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Estimation of heterosis and combining ability for oil and protein content in soybean [*Glycine max* (L.) Merrill]

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Abstract

The analysed the heterosis and combining ability for protein content and oil content in soybean. 21 F₁ hybrids were developed from crosses between seven line and three tester of soybean in line x tester mating design. These 21 crosses along with parent including check JS 95-60 were evaluated in Randomized Block design with three replications. In present study on mean performance, heterosis and combining ability, crosses viz., RKS 18 x JS 20-98, RVS 2011-10 x NRC 150, RVS 2011-10 x NRC 130 and AUKS 238 x JS 20-98 were identified for quality traits. The results of present study suggested that heterosis coupled with high SCA effects might be considered as a criteria for selecting crosses for further improvement with respect to quality traits.

Keywords: Heterosis, combining ability, soybean, protein content, oil content, F₁ hybrids

Introduction

Soybean [*Glycine max* (L.) Merrill.] is energy rich oil seed crop. It contains 40-42% high quality protein and 18-20% vegetable oil in which 85% unsaturated acid. Soybean not only contains high quality protein but higher than other legume crops. Soybean like other legume, is useful for crop rotation due to ability to fix nitrogen from the air. Soybean is self-pollination crop having $2n = 2x = 40$. Its member of Fabaceae family and sub-family Papilionaceae and originated in North Eastern China. Soybean is cheapest, richest and easiest sources of best quality protein. Multiple uses of as food and industries products, soybean is called as "wonder crop" or "Miracle crop of the world". As compared to other legumes and cereals it has highest protein content of 42% where as other legumes have a protein content of 20-30% and cereals have protein content ranged approximately 8-15%. Soybean has second highest oil content among all food legumes, with peanut having oil content of approximately 48% on dry matter basis and chickpea as third highest (5% oil content) Salunkhe ^[1]. Other nutritionally important components found in soybeans include phospholipids, vitamins, and minerals. In addition to this, soybean also contains minor substance such as phytates, trypsin inhibitors, and oligosaccharides, in biologically active form.

To develop elite and better nutritional quality varieties through a systematic approach has to be adopted. Protein and oil are polygenic character and its improvement is basically based upon identification of quality traits as well as selection of parents or lines, which can be effectively used for developing superior quality genotypes for any breeding programme. The first step in a successful breeding program is to select appropriate parents. However, a major issue is selection of parents based on per se performance which lacks fidelity and obvious failures to identify better parents. Therefore, it is essential to identify parents based on nicking ability in cross combinations rather than per se performance only. In order to choose appropriate parents and crosses, and to determine the combining abilities of parents in early generation.

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 heterosis over the better parent and the check. Latter a commercially exploitable heterosis exhibits by the cross commercial exploitation of heterosis has not

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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. The technique of Line x tester analysis Kempthorne ^[2] 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. This information can be utilized for adoption of appropriate breeding methods for improving the crop.

Materials and Methods

The study was conducted at Agricultural Research Station, Kota Agriculture University, Kota. The material used for the present study was developed by crossing seven soybean genotypes viz., AUKS 224, RKS 18, AUKS 207, AUKS 234, AUKS 238, RVS 2011-10, JS 20-116 as line and three genotypes viz., NRC 130, NRC 150 and JS 20-98 as testers. Crossing was taken up in a line x tester fashion as proposed by Kempthorne, ^[2]. The 21 crosses along with their parents were raised in randomized block design with three replications. 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. The protein content was estimated by using the method described by Lowry ^[3]. While oil content in seed samples was analysed by Soxhlet ^[4] extraction method at the central laboratory of Ummedganj Kota. Different types of heterosis viz. heterosis over mid parent (MP), heterosis over better parent (Heterobeltiosis) and economic heterosis over standard check (JS 95-60) were estimated using mean values. Analysis of Line x Tester data for combining ability was done according to Kempthorne ^[2] and Arunachalam ^[5].

Results and Discussion

Mean square due to genotypes was significant for the traits of quality such as protein content and oil content that is indicating the experimental material has sufficient genetic variability for above mention the traits. Average heterosis, hetero-beltiosis and standard heterosis (JS 95-60 as check) were estimated and result are represented in table 1 to 3. Out of among the 21 F_1 crosses, ten crosses, four crosses and sixteen crosses were observed highly significant of average heterosis, heterobeltiosis and standard heterosis for protein content respectively. Four crosses viz., AUKS 238 x NRC 130, JS 20-116 x NRC 130, AUKS 207 x NRC 150 and RVS 2011-10 x NRC 150 were found positively significant for all three types of heterosis such as average heterosis, hetero-beltiosis and standard heterosis for protein content. Similar result were reported earlier by Samant ^[6], Indu ^[7] and Nag ^[8]. For oil content, eleven and five crosses viz. AUKS 238 x NRC 130, RVS 2011-10 x NRC 130, AUKS 224 x NRC 150, RKS 18 x JS 20-98 and AUKS 238 x JS 20-98, showed significant and positive heterosis over mid parent and standard check, respectively. Only one cross RVS 2011-10 x NRC 130 was found highly significant for all three types of heterosis such as average heterosis, heterobeltiosis and standard heterosis. Bhavani ^[9], Indu ^[7] and Nag ^[8] also reported earlier for oil content in soybean. over all study on standard heterosis, eight crosses were found superior while two crosses AUKS 238 x JS 20-98 and RVS 2011-10 x NRC 150 were observed highest standard heterosis for both protein and oil content with high per se performance.

In self-pollinated crops, difficult in obtaining hybrids seed are hindrance to extensive crossing. However, the crosses attempted, in order to be rewarding, should be made between well-chosen parents. Joshi ^[10] while reviewing breeding methodology in autogamous crops emphasised that besides *per se* performance the parents should be selected on consideration of genetic diversity, phenotypic stability, combining ability and genetic analysis of targeted. In this context combining ability studies provide required information about the nature and magnitude of genetic variation along with the nicking ability of genotypes. It will be help in identifying superior parents and crosses that could be effectively utilized in breeding programme. Such study may also reflect the possibility of obtaining rare favourable combinations of characters in segregating generations.

Table 1: Heterosis (MP), Hetero-beltiosis (BP) and Standard heterosis (SC) for quality traits in soybean.

Crosses	Protein content (%)			Oil content (%)		
	MP	BP	SC	MP	BP	SC
AUKS 224 x NRC 130	1.83**	1.61	5.65**	2.09	0.22	5.12**
RKS 18 x NRC 130	0.26	-0.62	3.31**	-3.94**	-7.28**	-3.83*
AUKS 207 x NRC 130	-3.47**	-5.55**	-1.53	1.10	0.62	4.79**
AUKS 234 x NRC 130	1.39*	0.41	4.62**	-0.71	-3.13*	1.41
AUKS 238 x NRC 130	3.68**	2.30**	5.96**	3.92**	0.63	12.83**
RVS 2011-10 x NRC 130	1.62*	-0.25	3.81**	7.60**	5.53**	10.77**
JS 20-116 x NRC 130	1.61*	1.62*	5.47**	-9.91**	-10.31**	-7.13**
AUKS 224 x NRC 150	1.37*	1.05	4.62**	2.62*	-0.79	7.62**
RKS 18 x NRC 150	-3.45**	-3.68**	-1.19	-2.37	-6.69**	0.79
AUKS 207 x NRC 150	2.07**	1.45*	3.79**	0.63	-1.62	6.45**
AUKS 234 x NRC 150	-0.80	-1.02	1.66*	-6.87**	-9.93**	-2.78
AUKS 238 x NRC 150	2.15*	1.09	3.75**	2.13	0.17	12.77**
RVS 2011-10 x NRC 150	3.74**	2.29**	4.84**	2.13	-2.17	5.90**
JS 20-116 x NRC 150	-6.63**	-7.50**	-3.39**	0.91	-2.23	5.53**
AUKS 224 x JS 20-98	-0.33	-0.80	3.36**	-0.15	-0.61	1.15
RKS 18 x JS 20-98	-0.45	-1.35	2.35**	3.23*	0.91	2.46
AUKS 207 x JS 20-98	-4.02**	-5.79**	-2.31**	2.29	1.33	5.05**
AUKS 234 x JS 20-98	-1.03	-1.61*	2.22*	-8.41**	-8.52**	-7.39**
AUKS 238 x JS 20-98	2.20**	0.53	4.14**	6.05**	0.49	12.79**
RVS 2011-10 x JS 20-98	0.61	-1.12	2.65**	2.11	0.76	2.51
JS 20-116 x JS 20-98	-4.12**	-3.91**	-0.11	1.47	1.37	3.45*

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

Analysis of variance for combining ability revealed that the variances due to GCA and SCA were significant for the trait, protein and oil content. This indicated existence of genetic variability in the parental lines and involvement of both additive and non-additive gene effects in the inheritance of these traits. Magnitude of GCA and SCA variances revealed that the SCA variances were higher than their respective GCA variances for all the traits. Ratio between GCA and SCA variance was less than unity indicating that nonadditive component plays relatively greater role in the inheritance of most of these traits.

The GCA effects of the genotypes (Table 2) indicated that there was close relationship between parental mean performance and GCA effects for the traits, protein and oil content. Thus, the perfect relationship could be established between *per se* performance and GCA effects of the parents. Three parental lines viz., AUKS 238 (0.92), AUKS 224 (0.71), RVS 2011-10 (0.42) and tester NRC 130 (0.59) were found to be good general combiners for protein content as they had significant and positive GCA effects for this trait. The GCA value of parents revealed that three lines viz., AUKS 238 (1.90), RVS 2011-10 (0.49), AUKS 207 (0.34) and tester NRC 150 (0.29) manifested significant and positive GCA effects and were good general combiners for

oil content. On the basis of overall performance (Table 2), lines AUKS 238 and RVS 2011-10 was found to be good general combiner with high per se performance for both traits, protein content and oil content.

As regard to specific combining ability effect (Table 3), four crosses exhibited significant and positive SCA effects for protein content. The cross combination AUKS 207 x NRC 150 (poor x average) recorded the highest SCA effect followed by JS 20-116 x NRC 130 (poor x good), RVS 2011-10 x NRC 150 (good x average) and RKS 18 x JS 20-98 (poor x poor) and were rated as good specific cross combinations for protein content and five cross combinations showed significant and positive SCA effects for oil content with the highest SCA effect AUKS 234 x NRC 130 (poor x average) followed by RVS 2011-10 x NRC 130 (good x average), JS 20-113 x NRC 150 (poor x good), RKS 18 x JS 20-98 (poor x poor) and JS 20-116 x JS 20-98 (poor x poor). Similar findings were reported by Sharma and Maloo^[11], Pankra *et al.*^[12], Indu *et al.*^[7] and Nag *et al.*^[13]. General Combining Ability effects of genotypes and SCA effects of their crosses indicated that the crosses between two high general combiners were not best specific combiners. The best specific combinations for different traits were either good x poor, average x average, average x good general combiners.

Table 2: General Combining Ability (GCA) effects for quality characters.

S. No.	Parents	Protein content (%)	Oil content (%)
Lines			
1	AUKS 224	0.71**	0.12
2	RKS 18	-0.45**	-0.83**
3	AUKS 207	-1.00**	0.34*
4	AUKS 234	0.07	-1.38**
5	AUKS 238	0.92**	1.90**
6	RVS 2011-10	0.48**	0.49**
7	JS 20-116	-0.72**	-0.63**
Testers			
1	NRC 130	0.59**	-0.08
2	NRC 150	-0.21	0.29**
3	JS 20-98	-0.39**	-0.20*

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

Cross AUKS 238 x JS 20-98 and RVS 2011-10 x NRC 150 possessed significant standard heterosis and SCA effect and non-additive gene action played important roles in expression of these traits, although non-additive genetic variance was predominant. The conventional methods may not be efficient in capitalizing the available genetic variability. The commercially viable source of cytoplasmic-genetic male sterility is available then presence of greater non-additive gene action offers scope for exploiting hybrid vigour through heterosis breeding in soybean. Therefore, These crosses involved geographically diverse parents and at least one parent of high GCA effects in this cross combination. Majority of soybean breeding work is based on pedigree method, which exploits the fixable additive type of gene effects. However, this alone may be inadequate in view of the large non-additive component for both quality traits. Further, high heterosis for oil and protein along with positive SCA effects was observed in these crosses, which might be due to dominance or epistasis.

Table 3: Specific Combining Ability (SCA) for quality traits in soybean.

S. No.	Crosses	Protein content (%)	Oil Content (%)
1	AUKS 224 x NRC 130	-0.07	0.16
2	RKS 18 x NRC 130	0.13	-0.66*
3	AUKS 207 x NRC 130	-1.25**	0.01
4	AUKS 234 x NRC 130	0.18	0.97**
5	AUKS 238 x NRC 130	0.08	0.11
6	RVS 2011-10 x NRC 130	-0.62*	0.91**
7	JS 20-116 x NRC 130	1.53**	-1.50**
8	AUKS 224 x NRC 150	0.23	0.32
9	RKS 18 x NRC 150	-0.86**	-0.08
10	AUKS 207 x NRC 150	1.85**	-0.08
11	AUKS 234 x NRC 150	-0.24	-0.28
12	AUKS 238 x NRC 150	-0.24	-0.34
13	RVS 2011-10 x NRC 150	0.74*	-0.32
14	JS 20-116 x NRC 150	-1.48**	0.78**
15	AUKS 224 x JS 20-98	-0.17	-0.48
16	RKS 18 x JS 20-98	0.73*	0.74**
17	AUKS 207 x JS 20-98	-0.61*	0.07
18	AUKS 234 x JS 20-98	0.06	-0.69*
19	AUKS 238 x JS 20-98	0.17	0.23
20	RVS 2011-10 x JS 20-98	-0.12	-0.59*
21	JS 20-116 x JS 20-98	-0.06	0.72*

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

Although heterosis breeding makes maximal use of the non-additive genetic effects appears to be difficult for improving soybean in view of the non-availability of mass pollination systems needed for hybrid seed production. Accordingly, the feasible alternative is to consider simultaneous exploitation of both additive and non-additive gene action by adopting recurrent selection procedures. Under similar situation Harer and Deshmukh^[14] recommended biparental mating in soybean followed by recurrent selection. Since crossing is tedious in soybean, genetic male sterility and single seed or single pod descent method could be employed to facilitate recurrent selection schemes Wilcox,^[15]. Therefore, these crosses could throw transgressive segregants in still advance generations. Further, the results of present study suggested that heterosis coupled with high SCA effects might be considered as criteria for selecting cross for further improvement with respect to quality traits. To conclude, combining ability mean squares estimated revealed that both the quality traits displayed preponderance of non-additive gene effects. Often the unfavorable association between protein and yield generally met with are due to tight linkages, which could be broken by raising a large population. In the present study RKS 18 x JS 20-98 revealed superiority for protein content, oil content as well as yield might be considered a new favorable combination resulted due to breaking of tight linkages. Through the use of recurrent selection suggested that such negative relationship may be caused by linkage and improvements can be made for such traits by enforcing simultaneous selection in large segregation population.

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