

Original Research Article

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Study of Genetic Variability in Different Soybean Genotypes Based on Yield and Yield Contributing Traits

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ABSTRACT

The present investigation was undertaken to study the extent of genetic variability, heritability (b.s.), genetic advance, genotypic and phenotypic coefficient of variation, correlation, path analysis, genetic divergence among thirty genotypes of soybean. These genotypes were evaluated during *Kharif*, 2018 in a randomized block design with three replications. Observations were recorded on days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g), SPAD value, protein content (%), oil content (%). The treatment differences were statistically significant for all the characters. The phenotypic coefficient of variation (PCV) was found to be marginally higher than the genotypic coefficient of variation (GCV) for all the characters, indicating the dominance of the genotypic coefficient of variation for expression of these traits. Number of seed yield per plant exhibited the high GCV as well as PCV followed Number of pods per plant, plant height, number of seeds per pod, and 100 seed weight. The oil content exhibited the least GCV and PCV. Maximum heritability observed for the number of pods per plant (94.96), followed by plant height (93.11) and days to 50 percent flowering (91.38). The highest genetic advance estimates for the number of pods per plant, followed by plant height and days to maturity. The highest genetic advance as a percentage of mean was observed seed yield per plant followed by the number of pods per plant and plant height.

Keywords

Soybean, Genetic variation, Genetic advance, Heritability, Soybean, Selection intensity, Traits

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Introduction

Soybean (*Glycine max* L. Merrill) is considered a miracle crop due to of its extraordinary qualities. It is grown in East and South East Asia mainly for food, feed, and medicinal purposes. This plant contains about 38-42% of high-quality protein, 6% ash, 29% carbohydrate, and 17 to 24% oil, comprising 85% polyunsaturated fatty acids with two

essential fatty acids. Soybean ($2n=40$) belongs to the Leguminosae family and is believed to have originated in northeastern China and distributed in the USA, Brazil, Argentina, China, India, etc. Today it ranks first in oilseed production (contribution 58 %) followed by rapeseed, groundnut, and sunflower. In India, it occupied an area of 10.97 mha with a production of 13.46 mt and a productivity of 1120 kg ha^{-1} (Anonymous,

2018-19). In India, major soybean-producing states are Madhya Pradesh, Maharashtra, Rajasthan, Karnataka, Gujarat, Andhra Pradesh Uttar Pradesh and Chhattisgarh.

The continuous improvement of soybean depends on the information about genetic variability, genetic parameters, and their application, that assists the breeders in the reliable selection process. Important genetic parameters include heritability and genetic advance that enable the plant breeders to select the best breeding strategy. In this study was designed to estimate the genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2), expected genetic advance.

Materials and Methods

Experimental materials

For the purposed study consisted of 30 different soybean genotypes available with soybean breeder, Agricultural Research Station, Kasbe-Digranj, Sangli. The details of the 30 genotypes of soybean were given in Table 1.

Experimental methods

Field experiment

The field experiment consisting of 30 soybean genotypes was undertaken at Agricultural Research Station, Kasbe-Digranj, Sangli. To study recommended agronomic practices were followed to raise good crops. The detail of the experiment is as follows.

- a) Season – *Kharif*, 2018
- b) Design – RBD (Randomized Block Design)
- c) Plot size – 5 X 2 meter
- d) Date of sowing – 12 July 2018
- e) Spacing – 45 X 5 cm

- f) Number of genotypes – 30
- g) Fertilizer Dose – 30: 60:30 Kg NPK/ha

Details of observations Recorded

Following observations on the five randomly selected plants from each experimental plot in each replication and averages were worked out *viz.*, days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g), SPAD value, protein content (%), oil content (%)

Results and Discussion

Analysis of variance

The analysis of variance for the eleven characters studied is presented in Table 2. The analysis revealed that all the genotypes exhibited highly significant differences for all the characters under study. These results confirmed the earlier findings of Chandrawat *et al.*, (2017), Joshi *et al.*, (2017), Desissa (2017), and Koraddi and Baswaraja (2019).

Variability and genetic parameters

Components of genetic variation

Range of variability, estimates of components of variation, estimates of genotypic and phenotypic coefficient of variation, heritability percentage in a broad sense, genetic advance and genetic advance expressed as percentage of the mean are presented in Table 3 and Fig. 1.

Estimates of components of variation

It was observed that the estimates for phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV) for all the characters studied.

Similarly, the result observed by Neelima *et al.*, (2018), the magnitude of genotypic coefficient variance was maximum for seed yield per plant (38.59) followed by the number of pods per plant (34.47). The phenotypic coefficient variance, however,

ranged between 3.14 and 40.49. It was of higher magnitude for seed yield per plant (40.49) followed by the number of pods per plant (35.37) While it was minimum for protein content percentage (3.14) followed by days to maturity (4.62).

Table.1 List of genotypes along with pedigree included in the studies

Sr.no.	Name of genotype	Pedigree
1	BAUS-100	JS 20-30/JS 335
2	CAUMS-1	Selection from NRC 2012-6-3-1-4-3
3	DS-3109	Pusa 12/F4C7-32
4	DS-3110	Pusa 12/F4C7-32
5	DSb-33	DSb 21/JS 95-60
6	GJS-3	Germ plasm line KB -85
7	Himso-1688	NRC 2007/B1-19
8	Himso-1689	NRC 2008/G-1-12
9	JS-21-71	JS 20-63/JS 95-60
10	JS-21-72	SL 738/JS 95-60
11	KDS-1009	AMS 99 33/EC 241780
12	KDS-1073	JS 20-05/EC 241780
13	KS-113	Selection from KS 103
14	MACS-1566	RKS 24/NRC 55
15	MACS-1620	RKS 25/NRC 55
16	NRC-138	JS 97-52/NRC 107
17	NRC-139	JS 97-52/NRC 101
18	NRC-146	Selection from 6A-34
19	NRC-147	Indigenous collection (IC 210)
20	NRC-148	NRC 7/AGS 191
21	NRCSL-2	JS 335/SL 525 EDV of JS 335
22	PS-1634	JS 9752/PS 1225
23	PS-1637	JS 9752/PK 472
24	RSC-11-15	JS 335/PS 1024
25	RSC-11-17	JS 97-52/JS 93-05
26	RVS-2007-4	RVS 2000-10/JS 95-60
27	RVS-2011-10	JS -335/PK 1042
28	KS-103	JS 335/EC 241780
29	KDS -726	JS 9305/EC 241780
30	KDS - 753	JS 9305/EC 241780

Table.2 Analysis of variance for different eleven characters in soybean

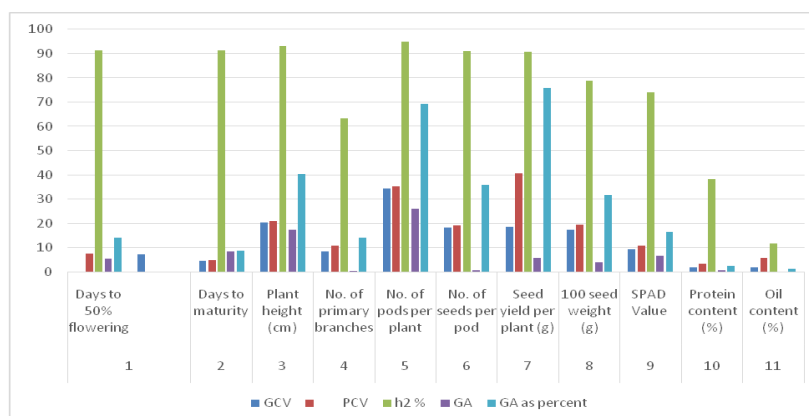
Sr. No.	Character	Mean sum of square		
		Replication	Treatment	Error
	Df	2	29	58
1	Days to 50% flowering	1.60	25.71**	0.78
2	Days to maturity	0.31	60.55**	1.85
3	Plant height (cm)	0.07	236.76**	5.69
4	Number of primary branches	0.04	0.30**	0.04
5	Number of pods per plant	9.26	514.20**	8.93
6	Number of seeds per pod	0.03	0.69**	0.02
7	Seed yield per plant (g)	2.79	28.62**	0.92
8	100 seed weight (g)	1.15	16.94**	1.40
9	SPAD Value	2.02	47.77**	5.01
10	Protein content (%)	2.52	2.79**	0.97
11	Oil content (%)	0.68	1.37**	0.98

* Significant at 5% level, ** Significant at 1% level, Values in parenthesis indicates the degrees of freedom

Table.3 Estimates of variability parameters for eleven different characters of soybean genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	h ² % (B.S.)	GA	GA as percent of mean (%)
1	Days to 50% flowering	40.86	35.33 -46.33	7.05	7.37	91.38	5.67	13.89
2	Days to maturity	99.97	88.00 -105.33	4.42	4.62	91.36	8.70	8.71
3	Plant height (cm)	43.32	32.06 -68.31	20.25	20.99	93.11	17.44	40.26
4	Number of primary branches	3.41	3.00 -4.00	8.60	10.80	63.42	0.48	14.10
5	Number of pods per plant	37.64	18.06 - 65.40	34.47	35.37	94.96	26.05	69.20
6	Number of seeds per pod	2.60	2.00 -3.00	18.27	19.13	91.18	0.93	35.93
7	Seed yield per plant (g)	7.87	3.71 - 14.80	38.59	40.49	90.87	5.96	75.79
8	100 seed weight (g)	13.11	10.01 - 18.31	17.34	19.55	78.69	4.15	31.70
9	SPAD Value	40.66	32.20 -48.83	9.28	10.79	73.99	6.68	16.44
10	Protein content (%)	40.00	38.10 - 41.66	1.94	3.14	38.24	0.99	2.47
11	Oil content (%)	18.91	18.00 - 20.63	1.90	5.57	11.66	0.25	1.33

Fig.1 Variability parameters for eleven different characters of soybean genotypes



The highest difference between GCV and PCV values were observed for oil content (1.90-5.57), followed by 100 seed weight (17.34-19.55) and primary branches per plant (8.60-10.80). Days to maturity showed the lowest difference between GCV and PCV estimates (4.42-4.62). Koraddi and Baswaraja (2019) recorded the highest GCV and PCV for seed yield per plant. Joshi *et al.*, (2017) reported the highest GCV and PCV for the number of branches and days to maturity. Chandel *et al.*, (2013) estimated the highest GCV and PCV for plant height, number of seeds per pod, seed yield per plant. Ghodrati (2013) observed the highest GCV and PCV for primary branches per plant, pods per plant and plant height.

Heritability (b.s.)

The estimates of heritability (b.s.) presented in Table 3 and Fig. 1 ranged from 11.66 to 94.96%. Maximum heritability observed for number of pods per plant (94.96), followed by plant height (93.11), days to 50 percent flowering (91.38) and minimum in case of oil content (11.66), followed by protein content (38.24) and number of primary branches per plant (63.42). Which confirmed with the finding of Jagdish *et al.*, (2000) for seed yield per plant, pods per plant, and plant height. Chamundeshwari and Aher (2003) for plant

height and number of pods per plant. Chandrawat *et al.*, (2017) for pods per plant, plant height and seed yield per plant. Desissa (2017) for plant height.

Genetic advance

The range of genetic advance was between 0.25 to 26.05 with the highest estimates for the number of pods per plant (26.05), followed by plant height (17.44) and days to maturity (8.70). The lowest genetic advance was observed for oil content (0.25), followed by the number of primary branches per plant (0.48) and the number of seeds per pod (0.93). A similar result reported by Mahawar *et al.*, (2013) recorded the low genetic advance for oil content. Mahbub and Shirazy (2016) recorded the highest genetic advance for the number of pods per plant, plant height, and number of branches per plant but in the present study, the number of primary branches per plant showed low genetic advance. Koraddi and Baswaraja (2019) recorded the highest genetic advance for plant height, number of pods per plant.

Genetic advance as percent of mean

The highest genetic advance as a percentage of mean was observed seed yield per plant (75.79) followed by the number of pods per

plant (69.20) and plant height (40.26). Jagdish *et al.*, (2000) and Neelima *et al.*, (2018) recorded high genetic advance as a percentage of the mean for the number of pods per plant and plant height. Joshi *et al.*, (2017) estimated high genetic advance as a percentage of the mean for plant height.

In the present investigation Phenotypic coefficient of variation (PCV) was found to be marginally higher than the genotypic coefficient of variation (GCV) for all the characters, indicating the dominance of the genotypic coefficient of variation for expression of these traits. Seed yield per plant exhibited the high GCV as well as PCV (38.59 and 40.49), number of pods per plant (34.47 to 35.37), plant height (20.25 and 20.99), number of seeds per pod (18.27 to 19.13) and 100 seed weight (17.34 and 19.55) respectively. Similarly, results observed by Neelima *et al.*, (2018).

In conclusion the High estimates of genotypic coefficient of variation among the genotypes indicates variability for the characters *viz.*, seed yield per plant, number of pods per plant, plant height, 100 seed weight. The magnitude of the phenotypic coefficient of variation was more than the genotypic coefficient of variation for all the characters. It can be concluded that the high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) coupled with high heritability indicates that there is a lesser influence of environment in the expression of characters which are amenable for selection. High heritability coupled with high genetic advance as percent of the mean indicated a preponderance of additive gene action in the inheritance of character like number of pods per plant and plant height and days to 50 % flowering, days to maturity scope for selection in these characters.

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