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Estimation of genetic variability, heritability, and genetic advance in soybean (*Glycine max* (L.) Merrill) genotypes

Pratik Kalamkhede, MK Rathod, Kevin Gawali, Deepak Sapkal, Praveen Gangasagar, Kartik Abhay Kharche

Pratik Kalamkhede
P.G. Scholar, Department of Genetics and Plant Breeding, GHRU, Saikheda, Madhya Pradesh, India

Dr. MK Rathod
Associate Professor
Department of Genetics and Plant Breeding GHRU, Saikheda, Madhya Pradesh, India

Dr. Kevin Gawali
Dean, School of Agricultural Sciences, GHRU, Saikheda, Madhya Pradesh, India

Dr. Deepak Sapkal
Associate Professor
Department of Genetics and Plant Breeding, GHRU, Saikheda, Madhya Pradesh, India

Praveen Gangasagar
Associate Professor
Department of Genetics and Plant Breeding, GHRU, Saikheda, Madhya Pradesh, India

Kartik Abhay Kharche
Assistant professor
Department of Botany
Dr. Ulhas patil college of agriculture Jalgaon, Maharashtra, India

Corresponding Author:
Pratik Kalamkhede
P.G. Scholar, Department of Genetics and Plant Breeding, GHRU, Saikheda, Madhya Pradesh, India

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Abstract

The current study examined seven genotypes of soybeans (*Glycine max* (L.) Merrill) and a standard check during the 2024 Kharif cropping cycle in order to evaluate genetic gain, genetic variability, and heritability on fourteen agronomic criteria, as well as yield-related ones. The study, which was conducted at the 'School of Agricultural Sciences, G.H. Raisoni University, Saikheda, Madhya Pradesh', used a Randomized Block Design (RBD) that was reproduced three times. All traits analysed varied significantly (p<0.01) among genotypes, confirming pronounced genetic divergence. The variables that were analyzed included the height of the plant, the number of primary and secondary branches, 50% pod development, number of nodes, number of pods each plant, number of pods each cluster, flowering as well as maturation intervals, seed yield per plant, 100-seed mass, and number of seeds per pod. For pods per cluster, seed weight, and major branches, the genetic as well as phenotypic coefficients of variation (GCV & PCV) were highest. A significant additive genetic effect was confirmed by the broad-sense heritability of most characteristics over 60%, with the highest values seen for seed yield per plant (85.73%), plant height (94.64%), and pods per cluster (87.28%). Significant findings were also found for 100-seed weight (28.3%), pods/plant (37.3%), and seed output per plant (48.8%), which are measures of advancement in genetics expressed as a percentage of the mean (GAM). These features are appropriate for selection in future soybean breeding projects targeted at increasing yield.

Keywords: Soybean, *Glycine max*, genetic variability, genetic gain, heritability

Introduction

Pulses are important food crops because of their high vegetable protein content (Guleria *et al*., 2019) [7]. *Glycine max* (L.) A vital legume crop for world nutrition, food security, while providing is merill, or soybean. It is thought to be the most significant legume throughout the world since it contributes to a wide variety of chemical compounds and produces essential proteins. Soybeans are widely used in the manufacturing of soy milk, meat alternatives, tofu, margarine, pharmaceuticals, cosmetics, and biodiesel due to their high protein (30-45%) and oil content (15-24%) (Smith, 1981; Fehr *et al*., 1992; Rao *et al*., 2002) [16, 6, 12]. Soybeans are also known for their biological nitrogen fixation, weed-suppressing capabilities, and adaptability to sequential and mixed cropping systems. Often referred to as the "wonder bean," "miracle bean," and "golden bean," soybeans' versatility underscores their importance in agricultural systems.

To fulfil changing production demands, ongoing phenotypic and genotypic evaluations of present germplasm are required to discover genetically varied lines with acceptable agronomic properties (Srishti *et al*., 2023) [17]. With an average yield of 26.07 q/ha, soybeans are currently produced on near 133.79 million hectares globally, producing 348.86 million tons. In India, the fifth-largest producer, soybeans are planted on 12.15 million hectares, yielding 12.99 million tons at a productivity rate of 10.69 q/ha (Anonymous, 2022a).

Successful crop improvement hinges on accessing genetic variation, which is the bedrock upon which effective breeding strategies must rest. Observations indicate that the success of selection efforts is closely tied to the magnitude of genetic diversity, especially the heritability of the trait of interest (Dubey *et al*., 2015) [5].

Investigating this variability mandates careful dissection of the total variation into heritable and nonheritable parts via key coefficients and metrics, specifically heritability, potential genetic gain, and the genotypic as well as phenotypic coefficients of variability (GCV and PCV). Understanding how these quantities relate allows breeders to estimate how much of the observed phenotype actually emanates from genetic differences and to steer breeding work toward traits harbouring high heritability (Sharma *et al*., 2016) [15]. The expected genetic advance (GA) as a percentage of the average phenotypic, provides quantifiable expectations for the magnitude of progress obtainable through selection and aids in reliably singling out superior genotypes. By judiciously concentrating on traits both high in heritability and promising marked genetic gain, programs can hasten the cycle of progress and attain breeding targets more efficiently.

Materials and Methods

The kharif season of 2024 served as the backdrop for the trial involving seven novel soybean genotypes plus a standard check cultivar. The genetic resources came from the genetics and plant breeding department of ‘G. H. Raisoni University's School of Agricultural Science’, which is situated in Saikheda, District Pandhurna, Madhya Pradesh. Layout of the field followed a Randomized Block Design replicated thrice, totaling 24 plots arranged in a single block of eight plots in four-row configurations. Uniform agronomic practices were applied universally to each treatment to achieve uniform crop establishment and progression. The cultivated area, with an inter-row spacing of 30 cm and an intra-row spacing of 5 cm, was 92.16 square meters. Five randomly selected plants to each plot were evaluated for the following agronomic traits: the duration from sowing to flower initiation, the interval from 50% flowering to physiological maturity, plant height, the count of primary as well as secondary branches each plant, the time until fifty percent pod set, the number of nodes, the total pod count, the average pod length, the number of pods per cluster, the mean seed yield per plant, the weight of 100 seeds, and the seed count per pod.

Statistical analysis

Recorded data underwent ANOVA in R Studio to confirm significant genotype effects, according to Panse and Sukhatme's (1976) [11] methodology. The Deshmukh *et al*. (1986) methodology was used to derive the basis genetic coefficients, what are the genotypic and phenotypic coefficients of variation (GCV and PCV)? Broad-sense heritability estimates were computed using Robinson's (1949) formula, and genetic advance as a percentage of mean was calculated according to the formula suggested by Johnson *et al*. (1955) [8]. The generated statistics were utilized to measure the degree of genetic variation, heritability, as well as selection effectiveness about yield-associated characteristics.

Result and Discussion

Variance Analysis

The research used a randomized full block design comprising three replications to assess seven new soybean lines in addition to a conventional check. A substantial degree of genetic diversity across the sample is confirmed by significant variation ($p<0.01$) for each of the fourteen assessed variables listed in Table 1. The parameters recorded included days to flowering, days to 50% flowering, days to physiological maturation, plant height, number of primary as well as secondary branches per plant, days to fifty percent pod setting, number of nodes, the pods, as well as clusters, pod length, seed yield per plant, 100-seed weight, and number of seeds per pod. Confirmatory findings are documented in Bairagi *et al*. (2023) [3] and Olorunfemi (2014) [10].

Mean performance of the studied soybean genotypes

Significant variation between soybean genotypes was found when mean performance across fourteen criteria was examined. The range of days to maturity was 96.93 to 105.13 days, with an average of 100.61 days; days to 50% flowering occurred between 36.53 and 45.53 days, with an average of 40.58 days. The average flower initiation time was 36.96 days, with a range of 34.40 to 42.00 days. The range of plant heights was 57.08 to 70.06 cm, with an average of 64.08 cm. With a mean of 7.95, secondary branches varied between 6.03 to 9.85, while main branches per plant ranged from 3.67 to 7.13, giving an average of 5.6. The proportion of 50% pod settings ranged from 77.07% to 84.00%, with an average of 80.11%. The range of nodes each plant was 13.53 to 22.67, with an average of 18.89. The parameters recorded included days to flowering, days to 50% flowering, days to physiological maturation, plant height, number of primary as well as secondary branches per plant, days to fifty percent pod setting, number of nodes, pods, as well as clusters, pod length, seed yield per plant, 100-seed weight, and number of seeds per pod.Each cluster had pods ranging in length from 3.13 to 4.93 cm, having an average of 3.96 cm, and pod sizes ranging from 5.47 to 10.87, having an average of 7.87. For yield components, the average weight of 100 seeds was 8.04 grams, ranging from 5.83 to 10.03 grams. With a range of 1.93 to 3.16, the average grain yield per pod was 2.55 g. The range of seed yield each plant were 7.23 to 12.75 g, with an average of 9.72 g. These results demonstrate substantial variation across genotypes, suggesting that there is a great deal of space for selection and improvement of soybean yield-related factors. Leite *et al*. (2018) [9], and Sharma *et al*. (2013) [14] all highlighted the significance of multi-trait selection for yield improvement, and these findings are consistent with their findings.

Determining the genotype and phenotypic coefficients of variation

The genotypic or phenotypic coefficients of variation (GCV & PCV) are important markers for studying genetic diversity. In this study, GCV and PCV ranged from 2.812% to 22.373% as well as 3.132% to 23.947%, respectively. For each attribute, PCV remained consistently higher than GCV, suggesting that the environment influences the expression of characteristics.

In Table 2, traits such as plant height, flower initiation, and 50% blooming showed moderate variability (10-20%), while days to maturity and 50% pod setting had minimal variability (<10%), suggesting modest genetic benefit from direct selection. The most variable pods per cluster (GCV: 22.373%, PCV: 23.947%) were followed by the number of major branches and seed yield/plant, both of which had substantial variability (>20%). Bairagi *et al*. also noted a similar outcome in 2023.

Heritability

All variables, with the exception of the number of major branches, showed high broad-sense heritability (>60%), according to the heritability estimates found in this study. This suggests that there is little environmental influence and significant genetic control. Pod yield per plant (85.73%), flower initiation (71.06%), days to 50% flowering (73.44%), days to maturity (80.61%), number of seeds/plant (85.73%), 50% pod setting (78.38%), plant height (94.64%), number of secondary branches (75.71%), plant number of pods (84.41%), plant number of pods (92.32%), and pod length (67.65%), and pods per cluster (87.28%), and grains per pod (68.60%) were all highly heritable. These characteristics are expected to respond favorably to selection. However, the number of primary branches (55.12%) showed a modest heritability. These results are in line with those of Thakur *et al*. (2024) [18] for 50% blooming, days to maturity, and plant height, and Bairagi *et al*. (2022) [2], who also discovered significant heritability for comparable yield-contributing variables in soybean, highlighting their significance for genetic gain.

Genetic advance percent mean

In this study, genetic advancement as a percentage of mean (GAM) was categorized as high (>20%), moderate (10-20%), and low (<10%). It varied from 3.3% to 48.8%. The high GAM in the number for secondary branches (22.69%), 100-seed weight (28.3%), pods/plant (37.3%), and seed output per plant (48.8%) suggested a considerable selection potential. The moderate GAM found for height of the plant (19.27%), number of important branches (12.60%), as well as grains per pod (14.54%) suggested modest improvement by selection. The low GAM values for days to 50% blooming (9.53%) as well as days to maturity (3.30%) indicate a modest expected growth.

Genetic advancement and heritability estimation

The genetic progress percent mean, pods per plant, as well as seed production/plant all demonstrated substantial heritability, making them prime candidates for efficient selection and genetic improvement in soybean breeding.

Table 1: Analysis of variance for yield and its attributing characters in Soybean genotypes

Character	Mean Squares			CD at 5%	CV (%)
	Replication df(2)	Treatments df(7)	Error df(14)		
Fi	4.002	16.350**	1.954	2.448	3.775
5f	0.540	22.604**	2.431	2.731	3.906
Dm	1.670	26.065**	1.935	2.436	1.379
Ph	2.455	73.145**	1.354	2.038	1.809
Npb	1.452	4.499**	0.960	1.716	17.630
Nsb	1.441	5.955**	0.575	1.328	9.527
50ps	3.652	17.746**	1.494	2.140	1.519
Npp	10.222	32.613**	1.890	2.408	7.355
Ppp	10.722	87.420**	2.358	2.689	2.983
Pl	0.114	1.072**	0.147	0.672	9.695
Ppc	2.102	9.356**	0.433	1.152	8.538
Sypp	1.468	11.879**	1.715	2.294	14.439
100sw	0.376	6.267**	0.489	1.224	8.848
Gpp	0.103	0.675**	0.089	0.523	11.881

** = Significant at 1% and * = Significant at 5% level of significance

Table 2: Genetic variability parameters for seed yield and its contributing characters in Soyabean genotypes.

Response Variable	SED	Heritability	GCV	PCV	Gen-Advance	Gen-Adv% Means
Fi	2.448	71.06	5.9	7.0	3.8	10.2
50%f	2.731	73.44	6.4	7.5	4.5	11.4
Dm	2.436	80.60	2.8	3.1	5.2	5.2
Ph	2.038	94.64	7.6	7.8	9.8	15.2
Npb	1.716	55.12	19.5	26.3	1.6	29.8
Nsb	1.328	75.71	16.8	19.3	2.4	30.1
50ps	2.140	78.38	2.8	3.2	4.2	5.2
Npp	2.408	84.41	17.1	18.6	6.0	32.4
Ppp	2.689	92.32	10.3	10.7	10.5	20.4
Pl	0.672	67.65	14.0	17.0	1.9	23.7
Ppc	1.152	87.28	22.3	23.9	3.3	43.0
Sypp	1.261	85.72	18.5	20.0	3.3	35.3
100sw	1.224	79.76	17.5	19.6	2.5	32.3
Gpp	0.523	68.60	17.5	21.2	0.7	29.9

Note: Fi: flower initiation, 50% F: days to 50% flowering, DM: Days to maturity, PH: Plant height, NPB: no. of primary branches, NSB: no. of secondary branches, 50 PS: 50% pod setting, NPP: node per plant, PPP: pods per plant, PL: pod length, PPC: Pod per cluster, SYPP: Seed yield per plant. 100sW: 100seed weight, GPP: Grain per pod.

Conclusion

Significant genetic heterogeneity was discovered in the evaluated soybean genotypes across all fourteen agronomic factors in the current study, suggesting the potential for efficient selection and genetic advancement. Measures including seed output per plant, pod count per plant, and 100-seed weight are appropriate as selection criteria for soybean breeding projects due to their strong genotypic and phenotypic coefficients of variation, high heritability, and genetic advancement. Given that hereditary factors predominate and environmental factors play a little role, these traits are likely to manifest consistently in many circumstances. Variables like plant height and grains per pod have been shown to exhibit moderate heritability and genetic progress, suggesting room for improvement through judicious selection. Overall, the results lend credence to the selective application of high-heritability, high-GAM traits to boost efficiency and production potential in soybean development initiatives.

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References

1. **Annual report.** Ministry of Agriculture, Government of India. New Delhi (India): Government of India; 2022.
2. Bairagi V, Chavan NA, Dalvi VV. Genetic analysis in soybean [*Glycine max* (L.) Merrill] for seed yield and its components. J Pharmacogn Phytochem. 2022;11(3):509-513.
3. Bairagi V, Dalvi V, Pawar P. Assessment of genetic variability in soybean (*Glycine max* L. Merrill). J Pharmacogn Phytochem. 2023;12(1):498-503.
4. Deshmukh SN, Basu MS, Reddy PS. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian J Agric Sci. 1986;56(8):816-821.
5. Dubey RB, Tiwari RS, Dubey DK. Genetic variability, heritability and genetic advance in soybean (*Glycine max* (L.) Merrill). An Int Q J Life Sci. 2015;10(1):161-163.
6. Fehr WR, Caviness CE, Burmood DT, Pennington JS. Stage of development descriptions for soybeans, *Glycine max* (L.) Merrill. Crop Sci. 1992;11(6):929-931.
7. Guleria S, Thakur KS, Sharma S. Genetic variability, heritability and genetic advance in chickpea (Cicer arietinum L.). Legume Res. 2019;42(4):496-499.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-318.
9. Leite RMVBC, Galvão JCC, Bellé ML. Agronomic performance of soybean cultivars under irrigation. Rev Ciênc Agron. 2018;49(2):278-285.
10. Olorunfemi DI. Genetic variability and trait association in some soybean genotypes. Int J Plant Soil Sci. 2014;3(10):1266-1275.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 3rd ed. New Delhi (India): Indian Council of Agricultural Research; 1976.
12. Rao PU, Devi KA, Ramesh HP. Chemical composition and nutritional evaluation of soybean. J Food Sci Technol. 2002;39(5):506-508.
13. Robinson HF. Estimation of heritability and the degree of dominance in corn. Agron J. 1949;41(8):353-359.
14. Sharma A, Singh A, Kumari J. Genetic variability and trait association studies in soybean (*Glycine max* L.). Bioscan. 2013;8(4):1407-1411.
15. Sharma A, Sharma M, Yadav SS. Genetic variability and character association in chickpea (Cicer arietinum L.). Legume Res. 2016;39(1):137-140.
16. Smith KJ. Soybeans: chemistry, technology, and utilization. New York (NY): Van Nostrand Reinhold Company; 1981.
17. Srishti D, Verma P, Kumar R. Genetic diversity studies in soybean (*Glycine max* L.) based on morphological and biochemical markers. J Plant Sci Res. 2023;39(2):149-157.
18. Thakur P, Tiwari DK, Chauhan MP. Estimation of genetic variability and heritability in soybean (*Glycine max* L.) for yield contributing traits. Int J Agric Sci. 2024;16(1):17-21.