Journal of Science Engineering Technology and Management Science *ISSN: 3049-0952*
Volume 01, Issue 01, May 2024 *www.jsetms.com*

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL]

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Abstract

Seventy genotype of soybean were evaluated to determine genetic variability, heritability and genetic advance for 14 contributing characters. The analysis of variance revealed significant variations for all the characters. The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation indicated that the values of PCV were slightly higher than that of GCV. This indicating less effect of environment on the expression of characters studied. High values of GCV and PCV were observed for plant height, number of pods per plant, seed yield per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod and biological yield per plant. High estimates of heritability coupled with high genetic advance as % of mean was observed for seed yield per plant, 100-seed weight, plant height, number of pods per plant, biological yield per plant, number of clusters per plant and pod length.

Keywords: Soybean [*Glycine max* (L.) Merrill], variability, heritability, genetic advance

Introduction

Soybean [*Glycine max* (L.) Merrill] being a potentially high yielding crop can play an important role in boosting oilseed production in the country. Linnaeous (1737) [17] proposed the name Glycine and described soybean plant as *Phaseolus max* in his book Genera plantarum. It belongs to family leguminoseae, sub family papilionaceae with chromosome number 2n=40. Soybean is a highly valued crop in terms of its contribution towards human nutrition. It has highest protein 42% and 20% oil (Gopalan *et al.*, 1994) [12]. In International market soybean oil trading is next only to palm oil. The crop contributes for nearly 25% of the world's total oil and fats production. There is good scope to improve the productivity of this crop by varietal improvement and adapting the improved production technology on larger areas of country. A successful breeding programme for yield improvement through phenotypic selection is mainly dependent on the nature and magnitude of variation in the available material and part played by the environment in the expression of the plant characters i.e. phenotype. This requires the partitioning of the overall variability into its heritable and non-heritable components with the help of suitable genetic parameters such as genetic coefficient of variation, heritability and genetic advance.

Materials and mathodology

The present investigation was carried out at the Sagdividi Farm, Department of Seed Science and Technology, College of Agriculture, Junagadh Agricultural University, Junagadh during *Kharif* 2019-20. Junagadh is situated at 21.5°N latitude and 70.5°E longitude with an elevation of 82.92 meters above the mean sea level. The soil of experimental site is medium black with pH 7.8. The weather during the growing season was favourable for normal growth and development of crop. The experimental material consisted of 70 diverse genotypes of soybean were sown on 8th August, 2019 in a randomized block design with three replications. The pure seeds of these genotypes were obtained from the Research Scientist (Oilseed), Agriculture Research Station, Junagadh Agricultural University, Amreli. Each genotype was sown in a single row plot of 2.0 m length with a spacing of 45 cm × 15 cm. The genotypes were randomly allotted to the plots in each replication. All the recommended agronomical practices along with necessary plant protection measures were followed timely for the successful raising of the crop. The observations were recorded on these five randomly selected plants in each replication and in each genotype for 14 characters *viz.*, days to flowering, days to maturity, number of branches per plant, plant height, number of pods per plant, number of seeds per pod, number of clusters per plant, number of pods per cluster, pod length, seed yield per plant, 100-seed weight, biological yield per plant, harvest index and oil content. But in case of days to flowering and days to maturity observations were counted on plot basis. Oil content in seed sample of each genotype was estimated by using Nuclear Infrared Reflectance (NRI).The analysis of variance for randomized block design (RBD) was done for each character as per Panse and Sukhatme (1985) [22]. The genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated according to the formula suggested by Burton and De Vane (1953). Heritability (h^2) in broad sense and genetic advance as % of mean (GA %) were calculated as per the formula suggested by Allard (1960) [3].

Table 1: Analysis of variance for 14 characters in soybean

Characters	**Mean sum of squares**		
	Replications	**Genotypes**	**Error**
d. f.	2	69	138
Days to flowering	1.34	19.74**	0.94
Days to maturity	16.72	247.42**	2.94
Number of branches per plant	0.71	0.89**	0.42
Plant height (cm)	106.08	469.66**	4.22
Number of pods per plant	1.43	260.21**	3.13
Number of seeds per pod	0.31	0.39**	0.16
Number of clusters per plant	4.86	21.61**	1.17
Number of pods per cluster	0.03	0.90**	0.36
Pod length (cm)	0.40	0.53**	0.02
Seed yield per plant (g)	0.04	3.56**	0.01
100-seed weight (g)	0.04	2.18**	0.006
Biological yield per plant (g)	5.00	14.71**	0.52
Harvest index (%)	9.77	14.16**	6.16
Oil content (%)	0.04	0.68**	0.04

* Significant at 5% and 1% levels, respectively.

Results and discussion

The analysis of variance for all the 14 characters studied is presented in Table 1. The analysis of variance revealed that mean square due to genotypes was highly significant for all the 14 characters indicating the presence of sufficient amount of variability in the experimental material used.

Genotypic and phenotypic coefficients of variation

GCV and PCV for all the characters are given in Table 2. The estimates of genotypic and phenotypic coefficient of variability indicated that the values of PCV were slightly higher than that of GCV for most of the traits studied, indicating less effect of environment on the expression of characters studied.

Highest GCV and PCV was observed for plant height followed by number of pods per plant, seed yield per plant and number of clusters per plant. High estimates of GCV and PCV in soybean have been reported for plant height by Mehetre *et al.* (1998) [19]; Shrivastava and Shukla (1998) [24]; Bangar *et al.* (2003) [5]; Hossain *et al.* (2004) [13]; Datt *et al.* (2011) [18] and Chandrawat *et al.* (2017) [9]. High estimates of GCV and PCV for number of pods per plant were reported by Akram *et al*. (2011) [2]; Reni and Rao (2013); Sureshrao *et al.* (2014) [25]; Mahbub *et al.* (2015) [18] and Kumar *et al.* (2018) [11]. High GCV and PCV was reported in soybean for seed yield per plant and number of clusters per plant by Das *et al.* (2001); Hossain *et al.* (2004) [18]; Akram *et al.* (2011) [2]; Baraskar *et al.* (2014) [6]; Kumar *et al.* (2015) [15]; Chandrawat *et al.* (2017) [9] and Kumar *et al.* (2018) [11].

The moderate values of GCV and PCV were observed for number of pods per cluster, number of seeds per pod, number of branches per plant, 100-seed weight and pod length, while low values of GCV and PCV indicated narrow genetic variation for these traits. These findings of low values of GCV and PCV were observed for days to flowering, harvest index, oil content and days to maturity in soybean by Chandrawat *et al.* (2017); Kumar *et al.* (2018) [11]; Neelima *et al.* (2018) and Koraddi & Basavaraja (2019). Graphical representation of PCV and GCV for various characters are given in Fig. 1.

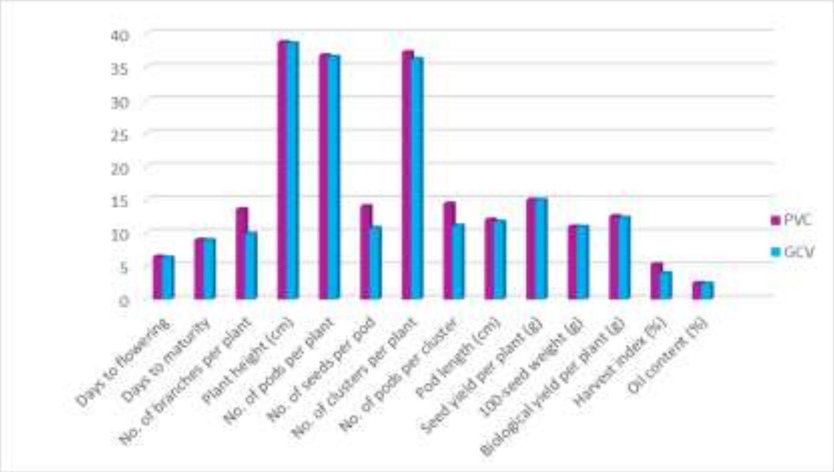

Fig 1: Graphical representation of phenotypic and genotypic coefficients of variation for various characters in soybean

Heritability

In the present study, the estimates of heritability were observed to be high for seed yield per plant (99.69%), 100- seed weight (99.69%), plant height (99.10%), days to maturity (98.81%), number of pods per plant (98.79%), biological yield per plant (96.44%), days to flowering (95.23%), pod length (cm) (94.74%), number of clusters per plant (94.58%) and oil content (%) (93.63%). Moderate heritability estimates were observed for number of pods per cluster (59.41%), number of seeds per pod (58.66%), harvest index (%) (56.44%) and number of branches per plant (52.71%). Heritability for all the characters are given in Table 2.

Table 2: Mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability (h^2) in broad sense and genetic advance (GA) as a % of mean for 14 characters in soybean

Characters	Mean	Range		PCV (%)	GCV (%)	h^2 (%)	GA as % mean
		Minimum	Maximum				
Days to flowering	39.69	36.33	47.00	6.46	6.31	95.23	12.68
Days to maturity	101.00	89.33	121.00	8.99	8.93	98.81	18.30
Number of branches per plant	4.02	3.00	5.66	13.60	9.88	52.71	14.77
Plant height (cm)	32.30	15.00	71.17	38.73	38.56	99.10	79.07
Number of pods per plant	25.33	14.00	52.00	36.76	36.54	98.79	74.81
Number of seeds per pod	2.59	2.00	3.00	14.05	10.76	58.66	16.98
Number of clusters per plant	7.21	4.00	14.66	37.23	36.20	94.58	72.54
Number of pods per cluster	3.80	2.66	5.00	14.42	11.11	59.41	17.65
Pod length (cm)	3.50	2.50	4.33	12.04	11.72	94.74	23.50
Seed yield per plant (g)	7.26	5.38	9.43	15.00	14.98	99.69	30.82
100-seed weight (g)	7.77	6.15	10.32	10.98	10.96	99.69	22.55
Biological yield per plant (g)	17.66	12.82	22.54	12.54	12.31	96.44	24.91
Harvest index (%)	40.93	28.44	44.09	5.30	3.98	56.44	6.17
Oil content (%)	19.20	18.19	20.24	2.48	2.40	93.63	4.79

High heritability for the above traits which were controlled by polygenes might be useful to the plant breeders for making effective selection. High magnitude of heritability has also been reported for seed yield per plant by (Kumar *et al.*, 2015 and Chandrawat *et al.*, 2017) [9]; 100-seed weight (Kumar *et al.*, 2018 [11] and Koraddi & Basavaraja 2019); plant height (Agrawal *et al.*, 2001; Hossain *et al.*, 2004 and Datt *et al.*, 2011) [18]; days to maturity Hossain *et al.*, 2004) [18]; number of pods per plant (Agrawal *et al.*, 2001; Hossain *et al.*, 2004; Bhat *et al.*, 2012; Amrita *et al.*, 2014 [4]; Baraskar *et al.*, 2014 and Neelima *et al.*, 2018) [6, 13]. High magnitude of heritability has also been reported for biological yield per plant (Amrita *et al.*, 2014 and Baraskar *et al.*, 2014) [6, 4]; days to flowering (Agrawal *et al.*, 2001 and Koraddi & Basavaraja 2019); days to maturity (Hossain *et al.*, 2004) [13] and number of clusters per plant (Baraskar *et al.*, 2014) [6].

Genetic advance expressed as % of mean

The genetic advance expressed as % of mean was highest for plant height, number of pods per plant, number of clusters per plant, seed yield per plant, biological yield per plant, pod length and 100-seed weight. The values were moderate for days to maturity, number of pods per cluster, number of seeds per pod, number of branches per plant and days to flowering. On the other hand, harvest index and oil content recorded low values of genetic advance expressed as percentage of mean. High values of genetic advance expressed as percentage of mean have been reported in soybean for plant height (Amrita *et al.*, 2014; Baraskar *et al.*, 2014; Chandrawat *et al.*, 2017 [9]; Kumar *et al.*, 2018[11] and Neelima *et al.*, 2018) [11]; number of pods per plant

(Bhat *et al.*, 2012; Sureshrao *et al.*, 2014 [25]; Chandrawat *et al.*, 2017 [9]; Kumar *et al.*, 2018 [11]; Neelima *et al.*, 2018 and Koraddi & Basavaraja 2019) [9]; number of clusters per plant (Baraskar *et al.*, 2014); seed yield per plant (Amrita *et al.*, 2014; Baraskar *et al.*, 2014; Sureshrao *et al.*, 2014 and Chandrawat *et al.*, 2017) [4, 25, 9]; biological yield per plant (Amrita *et al.*, 2014 and Baraskar *et al.*, 2014) [6] and 100-seed weight (Amrita *et al.*, 2014; Chandrawat *et al.*, 2017; Kumar *et al.*, 2018[9, 11] and Koraddi & Basavaraja 2019) [9]. Genetic advance as % of mean for all the characters are given in Table 2.

In the present study, high estimates of heritability coupled with high to moderate genetic advance as % of mean was observed for seed yield per plant, 100-seed weight, plant height, days to maturity, number of pods per plant, biological yield per plant, days to flowering, number of clusters per plant, number of pods per cluster, number of branches per plant, number of seeds per pod and pod length which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on these characters for their rationale improvement (Panse, 1957). Graphical representation of heritability and genetic advance as % of mean for various characters are given in Fig. 2.

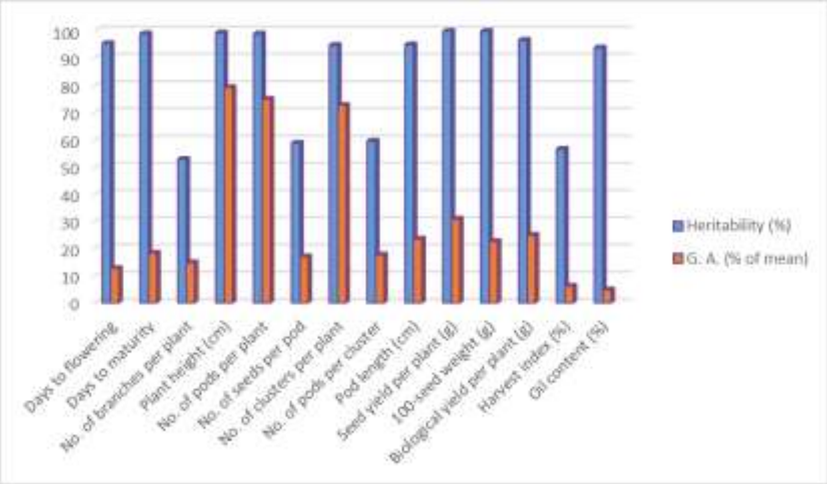

Fig 2: Graphical representation of heritability and genetic advance expressed as % of mean for various characters in soybean

Similar kinds of results were also reported by Agrawal *et al.* (2001); Hossain *et al.* (2004) [1] [3]; Amrita *et al.* (2014) [4]; Baraskar *et al.* (2014) [6]; Chandrawat *et al.* (2017) [9] and Neelima *et al.* (2018) for plant height, seed yield per plant and number of pods per plant. Amrita *et al.* (2014); Chandrawat *et al.* (2017) [9] and Kumar *et al.* (2018) [11] for 100-seed weight. Amrita *et al.* (2014) [4] and Baraskar *et al.* (2014) [6] for biological yield per plant. Moderate estimates of heritability coupled with low genetic advance as % of mean was expressed by harvest index may be inferred that these trait were regulated by non-additive gene action and presence of high genotype x environment interaction.

Conclusions

The analysis of variance revealed highly significant differences among the mean square due to genotypes for all the characters studied, suggesting the presence of sufficient amount of variability in the material used. The estimates of GCV and PCV indicated that the values of PCV were slightly higher than that of GCV for most of the traits studied, indicating the effect of environment on the expression of characters studied. High heritability coupled with high to moderate genetic advance expressed as per cent of mean were observed for seed yield per plant, 100-seed weight, plant height, days to maturity, number of pods per plant, biological yield per plant, days to flowering, number of clusters per plant, number of pods per cluster, number of branches per plant, number of seeds per pod and pod length suggesting the existence of sufficient heritable variation and wider scope for effective selection.

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