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Estimation of genetic variability in segregating populations of soybean (*Glycine max* L. Merrill)

Madhuri Singh, SK Nag and RK Yadav

Abstract
Genetic variation were estimated in three crosses *viz.*, RSC11-42 × PS1475, CG Soya11-15 × MACS5171 and CG Soya11-15 × PS1475. Additive gene effects were important for plant height, number of pods per plant, pod bearing length, number of seeds per pod, 100 seed weight, oil content and seed yield per plant in all crosses. All these traits indicates that emphasis should be given to these traits for seed improvement in soybean. High heritability with high genetic advance as percentage of mean further confirm it. Non-additive with appreciable additive gene effects were predominant for days to 50% flowering, days to maturity and protein content. It is suggested that better utilization of fixable and non-fixable genetic variances, biparental intermating can be followed in these segregating populations.

Keywords: Genetic variability, populations, soybean, yield components

Introduction
Soybean (*Glycine max* L. Merrill) is one of the world's most important economic legume crops. Soybean is also known as Golden Bean or Miracle Crop, as they contain a complete source of protein and oil. Soybean is considered as a wonder crop due to its dual qualities *viz.*, high protein (40-44%) and oil content (20%) (Baraskar *et al*., 2014) [1]. It contributes about 25% to the global edible oil production, about two thirds of the world's protein concentrate for livestock feeding and is a valuable ingredient in formulated feeds for poultry and fish. It is also an important raw material for food, fodder, pharma and other industries. Soybean seed consists of 35% carbohydrate, 5% ash, 40% protein and 20% oil and is a major source of protein and oil for commercial products. About 40% of the world's edible vegetable oil comes from soybeans (Hildebrand *et al*., 1986) [8]. The soya proteins have the highest nutritional value of all the plant proteins for human food, being particularly high in lysine.

Soybean is mainly grown for their seeds and is the second largest oil seed after groundnut in India. The estimation of genetic parameters like coefficient of variances, heritability and expected genetic advance as percentage of mean from selection has a prime role in genetic breeding programs. The continuous improvement of genetic breeding of soybean depends on the information about genetic variability, genetic parameters and their application, that assists the breeders in reliable selection process.

Materials and Methods
Crosses between RSC11-42 x PS1475, CG Soya11-15 x MACS5171, CG Soya11-15 x PS1475 were made at IGKV, Raipur during *kharif* 2020. The experiment consisted of three crosses which were evaluated in randomized block design with three replications. Crop was raised as per recommended package of practices.

Data were recorded on twelve quantitative characters for days to 50% flowering, Plant height (cm), number of primary branches per plant, number of pods per plant, pod bearing length (cm), number of seeds per pod, number of seeds per plant, 100 seed weight (g), protein content (%), oil content (%). Analysis of variance was done based on RBD for each of the crosses separately. The genotypic and phenotypic coefficient of variance, heritability in broad sense (Burton and Devane, 1953) [3] and genetic advance were estimated as per the method of Johnson *et al.*, (1955) [19].

Results and Discussion
The analysis of variance was calculated for twelve characters for three different crosses and is presented in Table No. 1. The data analysis of all the crosses *viz*., RSC11-42 × PS1475, CG

Soya 11-15 × MACS5171, CG Soya 11-15 × PS1475 revealed that there was high variability for all the characters as the mean sum of squares due to generations was significant. This indicated presence of high variability among the crosses, which provide ample scope for selection for different quantitative characters for soybean improvement.

Table 1: Analysis of variance for yield and its component in three crosses of soybean

Source of Variation	d.f	Characters											
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Pod bearing length(cm)	Number of seeds per pod	Number of seeds per plant	100 seed weight (g)	Oil content (%)	Protein content (%)	Seed yield per plant (g)
RSC11-42 × PS1475													
Replication	2	0.12	0.79	2.68	0.49	2.63	2.83	0.01	0.79	0.01	0.15	0.08	0.22
Treatment	5	1.70**	10.58**	97.58**	0.42**	146.69**	91.59**	0.24**	2810.11**	3.29**	3.96**	1.88**	10.24**
Error	10	0.14	0.41	1.03	0.09	1.22	0.81	0.00	0.91	0.03	0.07	0.10	0.25
CG Soya 11-15 × MACS5171													
Replication	2	0.41	0.03	1.44	0.00	2.41	3.50	0.01	2.56	0.01	0.17	0.25	0.41
Treatment	5	0.95**	20.57**	286.38**	0.38**	250.29**	182.79**	0.06**	4936.12**	9.50**	4.80**	3.62**	30.29**
Error	10	0.28	0.60	0.47	0.06	1.83	1.50	0.01	6.19	0.04	0.05	0.14	0.45
CG Soya 11-15 × PS1475													
Replication	2	0.17	6.49	2.24	0.03	4.93	1.26	0.01	2.76	0.00	0.16	0.33	0.26
Treatment	5	0.75**	33.02**	178.28**	0.1**	69.54**	67.31**	0.06**	2689.40**	6.64**	4.57**	5.99**	93.10**
Error	10	0.42	5.94	0.75	0.07	1.71	0.42	0.00	0.60	0.04	0.06	0.09	0.17

Table 2: Estimation of genetic variability for yield and its component in crosses of soybean

Name of Crosses	GCV (%)	PCV (%)	h^2 bs (%)	Genetic Advance	Genetic Advance as % mean
Days to 50% flowering					
RSC11-42 × PS1475	1.72	1.93	79.06	1.33	3.15
CG Soya 11-15 × MACS5171	1.10	1.66	44.23	0.65	1.51
CG Soya 11-15 × PS1475	0.78	1.72	20.61	0.31	0.73
Days to maturity					
RSC11-42 × PS1475	1.94	2.05	89.21	3.58	3.77
CG Soya 11-15 × MACS5171	2.70	2.82	91.74	5.09	5.32
CG Soya 11-15 × PS1475	3.16	4.07	60.33	4.81	5.06
		Plant height			
RSC11-42 × PS1475	11.41	11.59	96.90	11.50	23.14
CG Soya 11-15 × MACS5171	16.30	16.34	99.51	20.06	33.49
CG Soya 11-15 × PS1475	13.18	13.27	98.76	15.75	26.99
Number of primary branches					
RSC11-42 × PS1475	8.07	10.87	55.17	0.51	12.36
CG Soya 11-15 × MACS5171	8.16	10.37	61.96	0.53	13.23
CG Soya 11-15 × PS1475	4.80	8.15	34.70	0.24	5.83
Number of pods per plant					
RSC11-42 × PS1475	8.68	8.78	97.55	14.17	17.65
CG Soya 11-15 × MACS5171	10.40	10.51	97.84	18.54	21.19
CG Soya 11-15 × PS1475	5.15	5.34	92.97	9.45	10.22
Pod bearing length (cm)					
RSC11-42 × PS1475	13.58	13.76	97.39	11.18	27.60
CG Soya 11-15 × MACS5171	16.54	16.74	97.58	15.82	33.66
CG Soya 11-15 × PS1475	10.12	10.22	98.14	9.64	20.65
Number of seed per pod					
RSC11-42 × PS1475	10.48	10.70	96.01	0.56	21.15
CG Soya 11-15 × MACS5171	5.22	5.92	77.51	0.24	9.46
CG Soya 11-15 × PS1475	5.38	5.61	92.06	0.28	10.64
Number of seed per plant					
RSC11-42 × PS1475	19.31	19.32	99.90	63.01	39.76
CG Soya 11-15 × MACS5171	22.43	22.48	99.63	83.35	46.12
CG Soya 11-15 × PS1475	17.17	17.18	99.93	61.65	35.36
100 seed weight (g)					
RSC11-42 × PS1475	8.80	8.91	97.40	2.12	27.89
CG Soya 11-15 × MACS5171	14.29	14.38	98.75	3.64	29.25
CG Soya 11-15 × PS1475	12.13	12.25	98.04	3.02	24.73
Oil content (%)					
RSC11-42 × PS1475	8.27	8.50	94.67	2.28	16.58
CG Soya 11-15 × MACS5171	8.72	8.86	96.98	2.55	17.69
CG Soya 11-15 × PS1475	8.54	8.70	96.43	2.48	17.27
Protein content (%)					

RSC11-42 × PS1475	1.93	2.08	85.87	1.47	3.68
CG Soya 11-15 × MACS5171	2.78	2.94	89.62	2.10	5.43
CG Soya 11-15 × PS1475	3.56	3.64	95.51	2.82	7.17
Seed yield per plant (g)					
RSC11-42 × PS1475	10.53	10.92	93.05	3.63	20.93
CG Soya 11-15 × MACS5171	16.54	16.91	95.65	6.35	33.32
CG Soya 11-15 × PS1475	25.79	25.86	99.46	11.49	52.99

GCV%= Genotypic coefficient of variation, PCV%= Phenotypic coefficient of variation, $h^2_{(bs)}$= Heritability in broad sense, GA%= Genetic advance as percent of mean

Genotypic and phenotypic coefficient of variation

The estimation of genotypic and phenotypic components of variation is of primary importance to get an idea of relative extent of heritable and non-heritable components of variation. The estimates of genotypic and phenotypic coefficient of variation for yield and its components is presented in Table No. 2.

CROSS RSC11-42 × PS1475

The moderate magnitude of GCV and PCV were recorded for number of seeds per plant (19.31) and (19.32) followed by pod bearing length (13.58) and (13.76) plant height (11.41) and (11.59), seed yield per plant (10.53) and (10.92), number of seeds per pod (10.48) and (10.70) respectively, whereas low GCV and PCV were recorded for days to 50% flowering (1.72) and (1.93) followed by protein content % (1.93) and (2.08), days to maturity (1.94) and (2.05), oil content % (8.27) and (8.50), number of pods per plant (8.68) and (8.78) and 100 seed weight (8.80) and (8.91) respectively.

CROSS CG Soya11-15 × MACS5171

The highest magnitude of GCV and PCV was recorded for number of seeds per plant (22.43) and (22.48). The moderate GCV and PCV were observed for seed yield per plant (16.54) and (16.91) followed by pod bearing length (16.54) and (16.74), plant height (16.30) and (16.34), 100 seed weight (14.29) and (14.38), number of pods per plant (10.40) and (10.51). whereas low GCV and PCV were also recorded for days to 50% flowering (1.10) and (1.66), days to maturity (2.70) and (2.82), protein content % (2.78) and (2.94), number of seeds per pod (5.22) and (5.92) and oil content % (8.72) and (8.86) respectively.

CROSS CG Soya11-15 × PS1475

The maximum value for GCV and PCV was recorded for seed yield/plant (25.79) and (25.86) respectively. The moderate value of GCV and PCV were recorded for number of seeds per plant (17.17) and (17.18), plant height (13.18) and (13.27), 100 seed weight (12.13) and (12.25), pod bearing length (10.12) and (10.22) respectively. whereas low GCV and PCV were observed for days to 50% flowering (0.78) and (1.78) days to maturity (3.16) and (4.07), protein content % (3.56) and (3.64), number of primary branches per plant (4.80) and (8.15), number of pods per plant (5.15) and (5.34), number of seeds per pod (5.38) and (5.61) and oil content % (8.54) and (8.70) respectively.

In the present study, Cross CG Soya 11-15 × PS1475 showed highest magnitude of genotypic and phenotypic coefficient of variation for seed yield per plant. Similar finding were also reported by Baraskar *et al.* (2014) [1], Mahbub *et al.* (2015) [11], Nagarajan *et al.* (2017) [13], Bisht *et al.* (2018) [2], Ghimire *et al.* (2019) [6], Jandong *et al.* (2020) [10], Swar *et al.* (2020) [17], Dutt *et al.* (2021) and Goonde *et al.* (2021) [7] for seed yield per plant.

Crosses *viz.*, RSC11-42 × PS1475 and CG Soya 11-15 × MACS5171 observed moderate magnitude of genotypic and phenotypic coefficient of variation for number of primary branches per plant. similar finding was reported by Tigga and Nag (2021) for number of primary branches per plant.

All the Crosses RSC11-42 × PS1475, CG Soya 11-15 × MACS5171 and CG Soya 11-15 × PS1475 estimated the lower magnitude of genotypic and phenotypic coefficient of variation for protein content and oil content. Similar finding was reported by Swar *et al.* (2020) [17] for these traits.

Heritability (bs) and Genetic Advance as percent of mean

Heritability and genetic advance are the important parameters for selecting a genotype that permits greater effectiveness of selection by separating out the environmental influence from total variability. Heritability estimates along with genetic advance are normally more useful in predicating the gain under selection than that heritability alone.

CROSS RSC11-42 × PS1475

The highest heritability estimates were observed for number of seeds per plant (99.90%) followed by number of pods per plant (97.55%), 100 seed weight (97.40%), pod bearing length (97.39%), plant height (96.90%), number of seeds per pod (96.01%), oil content (94.67%), seed yield per plant (93.05%), days to maturity (89.21%), protein content (85.87%), days to 50% flowering (79.06%) and number of primary branches per plant (55.17%).

The highest amount of genetic advance as percentage of mean were observed for number of seeds per plant (39.76%); moderate for pod bearing length (27.60%) plant height (23.14%), number of seed per pod (21.15%), seed yield per plant (20.93%), 100 seed weight (17.89%), number of pods per plant (17.65%), oil content (16.58%), and number of primary branches per plant (12.36%); and lowest for days to 50% flowering (3.15%), protein content (3.68%), days to maturity (3.77%).

The high heritability estimates coupled with high genetic advance as percentage of mean was observed for number of seeds per plant followed by pod bearing length, number of seeds per pod, seed yield per plant. High heritability coupled with moderate genetic advance as percentage mean were recorded for number of pods per plant followed by 100 seed weight, oil content (%), whereas moderate heritability with moderate genetic advance as percentage of mean only number of primary branches per plant. The high heritability with low genetic advance as percentage of mean was observed for days to maturity, protein content (%) and days to 50% flowering.

CROSS CG Soya 11-15 × MACS5171

The highest heritability estimates were observed for number of seeds/plant (99.63%) followed by plant height (99.51%), 100 seed weight (98.75%), number of pods per plant (97.84%), pod bearing length (97.58%), oil content (96.98%),

seed yield per plant (95.65%), days to maturity (91.74%), protein content (89.62%), number of seeds per pod (77.51%), number of primary branches per plant (61.96%) and days to 50% flowering (44.23%).

Genetic advance as percentage of mean were high for number of seed per plant (46.12%) followed by plant height (33.49%), pod bearing length (33.66%), seed yield per plant (33.32%); moderate for 100 seed weight (29.25%) followed by number of pods per plant (21.19%), oil content (17.69%), and number of primary branches per plant (13.23%); lowest genetic advance as percent of mean was observed for number of seeds per pod (9.46%), protein content (5.43%), days to maturity (5.32%) and days to 50% flowering (1.51%).

The high heritability coupled with high genetic advance as percentage of mean was observed for number of seeds per plant followed by plant height (cm), pod bearing length and seed yield per plant; moderate for 100 seed weight, number of pods per plant, oil content (%), number of primary branches per plant; and low for days to maturity protein content (%) and number of seeds per pod.

CROSS CG Soya 11-15 × PS1475

The highest amount of heritability estimates were observed for number of seeds per plant (99.63%) followed by seed yield per plant (99.46%), plant height (98.76%), pod bearing length (98.14%), 100 seed weight (98.04%), oil content (96.43%), protein content (95.51%), number of pods per plant (92.97%) and number of seeds per pod (92.06%).

Genetic advance as percentage of mean were observed high for seed yield per plant (52.99%) and number of seeds per plant (35.36%); moderate for plant height (26.99%) 100 seed weight (24.73%), pod bearing length (20.65%), oil content (17.27%), number of seeds per pod (10.64%) and number of pods per plant (10.22%); and low for protein content (7.17%) followed by number of primary branches per plant (5.83)%, days to maturity (5.06%) and days to 50% flowering (0.75%).

The high heritability coupled with high genetic advance as percentage of mean was observed for number of seeds per plant followed by seed yield per plant, plant height, 100 seed weight and pod bearing length; moderate for oil content (%), number of pods per plant, number of seeds per pod; Protein content (%) and days to maturity showed high heritability with low genetic advance as percentage of mean.

In the present study, All the Crosses RSC11-42 × PS1475, CG Soya 11-15 × MACS5171 and CG Soya 11-15 × PS1475 estimated high heritability coupled with high genetic advance as percentage of mean was observed for seed yield per plant. Similar finding were also reported by Baraskar *et al.* (2014) [1], Bisht *et al.* (2018) [2], Neelima *et al.* (2018) [15], Ghimire *et al.* (2019) [6], Sonkamble *et al.* (2020) [16], Swar *et al.* (2020) [17], Camelia *et al.* (2021) [4], Dutt *et al.* (2021), Yamgar *et al.* (2021) [20] for seed yield per plant.

Cross CG Soya 11-15 × MACS5171 and CG Soya 11-15 × PS1475 showed high heritability coupled with high genetic advance as percentage of mean was observed for plant height. Similar finding were also reported by Baraskar *et al.* (2014) [1], Malek *et al.* (2014) [12], Bisht *et al.* (2018) [2], Jain *et al.* (2018) [9], Neelima *et al.* (2018) [15], Ghimire *et al.* (2019) [6], Jandong *et al.* (2020) [10], Naryana and Fakrudin (2020), Sonkamble *et al.* (2020) [16], Dutt *et al.* (2021) for plant height.

Number of seeds per pod in RSC11-42 × PS1475 showed high heritability coupled with high genetic advance as percentage of mean. Similar finding were also reported by Dutt *et al.* (2021) for number of seeds per pod. CG Soya 11-15 × PS1475 showed high heritability coupled with high genetic advance as percentage of mean was observed for 100 seed weight, pod bearing length, number of seeds per plant. Similar findings were also reported by Malek *et al.* (2014) [12], Ghimire *et al.* (2019) [6], Swar *et al.* (2020) [17], Dutt *et al.* (2021) for 100 seed weight. Naryana and Fakrudin (2020) for pod bearing length and Sonkamble *et al.* (2020) [16] for number of seeds per plant.

The high heritability coupled with high genetic advance as percentage of mean which indicated that the predominance of additive gene action in the expression of these characters in specific crosses which could be utilized through selection for the genetic improvement of these characters. Rest of the crosswise traits have shown high to low heritability estimates coupled with low to high genetic advance as percentage of mean indicated the role of non additive (dominance and epistatic) gene action in their expression.

Conclusion

An attempt was made to identify the quantitative traits among three crosses of soybean. significant amount of variability was observed for all the crosses. Crosses *viz.*, RSC11-42 × PS1475, CG Soya11-15 × MACS5171 and CG Soya11-15 × PS1475 had major contribution for the improvement of plant height, number of pods per plant, pod bearing length, number of seeds per plant, 100 seed weight, oil content and seed yield per plant. High heritability with high genetic advance as percentage of mean further confirm it. Other traits show medium to low heritability accompanied with medium to low genetic advance as percentage of mean in all crosses. As a result, direct selection based on these traits among crosses will be extremely capable increasing seed yield in soybean

References

1. Baraskar V, Kachhadia V, Vachhani Jivanlal, Barad Hitesh, Patel M, Darvhankar Mayur. Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. Electronic Journal of Plant Breeding. 2014;5:802-806.
2. Bisht M, Singh K, Bhatt P, Kunduru B, Chourasia KN. Studies on variability parameters in early generation of soybean [*Glycine max* (L.) Merrill]. Int J Chem Stud. 2018;6(3):208-211.
3. Burton GW, Devene EH. Estimating heritability in Jali Fesche. (*Festuca arundinaces*) from replicated clonal material. Agronomical J. 1953;45:478-481.
4. Camelia U, Vasilena S, Teodor R, Luana P, Raluca R, Nicolae T, *et al*. Variability and heritability of some agronomical and quality characters of soybean (*Glycine max* (L.) Merrill.) cultivars. Life Sci. Sustain. Dev. 2021;2(2):120-126.
5. Datt S, Noren SK, Bhadana VP, Sharma PR. Gene action for yield and its components in soybean (*Glycine max* (L.) Merrill). Vegetos. 2011;24(1):89-92.
6. Ghimire NH, Sah RP. Performance of advanced breeding lines of soybean [*Glycine max* (L.) Merrill] at Mid Western Terai of Nepal. Int. J Adv. Res. Biol. Sci. 2019;6(12):118-125.
7. Goonde DB, Ayana NG. Genetic diversity and character association for yield and yield related traits in Soybean (*Glycine Max* L.) genotypes. J Agri. Sci. Food Res.

2021;12(1):280-285.
8. Hildebrand DF, Phillips GC, Collins GB. Soybean [*Glycine max* (L.) Merr.]. In: Bajaj, Y.P.S. (eds) Crops I. Biotechnology in Agriculture and Forestry. Springer, Berlin, Heidelberg; c1986. p. 2.
9. Jain R, Joshi A, Chaudhary H, Dashora A, Khatik C. Study on genetic variability, heritability and genetic advance in Soybean [*Glycine max* (L.) Merrill]. Legume Research an International Journal. 2018;41:10.18805/LR-3874.
10. Jandong EA, Uguru MI, Okechukwu EC. Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.); c2020.
11. Mahbub MM, Rahman MM, Hossain MS, Mahmud F, Kabir MM. Genetic variability, correlation and path analysis for yield and yield components in soybean. American-Eurasian J Agric & Environ. Sci. 2015;15(2):231-236.
12. Malek MA, Rafii MY, Afroz SS, Nath UK, Mondal M. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. The Scientific World Journal; c2014.
13. Nagarajan D, Kalaimagal T, Murugan E. Evaluation of Genetic Parameters in M_4 Generation of Soybean Mutant Lines. Int. J Curr. Microbiol. App. Sci. 2017;6(11):2902-2906.
14. Nayana RS, Fakrudin B. Genetic variability, heritability and correlation studies in soybean (*Glycine max*). Indian J Agric. Sci. 2020;90(4):256-264.
15. Neelima G, Mehtre SP, Narkhede GW. Genetic Variability, Heritability and Genetic Advance in Soybean, Int. J Pure App. Biosci. 2018;6(2):1011-1017.
16. Sonkamble P, Nandanwar RS, Sakhare SB, Jadhav PV, Varghese P. Genetic variability for yield and its component traits in grain and vegetable type soybean. IJCS. 2020;8(6):2287-2290.
17. Swar BR, Latha VS, Reddy MR, Vanisri S. Assessment of genetic variability parameters in magic population of soybean [*Glycine max* (L.) Merrill]. The Bioscan. 2020;15(2):271-274.
18. Tigga A. Genetic variability and diversity analysis for yield and its contributing in soybean (*Glycine max* (L.) Merrill). M.Sc. Thesis, Indira Gandhi Krishi Vishwavidyalaya, Raipur; c2021. p. 1-88.
19. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. Agronomy Journal. 1955 Jul;47(7):314-8.
20. Yamgar SV, Pawar SV, Chimote VP, Deshmukh MP, Shinde GC, Nimbalkar CA. Expression of heterosis, residual heterosis and specific combining ability in yield and yield contributing characters of soybean (*Glycine max* (L.) Merrill). J Pharmacogn Phytochem. 2021;10(1):2711-4.