



GENETIC VARIABILITY PARAMETERS STUDY IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL] GENOTYPES

Kamna Parindiyal, Rajneesh Bhardwaj*, Arvind Singh Negi,
Kavya Parindiyal, Akriti Rawat, Shagufta Gulzar, Sachin Prakash

Department of Genetics and Plant Breeding, School of Agriculture
Graphic Era Hill University, Uttarakhand-248002

Research Paper

Received: 13.04.2023

Revised: 22.04.2023

Accepted: 06.05.2023

ABSTRACT

The present investigation was conducted during Kharif, 2022 at Research Farm, School of Agriculture, Graphic Era Hill University, Dehradun. The experimental material consist of fifteen genotypes along with three checks of soybean which were sown in a randomized block design with three replications. The analysis of variance revealed a highly significant difference for most of the traits studied viz., days to 50% flowering, number of pods per plant, number of nodes per plant, plant height at maturity (cm), number of primary branches, number of pod clusters per plant, number of seeds per plant, hundred seed weight (g), and seed yield per plant (g). High magnitudes of PCV and GCV were observed for the traits viz., plant height at maturity (cm), number of pods per plant, number of pod cluster per plant, number of nodes per plant and hundred seed weight (g). High heritability coupled with high genetic advance as per cent of mean was reported for plant height (g), nodes per plant, number of primary branches, pods per plant, pod cluster per plant, number of seeds per pod, hundred seed weight (g), number of seeds per plant and yield per plant (g).

No. of Pages: 11

References: 17

Keywords: Heritability, Soybean, PCV, GCV, Genetic advance.

INTRODUCTION

Soybean (*Glycine max*) is a member of the family *Leguminosae* subfamily *dae* and genus *Glycine*. It is renowned as the "Golden Bean" and "Miracle Crop" of the 21st century. Soybean originated in eastern Asia or China. The wild form is an annual procumbent or slender, twiner, exhibiting an erect growth habit. Soybean has been known by various names in India, such as Bhat, Bhut, Kalitur, Taliakuth, Bhatman, Ramkulthi and Garryakalay (Prasad, 2013). Soybean possesses a very high nutritional value. It contains about 21% oil and 41% high quality protein. Soybean protein is rich in the valuable amino acid lysine (5%) in which most cereals are deficient. It contains a good amount of minerals, salts, and vitamins (thiamin and riboflavin) and considering amount of vitamin C (Singh *et al.*, 1983).

At present, soybean has acquired global importance, second ranked oilseed contributing 28% in oil seed production. India ranked 5th after Argentina in production worldwide (FAO, 2022). In India, major soybean producing states are Maharashtra, Madhya Pradesh and Rajasthan (Agricultural Statistics at a Glance, 2022). Soybean is grown in an area of 12.50 million hectare with an annual production of 12 million ton and an average productivity of 0.96 tonnes per hectare in India (USDA, 2023). The Genetic variability present in the soybean helps in the utilization of plant characters for developing suitable variety for higher yield. Genetic variability study enables the breeder in determining most suitable genotypes for selection using genetic parameters like, genetic coefficient of variation, heritability and genetic advance. The present investigation was

*Corresponding author: rajneeshbhardwaj8@gmail.com

carried out by realizing the importance of the above facts, to estimate the genetic variability among soybean genotypes for yield and its component traits (Sonkamble *et al.*, 2020).

MATERIAL AND METHODS

The investigation was carried out during *Kharif*, 2022 at Research farm, School of Agriculture, Graphic Era Hill University, Dehradun, India. The experimental material comprised of 15 germplasms along with 3 check varieties. The material was sown in Randomized Block Design (RBD) with three replications. Each genotype was sown in three rows, 5m long at 30 x 45 cm apart. The 12 quantitative characters observed were plant height at maturity (cm), number of nodes per plant, number of primary branches, number of pods per plant, number of pod cluster per plant, pod length (cm), days to 50% flowering, days to maturity, number of seeds per pod, hundred seed weight (g), number of seeds per plant and seed yield per plant (g). Data were analysed for the variability, heritability, genetic advance for the characters.

RESULT AND DISCUSSION

The genetic variability is the raw material of plant breeding on which selection acts to evolve superior genotypes. Thus, higher the amount of variation present for a concerned trait in the breeding materials, greater is the scope for its improvement through selection (Uikey *et al.*, (2020). Analysis of variance of different character are presented in Table 1, which showed that the variances due to genotypes were highly significant for most of the traits studied viz., days to 50% flowering, number of pods per plant, number of nodes per plant, plant height at maturity (cm), number of primary branches, number of pod clusters per plant, number of seeds per plant, hundred seed weight (g), and seed yield per plant (g). Similar results were reported for most of traits by Kumari *et al.*, (2019), Jandong *et al.*, (2020), Baria *et al.*, (2022), Kumari *et al.*, (2022), Khan *et al.*, (2022), Yirga *et al.*, (2022) and Bairagi *et al.*, (2023).

Table 1: ANOVA showing mean sum of squares for yield and yield attributing characters of Soybean.

Source	d.f	Plant height at maturity (cm)	Number of nodes per plant	Number of primary branches	Number of pods per plant	Number of pod cluster per plant	Pod length (cm)	Days to 50% flowering	Days to maturity	Number of seeds per pod	Hundred seed weight (g)	Number of seeds per plant	Seed yield per plant (g)
Replications	2	0.712	1.448	0.207	5.765	0.326	0.002	0.794	0.020	0.024	0.016	40.379	0.605
Treatments	17	5,721.515**	55.297**	2.905**	843.314**	88.510**	0.308	60.911**	0.507	0.478	17.066**	3,166.626**	32.270**
Error	34	3.035	0.656	0.110	17.202	2.065	0.012	0.302	0.015	0.018	0.008	157.858	2.871

**Significant at 1% L.O.S

*Significant at 5% L.O.S

Table 1: ANOVA showing mean sum of squares for yield and yield attributing characters of Soybean.

S.No.	Name of the character	Mean	Range	GCV (%)	PCV (%)	Heritability	Genetic	Genetic Advance (GA) (%)
1.	Plant height at maturity(cm)	132.43	55.52-195.28	32.96	32.99	99.84	89.86	67.86
2.	Number of nodes per plant	17.99	10.06-23.20	23.71	24.13	96.52	8.63	47.99
3.	Number of primary branches	8.14	5.93-9.73	11.85	12.53	89.40	1.88	23.08
4.	Number of pods per plant	66.54	39.60-105.13	24.93	25.70	94.12	33.16	49.83
5.	Number of pod cluster per plant	21.88	13.16-34.76	24.52	25.38	93.31	10.68	48.80
6.	Pod length (cm)	3.79	3.08-4.09	8.28	8.76	89.49	0.61	16.15
7.	Days to 50% flowering	52.75	46.33-59.60	8.52	8.58	98.52	9.19	17.42
8.	Days to maturity	126.50	116.00-136.66	5.23	5.26	98.91	13.56	10.72
9.	Number of seeds per pod	2.57	3.00-2.00	15.70	16.41	91.46	0.79	30.93
10.	Hundred seed weight (g)	10.53	8.20-16.38	22.63	22.65	99.85	4.90	46.59
11.	Number of seeds per plant	168.17	112.46-211.50	18.83	20.25	86.40	60.64	36.05
12.	Seed yield per plant (g)	17.28	12.83-23.33	18.11	20.59	77.33	5.67	32.81

The estimate of component of variation including genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for all the traits under study are presented in Table 2. The estimates phenotypic coefficient of variation (5.26% to 32.99%) slightly higher than of genotypic coefficient of variation (5.23% to 32.96%) indicated less effect of environment in expression of traits. Among the different yield attributing characters, plant height at maturity (cm) had the highest magnitude of genotypic coefficient of variation (32.96%). The high magnitude of genotypic coefficient of variation were recorded for number of nodes per plant (23.71%), number of pods per plant (24.93%), number of pod cluster per plant (24.52%) and hundred seeds weight (g) (22.63%). The highest magnitude of phenotypic coefficient of variation were recorded for plant height at maturity (cm) (32.99%), number of nodes per plant (24.13%), number of pods per plant (25.70%), number of pod cluster per plant (25.38%), hundred seeds weight (g) (22.65%), number of seeds per plant (20.25%) and seed yield per plant (g) (20.59%). Sonkamble *et al.*, (2020), Yirga *et al.*, (2022), also reported high values of GCV and PCV for plant height (cm), number of pods and hundred seed weight. Similar results were reported for high GCV and PCV by Khan *et al.*, (2022), Mahbub and Shirazy (2016), Kumari *et al.*, (2022), Kumari *et al.*, (2019), Uiskey *et al.*, (2020), Bairagi *et al.*, (2023), Belay *et al.*, (2022) and Jandong *et al.*, (2020).

High heritability coupled with high genetic advance as per cent of mean was reported for plant height (g), nodes per plant, number of primary branches, pods per plant, pod cluster per plant, number of seeds per pod, hundred seed weight (g), number of seeds per plant and yield per plant (g). High heritability coupled with high genetic advance of mean per cent by Baraskar *et al.*, (2014), Mahbub and Shirazy (2016), Joshi *et al.*, (2018), Uiskey *et al.*, (2020) and Bairagi *et al.*, (2023).

CONCLUSION

The study implied the presence of high genetic variability among most of the genotypes. Thus, there is an opportunity to bring about improvement through direct selection or hybridization. For the traits *viz.*, plant height at maturity (cm), number of pods per plant, number of pod cluster per plant, number of nodes per plant and hundred seed weight (g) had high phenotypic (PCV) and genotypic coefficient of variability (GCV) values. High heritability coupled with high genetic advance as per cent of mean was reported for plant height (g), nodes per plant, number of primary branches, pods per plant, pod cluster per

plant, number of seeds per pod, hundred seed weight (g), number of seeds per plant and yield per plant (g).

ACKNOWLEDGEMENT

Authors are highly thankful to the Vice Chancellor, Graphic Era Hill University for providing necessary facilities to perform experiments and other facilities.

REFERENCES

1. **Agricultural Statistics at a Glance** (2021). Directorate of Economics and Statistics, Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Government of India, 87-89.
2. **Baria, A.R., Akabari, V.R. and Gohil, V.N.** (2022). Variability studies for seed for seed yield and its components in soybean. *Journal of Genetics, Genomics and Plant Breeding*, 6(2): 54-59.
3. **Bairagi, V., Mishra, S., Sen, R., Dixit, S. and Tyagi, D.B.** (2023). Assessment of Genetic Variability in Soybean (*Glycine max* L., Merrill). *Biological Forum - An International Journal*, 15(5): 258-263.
4. **Belay, T., Tesfaye, A. and Alamerew, S.** (2022). 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*, 12(2): 14-17.
5. **Baraskar, V.V., Kachhadia, V.H., Vachhhanl, J.H., Barad, H.R., Patel, M.B. and Darwankar, M.S.** (2014). Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Electronic Journal of Plant Breeding*, 5(4): 802-806.
6. **FAO.** 2022. World Food and Agriculture- Statistical yearbook 2021. Rome. 13:165-166.
7. **Jandong, E.A., Uguru, M.I. and Okechukwu, E.C.** (2020). Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.). *African Journal of Biotechnology*, 19(4): 201-206.
8. **Joshi D., Pushpendra S.K. and Adhikari S.** (2018). Study of genetic parameters in soybean germplasm based on yield and yield contributing traits. *International Journal of Current Microbiology and Applied Sciences*, 7(1): 700-709.
9. **Kumari, S., Meena, B.L., Sharma, S.C., Koli, N.R., Tak, Y. and Fozdar, P.** (2022). Study on genetic variability parameters in soybean [*Glycine max* (L.) Merrill] genotypes. *Journal of Agriculture and Ecology*, 14: 72-76.
10. **Kumari, S., Sreenivasa, V., Lal, S.K., Singh, S.K. and Singh, K.P.** (2019). Analysis of genetic

- diversity of 120 genotypes of *Glycine max* (L.) Merrill by using D^2 analysis. *Journal of pharmacognosy and phytochemistry*, 8(4): 1324-1329.
11. **Khan, N.A., Rana, M.S., Sen, A., Hasan, M.M., Sikder, R., Malek, M.A. and Islam, M.S.** (2022). Estimation of genetic parameters, interrelation and path coefficient analysis for seed yield and its component traits in soybean. *Bulgarian Journal of Agricultural Science*, 28(5): 889–895.
 12. **Mahbub, M.M. and Shirazy, B.J.** (2016). Evaluation of genetic diversity in different genotypes of soybean (*Glycine max* (L.) Merrill). *American Journal of Plant Biology*, 1(1): 24-29.
 13. **Prasad, R.** (2013) Textbook of Field Crops Production Commercial Crops. *Indian Council of Agricultural Research*, 2(2): 1-11.
 14. **Singh, C., Singh, P. and Singh, R.** (1983). *Modern Techniques of Raising Field Crops*. 2nd edition, 273-278.
 15. **Sonkamble, P., Nandanwar, R.S., Sakhare, S.B., Jadhav, P.V. and Varghese, P.** (2020). Genetic variability for yield and its component traits in grain and vegetable type soybean. *International Journal of Chemical Studies*, 8(6): 2287-2290.
 16. **Uikey, S., Sharma, S., Shrivastava, M.K. and Amrate, P.K.** (2021). Genetic studies for pod traits in soybean. *Journals of Pharmacognosy and Phytochemistry*, 10(1): 2418-2424.
 17. **USDA.** Foreign Agricultural Service, Global Market Analysis, World agricultural production. US Department of Agriculture, 2023, 43-44.
 18. **Yirga, M., Sileshi, Y., Tesfaye, A. and Hailemariam, M.** (2022). Genetic Variability and Association of Traits in Soybean (*Glycine max* (L.) Genotypes in Ethiopia. *Ethiopian Journal of Crop Science*, 9(2): 49-7.