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Studies on variability parameters in early generation of soybean [*Glycine max* (L.) Merrill]

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Abstract

Thirty six genotypes of soybean with twelve quantitative characters were analyzed for the variability parameters in Randomized Complete Block Design during *Kharif* 2015. In the study, the genotypes exhibited wide range of variability among the twelve characters. The magnitude of PCV was found to be higher than the value of GCV and ECV. High value of PCV along with GCV was exhibited by seed yield per plant, harvest index, number of pods per plant, basal pod height, basal node height and dry matter weight per plant indicates the minimal role of environment and maximum role of genetic factors in expression of these characters. High heritability coupled with high genetic advance (%) was observed in dry matter weight per plant, plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, yield per plant and harvest index, indicating the preponderance of additive gene action involved in the expression of these characters which could be highly rewarding during selection.

Keywords: Genotype, genetic variability, heritability, genetic advance and soybean

1. Introduction

Soybean (*Glycine max* (L.) Merrill) is the world's most important and one of the oldest seed legume, which contributes around 25 % of the global edible oil production, about two-thirds of the world's protein concentrate for livestock feeding. It is a miracle and premier oilseed crop with its 40 per cent protein and 20 per cent oil proving that it's a nature's gift to mankind. Owing to its amino acids composition, the protein of soybean is called a 'complete protein'. Soybean produces about three times more protein than rice, wheat and maize on per hectare production basis. It is also known an excellent source of good quality unsaturated fatty acids (about 85%) and is very high in the essential fatty acids such as oleic acid (23%) linoleic acid (53%) and linolenic acid (7%) [1]. The contribution of India in the world soybean area is around 10 %, but the contribution to total world soybean grain is only 4.12 % indicating the poor levels of productivity of the crop in India (1.2 t/ha) as compared to the world average (2.81 t/ha) [2]. The effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and extent to which it is heritable [3]. Furthermore, heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into next generations [4]. In addition, high genetic advance coupled with high heritability estimate offers the most effective condition for selection for a particular trait [5]. In the backdrop, the present study was undertaken to assess and estimate the magnitude and nature of variability among thirty six genotypes of soybean with respect to the twelve quantitative characters.

2. Materials and Methods

2.1 Experimental site

The investigation was conducted during *Kharif* 2015 at, N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. Geographically, Pantnagar is situated at the latitude of 29° N, longitude 79.3° E and at an altitude of 243.84 meters above the mean sea level. The university falls under the subtropical zone and situated in the *Tarai* region at the foothills of *Shivalik* range of the Himalayas.

2.2 Experimental material

Thirty six genotypes were used as experimental materials, which includes fourteen F₂ crosses, twenty parents and two standard checks PS 19 and SL 688. The names of the genotypes are summarized in Table 1. The genotypes were

planted in a Randomized Block design with two replications in *Kharif* 2015. F₂s were planted as bulk in 10 rows along with parents and check in 3 rows of 4 meter with row to row distance of 45cm. Plant to plant distance was maintained at 5 to 7 cm after thinning.

Table 1: List of thirty-six genotypes of soybean planted in RBD in *kharif* 2015

S. No.	Crosses	S. No.	Parents/ Checks	S. No.	Parents/ Checks
1.	PS 1583 x Pb1	1	PS 1583	15	JS 97-52
2.	PS 1583 x JS 335	2	PS 1584	16	JS 20-59
3.	PS 1583 x DS 12-5	3	PS 1042	17	JS 20-64
4.	PS 1583 x JS 20-29	4	PS 1347	18	JS 20-54
5.	PS 1583 x Bragg	5	PS 1092	19	JS 20-55
6.	PS 1584 x JS 20-69	6	PS 1225	20	RVS 200-1
7.	PS 1584 x JS 20-41	7	Bragg	21	PS 19 (Check)
8.	PS 1042 x PS 1347	8	JS 335	22	SL-688(Check)
9.	RVS 200-1 x PS 1092	9	Pb1		
10.	JS 20-63 x JS 97-52	10	DS 12-5		
11.	JS 20-69 x JS 20-59	11	JS 20-69		
12.	JS 20-64 x JS 20-54	12	JS 20-41		
13.	JS 20-29 x JS 20-55	13	JS 20-29		
14.	PS 1225 x PS 1347	14	JS 20-63		

2.3 Characters studied

A total of twelve quantitative characters traits were taken up for the present investigation which included discrete as well as continuous measurements for data recording. All the necessary observations were recorded at appropriate stages of crop growth which include plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, dry matter weight per plant, yield per plant and 100 seed weight. Observation on days to 50% flowering was recorded on whole plot basis and observation on derived character i.e. harvest index was also recorded for the genotypes.

2.4 Statistical Analysis

The analysis of variance for each character was carried out for the randomized complete block design as suggested by [6]. Genotypic and phenotypic coefficient of variation (GCV and PCV) were calculated as per the procedure given by [7] Burton and Devane (1952) while heritability in broad sense and expected genetic advance were worked out using the formula of [8] Johnson *et al.* (1955).

3. Results and Discussion

The Analysis of Variance (ANOVA) exhibited highly significant differences for all the traits among the soybean genotypes (Table 2). High genotypic coefficient of variation was observed for harvest index (31.75), seed yield per plant (35.26), basal node height (25.82), basal pod height (24.70), number of pods per plant (24.59) and dry matter weight per plant (22.82) while plant height, number of nodes per plant and number of primary branches per plant displayed moderate value of GCV. Days to 50% flowering, number of pods per plant and hundred seed weight showed low value of GCV. Similar trends were observed for PCV except for two characters, number of seeds per pod and hundred seed weight which showed moderate value of PCV (Table 3). High value of genotypic and phenotypic coefficient of variation were reported in soybean for number of pods per plant by [9] Manav and Arora, 2017, for yield per plant by [10] Baraskar *et al.* 2014, for harvest index by [3] Reni and Rao, 2013 whereas low

value for days to 50% flowering and moderate value of 100 seed weight were reported by [11] Chandrawat *et al.* 2017.

The estimation of genotypic coefficient of variation is not enough alone to predict the heritable nature of the character. Therefore, estimation of heritability is pre-requisite to measure the genetic relationship between parent and offspring. The estimates of heritability was found to be high for dry matter weight per plant, plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches per plant, number of pods per plant, yield per plant, hundred seed weight and harvest index whereas, number of seeds per pod exhibited moderate value of heritability. A similar finding of high heritability was also reported by [13] Aditya *et al.* 2011 for yield and yield contributing characters. The estimates of genetic advance were found to be highest for number of pods per plant followed by dry matter weight per plant, plant height, while moderate value of genetic advance was observed for harvest index and seed yield per plant. The estimates of genetic advance expressed as per cent of mean were observed to be highest for seed yield per plant, harvest index, basal node height, number of pods per plant, basal pods height, dry matter weight per plant, plant height, number of nodes per plant and number of primary branches per plant. High estimates of genetic advance as per cent mean indicated the preponderance of additive genetic effects in expression of the traits.

The estimate of heritability along with genetic advance gives the idea about the genetic architecture of the population [10]. High heritability coupled with high genetic advance as per cent mean was recorded for dry matter weight per plant, plant height, basal node height, basal pod height, number of nodes per plant, number of primary branches plant, number of pods per plant, seed yield per plant and harvest index. This indicates that these characters are governed by additive genes and direct selection for these characters can bring the desired improvement. Similar finding were also reported by [12] Suresh Rao *et al.* 2014 for plant height, pods per plant, biological yield, harvest index and yield per plant. [3] Reni and Rao (2013) also reported the findings of high heritability accompanied with high genetic advance for plant height, days to 50% flowering, branches per plant, pods per plant, hundred

seed weight, dry matter weight per plant, harvest index and yield per plant.

4. Conclusion

The analysis of variance showed significant difference among the genotypes of all characters studied indicating the prevalence of high amount of variability among the thirty-six genotypes. Narrow differences observed between PCV and GCV for most of the traits indicate less influence of environmental factors on the expression of these traits and the chance of higher improvement through phenotypic selection.

Heritability and GA along with GCV could provide the actual picture of the amount of selection gain to be expected through phenotypic selection. Thus, high values of heritability and GA (%) accompanied with high GCV for the characters like dry matter weight per plant, basal node height, basal pod height, number of pods per plant, yield per plant and harvest index can be considered as the traits for soybean which are favourable in improvement through phenotypic selection. These characters are under the control of additive gene action and would respond positively to the selection thus aids in bringing the desired improvement in breeding programme.

Table 2: Analysis of variance for yield and other characters in F₂ generation of soybean

Source of variation	df	Mean Sum of square											
		Days to 50% Flowering	Dry matter weight (g)	Plant height (cm)	Basal node height (cm)	Basal Pod height (cm)	Number of nodes per plant	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Seed yield per plant (g)	100 seed weight (g)	Harvest Index (%)
Replication	1	0.125	2.24	0.862	0.008	0.771	0.155	0.106	39.216	0.028	0.891	0.008	7.498
Treatments	35	8.738**	399.879**	229.425**	2.417**	11.522**	7.662**	0.926**	542.979**	0.094**	81.82**	2.365**	189.933**
Error	35	1.296	19.679	4.646	0.136	0.661	0.94	0.14	22.513	0.038	1.741	0.244	8.105

**significant at 1% probability

Table 3: General Mean (GM), Range, Standard Error of Mean (SEm) and Variability parameters in F₂ generation of soybean

Character	GM	Range	SEm±	PCV	GCV	ECV	h ²	GA	GA%
Days to 50% Flowering	50.15	44.50-56.00	0.57	4.47	3.85	16.08	0.74	3.42	6.82
Dry matter weight per plant	60.43	39.17-97.50	2.22	23.97	22.82	57.07	0.91	27.04	44.75
Plant height	59.43	39.64-81.50	1.08	18.21	17.84	27.96	0.96	21.40	36.01
Basal node height	4.14	2.15-6.36	0.18	27.33	25.82	18.13	0.89	2.08	50.27
Basal pod height	8.90	3.88-13.79	0.41	26.34	24.70	27.25	0.88	4.25	47.73
Number of nodes per plant	11.61	7.84-15.22	0.48	17.87	15.80	33.12	0.78	3.34	28.76
Number of primary branches per plant	3.93	2.50-5.92	0.19	18.59	15.96	18.88	0.74	1.11	28.23
Number of pods per plant	65.61	44.82-110.83	2.37	25.63	24.59	58.58	0.92	31.88	48.60
Number of seeds per pod	2.39	1.99-2.83	0.1	10.78	6.99	12.61	0.42	0.22	9.35
Seed yield per plant	17.87	7.79-29.76	0.66	36.03	35.26	31.21	0.96	12.71	71.10
100-seed weight	10.98	8.60-13.00	0.25	10.40	9.38	23.74	0.81	1.91	17.41
Harvest Index	30.03	14.86-57.00	1.42	33.14	31.75	51.95	0.92	18.82	62.68

Whereas, GM= General Mean, SEM±= Standard Error of Mean, PCV=Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation, ECV= Environmental Coefficient of Variation, h²= Heritability, GA= Genetic advance (5%) and GA (%) =Genetic advance as % of mean.

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