



P-ISSN: 2349-8528

E-ISSN: 2321-4902

www.chemijournal.com

IJCS 2020; 8(1): 3124-3126

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Received: 20-11-2019

Accepted: 23-12-2019

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Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]

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DOI: <https://doi.org/10.22271/chemi.2020.v8.i1au.12035>

Abstract

An experiment was conducted to estimate the genetic parameters for different traits in soybean. The crop was sown during June, 2015 at Research cum Instructional Farm Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.). The experiment was laid out in RCBD with two replications. The results of genetic variability analysis revealed the existence of moderate genotypic coefficient of variance (GCV) for character number of primary branches per plant revealing opportunity of isolating desirable genotypes through intensive selection. The phenotypic coefficient of variance was noted to be moderate for characters seed yield per plant followed by number of pods per plant, number of primary branches per plant. The highest heritability estimate was observed for number of primary branches per plant. High heritability coupled with moderate genetic advance as percentage mean was recorded for number of primary branches per plant. Days to 50% flowering and plant height showed moderate heritability with low genetic advance as percentage of mean. Moderate heritability with moderate genetic advance as percentage of mean were recorded for plant height followed by 100 seed weight, pod bearing length, number of seeds per pod and protein content.

Keywords: Genetic variability, heritability, genetic advance and soybean

Introduction

Soybean [*Glycine max* (L.) Merrill] is a wonderful crop gifted by the nature to mankind which is one of the richest sources of oil as well as protein. It belongs to the family Leguminosae and is a self-pollinated crop having chromosome number of $2n=40$. Genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and extent to which it is heritable. Soybean is a dominant oil seed crop in the world trade accounting about 25% world's total oil and fats production. India stands at fifth place in area and production in soybean at global level. Currently, soybean is at first place among the nine oil seed crops in India with a mean national productivity 1.2 t/h. Soybean has become the major source of edible vegetable oil and high quality proteins for food and feed supplement all over the world. 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 required the partitioning of the overall variability into its heritable and non-heritable components with the help of suitable genetic parameters such as heritability and genetic advance.

Materials and Methods

The experimental material used in the present study was obtained from All India Coordinated Research Project on Soybean, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.) which consisted of 8 diverse genotypes viz., RSC 10-04, RSC 10-17, RSC 10-30, RSC 10-46, JS 97-52, JS 93-05, JS 335 and NRC 37. The experiment was comprised of 4 lines and 4 testers of soybean and cross were attempted using L x T design (Kempthorne, 1957)^[5]. Two varieties were used as a check. The F₁ were obtained by crossing each of the 4 lines with 4 testers during the *Kharif* season 2014-15 and evaluated in RCBD with 2 replication during *Kharif season* 2015-16.

Each entry was grown in a single row of 2 m length spaced at 30 cm and 20 cm between plants. The data were recorded on days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, pod bearing length, number of pod bearing nodes, number of pods per plant, number of seeds per pod, 100 seed weight (g), protein content (%), oil content (%) and seed yield per plant (g).

Results and Discussion

The results of variance revealed highly significant differences among the all characters studied.

Genotypic and phenotypic coefficient of variation

The estimation of genotypic and phenotypic components of variation is of most important to get an idea of relative extent of heritable and non-heritable components of variation. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. The phenotypic coefficients of variation were in general higher than the corresponding genotypic coefficient of variation, demonstrating the influence of environment in the expression of the characters studied. The moderate GCV was recorded for characters number of primary branches per plant (10.32%) while, lowest GCV were recorded for seed yield per plant (9.67) followed by number of pods per plant (9.01), 100 seed weight (8.93%), pod bearing length (8.25%), plant height (7.54), oil content (5.97), number of pods bearing nodes (5.84), number of seeds per pod (5.45%), protein content (2.58%) and days to maturity (2.07%). The moderate magnitude of PCV was recorded for characters seed yield per plant (14.11%) followed by number of pods per plant (12.93%), number of primary branches per plant (12.13%), number of seeds per pod (11.75%), 100 seed weight (11.62%), number of pod bearing nodes (10.74%) pod bearing length (10.26%) and plant height (10.25%) whereas, the lowest PCV were recorded for characters followed by oil content (7.14%), days to 50% flowering (6.88%), protein content (4.46%) and days to maturity (2.88%).

The magnitude of PCV was higher than the corresponding GCV for all the traits. This might be due to the interaction of the genotypes with the environment to some degree or environmental factor influencing the expression of these traits. Close correspondence between phenotypic and genotypic coefficient of variation were observed *i.e.* sufficient variability among the traits is present among the genotype. Hence, the enough scope of improvement of these traits. These results are in general accordance with the findings of Yadav (2007)^[11], Showkat and Tyagi (2010)^[10] and Reni and Rao (2013)^[9].

Heritability and Genetic Advance

The nature and extent of inherent capacity of a genotype for a character is an important parameter that determines the extent of any crop species. Genetic improvement of any character is difficult without having sufficient heritability, genetic advance and genetic variability. Hence, heritability and genetic advance are the important parameters for selecting a genotype that permits greater effectiveness of selection by separating out the environmental influence from total variability. Heritability estimates along with genetic advance are normally more useful in predicating the gain under selection than that heritability alone. However it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.* 1955)^[4].

Estimates of heritability give some idea about the gene action involved in the expression of various polygenic traits. The success of genetic advance depends on; genetic variability, heritability, selection intensity. The heritability and genetic advance of the experiment is being presented in Table-2 and discussed as under. The highest heritability estimate was observed for number of primary branches per plant (72.33%). Present findings are in agreement with the studies of Malik *et al.* (2006)^[6] and Aditya *et al.* (2011)^[11].

The moderate heritability was observed for oil content (69.98%) followed by seed yield per plant (65%) followed by pod bearing length (64.58%), 100 seed weight (59.11%), plant height (54.02%), number of seeds per pod (55.58%), days to 50% flowering (52.39%) and days to maturity (51.35%) whereas, the lowest heritability were observed for number of pods per plant (48.53%) followed by seed yield per plant (46.98%), protein content (33.99%) and number of pod bearing nodes (29.60%). The heritability values alone however, provide no information of the amount of genetic improvement that would results from selection of superior genotypes. The heritability estimates would be more reliable if its limitation in a broad sense, additive and non additive genes where accompanied with high genetic advance (Ramanujam and Tirumalachar 1967)^[7].

The magnitude of genetic advance as percentage of mean was categorized as high (> 20%), moderate (10-20%) and low (< 10%) (Johnson *et al.*, 1955)^[4]. The moderate genetic advance as percentage of mean were observed for number of primary branches per plant (18.07 %) followed by 100 seed weight (14.15%), pod bearing length (13.65%), number of seeds per pod (13.45%), number of pods per plant (12.93%), plant height (11.41%) and oil content (10.29%) whereas, lowest genetic advance as percent of mean was observed for days to 50% flowering (7.42%) followed by protein content (3.07 %) and days to maturity (3.05%).

Genetic Advance as percentage of mean

Genetic advance is considered to be a powerful measure to predict genetic gain at the specified selection intensity *i.e.* 2.06 at 5 per cent selection intensity considered in the present study. But, when it is considered along with heritability it becomes more valuable to predict response to selection than considered alone (Johnson *et al.*, 1955)^[4].

The expected genetic gains expressed as percentage of mean were estimated for all the traits. It was recorded moderate for characters number of primary branches per plant (18.07%), 100 seed weight (14.15%), seed yield per plant (13.66%), pod bearing length (13.65%), number of seeds per pod (13.45%), number of pods per plant (12.93%), plant height (11.41%) and oil content (10.29) whereas, lowest genetic advance as percentage of mean recorded for characters days to 50% flowering (7.42%), number of pod bearing nodes (6.55%), protein content (3.07%) and days to maturity (3.05%).

High heritability coupled with moderate genetic advance as percentage mean was recorded for number of primary branches per plant. Days to 50% flowering and plant height showed moderate heritability with low genetic advance as percentage of mean. Moderate heritability with moderate genetic advance as percentage of mean were recorded for plant height followed by 100 seed weight, pod bearing length, number of seeds per pod and protein content. The low heritability coupled with moderate genetic advance as percentage of mean were recorded for number of pod bearing nodes followed by number of pod per plant and yield per plant. The low heritability coupled with low genetic advance

as percentage of mean was recorded for oil content. The characters showing low heritability coupled with low in genetic advance are of less use in the breeding programme due to poor transferability or transmission of genetic materials

from one generation to another. Similar findings were also reported by authors viz. Reni and Rao (2013) [9], Ghodrati (2013) [3], Adity, *et al.*, (2011) [1], Ramteke *et al.*, (2010) [8] and Malik, *et al.*, (2006) [6].

Table 1: Analysis of variance for yield and yield attributing characters of soybean

Source	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant ⁻¹	Pod bearing length (cm)	Number of pod bearing nodes	Number of pods per plant	number of seeds per pod	100 seed weight (g)	Protein content (%)	Oil content (%)	Seed yield per plant (g)
Replication	1	10.739	9.909	25.71	0.027	18.426	0.425	9.064	0.004	1.084	3.541	1.119	2.008
Treatment	23	13.268	12.75	54.22	0.194	50.740	1.697	45.876	0.142	2.356	4.221	3.513	3.426
Error	23	4.145	4.106	14.91	0.031	10.891	0.922	15.900	0.041	0.607	2.106	0.620	1.236

Table 2: Genetic parameters of variation for yield and its components in soybean

S. No.	Characters	Mean	Range		Coefficient of variation		Heritability 'h ² (bs)'	Genetic advance	GA as % of mean
			Minimum	Maximum	GCV	PCV			
1	Days to 50% flowering	42.90	38.84	47.94	4.98	6.88	52.39	3.18	7.42
2	Days to maturity	100.7	96.70	104.59	2.07	2.88	51.35	3.07	3.05
3	Plant height (cm)	57.32	46.80	64.95	7.54	10.25	54.02	6.54	11.41
4	Number of primary branches plant ⁻¹	2.76	2.09	3.11	10.32	12.13	72.33	0.50	18.07
5	Pod bearing length (cm)	52.01	42.91	58.41	8.25	10.26	64.58	7.12	13.65
6	Number of pod bearing nodes	10.65	8.92	12.35	5.84	10.74	29.60	0.70	6.55
7	Number of pods per plant	42.97	36.51	52.14	9.01	12.93	48.53	5.56	12.93
8	number of seeds per pod	2.57	1.95	3.00	8.76	11.75	55.58	0.35	13.45
9	100 seed weight (g)	10.47	9.12	12.84	8.93	11.62	59.11	1.48	14.15
10	Protein content (%)	39.93	37.73	42.15	2.58	4.46	33.41	1.22	3.07
11	Oil content (%)	20.14	18.00	22.81	5.97	7.14	69.99	2.07	10.29
12	Seed yield per plant (g)	10.70	9.40	13.71	9.67	14.11	46.98	1.48	13.66

Conclusion

The analysis of variance showed significant difference among the genotypes of all characters studied indicating that the data generated from the above diverse material shall represent wide variability. The phenotypic coefficients of variation were comparatively higher than the genotypic coefficient of variation, indicates the influence of environmental factors on the expression of the characters. Results of the genetic variability analysis revealed the existence of moderate genotypic coefficient of variance (GCV) for character number of primary branches per plant while, lowest GCV were recorded for seed yield per plant followed by number of pods per plant, 100 seed weight, pod bearing length, plant height, oil content, number of pods bearing nodes, number of seeds per pod, protein content and days to maturity. The phenotypic coefficient of variance was noted to be moderate for characters seed yield per plant followed by number of pods per plant, number of primary branches per plant, number of seeds per pod, 100 seed weight, number of pods bearing nodes, pod bearing length and plant height whereas, the lowest PCV were recorded for characters followed by oil content, days to 50% flowering, protein content and days to maturity. The wide range genetic variability obtained for most of the characters as evidenced by significant variances due to genotypes suggesting that, it could be helpful in isolation of better genotypes. The high heritability was noted in character number of primary braches per plant.

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