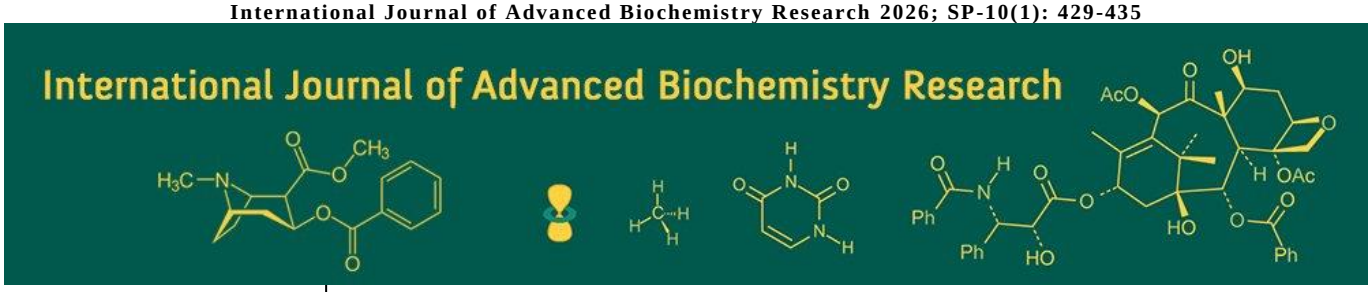

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(1): 429-435
www.biochemjournal.com
Received: 05-10-2025
Accepted: 09-11-2025

Debolina Sinha
Assistant Professor, Department of Agriculture, Netaji Subhas University, Jamshedpur, Jharkhand, India

Akashi Sarma
Professor, Department of Plant Breeding and Genetics, Assam Agricultural University, Assam, India

Zafar Ullah
Retd. Principal Scientist, Department of Plant Breeding & Genetics, Assam Agricultural University, Assam, India

Vijay Kant Pandey
Associate Professor, Department of Life Science, Netaji Subhas University, Jharkhand, India

Corresponding Author:
Vijay Kant Pandey
Associate Professor, Department of Life Science, Netaji Subhas University, Jharkhand, India

Analysis of genetic variability and the pattern of genetic divergence among soybean [*Glycine max* (L.) Merrill] genotypes

Debolina Sinha, Akashi Sarma, Zafar Ullah and Vijay Kant Pandey

DOI: https://www.doi.org/10.33545/26174693.2026.v10.i1Sf.6974

Abstract
Forty soybean genotypes were evaluated following randomized block design with three replications at the ICR experimental farm of AAU, Jorhat, Assam in order to achieve genetic variability and diversity patterns. Eleven quantitative traits showed considerable variability and high GCV and PCV for seed yield per plant and 100-seed weight. High heritability and high genetic advance associated with days to 50% flowering, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, harvest index and seed yield per plant were observed depicting the usefulness for selection. D^2 statistics of Mahalanobis was used for clustering the genotypes in to four clusters. The greatest distance between clusters (2572.391) was found between Clusters II and IV, both the most divergent in the analysis. 100-seed weight, seed yield per plant and protein content made the maximum contribution to genetic divergence. Principal component analysis showed that PC1 and PC2 explained 74.931% of total variability, in which PC1 contributed to 59.858%, mainly contributed by yield-related traits, as well as serving as important information for future breeding practices.

Keywords: Genotypic variation; heritability, phenotypic variation, cluster, genetic advance

Introduction
Soybean [*Glycine max* (L.) Merrill] commonly known as 'wonder crop' is known to be one of the richest sources of both oil and protein and, therefore, sometimes identified as 'gold from soil'. One of the first domesticated crops, rice was grown in central China approximately 7000 B.C. It belongs to the Fabaceae family and is a self-pollinated crop with chromosome no. 2n = 40. It is considered a 'miracle crop' due to its versatility, (its oil as edible oil is being used extensively in the world and soybean meal known to be an important source of protein and metabolizable energy for human diets and animal feeds). As one of the major oilseed crops worldwide, soybean is top in world market (Chung and Singh, 2008) [15]. Soybean is not only an oil crop but is also endowed with significant medicinal and nutritional value. They contribute several vitamins and minerals as well as a diverse range of bioactive plant compounds such as isoflavonoids, phytic acid and saponins.
The genetic diversity and variability that are available today determine the extent to which most crops can be genetically improved. Genetic variability and diversity are critically important for a successful breeding program. Study of genetic diversity helps assessing amount of diversity existing in the genotypes and also provides a means to identify parents for the strengthening as well as broadening of genetic base and heterosis through hybridization. Sufficient understanding of genetic diversity will enable the plant breeders to evolve superior cultivars with desired traits.
Multivariate analysis is one of the most useful technique for studying genetic variability and pattern of diversity in germplasm collections. Related to this r the two most preferred singletons for exploring the pattern of genetic diversity among genotypes based on morphometric characters are: cluster analysis and principle component analysis (PCA). Another use of genetic diversity study among different germplasm collections is to enable the accurate classification of accessions and reveal subgroups in core collection. This also shows the contribution of individual characters to the total divergence among them. Furthermore, discrimination of crop genotypes on the basis of genetic diversity can be useful for broadening the germplasm base in crop improvement programmes.

Materials and Methods

Experimental material and plan

The experiment was conducted at the Instructional cum Research (ICR) farm of Assam Agricultural University, Jorhat, Assam during Kharif 2022-23. The study site was situated at 26°45' N latitude and 94° 12' east, with an altitude of 91.00 m above MSL. The experimental material comprised forty soybean genotypes including 2 checks (described in Table 1), were procured from ICAR-Indian Institute of Soybean Research, Indore, India. The experiment was conducted in randomised block design with three replications. Each genotype was planted into tows of 2 lengths 4m spaced at a distance of 45×10 cm. The recommended agronomic practices were adopted to obtain good crop growth.

Methodology

The observations were recorded on 40 soybean genotypes (Table 1) which were received from IISR, Indore and for each variety index plant i.e.5 plants per row of selected variety was taken randomly. Readings were taken for 11 quantitative characters such as days to 50% flowering (in days), plant height (cm), no. of primary branches/plant, no. of pods/plant, no. of seeds/pod, harvest index (%), oil content (%), protein content (%), days to maturity and yield/plant (g). Observations from 40 genotypes of soybean were analyzed for variance and estimation of different variability parameters viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2 bs) and per cent genetic advance as mean (PGAM).

To understand the pattern of genetic diversity among 40 soybean genotypes, cluster analysis using Mahalanobis D^2 method (1936) and principal component analysis were employed based on 11 quantitative characters in the present investigation. Wilk's criterion derived by Rao (1952) was used to test the significance of difference in the mean values for all characters.

Results and Discussion

The analysis of variance (Table 2) revealed significantly high magnitude of mean sum squares for genotypes with respect to all quantitative characters under investigation including days to fifty per cent flowering, no. primarily branches/plant, no.of pods/plant, no of seeds/pod, Plant Height (cm), Hundred Seed Weight (g), Harvest Index (%), days to maturity protein contents % oil content (%) and seed yield plant.

The PCV were higher as compared to the GCV for all 11 quantitative characters (Table 3) suggesting environmental effects on expression of these characters. Similar remarks were documented by Guleria *et al.* (2019) [23]. The traits seed yield per plant and 100-seed weight recorded high GCV and PCV (>20%) indicating the predominance of wider variability for these two characters. Malek *et al.* (2014) who found consistent results for 100 seed weight with Hossain *et al.* (2004) [25] for seed yield per plant and 100 seed weight and by Saicharan *et al.* (2022) [46] for seed yield per plant. A moderate to narrow range of GCV and PCV (10-20%) were noticed for number of primary branches/plant, number of seeds/pod, number of pods/plant, days to 50% flowering, harvest index and oil content suggesting that variability present in these traits can be improved by use of breeding methods for effective selection. Similar finding was also reported by Reni and Rao (2013) [45] on number of seed per pod and days to 50% flowering; Saicharan *et al.*, (2022) [46] for number of branches per plant.

Estimates of Heritability in % Relative in all the 40 soybean genotypes for Eleven quantitative traits ranged from 73.12% to 97.60%. High heritability alongwith high genetic advance as per cent of mean (>20%) was observed for characters days to 50% flowering, number of primary branches/plant, number of pods/plant, number of seed/pod 100 seed weight, harvest index oil content & seed yield/plant. This revealed the importance of additive gene action and direct selection for genotypic expression may be beneficial for their future exploitation. Hossain *et al.* (2004) [25] also recorded similar observation for high heritability along with high genetic advance as % of mean. for 100 seed weight, pods per plant and seed yield per plant, Khumukcham *et al.* (2022) [32] for number of pods per plant, 100 seed weight, harvest index and seed yield per ha.

Multivariate analysis was used to analyse the pattern of genetic divergence among soybean genotypes. Based on 11 quantitative traits, the 40 soybean genotypes were divided into four clusters (Table 4), utilizing Tocher's method of cluster analysis. This indicates that the genotypes of soybean under investigation reveal considerable divergence with respect to various morphological characters. Among the four clusters thus formed, cluster I harboured largest genotype (25), followed by Cluster III (8), Cluster II (6) and Cluster IV represented by single varieties. Marconato *et al.* also observed the formation of various number of clusters on the basis of different morphological characters in various genotypes of soybean. (2016) to classify 93 soybean genotypes into 8 clusters and Upadhyay *et al.* (2022) [54] for partitioning 50 genotypes of soybean into five clusters. The inter and intra cluster distances (Table 5), revealed that the most dissimilar clusters were cluster II and IV with a value of 2572.391 between these two clusters also reflected the diverse nature of genotypes among these two clusters. Table 6 presenting percentage contribution of all the 11 characters towards genetic divergence The microdiasim figure (table7) which depicts percentage accumulated variance for each character to genetic diversity revealed that hundred seed weight contributed maximum toward divergence followed by per plant seed yield and protein content. Characters number of primary branches per plant, oil content, number of pods per plant and days to maturity contributed almost equally in divergence. Therefore, it is better to intermate the genotypes under investigation by choosing extreme parents for those characters which are contributing significantly towards total divergence. This may facilitate a range of satisfactory levels of genetic variation towards yield improvement in soybean. Significant contribution of seed yield per plant towards genetic divergence was reported by Shinde *et al.* (2013) [49] and 100 seed weight as reported by Alpna *et al.* (2015) [2] and 100 seed weight and seed yield per plant by Mounika *et al.* (2022) [40].

The PCA result (Table 7) reflected the genetic diversity of soybean germplasm accessions. Scores and loadings analysis On the basis of scree plot out of 11 components (11 characters) two principal elements (PC 1 and PC 2) were observed above eigen value one, contributing about 74.93% of total variability. Accordingly, these two principal components were chosen for further interpretation. The PC 1 which contributed maximum to the variability (59.86%)

had strong associations with 100 seed weight, seed yield per plant, oil content, number of pods per plant, number of primary branches per pant and harvest index on the basis of highly loaded factors. Semi curve trend observed after second PC, showed by scree plot (Fig 1) and less fluctuation within the each PC revealed that more maximum variation was loaded on PC1 so the selection of lines for characters under PC 1 may be useful for future prospects. Ghiday *et al.* (2015) [20] found for number of pods per plant and seed yield per plant, El-Hashash (2016) [18] for pods/plant, seed yield/plant and harvest index and Verma *et al.*, (2021) [55] for number of pods/plant, number of primary branches/plant and also for number of seeds/pod.

Table 1: List of genotypes used in the experiment:

S. No.	Name of genotypes
1	VLS 104
2	NRCSL 5
3	JR 24-26
4	NRCSL 7
5	RVS 12-8
6	KDS 1203
7	NRC 253
8	MACS 1756
9	Lok Soya-2
10	AMS 2021-3
11	Himso 1695
12	TS-156
13	NRCSL 8
14	JS 24-34
15	DS 1510
16	KSS 213
17	MAUS 824
18	NRC 254
19	AMS 2021-4
20	Himso 1696
21	DS 1529
22	KDS 1188
23	Acb 93
24	NRCSL 4
25	Himso 1694
26	MAUS 814
27	Asb 85
28	NRC 191
29	NRC 256
30	BAUS 124
31	NRC 258
32	AUKS 212
33	RVSM 12-21
34	NRC 259
35	RSC 1172
36	AS 55
37	NRC 260
38	NRC 196
39	JS 20-116 (C)
40	Macs 1407 (C)

Table 2: Analysis of variance for eleven quantitative characters

	Sources of Variance			
	Replications	Genotypes	Error	CV %
DF(degrees of freedom)	2	39	78	
Days to 50% flowering	0.158	72.448**	3.475	4.744
No. of primary branches/plant	0.14	9.479**	0.503	7.341
No. of pods/plant	5.29	733.510**	15.16	3.737
No. of seeds/pod	0.042	0.495**	0.054	9.112
Plant height (cm)	0.147	109.645**	5.818	
100 seed weight(g)	0.454	21.657**	0.176	3.305
Harvest index	3.861	75.535**	4.085	4.655
Days to maturity	5.025	79.141**	2.512	1.557
Oil content (%)	0.031	8.820**	0.254	3.248
Protein Content (%)	0.168	47.409**	0.623	1.901
Seed yield/plant(g)	1.19	70.945**	0.674	3.658

** represents significance at 1% level

Table 3: Genetic variability parameters for the eleven characters

	Range	GCV %	PCV%	h^2(broad sense)	G.A. %
DF	31.33-47.66	12.2	13.09	86.87	23.43
NPB	6.22-12.80	17.9	19.35	85.59	34.11
NPP	59.66-122.53	14.85	15.31	94.05	29.67
NSP	2.00-3.26	15.02	17.57	73.12	26.46
PH	45.77-71.52	4.04	9.87	85.61	18.8
SW	7.27-19.12	21.08	21.34	97.6	42.9
HI	32.32-50.58	11.24	12.16	85.36	21.39
DM	93.33-109.00	4.96	5.2	91.05	9.76
OC	12.67-18.93	10.89	11.36	91.82	21.5
Pc	33.78-46.20	9.51	9.7	96.16	19.21
SY	12.70-31.92	21.56	21.87	97.2	43.8

DF = Days to 50% flowering NPB = No. of primary branches per plant NPP = No. of pods per plant NSP = No. of seeds per pod PH = Plant height SW = 100 seed weight HI = Harvest index DM = Days to maturity OC = Oil content Pc = Protein content SY = Seed yield per plant

Table 4: Constituents of each cluster accordance to Tocher's clustering pattern

Cluster No.	No. of varieties	Varieties included
Cluster I	25	TS-156, NRC 259, MACS 1756, JS 20-116, RVSM 12-21, NRC 256, Himso 1695, AUKS 212, JS 24-34, Himso 1694, Lok Soya-2, Acb 93, DS 1529, Himso 1696, NRC 254, KDS 1203, VLS 104, Macs 1407, MAUS 814, NRCSL 4, JR 24-26, NRC 253, Asb 85, NRCSL 8, BAUS 124
Cluster II	6	AMS 2021-4, NRC 258, NRC 196, AMS 2021-3, RSC 1172, DS 1510
Cluster III	8	KSS 213, MAUS 824, KDS 1188, NRCSL 7, AS 55, NRC 260, NRC-191, RVS 12-8
Cluster IV	1	NRCSL 5

Table 5: Intra (bold) and inter-cluster distance (D^2) among four clusters

Cluster distances	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	130.895	389.924	388.386	1227.517
Cluster II		81.119	1176.999	2572.391
Cluster III			124.788	454.138
Cluster IV				0

Table 6: Percentage contribution of 11 characters towards genetic divergence

Name of characters	% Contribution towards divergence
100 seed weight (g)	29.90%
Seed yield/plant	17.50%
Protein content %	13.60%
No. of primary branches per plant	6.90%
Oil content %	6.40%
No. of pods per plant	6.30%
Days to maturity	6.00%
Plant height (cm)	5.40%
Days to 50 % flowering	4.40%
Harvest index %	2.50%
No. of seeds per pod	1.10%

Table 7: Eigenvalues and extracted Sum of Squared Loadings for 11 characters (Extraction Method: Principal Component Analysis)

Total Variance Explained						
Component	Initial Eigenvalues			Extraction Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	6.584	59.858	59.858	6.584	59.858	59.858
2	1.658	15.073	74.931	1.658	15.073	74.931
3	0.647	5.881	80.812			
4	0.516	4.695	85.507			
5	0.485	4.405	89.912			
6	0.333	3.029	92.941			
7	0.241	2.193	95.134			
8	0.198	1.802	96.935			
9	0.153	1.391	98.327			
10	0.122	1.106	99.433			
11	0.062	0.567	100			

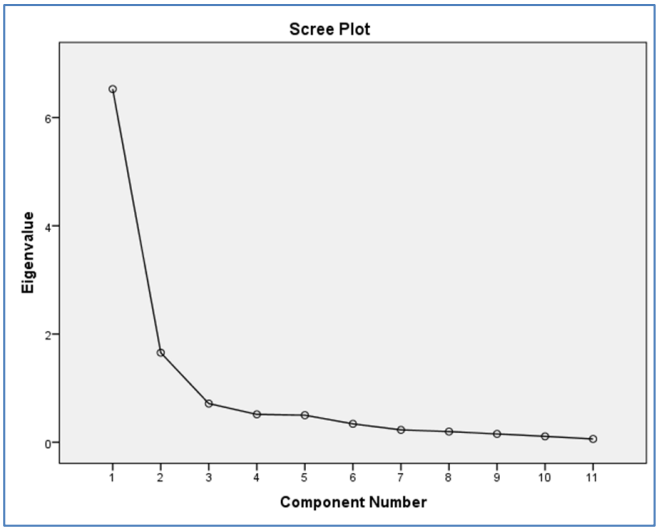

Fig 1: Scree plot

Conclusion

In the present study highly significant genetic variability was recorded among 40 genotypes of soybean on eleven quantitative traits. ANOVA detected genetic distinctions for breeding purposes. Yield potential (seed yield per plant and 100-seed weight) and number of primary branches per plant, seeds per pod, pods per plant, days to 50% flowering harvest index and oil content showed high (GCV & PCV >20%), moderate (10-20%) variability. The characters viz, days to 50% flowering, primary branches per plant, seed yield per plant and 100-seed weight exhibited high heritability along with high genetic advance indicating preponderance of additive gene action, thus direct selection will be effective. Based on cluster analysis, the genotypes were classified into four clusters and Cluster I included 25 genotypes. Between Cluster II and IV, the maximal divergence was observed. The traits that most contributed to divergence were 100-seed weight, seed yield and seed protein. PC analysis showed that PC1 and PC2 were able to explain 74.93% of the variance with significant association with yield traits. For the purpose of breeding better soybean cultivars, hybrids between different genotypes separated from Clusters II and IV should be developed.

References

1. Akram S, Hussain BN, Al Bari MA, Burritt DJ, Hossain MA. Genetic variability and association analysis of soybean (*Glycine max* (L.) Merrill) for yield and yield attributing traits. Plant Gene and Trait. 2016;7(13):1-11.
2. Alpna, Arora RN, Yadava RK. Genetic divergence analysis in soybean (*Glycine max* (L.) Merrill). Res on Crops. 2015;16(1):110-116.
3. Anupam B, Pushpendra, Meenakshi J. Bhat: a new source of genetic divergence for soybean improvement. African Journal of Agricultural Research. 2014;9(1):119-124.
4. Ao J, Fu J, Tian J, Yan X, Liao H. Genetic variability for root morph-architecture traits and root growth dynamics as related to phosphorus efficiency in soybean. Functional Plant Biology. 2010;37(4):304-312.
5. AOAC. AOAC official methods of analysis. Association of Official Analytical Chemists, Arlington, Virginia; 1990.
6. Arora RN. Assessment of genetic diversity for yield and seedling traits in soybean (*Glycine max* L. Merrill). Electronic Journal of Plant Breeding. 2018;9(1):355-360.
7. Baraskar VV, Vachhani JH, Kachhadia VH, Patel MB, Barad HR. Correlation and path analysis for seed yield in soybean (*Glycine max* (L.) Merrill). Electronic Journal of Plant Breeding. 2015;6(2):570-573.
8. Begum T, Kumar D. Usefulness of morphological characteristics for DUS testing of jute (*Corchorus olitorius* L. and *C. capsularis* L.). Spanish Journal of Agricultural Research. 2011;9(2):473-483.
9. Bekele A, Alemaw G, Zeleke H. Genetic divergence among soybean (*Glycine max* (L.) Merrill) introductions in Ethiopia based on agronomic traits. Journal of Biology, Agriculture and Healthcare. 2012;2(6):6-13.
10. Belay T, Tesfaye A, Alamerew S. Genetic variability, genetic advance and heritability of black and brown seeded soybean (*Glycine max* (L.) Merrill) lines in Jimma and Bonga Southwest Ethiopia. International Journal of Agricultural Research, Innovation and Technology. 2022;12(2):14-17.
11. Bhandari HR, Bhanu AN, Srivastava K, Singh MN, *et al.* Assessment of genetic diversity in crop plants—an overview. Advances in Plants & Agriculture Research. 2017;7(3):279-286.
12. Cantelli DAV, Hamawaki OT, Rocha MR, Nogueira APO, Hamawaki RL, *et al.* Analysis of the genetic divergence of soybean lines through hierarchical and Tocher optimization methods. Genetics and Molecular Research. 2016;15(4):1-13.
13. Chakraborty S, Patel DA, Parmar H, Dhaduk HL, Sasidharan N. Genetic diversity analysis in soybean (*Glycine max* (L.) Merrill) using SSR markers. Journal of Pharmacognosy and Phytochemistry. 2018;7(3):2380-2384.
14. Chandrawat KS, Baig KS, Hashmi S, Sarang DH, Kumar A, *et al.* Study on genetic variability, heritability and genetic advance in soybean. International Journal of Pure and Applied Bioscience. 2017;5(1):57-63.
15. Chung G, Singh RJ. Broadening the genetic base of soybean: a multidisciplinary approach. Critical Reviews in Plant Sciences. 2008;27(5):295-341.
16. Dhillon SK, Singh G, Gill BS. Genotypic and phenotypic variability and heritability of some yield and quality characters in soybean (*Glycine max* (L.) Merrill). Legume Research—An International Journal. 2005;28(4):276-279.
17. Dubey N, Avinashe HA, Shrivastava AN. Principal component analysis in advanced genotypes of soybean (*Glycine max* (L.) Merrill) over seasons. Plant Archives. 2018;18(1):501-506.
18. El-Hashash E. Genetic diversity of soybean yield based on cluster and principal component analyses. Journal of Advances in Biology & Biotechnology. 2016;10(3):1-9.
19. Getnet BE. Genetic variability, heritability and expected genetic advance in soybean (*Glycine max* (L.) Merrill) genotypes. Agriculture, Forestry and Fisheries Journal. 2018;7(5):108-112.
20. Ghiday T, Sentayehu A. Genetic divergence analysis on some soybean (*Glycine max* L. Merrill) genotypes grown in Pawe, Ethiopia. American-Eurasian Journal of Agriculture and Environmental Science. 2015;15(10):1927-1933.
21. Gohil VN, Mehta DR, Pandya HM. Genetic divergence in soybean (*Glycine max* (L.) Merr.). Legume Research—An International Journal. 2007;30(3):224-226.
22. Govindaraj M, Vetriventhan M, Srinivasan M. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. Genetics Research International. 2015;Article ID 431487.
23. Guleria SK, Sharma A, Gupta OP. Genetic variability and association studies for plant architecture and yield traits in soybean (*Glycine max* L. Merrill). Journal of Farm Sciences. 2019;32(3):267-270.
24. Hormichon S, Devi HN, Devi THR, Devi TS, Nilima K, *et al.* Genetic diversity analysis among soybean (*Glycine max*) genotypes based on agro-morphological characters. Indian Journal of Agricultural Sciences. 2018;88(12):1839-1842.

25. Hossain MA, Naz S, Rahman L. Genetic variability, heritability and genetic advance of yield and related traits of soybean (*Glycine max* L.). Journal of the Bangladesh Agricultural University. 2004;2:9-14.
26. Hou A, Chen P, Alloatti J, Li D, Mozzoni L, *et al.* Genetic variability of seed sugar content in worldwide soybean germplasm collections. Crop Science. 2009;49(3):903-912.
27. 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;41(4):532-536.
28. Jandong EA, Uguru MI, Okechukwu EC. Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.). African Journal of Biotechnology. 2020;19(4):201-206.
29. Kachhadia VH, Baraskar VV, Vachhani JH, Patel MB, Barad HR. Genetic divergence in soybean (*Glycine max* (L.) Merrill). Electronic Journal of Plant Breeding. 2014;5(3):563-566.
30. Kayande NV, Patil SP. Genetic divergence in soybean (*Glycine max* (L.) Merril). International Journal of Plant Sciences. 2009;4(1):218-220.
31. Khan S, Latif A, Ahmad SQ, Ahmad F, Fida M. Genetic variability analysis in some advanced lines of soybean (*Glycine max* L.). Asian Journal of Agricultural Sciences. 2011;3(2):138-141.
32. Khumukcham JD, Tandekar K, Nag S, Shrivastava R. Genetic variability analysis in soybean genotypes based on yield and yield contributing traits. The Pharma Innovation. 2022;11(7):3233-3236.
33. Koraddi S, Basavaraja GT. Genetic variability studies on yield and yield component traits of soybean. International Journal of Current Microbiology and Applied Sciences. 2019;8(2):1269-1274.
34. Kumar A, Pandey A, Aochen C, Pattanayak A. Evaluation of genetic diversity and interrelationships of agro-morphological characters in soybean (*Glycine max*) genotypes. Proceedings of the National Academy of Sciences, India Section B. 2015;85(2):397-405.
35. Kumar M, Nadarajan N. Genetic divergence studies in soybean (*Glycine max* (L.) Merrill). Indian Journal of Genetics and Plant Breeding. 1994;54(3):242-246.
36. Mahalanobis PC. On the generalized distance in statistics. Sankhyā: The Indian Journal of Statistics. 2018;80(1):S1-S7.
37. Mahbub MM, Rahman MM, Hossain MS, Nahar L, Shirazy BJ. Morpho-physiological variation in soybean (*Glycine max* (L.) Merrill). American-Eurasian Journal of Agricultural and Environmental Sciences. 2016;16(2):234-238.
38. Marconato MB, Pereira EM, Silva FM, Bizari EH, Pinheiro JB, *et al.* Genetic divergence in a soybean (*Glycine max*) diversity panel based on agro-morphological traits. Genetics and Molecular Research. 2016;15(4):1-10.
39. Marega Filho M, Destro D, Miranda LA, Spinosa WA, Carrão-Panizzi MC, *et al.* Relationships among oil content, protein content and seed size in soybeans. Brazilian Archives of Biology and Technology. 2001;44(1):23-32.
40. Mounika KLS, Devi TR, Devi HN, Kammela SR, Masadi SK, *et al.* Genetic diversity study in soybean (*Glycine max* L. Merrill) based on agro-morphological characters. Electronic Journal of Plant Breeding. 2022;13(3):1005-1011.
41. Neelima G, Mehtre SP, Narkhede GW. Genetic variability, heritability and genetic advance in soybean. International Journal of Pure Applied Bioscience. 2018;6(2):1011-1017.
42. Patil SS, Naik MR, Patil AB, Ghodke UR. Genetic diversity in soybean. Legume Research—An International Journal. 2011;34(1):68-70.
43. Pearson K. Principal components analysis. Philosophical Magazine. 1901;6(2):559.
44. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria; 2020.
45. Reni YP, Rao YK. Genetic variability in soybean (*Glycine max* (L.) Merrill). International Journal of Plant, Animal and Environmental Sciences. 2013;3(4):35-38.
46. Saicharan G, Dhuppe MV, Rathod ST, Sargar PR, Venkateshwara M. Studies on genetic variability, heritability, and genetic advance for yield and yield contributing traits in soybean (*Glycine max* (L.) Merrill). The Pharma Innovation. 2022;11(12):3131-3133.
47. Sareo H, Devi HN, Devi TR, Devi TS, Karam N, *et al.* Genetic diversity among soybean (*Glycine max* (L.) Merrill) genotypes based on agro-morphological characters under rainfed condition of Manipur. Climate Change and Environmental Sustainability. 2018;6(1):41-45.
48. Shadakshari TV, Kalaimagal T, Senthil N, Boranayaka MB, Kambe Gowda R, *et al.* Genetic diversity studies in soybean (*Glycine max* (L.) Merrill) based on morphological characters. Asian Journal of Bio Science. 2011;6(1):7-11.
49. Shinde SR, Chavan RB, Pawar RM. Genetic divergence in soybean (*Glycine max* (L.) Merrill). Asian Journal of Bio Science. 2013;8(2):225-228.
50. Shwe UH, Murthy BR, Singh AB, Rao UMS. Genetic divergence in recent elite strains of soybean and groundnut in India. Indian Journal of Genetics and Plant Breeding. 1972;32(2):285-298.
51. Subhash R, Devidas P, Gupta MK, Vani DK. Assessment of genetic variability, correlation and path analyses for yield and its components in soybean. Trends in Biosciences. 2017;10(23):4587-4591.
52. Sultana D, Bari MN, Karim MA, Mia MAB, Sarker RR. Variation in morphological characters and yield attributes of five selected soybean genotypes. Journal of Environmental Science and Natural Resources. 2015;8(2):93-96.
53. Uikey S, Sharma S, Shrivastava MK, Amrate PK. Genetic studies for pod traits in soybean. Journal of Pharmacognosy and Phytochemistry. 2021;10(1):2418-2424.
54. Upadhyay P, Shrivastava MK, Amrate PK, Sharma S, Thakur S, *et al.* Assessing genetic diversity of exotic lines of soybean based on D^2 and principal component analysis. The Pharma Innovation Journal. 2022;11(5):89-93.
55. Verma V, Shrivastava MK, Mehra S, Amrate PK, Yadav RB. Estimation of genetic parameters for yield associated traits and principal component in advanced

breeding lines of soybean (*Glycine max* (L.) Merrill). International Journal of Current Microbiology and Applied Sciences. 2021;10(1):2704-2710.
56. Wilcox JR. Increasing seed protein in soybean with eight cycles of recurrent selection. Crop Science. 1998;38(6):1536-1540.