



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(12): 1999-2001
© 2023 TPI
www.thepharmajournal.com
Received: 02-10-2023
Accepted: 07-11-2023

VA Dhengle
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

MV Dhuppe
Oilseeds Specialist, Oilseeds
Research Station, Latur,
Maharashtra, India

PM Salunke
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

SG Dhawale
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

MR Sawadadkar
Department of Agronomy,
College of Agriculture, Latur,
Maharashtra, India

Corresponding Author:
VA Dhengle
Department of Genetics and
Plant Breeding, College of
Agriculture, Latur, Maharashtra,
India

Genetic variability, heritability and genetic advance of yield and yield contributing traits in soybean (*Glycine max* L.)

VA Dhengle, MV Dhuppe, PM Salunke, SG Dhawale and MR Sawadadkar

Abstract

The present investigation was conducted to estimate the extent of genetic variability, heritability, genetic advance. The experimental material comprising of 26 genotypes were evaluated at Oilseeds Research Station, Latur during *kharif-2022*. The material was sown in randomized block design with three replications, on 25th June, 2022, observations were recorded for nine characters. Mean sum of square of genotype revealed highly significant for most of the characters under study which show the presence of sufficient amount of variability among the germplasm lines (experimental material) and hence provide an opportunity to improve the character through 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, number of pods per plant, showed presence of high amount of variability among the genotypes and offer the scope for different yield contributing characters improvement in soybean. The estimates of GCV and PCV were recorded high for number of pods per plant, number of branches per plant, number of pod per cluster 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 noted for characters like number of pods per plant, days to 50% flowering, days to maturity, number of branches per plant, seed yield per plant, plant height number of pod per cluster and low to moderate for 100 seed weight, oil content.

Keywords: Genetic variability, heritability, genetic advance, GCV, PCV

Introduction

Soybean (*Glycine max* (L.) Merrill) occupies a unique position among edible legume. *Glycine max* (L.) Merrill is a self-pollinated crop belonging to the Leguminaceae family and sub family Papilionideae tribe phaseolae and genus glycine. There are 1200 species in the *Glycine* genus. Normally, the plant is diploid, with $2n=40$ chromosomes. The sub genera *Glycine* and *Soja* make up the genus *Glycine*. *Glycine* has 16 perennial species, while *Soja* (Moench) contains the cultivated soybean, *Glycine max* (L.) Merrill, as well as two annual species, *Glycine soja* Siebold and *Zucc*. The cultivated species, *G. max*, hybridizes easily with its wild annual relative and most likely progenitor *G. soja*, but it has a low cross ability rate with perennial relatives (Singh and Hymowitz, 1999) [13]. Soybean is an important oil seed crop with a high protein (40-42%), high lysine content, and oil content (20-22%) also rich in vital fatty acids. It also contains isoflavones, which protect the human body from cancer, diabetes, osteoporosis, high blood pressure, and heart disease, among other things. Soybean is the most common source of oil in the world, and De Oil Cake (DOC) is utilised in animal feed and as a food processing unit for new food product development. Because of its many uses, soybean is aptly referred to as the "Golden Bean" or "Miracle Crop" of the twentieth century. Because soybean contains 40 percent protein and 20 percent oil, it is classed as an oil seedcrop rather than a pulse crop. The growing demand for soya meals highlights the importance of locating and developing high-quality sources. (Fasoula and Boerma, 2007) [7].

Materials and Methods

Twenty six soybean genotypes provided from the Oilseed Research Station in Latur were grown in a rainfed Randomised block design at an experimental farm during *Kharif-2022*. Each genotype was seeded with 45cm between rows and 5 cm between plants. Dibbling was the method that was used for sowing.

Thinning done 20 days after sowing kept one plant per hill, and RDF for soybean is 30 kg N, 60 kg, 60 kg K and 20kg S P/ha was applied at the time of seeding. Observations were made on five randomly chosen plants from each genotype, and the mean value was used for statistical analysis for nine characters *viz.*, days to 50 percent flowering, plant height, days to maturity, number of branches per plant, number of pods per plant, number of pods per cluster, 100- seed weight (g), seed yield per plant (kg), and oil content (%). The formula of Panse and Sukhatme (1985) ^[11] will be used to calculate variation for all of the features under consideration. The mean squares from the variance table will be used to determine genotypic and phenotypic variances (Johnson *et al.*, 1955) ^[8]. The GCV and PCV will be determined using Burton (1952) ^[4] approach. Heritability (in the broad sense) will be calculated using the method proposed by Allard (1960) ^[2]. Johnson *et al.* (1955) ^[8] proposed a formula for calculating genetic advance.

Results and Discussion

The data investigated on different characters for various entries were averaged and subjected to statistical analysis of variance (Table 1) revealed that, the significant differences among the experimental material for all the characters studied. The significance was marked by applying 'F' test. The variation due to genotypes were 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), genetic advance and genetic advance as percentage of mean (GAM) were reported in table 2. Wide range of variability was observed among twenty six genotypes for yield and yield contributing and quality traits under which indicates good scope for selection of genotypes for particular traits. Genotypic variance was found to be lower than phenotypic variance for all the characters. However, higher magnitude of genotypic variance was recorded for number of pods per plant (506.42), followed by plant height (130.78). While moderate genotypic variance observed in days to maturity (50.99), Days to 50% flowering (11.52), seed yield per plant (7.37). Whereas, the relatively lower genotypic variance observed in 100 seed weight (2.92), oil content (1.97), number of pod per cluster (0.58), number of branches per plant (0.58). Similar result reported by Aditya *et al.* (2011) ^[1].

Higher phenotypic variance was observed for number of pod per plant (550.95), plant height (169.41), days to maturity (55.95). while, moderate phenotypic variance observed for days to 50% flowering 12.92, seed yield per plant (9.34), 100 seed weight (5.46), oil content (5.00), Whereas, the lower genotypic variance number of pod per cluster (0.76), number of branches per plant (0.68). Similar result reported by Lukman *et al.* (2014) ^[9].

High magnitude of Genotypic coefficient of variation was observed in trait number of pods per plant (33.71), number of branches per plant (24.27), number of pod per cluster (20.11), seed yield per plant (19.34), while, moderate genotypic variance observed in plant height (17.06), 100 seed weight (9.82), While lower genotypic coefficient of variance was observed days to 50% flowering (8.42), days to maturity (7.30), oil content (6.46).

High magnitude of Phenotypic coefficient of variation was observed in trait number of pods per plant (35.16), number of branches per plant (26.38), number of pod per cluster (23.06), seed yield per plant (21.77). While moderate genotypic coefficient of variance was observed in plant height (19.41), 100 seed weight (13.41), whereas, the lower genotypic variance oil content (10.27), days to 50% flowering (8.82), days to maturity (7.64). The character of number of pod per plant, number of branches per plant, number of pod per cluster, seed yield per plant showed higher value of GCV and PCV indicating the presence of considerable amount of genetic variability and less influence of environment and suitable for selection. This character can be relied upon and simple selection can be practiced for further improvement. Similar result recorded as Neelima *et al.* (2018) ^[10].

The traits plant height, seed weight show moderate value of GCV and PCV indicating medium range of variability and influence of environment and unsuitable for selection. Similar result agreement with Chandrawat *et al.*, (2017) ^[6] The character days to 50% flowering, days to maturity, oil content show lower value of GCV and PCV indicating low variability, high influence of environment and unsuitable for selection. Similar result were found with Saicharan *et al.* (2022) ^[12]. The character plant height, number of pod per plant, number of pod per cluster, 100 seed weight, oil content showed wider difference between GCV and PCV indicating that, this characters were highly influenced by environment factor. Similar result were recorded as Chandel *et al.* (2017) ^[5] The character days to 50% flowering, days to maturity, number of branches per plant, seed yield per plant showed lower difference between GCV and PCV indicating that, this character were low influenced by environment factor. Similar result recorded as Aditya *et al.* (2011) ^[1].

The high heritability estimates were observed in trait number of pods per plant (91.90%), followed by days to 50% flowering (91.30%), days to maturity (91.10%), no.of branches per plant(84.70%), Seed yield per plant (79.00%), plant height (77.20%), no. of pod per cluster (76%). While moderate heritability was found in 100 seed weight (53.60%) followed by oil content (39.50%).

The highest genetic advance (%) was observed in character number of pods per plant (44.4), followed by plant height (20.70), While moderate heritability was observed in days to maturity (14.04), While least genetic advance was observed in days to 50% flowering (6.68) followed by seed yield per plant (4.97), 100 seed weight (2.58), oil content (1.82), no. of branches per plant (1.44), no. of pods per cluster (1.37.)

The highest Genetic advance as percent of mean (%) was observed in character number of pods per plant (66.58), number of branches per plant per plant (46.02), number of pod per cluster (36.11), seed yield per plant (35.42), plant height (30.88), while moderate Genetic advance as percent of mean (%) was observed in character days to 50% flowering (16.58), 100 seed weight (14.81), days to maturity (14.35), whereas, least advance as percent of mean (%) was observed in character oil content (8.36).

The traits number of pod per plant, number of branches per plant, number of pod per cluster, seed yield per plant, plant height showed high heritability coupled with high genetic advance as percent of mean. It indicating that most likely the heritability is due to additive gene effect and selection be effective. Similar result recorded by Chandel *et al.* (2017) ^[5], Saicharan *et al.* (2022) ^[12], Chandrawat *et al.* (2017) ^[6]. The

traits 100 seed weight showed moderate heritability coupled with moderate genetic advance as percent of mean. This indicates involvement of additive gene action and there is further scope for improvement of this character through for selection. The traits days to 50% flowering, days to maturity show high heritability coupled with moderate genetic advance

as percent of mean. This indicates selection may be rewarding because of both additive and non-additive gene action play important role in the expression of these traits and improvement can be done though diallel selection mating followed by selection. Similar result recorded as Baraskar *et al.* (2014)^[3].

Table 1: Analysis of variance (ANOVA) for yield and yield component traits studied in soybean (*Glycine max* [L.]

Sr. No.	Source of Variation	D. F.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	No. of pods per cluster	100 seed weigh (g)	Seed yield per plant (g)	Oil content (%)
1	Replication	2	1.397	1.3205	35.895	0.0866	100.736	0.319	3.576	0.431	4.501
2	Treatment	25	35.672**	157.95**	430.98	1.852**	1563.81**	1.938**	11.321**	24.100**	8.953**
3	Error	50	1.104	4.9605	38.623	0.105	44.531	0.184	2.536	1.96	3.025

* Indicates significance at 5% level

** Indicates significance at 1% level

Table 2: Parameters of genetic variability for yield and yield contributing traits in soybean (*Glycine max* [L.]

Name of the Character	Range	Mean	GV (σ^2_g)	PV (σ^2_p)	EV (σ^2_e)	GCV	PCV	ECV	Heritability (%)	Genetic advance	GAM (%)
Days to 50% flowering	31.33-47	40.28	11.52	12.62	1.10	8.42	8.82	2.60	91.30	6.68	16.58
Days to maturity	84.66-110.66	97.82	50.99	55.95	4.96	7.30	7.64	2.27	91.10	14.04	14.35
Plant height(cm)	48.80-91.33	67.03	130.78	169.41	38.62	17.06	19.41	9.27	77.20	20.70	30.88
No. of branches per plant	2.00-4.60	3.14	0.58	0.68	0.10	24.27	26.38	10.32	84.70	1.44	46.02
No. of pods per plant (g)	36.46-97.66	66.74	506.42	550.95	44.53	33.71	35.16	9.99	91.90	44.44	66.58
No. of pod per cluster	2.56-6.42	3.80	0.58	0.76	0.18	20.11	23.06	11.29	76.00	1.37	36.11
100 Seed weight (g)	14.33-22.33	17.42	2.92	5.46	2.53	9.82	13.41	9.14	53.60	2.58	14.81
Seed yield per plant (kg)	11.26-23.66	13.47	7.37	9.34	1.96	19.34	21.77	9.97	79.00	4.97	35.42
Oil content (%)	18.20-24.10	21.76	1.97	5.00	3.02	6.46	10.27	7.99	39.50	1.82	8.36

GV- Genotypic variance, PV- Phenotypic variance, EV- Environmental variance, GCV- Genotypic coefficient of variation, PCV- phenotypic coefficient of variation, ECV- environmental coefficient of variation, GAM - Genetic advance as % mea

References

- Aditya JP, Bhartiya P, Bhartiya A. Genetic variability, heritability and character association for yield and component characters in soybean (*Glycine max* (L.) Merrill). J Cent Eur. Agric. 2011;12(1):27-34.
- Allard RW. Principles of Plant Breeding. New York: John Wiley and Sons, Inc; c1960.
- Baraskar VV, Kachhadia VH, Vachhani JH, Barad HR, Patel MB, Darwankar MS. Genetic variability, heritability and genetic advance in soybean (*Glycine max* (L.) Merrill). Electron J Plant Breed. 2014;5(4):802-806.
- Burton GW. Quantitative inheritance in grasses. Proceeding of International 6th Grassland Congress. 1952;1:277-283.
- Chandel KK, Patel NB, Sharma LK, Suresh G. Genetic variability, correlation coefficient and path analysis for yield and yield contributing characters in soybean (*Glycine max* (L.) Merrill). Green Farming. 2017;8(3):547-551.
- Chandrawat KS, Baig KS, Sarang DH, Dumai PK, Dhone PU, Kumar A. Association analysis for yield contributing and quality parameters in soybean (*Glycine max* (L.) Merrill). Ecoscan. 2015;7:113-118.
- Fasoula VA, Boerma HR. Intra-cultivar variation for seed weight and other agronomic traits within three elite soybean cultivars. Crop Sci. 2007;47(1):367-373.
- Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybean and their implication in selection. Agron J. 1955;47(10):477-483.
- Lukman, H, Suyanto, Eman P. Genetic variability, heritability and expected genetic advances of quantitative characters in F2 progenies of soybean crosses. Indones J Agric Sci. 2014;15:11-16.
- Neelima G, Mehetre SP, Narkhede GW. Genetic variability, heritability and genetic advance in soybean. Int. J Pure Appl. Biosci. 2018;6(2):1011-1017.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: ICAR; 1985.
- Saicharan G, Dhuppe MV, Rathod ST, Sargar PR, Venkateshwara Rao M. Studies on genetic variability, heritability and genetic advance for yield and yield contributing traits in soybean (*Glycine max* (L.) Merrill). Pharma Innov J. 2022;11(12):3131-3133.
- Singh RJ, Hymowitz T. Soybean genetic resources and crop improvement. Genome; c1999. p. 42.