1.08
AUKS 234 x NRC 130	3.10**	2.33*	2.58	1.05**	-3.46	0.04	0.13	-0.14	-0.75	-1.47	-0.67
AUKS 238 x NRC 130	-3.57**	-2.22*	-4.75	-0.05	-0.78	0.05	0.01	-0.07	0.05	-3.16*	1.85
RVS 2011-10 x NRC 130	-1.13	1.22	7.28*	1.15**	-0.29	0.04	-0.11	0.46*	1.01	3.12*	-0.09
JS 20-116 x NRC 130	-0.24	-1.00	-1.32	0.23	-0.21	-0.09	-0.04	-0.13	1.00	-0.38	1.70
AUKS 224 x NRC 150	-2.95**	-2.67**	4.17	-0.28	-0.44	0.06	-0.00	0.08	0.90	1.04	0.77
RKS 18 x NRC 150	1.27	0.00	2.24	-0.16	-14.07**	-0.15	-0.01	0.17	-5.18**	-7.97**	-4.25**
AUKS 207 x NRC 150	-0.62	0.67	2.95	0.56*	-0.77	0.01	-0.06	-0.23	0.99	0.72	1.42
AUKS 234 x NRC 150	-3.95**	-3.33**	-1.81	-1.02**	6.40	-0.01	-0.01	0.03	1.31	2.86	0.70
AUKS 238 x NRC 150	3.71**	3.44**	0.73	0.02	0.71	0.02	0.12	-0.14	-1.02	0.13	-1.65
RVS 2011-10 x NRC 150	1.49	-0.44	-9.23**	0.01	2.13	0.08	-0.03	0.03	1.96*	2.73	1.30
JS 20-116 x NRC 150	1.05	2.33*	0.96	0.88**	6.04	-0.02	-0.00	0.06	1.04	0.48	1.71
AUKS 224 x JS 20-98	1.86*	0.67	-4.37	0.37	1.45	-0.12	0.03	0.08	-0.28	-2.48	0.91
RKS 18 x JS 20-98	1.41	5.33**	-3.63	1.03**	16.06**	0.44**	0.06	-0.33	7.71**	11.37**	6.45**
AUKS 207 x JS 20-98	-2.81**	-3.67**	2.43	0.87**	-6.96	-0.20*	-0.02	0.34	-2.83**	-4.57**	-2.51
AUKS 234 x JS 20-98	0.86	1.00	-0.76	-0.03	-2.94	-0.03	-0.11	0.11	-0.56	-1.38	-0.03
AUKS 238 x JS 20-98	-0.14	-1.22	4.02	0.04	0.08	-0.07	-0.14	0.21	0.97	3.03	-0.21
RVS 2011-10 x JS 20-98	-0.37	-0.78	1.96	-1.16**	-1.85	-0.12	0.14	-0.49*	-2.97**	-5.86**	-1.21
JS 20-116 x JS 20-98	-0.81	-1.33	0.36	-1.11**	-5.83	0.11	0.04	0.07	-2.04**	-0.10	-3.41*
SE	0.81	0.90	3.46	0.24	4.76	0.09	0.12	0.18	0.76	1.55	1.45
Sij-Sjk	1.13	1.26	4.82	0.33	6.62	0.13	0.17	0.26	1.06	2.16	2.02

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

of these genotypes in the crossing programme would result in the identification of superior segregants with favourable genes for seed yield and its contributing traits.

Specific combing ability is the deviation from the performance predicted on the basis of general combing ability, Allard [11]. High sca effects alone may not be the appropriate choice of hybrids for heterosis exploitation because the hybrids with low mean value may also posses high sca effects, even if the gca effects of parents were very low or even negative, Grakh and Chaudhary [12]. In present studies, the specific combining ability effects of 21 F_1 crosses for eleven quantitative traits were computed in Table-3. Three cross combinations *viz*., RKS 18 x JS 20-98 (good x average), RVS 2011-10 x NRC 150 (good x average) and AUKS 207 x NRC 130 (poor x poor) were identified as best cross for most of the traits among all 21 F_1 crosses. A combination of good general combiners was not necessarily the best cross nor was poor x poor cross always a poor combination. Accumulation of favourable genes might be the cause of parents with poor *gca* effects giving rise to crosses with higher *sca* effects. Similar finding also observed earlier by Raju *et al.*[13], Fasahat *et al.*[14] and Painkra *et. al*. [15]. Therefore, theses crosses may be utilized for heterosis breeding as well as for isolating the promising segregates in advanced generation for seed yield as these crosses are under the control of additive gene action which are fixable. However, the ratio of GCA/SCA variance indicated the preponderance of non-additive or dominance effects for seed yield in soybean. Datta *et.al*. [16], Samant *et. al*[17] and Nag *et.al*[6] and Tadesse *et.al*. [18] reported earlier in soybean. Hence, the lines AUKS 238, RVS 2011-10 and AUKS 234 were identified as good general combiner with high *per se* performance for most of the quantitative traits. The *gca* effect is confined to additive gene action which is fixable in nature therefore, selection of these parents might be useful for recombination breeding programme as parents for yield improvement in soybean. Cross combinations RKS 18 x JS 20-98 and RVS 2011-10 x NRC 150 were exhibited significant *sca* effects and high *per se* performance for most of the quantitative traits. These crosses could be utilized for selection of superior segregants for developing improved cultivars in future.

CONCLUSION

Line x tester analysis is used in predicting *gca* effects of parents and *sca* effects of their crosses and understand the nature of gene action. The lines AUKS 238, RVS 2011-10 and AUKS 234were identified as good general combiner with high *per se* performance for most of the quantitative traits. The *gca* effect is confined to additive gene action which is fixable in nature. Therefore, selection of these parents might be useful for recombination breeding programme as parents for yield improvement in soybean and cross combinations

RKS 18 x JS 20-98 andRVS 2011-10 x NRC 150 were exhibited significant *sca* effects and high *per se* performance for most of the quantitative traits. These crosses would produce superior recombinants for seed yield.

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