Assessment of Genetic Variability of Parameters for Yield and its Components in Soybean [*Glycine max* (L.) Merrill]

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Authors' contributions

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

Original Research Article

ABSTRACT

An experiment was conducted with 9 crosses of soybean in compact family block design for 14 quantitative traits during *kharif* 2019 at N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Udham Singh Nagar, Uttarakhand, India to assess genetic variability, heritability and genetic advance. Genetic variability were found among the experimental materials for all traits. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for most of the traits. Seed yield per plant showed highest genotypic coefficient of variation (29.1%). The highest heritability was exhibited by plant height followed by number of pods per plant, seed yield per plant and harvesting index. The value of genetic advance ranged from 0.06 (number of seeds per pod) to 89.45 (seed yield per row). The highest value of heritability coupled with high genetic advance as per cent mean exhibited by seed yield per plant followed by dry matter weight per plant, seed yield per row, number of pods per plant, seed yield efficiency which ensured additive gene action.

Keywords: GCV; PCV; genetic variability parameters; heritability; genetic advance.

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1. INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] (2n=40) 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 [1]. In the world level, 25 percent of the global edible oil and two-thirds concentrated livestock fodder contributed by soybean [2]. It also fixes the atmospheric nitrogen in soil through symbiotic relationship with biological nitrogen fixing bacteria namely *Bradyrhizobium japonicum* and *Bradyrhizobium diazoefficiens* found in the root nodules of soybean plant [3].

Soybean is called "Golden bean" of 20th century and "Miracle crop" with hundreds of uses including animal feed, fertilizer, cleaning products, cosmetics, candle wax, bio-fuel and a protein source *etc.* The protein and oil contents in soybean are 30-45% and 15-24% respectively with tremendous amount of unsaturated fatty acids contents [4]. Soybean oil has high amount of minerals like copper, manganese, potassium along with 85% unsaturated fatty acids of zero cholesterol content which is very sensible for human health [5]. Recent research revealed that soybean proteins prevent 70% for liver cancer, 73% for colon cancer, and 68% for lung cancer cells using human cell line [6].

The present trend of soybean yield can't meet the 50% targeted soybean production in 2030 without expanding soybean production area [7]. Hence, the recent research was conducted to create genetic variability with respect to high yield among different quantitative traits in advance breeding materials of soybean.

2. 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 consisted of nine crosses which were planted in compact family block design with three replications (comprising 9 F_6 crosses and each cross containing 5 lines of high yielding, 5 lines of low yielding and 5 lines of bulk). 15 rows (5 progeny rows of high yielding, 5 progeny rows of low yielding and 5 rows of bulk progeny) of 4 meter with 45 cm row to row spacing for each F_6 cross was planted. 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 and low yielding progeny. But 5 randomly competitive plants from 5 bulk rows of each cross were selected for recording data. A total of fourteen quantitative characters were recorded such as days of 50% flowering, days of 90% maturity, plant height, number of nodes per plant, number of pods per plant, number of seeds per pod, number of primary branches per plant, dry matter weight per plant, seed yield per plant, 100-seed weight, harvesting index, seed yield per row, seed yield per hectare and seed yield efficiency were taken for data recording.

The analysis of variance for each character was carried out for compact family block design suggested by Hutchinson and Panse [8] and Federer [9]. The genotypic, phenotypic and environmental coefficients of variability were computed for each character as per method explained by Singh and Chaudhary [10]. Heritability coefficient (h^2) for each quantitative traits was estimated which explains heritable genetic variance from total variance [11]. The expected genetic advance under selection for each quantitative character was computed by formula proposed by Johanson et al. [12].

3. RESULTS AND DISCUSSION

Analysis of variance for the compact family block design for fourteen undertaken characters is presented in Table-1 for nine crosses. The mean of squares due to families were found to be highly significant for all the fourteen characters studied as well as for all the progenies of the respective families. However, the replication variances for all the traits were found to be non-significant.

The mean performance of nine crosses and the range of variation among them for the characters studied are summarized in Table-2. The range was for plant height (53.79-79.51 cm), number of nodes per plant (13.12-14.56), number of pods per plant (26.27-93.19), number of seeds per pod (2.03-2.29), number of primary branches per plant (2.14-3.76), dry matter weight per plant (15.39-31.16 g), seed yield per plant (1.89-16.85 g), 100-seed weight (8.32-10.36 g), harvesting index (13.41-35.1 %), seed yield efficiency (16.2-54.72%), seed yield per row (67.83-395.59 g), seed yield per hectare (3.77-12.18 q/ha), days to 50% flowering (46.67-52.78 days) and days to 90% maturity (107.56-118.67 days).

Table 1. Analysis of variance for yield and other characters in F$_6$ generation of soybean

Mean Squares / Source of Variation	Replication	Family	Error(a)	Progeny within crosses	Error(b)
DF	2	8	16	30	60
Plant height(cm)	2.822	1884.599**	3.073	741.765**	4.084
Number of nodes per plant	1.498	12.162**	0.783	12.158**	2.178
Number of pods per plant	0.157	6409.358**	3.89	3292.611**	6.16
Number of seeds per pod	0.024	0.171*	0.031	0.083**	0.014
Number of primary branches per plant	0.144	8.523**	0.259	6.229**	0.135
Dry matter weight per plant (g)	0.318	2627.599**	3.273	933.556**	4.08
Seed yield per plant (g)	0.084	553.424**	0.298	202.085**	0.407
100-seed weight (g)	0.101	8.664**	0.256	13.099**	0.227
Harvesting index (%)	0.274	643.584**	0.201	413.476**	0.577
Seed yield efficiency (%)	0.835	2353.873**	0.94	1861.008**	2.697
Seed yield per row(g)	280.038	226702.876**	99.781	120836.479**	315.913
Seed yield per hectare(q/ha)	0.865	699.708**	0.308	372.958**	0.975
Days to 50% flowering	2.67	147.657**	1.034	34.415**	1.535
Days to 90% maturity	8.327	580.657**	2.247	66.884**	1.068

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

Table 2. Mean performance of yield and other characters in F_6 generation of soybean

S. No.	Genotype	Plant height (cm)	Number of nodes per plant	Number of pods per plant	Number of seeds per pod	Number of primary branches per plant	Dry matter weight per plant(g)	Seed yield per plant (g)	100-seed weight (g)	Harvesting index (%)	Seed yield efficiency (%)	Seed yield per row (g)	Seed yield per hectare (q/ha)	Days to 50% flowering	Days to 90% maturity
1	JS 20-29 × JS 20-55	62.29	13.51	52.37	2.15	3.76	30.02	10.62	10.12	35.1	54.72	217.76	12.09	47.17	108.67
2	PS 1584 × JS 20-41	72.37	14.07	52.92	2.23	3.57	27.53	6.8	9.24	24.66	33.02	152.41	8.47	50.5	115.45
3	JS 20-69 × JS 20-59	79.51	14.21	59.3	2.26	2.57	36	12.36	8.46	33.37	50.54	296.52	16.47	50.89	107.56
4	PS 1584 × JS 20-69	72.41	13.45	66.48	2.29	2.82	47.56	15.49	10.36	32.24	48.83	347.63	19.31	49.83	118.67
5	JS 20-64 × JS 20-54	67.88	13.59	58.28	2.25	3.22	32.61	10.97	8.68	34.01	51.85	266.69	14.82	52.78	115.67
6	PS 1042 × PS1347	61.13	14.56	45.32	2.2	2.88	22.56	5.78	8.32	27.28	38.83	131.56	7.31	53.4	108.89
7	PS 1583 × Bragg	69.05	14.14	93.19	2.25	3.45	45.67	16.85	9.15	33.97	54.37	395.59	21.98	51.67	117.45
8	PS 1583 × JS 20-29	60.18	13.12	52.43	2.26	2.14	22.22	6.94	10.25	32.01	48.11	222.97	12.39	46.67	108.12
9	RVS 2000-1 × PS1092	53.78	13.81	26.27	2.03	2.26	15.39	1.89	8.62	13.42	16.02	67.83	3.77	47.5	108.06
	GM	65.78	13.93	57.02	2.23	2.95	31.16	10.17	9.08	30.91	46.77	219.31	12.18	49.78	111.58
	S.Em±	0.58	0.29	0.66	0.06	0.17	0.6	0.18	0.17	0.15	0.32	3.33	0.18	0.34	0.5
	SE(d)	0.83	0.42	0.93	0.08	0.24	0.85	0.26	0.24	0.21	0.46	4.71	0.26	0.48	0.71
	C.D. (5%)	1.75	0.88	1.97	0.18	0.51	1.81	0.55	0.51	0.45	0.97	9.8	0.56	1.01	1.49
	C.D. (1%)	2.41	1.22	2.72	0.24	0.7	2.49	0.75	0.69	0.62	1.33	13.75	0.76	1.4	2.06
	C.V. (5%)	0.4	2.3	0.9	1.1	2.3	1	0.9	0.9	0.5	0.7	1.8	1.8	0.5	0.2

GM= General mean, S.Em = Standard error mean, SE(d)= Standard deviation, CD= Critical difference, C.V=Coefficient of variation

The quantitative traits under investigation were analyzed for phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation along with heritability, genetic advance and genetic advance as per cent mean (GAM) which are summarized in Table -3 and the histogram of genetic variability parameters are mentioned in Fig. 1. In general the result obtained from the analysis exhibited that PCV was higher for most of the traits than GCV and ECV. In some characters PCV exhibited similar values as GCV but higher than ECV values. It was indicated that traits studied in present investigation was influenced by genetic makeup of the plant rather than environment. The phenotypic coefficient of variance and genotypic coefficient of variance were grouped into 3 categories as proposed by Sivasubramanian and Menon [13] *i.e.* low (0-10%), moderate (10-20%) and high (20% and above).

The highest value for PCV (%) was 29.1% (seed yield per plant) followed by 20.8% (dry matter weight per plant), 20% (seed yield per row) and 20% (seed yield per hectare). Whereas, moderate PCV (%) values were 19.6%, 14.9%,

11.9% and 10.4% recorded for the traits *viz.* number of pods per plant, seed yield efficiency, number of primary branches per plant and harvesting index, respectively. The lowest estimate PCV (%) were 5.3%, 4.2%, 3.9%, 2%, 1.3% and 1% recorded for 100-seed weight, plant height, number of nodes per plant, number of seeds per pod, days to 50% flowering and days to 90% maturity, respectively.

Majority of characters under study showed moderate to low GCV values. The highest GCV (%) was estimated for the characters seed yield per plant (29.1%) followed by dry matter weight per plant (20.7%) whereas, moderate GCV (%) values were recorded for seed yield per row (19.9%), seed yield per hectare (19.9%) followed by number of pods per plant (19.5%), seed yield efficiency (14.9%), number of primary branches per plant (11.7%) and harvesting index (10.4%). However , the lowest GCV(%) value was exhibited by days to 90% maturity (1%), followed by days to 50% flowering (1.2%), number of seeds per pod (1.6%), number of nodes per plant (3.2%), plant height (4.2%) and 100-seed weight (5.2%).
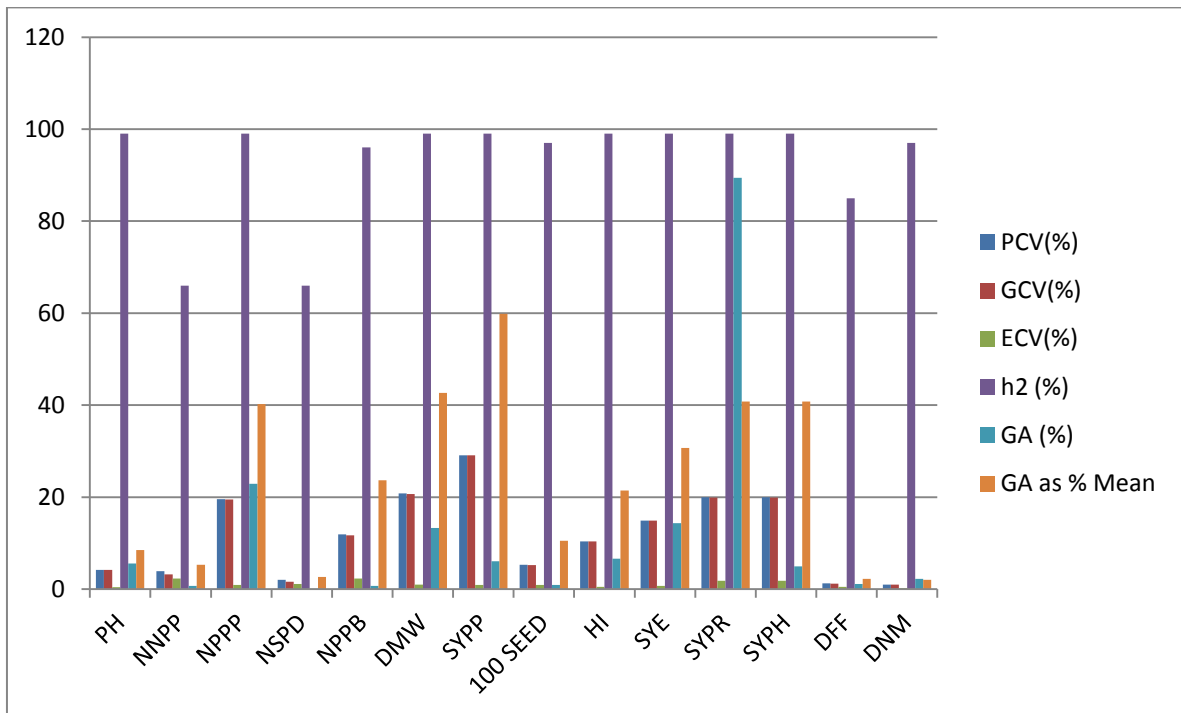

Fig. 1. Genetic variability parameters for different quantitative characters in soybean
PH- Plant height, NNPP- Number of nodes per plant, NPPP- Number of pods per plant, NSPD- Number of seeds per pod, NPPB- Number of primary branches per plant, DMW- Dry matter weight per plant (g), SYPP- Seed yield per plant (g), 100-SEED- 100-seed weight (g), HI- Harvesting index (%), SYE- Seed yield efficiency (%), SYPR-Seed yield per row (g), SYPH- Seed yield per hectare(q/ha), DFF- Days to 50% flowering, DNM- Days to 90% maturity

Table 3. General mean (GM), range, Standard Error of Mean (SEm) and variability parameters in F$_6$ generation of soybean

Character	GM	Range	SEm±	PCV (%)	GCV (%)	ECV (%)	h^2	GA	GA value % mean
Plant height (cm)	65.78	53.79-79.51	0.58	4.2	4.2	0.4	0.99	5.61	8.53
Number of nodes per plant	13.93	13.12-14.56	0.29	3.9	3.2	2.3	0.66	0.74	5.28
Number of pods per plant	57.02	26.27-93.19	0.66	19.6	19.5	0.9	0.99	22.93	40.22
Number of seeds per pod	2.23	2.03-2.29	0.06	2	1.6	1.1	0.66	0.06	2.68
Number of primary branches per plant	2.95	2.14-3.76	0.17	11.9	11.7	2.3	0.96	0.69	23.69
Dry matter weight per plant (g)	31.16	15.39-47.56	0.6	20.8	20.7	1	0.99	13.29	42.66
Seed yield per plant(g)	10.17	1.89-16.85	0.19	29.1	29.1	0.9	0.99	6.09	59.84
100-seed weight (g)	9.08	8.32-10.36	0.17	5.3	5.2	0.9	0.97	0.95	10.51
Harvesting index (%)	30.91	13.42-35.1	0.15	10.4	10.4	0.5	0.99	6.63	21.45
Seed yield efficiency (%)	46.77	16.03-54.72	0.32	14.9	14.9	0.7	0.99	14.36	30.71
Seed yield per row (g)	219.31	67.83-395.59	3.33	20	19.9	1.8	0.99	89.45	40.79
Seed yield per hectare (q/ha)	12.18	3.77-21.98	0.18	20	19.9	1.8	0.99	4.97	40.79
Days to 50% flowering	49.78	46.67-52.78	0.34	1.3	1.2	0.5	0.85	1.12	2.25
Days to 90% maturity	111.58	107.56-118.67	0.5	1	1	0.2	0.97	2.24	2.01

It has been observed from the results obtained in F_6 crosses that the values of ECV (%) were comparatively lower than those of PCV (%) and GCV (%) for majority of characters under study. The highest value for ECV (%) was observed for number of primary branches per plant (2.3%) followed by seed yield per row (1.8%), seed yield per hectare (1.85), number of seeds per pod (1.1%), dry matter weight per plant (1%), whereas, the lowest value for ECV was recorded for the traits *viz.* number of pods per plant (0.9%) seed yield per plant (0.9%), 100-seed weight (0.9%) succeeded by seed yield efficiency (0.7%), harvesting index (0.5%), days to 50% flowering (0.5%), plant height (0.4%) and days to 90% maturity (0.2%). All the traits except number of nodes per plant showed a greater contribution of GCV values towards PCV values with a negligible impact of ECV. This indicated a minimal influence of environment and hence, a maximum role of genetic factors in the character expression, which could make the selection process more effective [14,15]. Earlier workers Jain et al. [16] and Bisht et al. [17] also reported high estimates of PCV and GCV as compare to ECV. Ghiday et al. (2017) also found that GCV and PCV were high for seed yield per plant, number of seeds per pod and biological yield. High values of GCV and PCV were reported by Chandrawat et al. [18] and Guleria et al. [19] for numbers of pod per plant and seed yield per plant.

Genotypic coefficient of variation only ensures the amount of variation in genetic materials without explaining its heritable portion of variation. Hence, current research was conducted to estimate heritability and genetic advance. The estimates of heritability were also classified into 3 categories, low (0-30%) moderate (30-60%) and high (>60%) as suggested by Robinson et al. [20]. Similarly, Genetic advance as per cent mean was also classified into 3 categories, low (0-10%) moderate (10-20%) and high (20% and above) as suggested by Johnson et al. [12].

All the characters under study showed high heritability in broad sense. The highest heritability value was exhibited by seed yield per plant (99.9%) followed by number of pods per plant (99.8%), harvesting index (99.8%), seed yield efficiency (99.8%). The highest and lowest genetic advance recorded for seed yield per row (89.44) and number of seed per pod (0.06), respectively. Majority of traits under

consideration including seed yield per plant (g), dry matter weight per plant (g),number of pods per plant, seed yield efficiency, number of primary branches per plant and plant height (g) exhibited high values of heritability along with high estimates of genetic advance as per cent mean in the F_6 generation which indicating the involvement of additive gene action in these characters expression and hence, it offers an ample scope to plant breeders to improve these traits further through selection. These results are in accordance with Chandrawat et al. [18] and Jain et al. [21].

High heritability coupled with moderate genetic advance per cent of mean was reported for 100-seed weight. Similar finding was reported by Pandey et al. [22]. High heritability combined with low genetic advance as per cent mean was found for plant height, days to 50 percent flowering and days to 90 percent maturity indicating the influence of dominant effects on the expression of such characters. Hence, progeny testing or heterosis breeding could be employed for the improvement of these characters in soybean. Similar findings are obtained by Ghodrati [23].

4. CONCLUSION

The analysis of variance found significant for all the characters which ensured presence of variability in experimental materials of F_6 generation. Seed yield per plant exhibited the highest values for both phenotypic coefficient of variation (29.21%) and genotypic coefficient of variation (29.1%). The highest heritability estimates were obtained for number of pods per plant followed by plant height, seed yield per plant, harvesting index and seed yield efficiency. The expected genetic advance ranged from 0.06 (number of seeds per pod) to 89.45 (seed yield per row).The highest genetic advance as percent of mean (5%) was 59.84% for the trait seed yield per plant. Majority of traits under consideration including seed yield per plant (g), dry matter weight per plant (g),number of pods per plant, seed yield efficiency, number of primary branches per plant and plant height (g) exhibited high values of heritability along with high estimates of genetic advance as per cent of mean. High heritability coupled with low genetic advance as per cent mean was observed for plant height followed by days to 50% flowering and days to 90% maturity indicating the influence of non additive effects on the expression of such characters.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Peerzada OH, Chaurasia AK, Naqueshbandilrshad A. Evaluation of chickpea germplasm (desi) (*Cicer arietinum L.*) for yield and yield contributing traits, The Bioscan. 2014;9(4):1805- 1809.
2. Agarwal DK, Billore SD, Sharma AN, Dupare BU, Srivastava SK. Soybean: introduction, improvement, and utilization in India—problems and prospects. Agricultural Research. 2013;2(4):293-300.
3. Siqueira AF, Ormeño-Orrillo E, Souza RC, Rodrigues EP, Almeida LGP, Barcellos FG, Hungria M. Comparative genomics of Bradyrhizobium japonicum CPAC 15 and Bradyrhizobium diazoefficiens CPAC 7: elite model strains for understanding symbiotic performance with soybean. BMC genomics. 2014;15(1): 1-21.
4. Akram RM, Fares WM, Fateh HAS, Rizk AMA. Genetic variability, correlation and path analysis in soybean. Egyptian Journal Plant Breed. 2011;15(1):89-102.
5. Antalina S. Modern processing and utilization of legumes. Recent Research and Industrial achievement for soybean food in Japan. Proceeding of RILET-JIRCAS. Workshop on Soybean Research., Malang-Indonesia; 2000.
6. Aizawa SI. Flagellar World. Elsevier, Incorporated; 2014.
7. Egli DB, Bruening WP. Flowering and fruit set dynamics at phloem-isolated nodes in soybean. Field Crops Research. 2002;79: 9–19.
8. Hutchinson JB, Panse VG, Apte N. Studies in plant breeding technique. Indian J. agric. Sci. 1937;7:531-564.
9. Federer WT. Experimental design: theory and application. 1955;(No. 001.434 F293). Macmillan.
10. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. New Delhi-Ludhiana, India. Kalyani publishers. 1977;318.
11. Hanson CH, Robinson HF, Comstock RE. Biometric studies of yield segregating population in Korean lespedeza. Agron. J. 1956;48:268-272.
12. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron. J. 1955;47 (7):314-317.
13. Sivasubramanian S, Menon PM. Genotypic and phenotypic variability in rice. Madras Agric. J. 1973;60(9-13):1093-1096.
14. Ekka NP, Lal GM. Study on genetic variability and character association in soybean [*Glycine max (L.)* Merrill] germplasm at vindhyan zone of Uttar Pradesh. Agricultural Science Digest-A Research Journal. 2016;36(1):69-71.
15. Chandel K, Patel N, Sharma L, Gali S. Genetic variability, correlation coefficient and path analysis for yield and yield attributing characters in soybean [*Glycine max (L.)* Merrill]. Green Farming. 2017;8(3):547-551.
16. Jain S, Srivastava SC, Singh SK, Indapurkar YM, Singh BK. Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max (L.)* Merrill]. Legume Research-An International Journal. 2015;38(2):182-184.
17. Bisht M, Singh K, Bhatt P, Kunduru B, Chourasia KN. Studies on variability parameters in early generation of soybean [*Glycine max (L.)* Merrill]. IJCS. 2018;6 (3):208-211.
18. Chandrawat KS, Baig KS, Hashmi, S., Sarang DH, Kumar A, Dumai PK. Study on genetic variability, heritability and genetic advance in soybean. Int. J. Pure App. Biosci. 2017;5(1):57-63.
19. Guleria H, Kumar P, Jyoti B, Kumar A, Paliwal A, Paliwal A. Genetic variability and correlation analysis in soybean *[Glycine max (L.)* Merrill] genotypes. IJCS. 2019;7(1):1928-1932.
20. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agron. J. 1949;41:353-359.

21. Jain RK, Joshi A, Chaudhary HR, Dashora A, Khatik CL. Study on genetic variability, heritability and genetic advance in Soybean [*Glycine max (L.)* Merrill]. Legume Research-An International Journal. 2018;4(4):532-536.

22. Pandey K, Singh K, Singh BV, Pushpendra Gupta MK, Yadav NS. Character association and path coefficient analysis in advance breeding lines of soybean [*Glycine max (L.)* Merrill.]. Soybean Research. 2008;45:34-38.

23. Ghodrati G. Study of genetic variation and broad sense heritability for some qualitative and quantitative traits in soybean [*Glycine max (L.)* Merrill] genotypes. Current Opinion in Agriculture. 2013;2(1): 31–35.

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