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Effectiveness of Selection for Yield and its Components in Soybean [*Glycine max* (L.) Merrill]

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ABSTRACT: An experiment was conducted with 9 F_6 crosses (each cross consists of 5 lines of high yielding, 5 lines of low yielding and 5 lines of bulk) of soybean in compact family block design for fourteen quantitative characters to identify the best method for selection and superior crosses in advance breeding lines through *per se* performance and inter correlation analysis. The inter correlation analysis within same family for the trait seed yield per plant and *per se* performance study exhibited that C_7 (PS 1583×Bragg) was best performing cross followed by C_4(PS1584×JS2069) and C_5 (JS20-64×JS20-54) through bulk method of selection. The inter cross correlation analysis for the character seed yield per plant and *per se* performance study revealed that among all high yielding lines, C_7 (18.04g) was the best cross. Among all low yielding lines, C_7 and C_3 both were the best performing crosses. Among bulk lines, C_7 and C_5 emerged as best crosses. Hence, recent study revealed that bulk method of selection in soybean would be a good alternative than pedigree method for high yielding variety development as it is inexpensive and little record keeping. It also showed that bulk method of selection not only help in handling large segregating population but also provides opportunity for natural selection of high yielding and disease resistant lines.

Keywords: Soybean, Bulk method, Pedigee method, *Per se* performance, Inter correlation analysis.

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is one of the most important oilseed crop in the world which is grown since ancient times and is one of the oldest grown crop known to mankind (Peerzada *et al.*, 2014). The North-eastern China region is believed to be the primary centre of origin of this crop. Introduction of soybean to the Indian subcontinent dates back to 1000 AD (Orf *et al.*, 1980). Soybean (2n=40) is botanically placed under the family Fabaceae. Soybean plant favours an optimum temperature of 30°C for its normal growth and development while an optimum temperature for seedlings emergence is found to be 25–33°C. It also fixes the atmospheric nitrogen in soil through symbiotic relationship with biological nitrogen fixing bacteria namely *Bradyrhizobium japonicum* and *Bradyrhizobium diazoefficiens* (Siqueira *et al.*, 2014). Soybean is an important multi-purpose leguminous crop known for its highly valued protein and oil, and its use in food, feed and industrial applications. Hence it is popularly known as the "Golden Bean" of the 20th century. Soybean has been typically used for preparation of traditional and as well as value added food products such as tofu, shoyu, okara, miso, natto, soy milk, soya sauce, tempeh, soy sprouts and soymilk yoghurt *etc*. which are being consumed on a regular basis in China, Japan, Korea and Southeast Asia **(**Muredzi, 2013). Soybean seeds have the highest protein content (30-45%) of all food crops and also contains a considerable oil content (15-24%) comprising high percent of unsaturated fatty acids (Akram *et al.*, 2011). The oil contains 85% unsaturated fatty acids which is free from cholesterol, along with ample mineral elements which is very desirable for human diet (Antalina, 2000).

A rapid increase in area under soybean has been observed which was just 0.03 million ha in 1970 to 12.05 million ha in 2021 (MOA and FW, GOI, 2022) and mean annual productivity has been increased from 430 kg per ha in 1970 to 1280 kg per ha with the production of 13.58 m tons in 2021 (SOPA, 2022). However, world productivity level has not yet been achieved in India. The major constraints for low productivity in India are low varietal stability and narrow genetic base. Therefore, soybean productivity can be enhanced through creating genetic variability and employing effective selection methods to recover superior transgressive segregation lines in advance generation. Hence, the present investigation was carried out to find out superior crosses and the best method for selection in advance breeding lines through *per se* performance and inter correlation analysis, respectively.

MATERIALS AND METHODS

The present investigation was conducted during *kharif* 2019 at N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. The experimental material in the present study consisted of nine F_6 crosses which were planted in compact family block design with three replications in *kharif* 2019 (each cross containing 5 lines of high yielding, 5 lines of low yielding and 5 lines of bulk). Bulk lines of each cross were handled through bulk method since F_3 generation. 15 rows (5 progeny rows of high yielding, 5 progeny rows of low yielding and 5 rows of bulk progenies) of 4 meter with 45 cm row to row spacing for each F_6 cross was planted in *Kharif* 2019, while two rows of parents were planted alongside the crosses. Plant to plant distance was maintained at 5 to 7 cm after thinning. Data was taken from 5 randomly selected competitive plants from each row of high yielding, low yielding progeny and parent of each cross. But 5 randomly competitive plants from 5 bulk rows of each cross were selected for recording data. Data was recorded from each line of all crosses for the most promising and variable character "seed yield per plant". The *per se* performance was calculated by taking mean seed yield per plant. The phenotypic inter correlations between all lines within same family as well as among the families were estimated according to the method given by Searle (1961).

RESULTS AND DISCUSION

Per se performance indicates the performance of plants by "itself". Therefore, performances of various crosses were selected in advance generation based on their mean seed yield per plant which is presented in Table 4. Among high yielding lines, the highest *per se* performance was shown by C_7 (18.04 g) followed by C_4 (17.13 g), C_3 (13.11 g), C_5 (10.81 g), C_1 (10.28 g), C_8 (6.94 g), C_2 (6.17 g), C_6 (5.27 g) and C_9 (1.84). Among low yielding lines, the highest *per se* performance was exhibited by C_7(14.10 g) followed by C_3(11.13 g), C_5(10.54 g), C_1(9.26 g), C_4(9.01 g), C_6(7.62 g), C_8(6.83 g), C_2(6.47 g) and C_9(5.63g) whereas among bulk lines, the highest *per se* performance was shown by the C_7(33.66 g) followed by C_5(23.26 g), C_6(19.24 g), C_3(18.79 g), C_4(18.75 g), C_9(16.56 g), C_2(11.07 g), C_8(7.83 g) and C_1(7.1 g). The mean seed yield of three lines of each cross was added and overall *per se* performance was estimated. The study of overall *per se* performance stated that C_7 was the most promising cross followed by C_4, C_5, C_3 and C_6 whereas C_9 was the poorest performing cross. Sharma *et al.* (2012) also reported the similar result.

In the present investigation, inter correlation among high yielding lines, low yielding lines and bulk lines within same family at phenotypic level was estimated for the trait "seed yield per plant (g)" to screen out the best method of selection in above promising crosses. It was indicated that there were significant and positive correlation found among different lines in different crosses which revealed that method of selection through inter correlation study played an important role in soybean in advance generation.

Inter correlation analysis within same family in F_6 generation for seed yield per plant at phenotypic level exhibited that there was significant and positive correlation was present between high yielding lines and bulk lines *viz.* HB(0.77) in C_1 (JS20-29 × JS20-55) which indicated that seed yield variation between these two line was really significant. The mean seed yield of high yielding lines was 10.28 g which was higher than bulk lines (7.1 g) which showed that pedigree method in high yielding lines was performing better than bulk method. In C_2 (PS 1584 × JS 20-41), high yielding lines was significant and positively correlated with low yielding lines for the trait seed yield per plant (0.54). Similarly, there was negative and significant correlation present between low yielding-bulk lines (-0.84). As mean seed yield of bulk lines was higher than high and low yielding lines thus bulk method was performing better than pedigree method. There was positive and significant correlation present between high yielding-bulk line in C_3 (JS 20-69 × JS 20-59) and mean seed yield of bulk lines was more than other lines; hence bulk method is better than pedigree method. In C_4 (PS 1584 × JS 20-69), a negative and significant correlation was present between high yielding- bulk lines (-0.68) and bulk lines had more mean seed yield per plant which indicated the predominance of bulk method over pedigree method. Similarly a positive significant correlation was found in high-low yielding lines (0.67) in C_5 (JS 20-64 × JS 20-54) and correlation between high yielding and bulk lines was negative. As bulk lines have high mean seed yield thus bulk method was better than pedigree method. The inter correlation study in C_6 (PS 1042 × PS1347) showed that high yielding and low yielding lines were negatively and significantly correlated with each other whereas low yielding and bulk lines were positively and significantly correlated. As bulk lines showed a negative correlation with high yielding lines and exhibited higher mean seed yield than other two lines thus bulk method was performing better than pedigree method. There was positive and significant correlation 0.92 and 0.61 were exhibited by high yielding-bulk and low yielding-bulk line, respectively in C_7(PS 1583 × Bragg). Bulk line had high mean seed yield than other two lines so bulk method was predominant than pedigree. All the lines in C_8(PS 1583 × JS 20-29) didn't show any significant correlation. Therefore, mean seed yield did not significantly differ among these lines of C_8. In C_9 (RVS 2000-1 × PS 1092), there was significant and negative correlation between low yielding and bulk lines (-0.56). Bulk lines also showed a negative correlation with high yielding lines. As bulk lines had more mean seed yield thus bulk method was performing superior than pedigree method. The above inter correlation analysis values within same family for the trait seed yield per plant is shown in Table 1.

Table 1: Inter correlation analysis within same family for seed yield per plant in F_6 generation.

Sr. No.	Code and Cross	Inter correlation analysis within same family		
		HL	HB	LB
1.	C_1(JS 20-29 × JS 20-55)	0.21	0.77**	-0.2
2.	C_2(PS 1584 × JS 20-41)	0.54*	-0.4	-0.84**
3.	C_3(JS 20-69 × JS 20-59)	0.42	0.76**	0.24
4.	C_4(PS 1584 × JS 20-69)	-0.17	-0.68**	-0.33
5.	C_5(JS 20-64 × JS 20-54)	0.67**	-0.04	-0.34
6.	C_6(PS 1042 × PS1347)	-0.71**	-0.29	0.57*
7.	C_7(PS 1583 × Bragg)	0.46	0.92**	0.61*
8.	C_8(PS 1583 × JS 20-29)	0.45	0.51	-0.14
9.	C_9(RVS 2000-1 × PS 1092)	-0.49	-0.16	-0.56*

** Significant at 1% level of probability; * Significant at 5% level of probability

HL=High yielding lines –Low yielding lines HB=High yielding lines –Bulk lines

LB=Low yielding lines –Bulk lines

The above inter correlation analysis within same family and overall *per se* performance study exhibited that C_1 was better performing through pedigree method of selection whereas in C_2, both pedigree and bulk lines were equally performing. The bulk method of selection was the best for C_7 followed by C_4, C_5, C_3 and C_6.

In the present investigation the inter correlation between high yielding- high yielding, low yielding-low yielding and bulk-bulk lines among different family at phenotypic level was carried out for the traits seed yield per plant. It was revealed that the significant correlation was present among different crosses in different lines which helped to find out the best cross among high yielding, low yielding and bulk lines through direct selection.

In F_6 generation, inter correlation analysis among different family at phenotypic level for the trait seed yield per plant revealed that among high yielding lines, C_1 exhibited positive and significant correlation with C_2 (0.49), C_3 (0.45), C_5 (0.51) and C_6 (0.39) and also showed a negative and significant correlation with C_4(-0.62). The positive and significant correlations exhibited by C2 with C_5 (0.54), C_6(0.83), C_7 (0.41) and a negative significant correlation with C_9 (-0.41). Similarly, C_3 showed positive and significant correlation with C_4 (0.81), C_7 (0.5) and negative significant correlation with C_8 (-0.9) and C_9 (-0.66). C_4 exhibited a positive significant correlation with C_7 (0.49) and negative significant correlation with C_5 (-0.71) and C_8 (-0.74). There was a positive significant correlation between C_5C_6 (0.43) and C_5C_8 (0.53) and a negative significant correlation between C_5C_9(0.61). C_7 showed a negative significant correlation with C_8 (-0.81). From the above correlation analysis and mean seed yield per plant study, it was revealed that among all high yielding lines, C_7 (18.04g) was the best cross followed by C_4 (17.13g) and C_3 (13.11g).

Among low yielding lines, the positive and significant correlation at phenotypic level exhibited by crosses *viz.* C_1C_6(0.9), C_4C_8(0.79), C_6C_9(0.77), C_2C_5(0.74), C_5C_8 (0.7), C_1C_9(0.65), C_3C_4(0.46), C_3C_8(0.46), C_7C_9(0.44) and C_2C_8(0.4). Similarly negative and significant correlations at phenotypic level exhibited by the crosses *viz.* C_5C_7(-0.83), C_1C_3(-0.74), C_2C_7(-0.74), C_3C_6(-0.69), C_4C_6(-0.55), C_2C_9(-0.46) and C_7C_8(-0.4). Among all low yielding lines, C_7 and C_3 both were best performing crosses as they had high mean seed yield per plant (14.1g) and they were not significantly correlated with each other.

Among bulk lines, the positive and significant correlation at phenotypic level exhibited by the crosses *viz.* C_2C_5 (0.99), C_2C_3 (0.97), C_1C_9 (0.95), C_6C_8 (0.95), C_3C_5 (0.94), C_5C_8 (0.93), C_2C_8 (0.9), C_7C_9 (0.89), C_5C_6 (0.77), C_3C_8 (0.75), C_1C_2 (0.74), C_1C_7 (0.71), C_2C_6 (0.71) and C_3C_6 (0.5). The negative and significant correlation at phenotypic level exhibited by the crosses *viz.* C_1C_6 (-0.99), C_1C_8 (-0.96), C_6C_9 (-0.96), C_8C_9 (-0.83), C_1C_5 (-0.8), C_6C_7 (-0.74), C_4C_7 (-0.71), C_2C_4 (-0.6), C_4C_5 (-0.6), C_5C_9 (-0.57), C_1C_2 (-0.56), C_2C_9 (-0.5) and C_7C_8 (-0.49). Among bulk lines, C_7 and C_5 exhibited high mean seed yield per plant (33.66g) and did not significantly correlated hence these two cross emerged as best crosses among all others followed by C_6 (19.24g). The above inter correlation study among different lines among different family is presented in Table 2.

The inter correlation analysis and mean seed yield per plant study revealed that among all high yielding lines C_7, C_4 and C_3 were best performing crosses whereas C_7 and C_3 were better performing crosses in low yielding lines. Similarly in bulk lines, C_7 and C_5 both were equally better performing crosses followed by C_6 which are given in Table 3.

Table 2: Inter correlation analysis among high yielding lines, low yielding lines and bulk lines in different family for the trait seed yield per plant in F_6 generation.

Cross		Inter correlation analysis among high yielding, low yielding and bulk lines in different family								
		C_1	**C_2**	**C_3**	**C_4**	**C_5**	**C_6**	**C_7**	**C_8**	**C_9**
C_1(JS 20-29 × JS 20-55)	r_{hy}	1	0.49**	0.45*	-0.62**	0.51**	0.39*	0.37	-0.003	0.1
	r_{ly}	1	0.16	-0.74**	-0.35	0.36	0.9**	0.09	0.14	0.65**
	r_b	1	-0.74**	-0.56**	-0.01	-0.8**	-0.99**	0.71**	-0.96**	0.95**
C_2(PS 1584 × JS 20-41)	r_{hy}		1	0.21	-0.16	0.54**	0.83**	0.41*	-0.36	-0.41*
	r_{ly}		1	-0.05	0.32	0.74**	-0.12	-0.74**	0.64**	-0.46*
	r_b		1	0.97**	-0.66**	0.99**	0.71**	-0.06	0.9**	-0.5**
C_3(JS 20-69 × JS 20-59)	r_{hy}			1	0.81**	-0.16	-0.14	0.5**	-0.9**	-0.66**
	r_{ly}			1	0.8**	-0.003	-0.69**	-0.1	0.46*	-0.2
	r_b			1	-0.83**	0.94**	0.5**	0.2	0.75**	-0.26
C_4(PS 1584 × JS 20-69)	r_{hy}				1	-0.71**	0.34	0.49**	-0.74**	-0.11
	r_{ly}				1	0.17	-0.55**	-0.05	0.79**	-0.12
	r_b				1	-0.6**	0.05	-0.71**	-0.26	-0.32
C_5(JS 20-64 × JS 20-54)	r_{hy}					1	0.43*	-0.22	0.53**	-0.61**
	r_{ly}					1	0.32	-0.83**	0.7**	0.06
	r_b					1	0.77**	-0.14	0.93**	-0.57**
-C_6(PS 1042 × PS1347)	r_{hy}						1	-0.05	-0.12	-0.07
	r_{ly}						1	0.07	-0.06	0.77**
	r_b						1	-0.74**	0.95**	-0.96**
C_7(PS 1583 × Bragg)	r_{hy}							1	-0.83**	-0.11
	r_{ly}							1	-0.41*	0.44*
	r_b							1	-0.49**	0.89**
C_8(PS 1583 × JS 20-29)	r_{hy}								1	-0.06
	r_{ly}								1	0.1
	r_b								1	-0.83**
C_9(RVS 2000-1 × PS 1092)	r_{hy}									1
	r_{ly}									1
	r_b									1

** Significant at 1% level of probability, * Significant at 5% level of probability

Table 3: Selection of the best cross based on inter correlation analysis and mean seed yield per plant (g).

Sr. No.		Best Cross
1.	**High yielding lines**	C_7(PS 1583×Bragg)
		C_4(PS1584×JS2069)
		C_3(JS20-69×JS20-59)
2.	**Low yielding lines**	C_7(PS 1583×Bragg)
		C_3(JS20-69×JS20-59)
3.	**Bulk lines**	C_7(PS 1583×Bragg)
		C_5(JS20-64×JS20-54)
		C_6(PS1042×PS1347)

Table 4: Summery table depicting mean seed yield of high yielding, low yielding and bulk lines of nine crosses in F_6 generation.

Mean seed yield per plant(g)					
Sr. No.	**Code**	**Cross**	**High yielding lines**	**Low yielding lines**	**Bulk lines**
1.	**C_1**	**JS 20-29 × JS 20-55**	10.28	9.26	7.10
2.	**C_2**	**PS 1584 × JS 20-41**	6.17	6.47	11.07
3.	**C_3**	**JS 20-69 × JS 20-59**	13.11	11.13	18.79
4.	**C_4**	**PS 1584 × JS 20-69**	17.13	9.01	18.75
5.	**C_5**	**JS 20-64 × JS 20-54**	10.81	10.54	23.26
6.	**C_6**	**PS 1042 × PS1347**	5.27	7.62	19.24
7.	**C_7**	**PS 1583 × Bragg**	18.04	14.1	33.66
8.	**C_8**	**PS 1583 × JS 20-29**	8.94	6.83	7.82
9.	**C_9**	**RVS 2000-1 × PS 1092**	1.84	5.63	16.56

Recent study showed the comparison between bulk method and pedigree method of handling of soybean lines. In advance generation (F_6), the bulk lines which were handled since F_3 exhibited superior performance for yield contributing characters especially seed yield per plant than those of pedigree lines. Hence, it not only gives us a great scope for natural selection of many traits including disease resistant but also enables us for screening large segregating population in advance generation.

CONCLUSION

Inter correlation analysis within same family for the traits namely, seed yield per plant (g) was revealed that the yield variation among high yielding, low yielding and bulk lines was found significant and direct selection within same family could be effective for increasing yield in later generations. From the inter correction analysis within same family as well as among different families and mean seed yield per plant, it was revealed that C_7 (PS 1583 × Bragg) and C_6 (PS 1584 × JS 20-69) were better performing crosses through pedigree method of selection in high yielding lines. In low yielding lines, C_7 (PS 1583 × Bragg) and C_3 (JS 20-69 × JS 20-59) were better performing crosses through pedigree method of selection. In bulk lines, C_7 (PS 1583 × Bragg) and C_6 (PS 1042 × PS1347) were better performing crosses through bulk method of selection.

FUTURE SCOPE

Soybean is an important oilseed crop in the world and it is also used as a good source of protein supplements. However, in India and other developing countries, it is a low productive crop and its *Bt* version is not commercialized. To increase soybean yield, we have to generate more genetic variability for various yield attributing traits along with stress resistance characters. Hence, recent study showed the comparison between bulk method and pedigree method of handling of soybean lines. In advance generation (F_6), the bulk lines which were handled since F_3 exhibited superior performance for yield contributing characters especially seed yield per plant than those of pedigree lines. Hence, it not only gives us a great scope for natural selection of many traits including stress resistant but also enables us for screening large segregating population in advance generation.

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Conflict of Interest. None.

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