



Genetic divergence analysis for yield and yield attributing traits in some genotypes of Soybean (*Glycine max*)

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Abstract

Genetic divergence was studied among eighteen germplasm lines Soybean (*Glycine max*) by using Mahalanobis D^2 analysis. Analysis of variances for dispersion showed significant differences among the genotypes and these genotypes were grouped into four clusters. The cluster I consisted of ten genotypes, cluster II has four genotypes, cluster III having three genotypes whereas cluster I has single genotype. Highest inter cluster distance observed among all clusters, while cluster III shown maximum intra cluster distance. Characters days to 50 % flowering (24.68 %) contributed maximum towards genetic divergence followed by number of pods per plant (21.84 %), plant height (g) (17.74 %), number of primary branches (15.68 %), number of seeds per pod (5.84 %) and 100 seed weight (5.79 %). All four clusters shown high cluster means for yield and yield components, therefore genotypes *viz.* JS-2098, MAUS-162, JS 95-60, MAUS-612, AKH081, SL-525 and JS- 20-29 of these diverse clusters may be used for further breeding programs.

Keywords: Soybean, *Glycine max*, genetic divergence, yield components

Introduction

Soybean (*Glycine max* L. Merrill) is an economically important oil-yielding crop, which is frequently referred to as the 'Golden Bean,' and stands among the most nutritionally beneficial leguminous crops grown universally (Mishra *et al.*, 2020) [9]. It is a critical component of the global food, feed and industrial sectors owing to its amusing seed composition, encompassing around 40% high-quality protein and 20% oil (Mishra., 2021a; Sharma *et al.*, 2021). Beyond its macronutrient significance, it is also an excellent source of bioactive compounds, for instance, isoflavones, essential amino acids, and vitamins, which enhance its value in functional foods and nutraceutical applications (Mishra *et al.*, 2021b and Mishra *et al.*, 2024). The crop is broadly adapted to an array of agroclimatic zones and plays a crucial role in sustainable agriculture through its symbiotic nitrogen fixation with *rhizobium spp.*, thereby enhancing soil fertility and reducing reliance on synthetic nitrogen fertilisers (Upadhyay *et al.*, 2020a; Nakei *et al.*, 2022; Hu *et al.*, 2023) [2, 6, 26].

In India, it is generally grown in the *kharif* season, particularly in central and western states, including Maharashtra, Madhya Pradesh, and Rajasthan (Mishra *et al.*, 2022). Maharashtra is the second-largest producer of soybeans in India. The crop subsidizes meaningfully to income generation, cropping system diversification, and livelihood security for millions of smallholder farmers (Mishra *et al.*, 2021c; Sharma *et al.*, 2023; Mishra *et al.*, 2024) [10, 11, 12, 13, 14, 15, 23]. Despite significant improvements in breeding and agricultural methods, achieving consistently high soybean yields remains challenging due to the polygenic nature of yield and its sensitivity to environmental conditions. (Mishra *et al.*, 2021; Vogel *et al.*, 2021; Mishra *et al.*, 2024; Vargas-Almendra *et al.*, 2024) [10, 11, 12, 13, 14, 15, 27, 28]. Soybean yield is a multifaceted trait influenced by various interacting elements and the interactions between genotype and environment, which makes it less effective to select directly for yield, especially in the earlier generations (Mishra *et al.*, 2021; Tripathi *et*

al., 2022) [10, 11, 12, 13, 14, 15, 25]. Therefore, it is crucial to understand the extent of genetic diversity and the relationships among traits that contribute to yield to develop effective breeding strategies. (Saroj *et al.*, 2021) [21].

Genetic enhancement is heavily dependent on the presence of significant genetic diversity and the success of selection processes. Characteristics that display a strong heritable nature combined with a significant genetic gain are usually governed by additive gene action, making them excellent candidates for direct selection. Moreover, correlation and path coefficient analyses are essential methods for pinpointing traits that have meaningful direct and indirect impacts on yield, which facilitates the creation of efficient selection indices (Khan & Dar, 2010; Mefsin *et al.*, 2018; Shrivastav *et al.*, 2023; Yadav *et al.*, 2023; Jain *et al.*, 2024) [3, 5, 8, 24, 29]. In light of these circumstances, the present study was conducted to evaluate genetic diversity, heritability, and genetic progress for important agronomic characteristics, as well as to examine the relationships between yield and its component traits in a varied collection of soybean genotypes. The main goal is to identify promising traits and genotypes that can be effectively utilized in breeding programs focused on improving productivity, stability, and adaptability in fluctuating agro-ecological conditions.

Materials and Methods

Eighteen genotypes of Soybean (*Glycine max*) were collected from various agricultural Research Institutes and grown in randomized block design with three replication and spacing of 30 x 10 cm at Research field in *kharif* 2024. Data were collected from five randomly chosen plants of each genotype for eight quantitative traits, including days to 50 percent flowering, plant height (cm), number of pods per plant, number of branches per plant, number of seeds per pod, 100 seed weight, and yield per plant. Genetic divergence was assessed using the Mahalanobis D^2 statistics method (1936) [7], and the genotypes were classified into clusters based on the Tocher's method outlined by Rao (1952) [20].

Results and Discussion

Analysis of variances exhibited significant differences among the eighteen genotypes for all studied characters. According to Wilk's criteria aggregate effects of all the traits tested. It showed significant differences among the genotypes. Twenty genotypes were grouped into four clusters (Table 1), 10 genotypes were grouped in to cluster I, 4 genotypes were grouped in cluster II, 3 genotypes were grouped in cluster III and cluster IV was solitary cluster with single genotype. Raina & Khan (2023) [18] and Xu *et al.* (2024) also reported similar type of distribution of genotypes. Distribution of the genotypes into different clusters was based on D^2 values, which ranged from 9.25 to 21.05 (Table 2). Highest inter cluster distance between cluster III and IV was 21.05. Highest intra cluster distance was shown by cluster III (10.40), followed by cluster II (10.12), followed by cluster I (9.25), while rest of the cluster having zero intra cluster distance. Genotypes for the hybridization should be selected from the more distant clusters as chances are more to obtain heterotic combinations. Cluster means indicates the variation for the quantitative traits among the cluster (Table 3).

All four clusters shown considerable cluster means for considering major yield contributing characters along with earliness to flowering and maturity, genotypes from these diverse clusters should be used for further hybridization and isolating transgressive segregants in later generations. The analysis of contribution of the characters for genetic diversity (Table 3) revealed that characters Days to 50% flowering (24.68 %) contributed maximum towards genetic divergence followed by number of pods per plant (21.84 %), plant height (g) (17.74 %), number of primary branches (15.68 %), number of seeds per pod (5.84 %) and 100 seed weight (5.79 %). Kanavi *et al.*, 2019 [4]; Sharma & Lal, 2020; proposed that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for further selection and choice of parents for hybridization. Zafar *et al.*, 2023 [30]; Patil *et al.*, 2024 [17] observed similar level of contribution phenotypic yield and yield contributing traits. On the basis of inter cluster distance, clusters I, II, III and IV were identified as divergent clusters, and genotypes *viz.* JS-2098, MAUS-162, JS 95-60, MAUS-612, AKH081, SL-525 and JS- 20-29 should be used for further improvement in yield targeted traits with creation of wider variability.

Table 1: Grouping of Eighteen genotypes into different clusters

Cluster	Number of Genotypes	Genotypes
I	10	JS-2098, DSB-23, Pusa-12, Raj Soya-24, MAUS-162, SL-688, RKS-18, TAMS-38, PS-1347, JS 95-60, DSB-1
II	4	MAUS-612, SL-958, SL-525,
III	3	DS-9712, NRC-86, KDS-344
IV	1	JS- 20-29

Table 2: Average intra (diagonal) and inter cluster distance (D^2) in Soybean

Cluster	I	II	III	IV
I	9.25	14.20	16.04	11.34
II		10.12	17.12	14.33
III			10.40	21.05
IV				00.00

Table 3: Cluster means and per cent contribution of different characters

Cluster	Days to 50% flowering	Plant height (cm)	Numbers of primary branches per plant	Numbers of pods per plant	Numbers of seeds per pod	100-seed weight (g)	Yield per plant (g)
I	42.20	48.5	8.09	22.04	2.80	10.03	15.12
II	41.08	40.02	7.50	23.01	3.00	10.60	13.12
III	45.00	46.12	8.01	21.01	3.10	10.50	14.23
IV	42.06	42.00	9.13	25.10	2.90	10.30	16.01
Contribution of individual characters towards total genetic divergence (%)	24.68	17.74	15.68	21.84	5.84	5.79	8.42

References

- Fang C, Du H, Wang L, Liu B, Kong F. Mechanisms underlying key agronomic traits and implications for molecular breeding in soybean. *Journal of Genetics and Genomics*,2024;51(4):379–393.
- Hu Y, Chen Y, Yang X, Deng L, Lu X. Enhancing soybean yield: The synergy of sulfur and rhizobia inoculation. *Plants*,2023;12(22):3911. <https://doi.org/10.3390/plants12223911>
- Jain N, Sikarwar RS, Tripathi MK, Tiwari S. Evaluation of genetic parameters for yield and its attributing traits in green gram [*Vigna radiata* (L.) Wilczek]. *International Journal of Environment and Climate Change*,2024;14(2):482–487. <https://doi.org/10.9734/ijec/2024/v14i23963>
- Kanavi MSP, Rangaiah S, Anusha CR. Genetic diversity analysis through d^2 statistic for quantitative traits in germplasm lines of green gram [*Vigna radiata* (L.) Wilczek]. *International Journal of Current Microbiology and Applied Sciences*,2019;8(06):847–855. <https://doi.org/10.20546/ijemas.2019.806.102>
- Khan M, Dar A. Correlation and path coefficient analysis of some quantitative traits in wheat. *African Crop Science Journal*,2010;18(1). <https://doi.org/10.4314/acsj.v18i1.54188>

6. Khan T, Dubey RB, Nagar KK, Bairwa LL. Studies on genetic variability in genotypes of black gram [*Vigna mungo* (L.) Hepper]. *International Journal of Current Microbiology and Applied Sciences*,2020;9(3):2736–2741. <https://doi.org/10.20546/ijcmas.2020.903.3.13>
7. Mahalanobis KC. On the generalized distance in statistics. *Proc. Nat. Inst. Sci. India*,1936;2:49-55.
8. Mefsin HH. Path analysis, genetic variability and correlation studies for soybean (*Glycine max* L.) Merrill for grain yield and secondary traits at Asosa, Western Ethiopia. *Greener Journal of Plant Breeding and Crop Science*,2018;6(3):35–46. <https://doi.org/10.15580/GJPBCS.2018.3.1.11418158>
9. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Trivedi HK. Morphological and molecular screening of soybean genotypes against yellow mosaic virus disease. *Legume Research*, 2020. <https://doi.org/10.18805/LR-4240>
10. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Gupta N, Sharma A, *et al.* Evaluation of diversity among soybean genotypes via yield attributing traits and SSR molecular markers. *Current Journal of Applied Science and Technology*,2021;40(21):9–24.
11. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Gupta N, Sharma A. *et al.* Morphological and physiological performance of Indian soybean [*Glycine max* L.) Merrill] genotypes in respect to drought. *Legume Research International Journal*, 2021, 4550.
12. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Sapre S, Ahuja A, *et al.* Cell suspension culture and *in vitro* screening for drought tolerance in soybean using polyethylene glycol. *Plants*,2021;10(3):517. <https://doi.org/10.3390/plants10030517>
13. Mishra N, Tripathi MK, Tripathi N, Tiwari S, Gupta N, Sharma A. *et al.* Validation of drought tolerance gene-linked microsatellite markers and their efficiency for diversity assessment in a set of soybean genotypes. *Current Journal of Applied Science and Technology*,2021;30: 48–57. <https://doi.org/10.9734/cjast/2021/v40i2531.515>
14. Mishra N, Tripathi MK, Tripathi N, Tiwari S, Gupta N, Sharma A. *et al.* Changes in biochemical and antioxidant enzymes activities play significant role in drought tolerance in soybean. *International Journal of Agricultural Technology*,2021;17:1425–1446.
15. Mishra R, Tripathi MK, Sikarwar RS, Singh Y, Tripathi N. Soybean *Glycine Max* L. *et al.* Merrill A multipurpose legume shaping our world. *Plant Cell Biotechnology and Molecular Biology*,2021;25(3–4):17–37. <https://doi.org/10.56557/pcbmb/2024/v25i3.48643>
16. Nakei MD, Venkataramana PB, Ndakidemi PA. Soybeannodulating rhizobia: Ecology, characterization, diversity, and growth promoting functions. *Frontiers in Sustainable Food Systems*, 2022, 6. <https://doi.org/10.3389/fsufs.2022.824444>
17. Patil MD, Pawar SB, Haloli S, Akhare MB. Unveiling genetic associations for enhanced grain yield in soybean [*Glycine max* L.) Merr.] germplasm. *International Journal of Advanced Biochemistry Research*,2024;8(7S):561–563. <https://doi.org/10.33545/26174693.2024.v8.i7Sg.1576>
18. Raina A, Khan S. Field assessment of yield and its contributing traits in cowpea treated with lower, intermediate, and higher doses of gamma rays and sodium azide. *Frontiers in Plant Science*, 2023, 14. <https://doi.org/10.3389/fpls.2023.1188077>
19. Rajput LS, Sikarwar RS, Tripathi MK, Tiwari S, Prajapati PK, Yadav RK, *et al.* Assessment of variability, heritability and genetic advance in peanut [*Arachis hypogaea* (L.)]. *International Journal of Advanced Biochemistry Research*,2024;8(5):1029–1031.
20. Rao CR. *Advanced statistical Method in Biometrical Research*. John Wiley and Sons, New York. 1952, 357–364.
21. Saroj R, Soumya SL, Singh S, Sankar SM, Chaudhary R, Yashpal Saini N, *et al* Unravelling the relationship between seed yield and yield-related traits in a diversity panel of Brassica juncea using multi-traits mixed model. *Frontiers in Plant Science*, 2021, 12. <https://doi.org/10.3389/fpls.2021.651936>
22. Sharma A, Tripathi MK, Tiwari S, Gupta N, Tripathi N, Mishra N, *et al.* Evaluation of soybean *Glycine max* L. genotypes on the basis of biochemical contents and anti-oxidant enzyme activities. *Legume Research*, 2021. <https://doi.org/10.18805/LR-4678>
23. Sharma S, Tripathi MK, Tiwari S, Solanki RS, Chauhan S, Tripathi N, *et al.* Discriminant function analysis for yield improvement in bread wheat (*Triticum aestivum* L.). *The Pharma Innovation Journal*,2023;12(5):224–232.
24. Shrivastav A, Tripathi MK, Tiwari S, Tripathi N, Tiwari PN, Bimal SS, *et al.* Evaluation of genetic diversity in Indian mustard (*Brassica juncea* var. rugosa) employing SSR molecular markers. *Plant Cell Biotechnology & Molecular Biology*,2023;24(3–4):10–21. <https://doi.org/10.56557/pcbmb/2023/v24i3.48245>
25. Tripathi N, Tripathi MK, Tiwari S, Payasi DK. Molecular breeding to overcome biotic stresses in soybean: Update. *Plants*,2022;11(15):1967. <https://doi.org/10.3390/plants11151967>
26. Upadhyay S, Singh AK, Tripathi MK, Tiwari S, Tripathi N. Validation of simple sequence repeats markers for charcoal rot and Rhizoctonia root rot resistance in soybean genotypes. *I.J.A.B.R*,2020;10(2): 137–144.
27. Vargas-Almendra A, Ruiz-Medrano R, Núñez Muñoz L A, Ramírez-Pool JA, Calderón-Pérez B, *et al.* Advances in soybean genetic improvement. *Plants*,2024 :13(21):3073. <https://doi.org/10.3390/plants13213073>
28. Vogel JT, Liu W, Olhoft P, Crafts-Brandner SJ, Pennycooke JC, Christiansen N. Soybean yield formation physiology – A foundation for precision breeding-based improvement. *Frontiers in Plant Science*,2021;12. <https://doi.org/10.3389/fpls.2021.719706>
29. Yadav RK, Tripathi MK, Tiwari S, Asati R, Chauhan S, Sikarwar RS, Yasin M, *et al.* Evaluation of genetic diversity through D2 Statistic in chickpea *Cicer arietinum* L. *International Journal of Environment and Climate Change*,2023;13(10):1598– 1611.
30. Zafar SA, Aslam M, Zaman Khan H, Sarwar S, Saad Rehman R, Hassan M, Masood Ahmad R, Gill RA, Ali B, AlAshkar I, Ibrahim A, Atikur Rahman M, El Sabagh A, *et al.* Estimation of genetic divergence and character association studies in local and exotic diversity panels of soybean (*Glycine max* L.) genotypes. *Phyton*,2023;92(6):1887–1906. <https://doi.org/10.32604/phyton.2023.0276.79>