



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(12): 3131-3133
© 2022 TPI
www.thepharmajournal.com
Received: 13-09-2022
Accepted: 20-10-2022

G Saicharan
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

MV Dhuppe
Associate Professor, College of
Agriculture, Ambajogai,
Maharashtra, India

ST Rathod
Assistant Professor, College of
Agriculture, Ambajogai,
Maharashtra, India

PR Sargar
College of Agriculture, Parbhani,
VNMKV, Parbhani,
Maharashtra, India

M Venkateshwara Rao
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

Corresponding Author:
G Saicharan
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

Studies on genetic variability, heritability, and genetic advance for yield and yield contributing traits in soybean [*Glycine max* (L.) Merrill]

G Saicharan, MV Dhuppe, ST Rathod, PR Sargar and M Venkateshwara Rao

Abstract

The purpose of the current study was to evaluate the genetic advance, heritability, and genetic variability of twenty-nine genotypes for ten traits. Plant height, days to maturity, number of branches per plant, and number of pods per plant showed a wide range of mean values among the genotypes, indicating the presence of a high amount of variability among the genotypes and providing the potential for different yield-contributing characters to be improved in soybean. For the number of pods per plant, several pods per cluster, seed yield per row, and seed yield per plant, high estimates of GCV and PCV were noted. All of the traits under study showed higher heritability estimates. The percentage of mean genetic advance was found to be high for traits like the number of pods per plant, plant height, and seed yield per plant and row, but low to moderate for traits like the number of branches per plant and oil content.

Keywords: Genetic advance, genetic variability, heritability, range, seed yield, soybean

Introduction

Soybean [*Glycine max* (L.) Merrill] is a self-pollinating crop in the Leguminaceae family, subfamily Papilionideae tribe phaseolae, and genus glycine, with a chromosome number of $2n=40$. Soybean is an important oil seed crop with a high protein content (40-42%), a high lysine content, and an oil rich in essential fatty acids (20-22%). It also contains isoflavones, which guard the body against conditions like diabetes, cancer, osteoporosis, high blood pressure, and heart disease. The most widely used oil source in the world is soybean, and De Oil Cake (DOC) is used in animal feed and as a food processing unit for the creation of new food products. Soybean is aptly known as the "Golden Bean" or "Miracle Crop" of the twentieth century due to its many uses. Soybean is classified as an oil seed crop as opposed to a pulse crop because it contains 40% protein and 20% oil. It is a good and affordable source of lysine, vitamins A, B, and D, calcium, phosphorus, and high-quality vegetable protein. The capacity of soybean to meet their nitrogen requirements through symbiotic nitrogen-fixing bacteria, rhizobium, and to deliver the ideal amount of nitrogen to the succeeding crop is equally important in this era of cataclysmically rising fertilizer prices.

The continuous improvement of soybean depends on knowledge about genetic diversity, genetic factors, and their application, which helps breeders in the reliable selection process. The complex polygenic variable of yield is the result of numerous interactions among different factors that affect yield (Korale *et al.*, 2021) [8]. Genetic variability is required for increasing yield because it is the source of variation and the raw material for yield improvement work (Shinde *et al.*, 2021) [14]. The analysis of genetic divergence can be used to quantify the genotypic level of genetic divergence between biological populations and to ascertain the relative contributions of various components to the overall genetic divergence, both within and between clusters. Breeders can determine the best genotypes for selection by using genetic parameters like the genetic coefficient of variation, heritability, and genetic advance (Sargar *et al.*, 2021) [13].

Materials and Method

The experimental material comprised of twenty-nine genotypes soybean. The experiment was carried out in Randomized Block Design with two replications at the experimental farm Oil seed Research Station, Latur. The crop was grown using all the agronomic methods advised for soybeans.

Each accession was grown in four rows of 3 m in length with a spacing of 45 cm between rows and 5 cm between plants within a row. A total of ten observations were recorded *viz.*, Days to 50% flowering, Days to maturity, Plant height (cm), No. of branches per plant, No. of pods per cluster, No. of pods per plant, 100 seed weight (g), Seed yield per plant (kg), Seed yield per row(kg), and Oil content (%).

The analysis of variance was done as suggested by Panse and Sukhatme (1962) [11]. Descriptive statistics were used to analyze the data, along with an analysis of variance (Cocheran and Cox, 1957) [4], and the genetic parameters were computed for any characters whose genotypes had a significant impact on the mean square. According to Burton's (1952) [3] recommendations, Lush's (1949) heritability (in the broad sense) and Johnson *et al* (1949)'s genetic advance were estimated for the phenotypic and genotypic coefficient of variation (1955). Heritability was rated as being less than 30% as low, 30%–60% as moderate, and more than 60% as high by Robinson H. F. *et al.* (1949) [12]. Johnson *et al.* (1955) [6] classified GAM as less than 10% low, 10-20% moderate, and more than 20% high.

Result and Discussion

Analysis of variance for ten quantitative characters revealed significant differences among the experimental material for all the characters studied presented in table 1. The significance was marked by applying F' test. The variation due to genotypes was significant for all the characters under study both at 5 and 1 percent probability levels which indicates the presence of variability among the germplasm accessions.

Genetic parameters *viz.* genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance as percentage of the mean (GAM) were reported in table 2. A wide range of variability was observed among twenty-nine genotypes for yield and yield contributing and quality traits which indicate good scope for selection of genotypes for particular traits. The genotypic variance was found to be lower than the phenotypic variance for all the characters. However, a higher magnitude of genotypic variance was recorded for the number of pods per plant (477.924), followed by plant height (286.235). While moderate genotypic variance was observed in days to maturity (13.931). The lowest genotypic variance was recorded in seed yield per row (0.016), and oil content (0.41), followed by several branches per plant (0.611). A similar result was reported by Aditya *et al.* (2011) [1].

A similarly higher phenotypic variance was observed the for trait number of pods per plant was 489.906, followed by plant

height (287.3). While moderate phenotypic variance was observed in days to maturity (16.735). While least phenotypic was variance observed in seed yield per row (0.016), oil content (0.471), and followed by the number of branches per plant (0.692). A similar result was reported by Lukman *et al.* (2014) [9].

A high magnitude of the Genotypic coefficient of variation was observed in the trait number of pods per plant (42.531), followed by plant height (31.23and 4), and seed yield per row (27.305). While moderate genotypic coefficient of variance was observed in seed yield per plant (20.647), followed by the number of pods per cluster (19.361), and the number of branches per plant (17.192). The least genotypic coefficient of variance was observed in oil content (3.364), followed by days to maturity (3.735), and days to 50% flowering (6.556). A similar result was reported by Swar *et al.* (2020) [15].

A high magnitude of Phenotypic coefficient of variation was observed in the trait number of pods per plant (43.061), followed by plant height (31.292), and seed yield per row (27.507). While moderate genotypic coefficient of variance was observed in seed yield per plant (21), followed by the number of pods per cluster (20.693), and the number of branches per plant (18.283). The least genotypic coefficient of variance was observed in oil content (3.605), followed by days to maturity (4.093), and days to 50% flowering (7.762). A similar result was reported by Ghodrati *et al.* (2013) [5].

The high heritability estimates were observed in trait plant height (99.60%), followed by 100 seed weight (99.2%), seed yield per row (98.5%), and the number of pods per plant (97.6%). While moderate heritability was found in the number of branches per plant (88.4%), followed by the number of pods per cluster (87.5%) and, days to maturity (83.2%). While least heritability was found in days to 50% flowering (71) the similar result was reported by Baraskar *et al.* (2014) [2].

The highest genetic advance (%) was observed in the character number of pods per plant (44.48), followed by plant height (34.787). While moderate heritability was observed in days to maturity (7.015), followed by days of 50% flowering (4.6). While least genetic advance was observed in seed yield per plant (0.007). A similar result was reported by Karnwal *et al.* (2009) [7].

The highest Genetic advance as percent of the mean (%) of mean was observed in character number of pods per plant (86.536), while moderate Genetic advance as percent of the mean (%) was observed in character plant height (64.223), followed by seed yield per row (55.836). The least Genetic advance as a percent of the mean (%) of mean was observed in character oil content (6.467), followed by days to maturity (7.01 the similar result was reported by Mahbub *et al.* (2016) [10].

Table 1: Analysis of variance for characters studied in genotypes of soybean.

Source of variation	D.F	Days to 50% flowering	Plant Height (cm)	Days to maturity	No. of Branches/ plant	No. of Pods/ plant	No. of Pods/ cluster	100 Seed Weight (gm)	Seed Yield/ Plant (kg)	Seed Yield/ Row (kg)	Oil Content %
Mean sum of squares											
Replication	2	6.425	4.269	30.494	0.196	89.721	0.115	0.050	0.008	0.005	0.061
Treatment	28	23.87**	807.77**	44.60**	1.91**	1445.75**	2.34**	14.73**	0.04*	0.48**	1.29**
Error	56	2.82	1.07	2.80	0.08	11.98	0.11	0.04	0.00	0.00	0.06
S. E±		0.97	0.60	0.97	0.16	2.00	0.19	0.12	0.00	0.01	0.14
C.D at 5%		2.755	1.688	2.739	0.463	5.662	0.532	0.327	0.001	0.025	0.403

Table 2: Parameters of genetic variability for yield and yield contributing characters in soybean

	Days to 50% flowering	Plant height (cm)	Days to maturity	No. of branches /plant	No. of pods /plant	No. of pods/ cluster	100 seed weight	Seed yield /plant (kg)	Seed yield /row (kg)	Oil content (%)
Range	36.33-45	28.66-103.73	93.33-106.66	3.06-6.10	29.9-110.46	2.967-6.33	10.10-16.91	0.013-0.0307	0.156-0.671	17.81-20.5
Mean	40.4023	54.1667	99.9425	4.5483	51.4013	4.454	13.2782	0.0169	0.4632	19.032
Var Environmental	2.818	1.065	2.804	0.08	11.983	0.106	0.04	0.001	0	0.061
ECV	4.155	1.905	1.675	6.22	6.734	7.303	1.505	3.835	3.327	1.296
Var Genotypical	7.016	286.235	13.931	0.611	477.924	0.744	4.895	0.003	0.016	0.41
GCV	6.556	31.234	3.735	17.192	42.531	19.361	16.663	20.647	27.305	3.364
Var Phenotypical	9.834	287.3	16.735	0.692	489.906	0.849	4.935	0.004	0.016	0.471
PCV	7.762	31.292	4.093	18.283	43.061	20.693	16.731	21	27.507	3.605
Heritability (%)	71.3	99.6	83.2	88.4	97.6	87.5	99.2	96.7	98.5	87.1
Genetic Advancement 5%	4.609	34.787	7.015	1.515	44.48	1.662	4.539	0.007	0.259	1.231
Genetic Advancement 1%	5.906	44.582	8.99	1.941	57.004	2.13	5.818	0.009	0.331	1.577
Gen. Adv. as % of Mean 5%	11.407	64.223	7.019	33.304	86.536	37.317	34.187	41.817	55.836	6.467
Gen. Adv. as % of Mean 1%	14.619	82.305	8.996	42.68	110.9	47.824	43.813	53.591	71.557	8.288

Conclusion

There is a lot of variation in the material for all of the characters that can be used in the future with a simple selection. A wide range of mean values among the genotypes for different characters *i.e.*, plant height, days to maturity, number of branches per plant, and number of pods per plant, so the presence of a high amount of variability among the genotypes offers the scope for different yield contributing characters improvement in soybean. The estimates of GCV and PCV were recorded as high for the number of pods per plant, the number of pods per cluster, seed yield per row, and seed yield per plant. Higher heritability estimates were observed for all the traits under the study. However, high genetic advance as percent of mean was recorded for characters a like number of pods per plant, plant height, seed yield per plant, seed yield per row, and low to moderate for days to 50% flowering, days to maturity, number of branches per plant, oil content.

References

- Aditya JP, Bhartiya P, Bhartiya A. Genetic variability, heritability, and character association for yield and component characters in soybean (*Glycine max* (L.) Merrill). Journal of Central European Agriculture. 2011;12(1):27-34.
- Baraskar VV, Kachhadia VH, VachhanI JH, Barad HR, Patel MB, Darwankar MS. Genetic variability, heritability, and genetic advance in soybean (*Glycine max* (L.) Merrill). Electronic Journal of Plant Breeding. 2014;5(4):802-806.
- Burton GW. Quantitative inheritance in grasses. Proc. Sixth International Grassland Congress. Pennsylvania State College, PA. US. 1952;1:24.
- Cochran WG, Cox GM. Experimental designs. 2nd ed. John Wiley and Sons., Inc., New York; c1957.
- Ghodrati GH. 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.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of Soybeans. Agronomy Journal. 1955;47:314-318.
- Karnwal Mukesh Kumar, Singh Kamendra. Studies on genetic variability, character association and path coefficient for seed yield and its contributing traits in soybean (*Glycine max* (L.) Merrill). Legume Research. 2009;32(1):70-73.
- Korale OD, Dhuppe MV, Bhosle GB, Sargar PR. Assessment of genetic variability, heritability and genetic advance for yield and yield contributing characters in groundnut (*Arachis hypogaea*. L.). Multilogic in science. 2021;12(40):123-126.
- Lukman Hakim, Suyamto, Eman Paturohman. Genetic variability, heritability and expected genetic advances of quantitative characters in F₂ progenies of soybean crosses. Indonesian Journal of Agricultural Science. 2014;15:11-16.
- Mahbub MM, Shirazy BJ. Evaluation of genetic diversity in different genotypes of soybean (*Glycine max* (L.) Merrill). American Journal of Plant Biology. 2016;1(1):24-29.
- Pansy VG, Sukhante PV. Statistical Methods for Agricultural Workers. I.C.A.R., New Delhi; c1967. p. 250-297.
- Robinson HF, Comstock RE, Harvey VH. Estimates of heritability and degree of dominance in corn. Agron. J. 1949;41:353-359.
- Sargar PR, Wadikar PB, Zade YA, Gorte AS. Genetic analysis for heritability and genetic advance studies in safflower (*Carthamus tinctorius* L.). Multilogic in science. 2021;11(38):1963-1966.
- Shinde RJ, Toprope VN, Sargar PR, Gavali RG, Samindre S. Heritability and genetic advance as indices for yield and yield components selection in Cowpea (*Vigna unguiculata* L. Walp). International journal of plant and environment. 2021;7(04):297-299.
- Swar BR, Latha VS, Reddy MR, Vanisri S. Assessment of Genetic variability parameters in magic population of soybean (*Glycine max* (L.) Merrill). Merrill Assessment. 2020;15(2):271-274.