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Research Article

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Genetic Variability, Heritability and Genetic Advance in Soybean

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ABSTRACT

The experiment was conducted to estimate the genetic variability in 124 diverse soybean germplasm accessions. The variability parameters like mean, range of variation, genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean were estimated for 13 different characters. The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors. The magnitude of heritability was observed to be high for all the characters under study indicated that the larger portion for total variation would be under genetic control and selection based on phenotypic levels would be useful for the improvement of these traits. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for plant height, number of branches per plant, number of pods per plant and seed yield per row 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 this character for their improvement.

Key words: *Genetic advance, GCV, PCV, Heritability.*

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is belonging to genus *Glycine*. The genus *Glycine* wild is divided into two sub genera, *Glycine* and *Soja*. North Eastern (Manchuria) region of the China is believed to be the center of origin and diversification center of the cultivated soybean. Soybean is considered as one of the important pulses and oilseed crops, because of high nutritional value, as it contains protein in range between 38-42 per cent and edible oil in the range of 18-25 per cent. Improvement of genetic architecture of any crop depends upon the nature and extent of genetic variability. Presence of genetic variability is one of the prerequisites to perform selection in any breeding program. Heritability estimates are considered in understanding the pattern of inheritance of quantitative character like seed yield. Similarly, genetic advance is also a useful measure to predict gain in specified selection intensity. However, when it is considered along with heritability becomes more valuable to predict response to selection than the heritability estimates alone[19].

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Keeping in view, different variability parameters like mean, range of variation, genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean were estimated for 13 different characters for 124 diverse soybean germplasm accessions.

MATERIAL AND METHODS

The present investigation was conducted to measure the different variability parameters like mean, range of variation, genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean using 124 diverse germplasm accessions including 8 checks of soybean. The experiment was laid-out in a Randomized Block Design with two replications at the All India Coordinated Research Project on Soybean, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during *kharif* 2015-2016. The observations were recorded for 13 different characters, *viz*., days to initial flowering, days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight (g), seed yield per plant, seed yield per row, protein content (%) and oil content (%). The genotypic and phenotypic coefficients of variation were computed as per the formula suggested by Burton[10]. Heritability in broad sense was calculated as per the formula suggested by Allard[5]. The expected genetic advance was calculated by the formula given by Johnson *et al*[19].

RESULTS AND DISCUSSION

Genetic variability is the pre-requisites for genetic improvement in a systematic breeding programme. Analysis of variance revealed that the mean squares due to genotype were found significant for all the traits under study, which indicated the enormous phenotypic variability was present among the genetic materials studied (Table 1).

In the present investigation, the accessions PP6, HARDER, CAT 3466, CAT 3468, CAT 449A, CAT 97B, CAT 2144B, CAT 3453, CAT 1979B, LEE-95, CAT 3470, CAT 1341B, G-620, F4 P21, G4 P17, G-688, VLS-75 gave significant higher seed yield per plant than the general mean (4.0g) hence could be utilized for improvement in the yield in soybean. All the 124 genotypes showed wide range of variation for most of the traits under study (Table 2), indicated the scope for selection of these traits for further breeding work. The estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variability indicated that the values of PCV were higher than GCV for all the traits partly due to interaction of the genotypes with the environment or other environmental factors influencing the expression of these characters (Table 2). Narrow differences observed between the PCV and GCV in certain cases indicated that these characters were less influenced by the environment. Similar results for high GCV and PCV for the characters Plant height, number of branches per plant, number of pods per plant and seed yield were obtained by Karnwal and Singh[21], Malik *et al.*[27], Ngalamu *et al.*[29], Athoni *et al.*[7], Pushpa Reni *et al.*[35], Sawale Swapnil *et al.*[40], Malek *et al.*[26], Chandel *et al.*[12], Osekita *et al.*[30], Malek *et al.*[26], Mahbub *et al.*[25] indicating the wider adapability of these traits in the genotypes studied. The character Days to initial flowering, Days to 50% flowering and number of nodes per plant were reported with moderate GCV and PCV values in the present investigation. These research findings are in accordance with the experimental findings of Dhillon *et al.*[15], Pushpa Reni *et al.*[35], Sawale Swapnil *et al.*[40], Lukman Hakim *et al.*[24], Mahbub *et al.*[25]. This suggests that there is scope to enrich the variation for these characters.

The characters Days to maturity, oil and protein content showed the lowest GCV in the present investigation. Similar kinds of results were obtained by Athoni *et al.*[7], Pushpa Reni *et al.*[35], Chandel *et al.*[12], and Pushpa Reni *et al.*[35], This may be due to the involvement of environment and genotype x environment effects in character expression. High values of heritability in broad sense are helpful in identifying the appropriate character for selection and in enabling the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits[37]. The GCV along with heritability estimates would provide a better picture of the amount of genetic advance expected by phenotypic selection[10].

Table 1: ANOVA for yield and yield contributing traits

SV	Df	Days to initial flowering	Days to 50% Flowering	Days to Maturity	Plant height (cm)	Number of branches per plant	No. of Nodes per plant	Number of pod clusters per plant	No. of Pods per plant	100 seeds weight (g)	Seed yield per plant(g)	Seed yield per row (g)	Oil %	Protein%
Replication	1	0.38	0.38	0.74	0.11	0.00	0.09	0.03	0.12	0.12	0.02	258.03	3.67	11.88
Treatment	131	53.57**	53.01**	65.02**	226.06**	0.61**	2.29**	3.35**	88.63**	8.65**	1.76**	6294**	6.12**	1.12**
Error	131	2.15	2.15	2.27	2.15	0.02	0.04	0.06	0.80	0.01	0.02	150.01	0.26	0.17

*,** significance at 5% and 1% respectively

Table 2: Estimation of Variability, Heritability and Genetic advance for seed yield and its component traits

S.N	Character	Range	General mean	Genotypic Variance $(\sigma^2 g)$	Phenotypic Variance $(\sigma^2 p)$	GCV (%)	PCV (%)	Heritability	Genetic advance	Genetic adv. as percent of mean
1	Days to initial flowering	25 – 57	36.2	25.70	27.85	14	14.57	92.28	10.03	27.71
2	Days to 50% Flowering	28 – 59	38.6	25.43	27.58	13.07	13.6	92.20	9.97	25.83
3	Days to Maturity	82 – 114	94.4	31.37	33.63	5.93	6.14	93.28	11.14	11.80
4	Plant Height	19.8 - 72.6	42.1	111.95	114.10	25.12	25.36	98.12	21.59	51.28
5	Number of branches /plant	0 - 3.5	1.5	0.29	0.31	35.43	36.63	93.55	1.07	71.33
6	Number of nodes/plant	4.9 - 11.9	8.2	1.12	1.15	12.9	13.1	97.39	2.15	26.22
7	Number of pods clusters/ plant	3.9 - 9.0	6.7	1.64	1.70	19	19.34	96.47	2.59	38.66
8	Number of pods/plant	7.0 - 39.5	26.8	43.91	44.70	24.72	24.94	98.23	13.5	50.37
9	100 seed weight	4.65 - 21.95	9.9	4.32	4.33	20.8	20.83	99.77	4.27	42.70
10	Seed yield per pant	1.57 – 5.92	4	0.86	0.88	23.12	23.39	97.73	1.88	47
11	Seed yield per row	15 – 314	136	3071.99	3222	40.77	41.75	95.34	111.48	82.03
12	Oil content	15.94-24.74	19.4	2.93	3.18	8.84	9.21	92.14	3.38	17.42
13	Protein content	38.36-41.03	39.7	0.47	0.64	1.72	2.01	73.44	1.21	3.05

In the present investigation, results indicated that the heritability estimates were high for all the traits under study. Aditya *et al*[22], Shiv Datt *et al.*[14] and Pushpa Reni *et al.*[35], observed the similar findings for the above traits while the characters days to 50% flowering, plant height, number of branches per plant, number of pods per plant, 100 seed weight and seed yield per plant observed high heritability coupled with high genetic advance. The same was reported by the research findings of Patil *et al.*[33], Shiv Datt *et al.*[14], Osekita *et al.*[30], Pushpa Reni *et al.*[35], Agdew Bekele *et al*[4], Dilnesaw *et al.*[16], Ghodreti *et al.*[17], Sawale Swapnil *et al.*[40], Lukman Hakim *et al.*[24], Mahbub *et al.*[25]

Genetic advance measures the expected genetic progress that would result from selecting the best performance genotypes for a given characters[5]. The genetic gain that can be obtained for a particular trait through selection is the product of its heritability, phenotypic standard deviation and selection differential[10]. Yield being a complex character is influenced by many factors. In the present study, high genetic advance was observed for plant height and seed yield. The results of Abady *et al.*[1], Baruah *et al.*[9] and Mahbub *et al.*[25] are comparable with the results reported in the present investigation. The genetic advance was found to be moderate for days to initial and

50% flowering, days to maturity and number of pods per plant. The same was reported by Mahbub *et al.*[25], Dilnesaw *et al.*[16], for moderate genetic advance. While low genetic advance was observed with the traits like number of branches per plant, number of nodes per plant, number of pod clusters per plant, 100 seed weight, Seed yield per plant, oil and protein content. The results of Mukesh *et al.*[28], Ramteke *et al.*[36], Chandel *et al*[12], Mahbub *et al.*[25], and Chandel *et al.*[12] were comparable with the findings of present investigation. High genetic advance as percent mean was observed for all traits except protein content and days to maturity. Similar results were obtained by Agarwal *et al.*[3], Bangar *et al.*[8], Karad *et al.*[20], Parameshwar[32] , Chandel *et al.*[12], Amit *et al.*[6], Saxesena *et al*[41] and Mahbub *et al.*[25], High heritability coupled with high genetic advance as per cent mean was observed for number of pods per plant, number of pod clusters per plant, plant height, number of nodes per plant, 100 seed weight, seed yield per plant, seed yield per row, number of branches per plant, days to initial flowering and days to 50% flowering suggesting that these traits are under the control of additive gene action and can be improved through simple selection procedure. Similar results were reported by Yadawad *et al*[44], Bangar *et al.*[8], Hina Kausar , Sahay *et al.*[38], Savita and Koti[39] , Abady *et al*[1], Chandel *et al.*[12], Amit *et al.*[6], and Mahbub *et al.*[25]. This indicates the lesser influence of environments in expression of characters and prevalence of additive gene action in their inheritance, since are amenable for simple selection.

High heritability with moderate genetic advance as per cent of mean was recorded for oil content and days to maturity. Similar results were obtained by Abady *et al.*[1], Khan *et al.*[22] and Chandel *et al.*[12] Results indicate that these characters were less influenced by environment but governed by additive and non-additive gene action. The character days to maturity and protein content showed high heritability but low genetic advance as per cent of mean, thereby indicating that expression of these characters may be due to non-additive gene action. Similar results were obtained by Vart *et al.*[43]. This indicated marked influence of the environment of these traits and limited gain is expected through the selection.

CONCLUSION

Analysis of variance revealed that enormous phenotypic variability was present among the genetic materials studied. The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for number of plant height, number of branches per plant, number of clusters per plant, number of pods per plant, 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 this character for their rationale improvement.

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