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Genetic variability studies for yield and seedling traits in soybean [*Glycine max* (L.) Merrill]

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ABSTRACT

Yield and seedling characters of Forty five germplasm accessions of soybean were studied for genetic variability at CCSHAU, Hisar during kharif, 2014. Accessions exhibited wide range of variability for different characters studied. Maximum variability was recorded for number of pods per plant and minimum variability was recorded for seedling dry weight. There were close agreement between GCV and PCV for number of days to maturity, plant height and number of branches per plant. Highest heritability was observed for number of pods per plant. Genetic advance as percent of mean was maximum for number of pods per plant. Thus, it may be concluded that a great amount of variability existed in the present material and it would be desirable to give emphasis on number of branches per plant, number of pods per plant and number of seeds per pod traits for selection of high yielding genotypes in soybean.

Key words: Variability, heritability, genetic advance.

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INTRODUCTION

Soybean (*Glycine max* (L.) Merril) is a member of Fabaceae family and believed to have originated in Northeastern China and distributed in Asia, USA, Brazil, Argentina etc. This crop is aptly called as "Golden Bean" or "Miracle crop" of the 20th century, because of its multiple uses. It is recognized as the most important grain legume in the world in terms of total production and international trade (Golbitz, 2007), being an important source of protein and oil which contains about 38 to 42 per cent high quality protein and 18 to 20 per cent oil, can meet present and future needs of the world for protein and edible oil. It is cultivated in 116.20 lac ha with a total production of about 86.426 lac ton and productivity 959 kg per hectare in India. Madhya Pradesh is the leading state in soybean area and production in which it is cultivated in 56.127 lac hectare with total production of 44 lac ton (Anonymous, 2013). It has also become prominent crop of Maharashtra followed by Rajasthan, Andhra Pradesh and Karnataka. Collection of genotypes and assessment of genetic variability is a basic step in any crop improvement programme. Genetic variability is the pre-requisite for selection because selection can be effective only when the population shows variability within itself. Yield being a complex character is influenced by a number of high yield contributing characters controlled by polygenes and also influenced by the environment. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance. With this background in view, the present study was undertaken to assess and estimate the magnitude and nature of variation among 45 genotypes of soybean with respect to various yield and seedling attributes which could be utilized in crop improvement programme.

MATERIALS AND METHODS

The experimental material comprised of 45 germplasm accessions of soybean collected from various sources, Pulses Section, Department of Genetics and Plant breeding, CCSHAU, Hisar during kharif, 2014. All these accessions were sown in randomized block design having three replications in single row of 3m length, keeping row to row distance of 45 cm and plant to plant distance of 10 cm. In each replication, 3 checks (PS 688, PS 1347 and PK 416) were also sown randomly in order to avoid block effect. The data were recorded on five randomly selected competitive plants for all the quantitative traits (listed in the tables). The analysis of variance was done following the method suggested by Panse and Sukhatme (1985). Genotypic and phenotypic co-efficient of variation (GCV and PCV) were calculated as per the procedure given by Burton and Devane (1952) while heritability in broad sense and expected genetic advance were worked out using the formula of Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance with respect to seed yield and its component characters (table 1) clearly indicates that mean sum of squares due to genotypes were highly significant for all the characters, thereby indicating the presence of sufficient genetic variability among various genotypes for all the characters studied, thus there is a lot of scope for selection. Genetic variability is a basic information needed for the breeders to improve the crops by adopting appropriate method of selection based on variability that exist in the material. In this regard, it is necessary to partition the total variability into heritable and non-heritable components viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and further to compute heritability and genetic advance for various metric traits. Comparison of variability between two traits is possible with coefficient of variation as it is free of units. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all 15 yield component traits. All the 45 genotypes showed wide range of variation for the traits *viz.* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, 100 seed weight, germination (%), root length, shoot length, fresh weight of seedlings, dry weight of seedlings, seedling vigour index and seed yield per plant (table). This variation indicated the scope for selection of these traits for further breeding work. The characters number of pods per plant and seed yield per plant showed higher values of PCV and GCV. Similar findings for number of pods per plant were reported by Gupta *et* *al.,* (2007), for seed yield per plant (g) by Yadav (2007), The results indicate a greater scope for selection to improve these characters. Moderate values of PCV and GCV were noticed for characters *viz.,* plant height (cm), 100 seed weight (g). Similar findings were reported by Dhillon *et al.,* (2005) whereas, number of days to maturity showed lower values of PCV and GCV. Similar kind of results was obtained by Gohil *et al.,* (2006). This suggests that there is scope to enrich the variation for these characters.

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. In present study, broad sense heritability, which includes both additive and non-additive gene effects was estimated. The estimation of heritability is important in determining the effectiveness of selection of a character provided it is considered in conjunction with the genetic advance as per method given by Johnson *et al,* (1955). In the present study, the estimates of heritability were observed to be high for number of pods per plant (97.78), root length (86.18), shoot length (86.12), fresh weight of seedlings (82.97), dry weight of seedlings (75.79) number of seeds per pod (72.56), seed yield per plant (68.09), 100-seed weight (67.46), number of branches per plant (67.20), plant height (65.30) and number of days to maturity (64.10) while medium for germination percentage (59.58) and number of days to 50% flowering (43.43). Similar observations were made for number of branches per plant by Parameshwar (2006), for plant height (cm) by Agarwal *et al.,* (2001), for number of days to maturity by Hina Kausar (2005), for number of pods per plant and 100- seed weight (g) by Bangar *et al.,* (2003).This indicated that selection based on phenotypic levels would be useful for the improvement of the traits. Earlier workers also reported high magnitude of heritability for seed yield and its components (Bangar *et al.,* 2003; Malik *et al.,* 2006). Genetic advance as percent of mean was maximum for number of pods per plant (60.81) followed by seed yield per plant (39.07), 100-seed weight (27.83), pod length (26.64), fresh weight of seedlings (25.10), root length (23.95), number of branches per plant (21.95), dry weight of seedlings (21.10), number of seeds per pod (20.33), plant height (19.99) and seedling vigour index (19.31) while rest of the traits showed lower values. High heritability associated with high genetic advance (table 2) for different characters were indicative of dominance and epistatic effects. High magnitude of genetic advance is helpful in identifying the appropriate character for selection and enabling the breeder to applying selection on said character. The estimate of heritability accompanied by genetic advance gives the idea about the genetic architecture of the population. In the present study, high heritability coupled with high genetic advance as percent mean was observed for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, root length, fresh weight of seedlings, dry weight of seedlings and seed yield per plant. Similar results were reported by Gohil *et al.,* (2006) for number of pods per plant, for number of branches by Bhandarkar *et al.,* (1999),for 100- grain weight (g) Sultana *et al.,* (2005). 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. For the remaining traits with low genetic advance over mean non additive gene effects appears to be more important. These traits can be improved by individual and family selection or by incorporation of selected individuals in recurrent breeding programme. In the present investigation, considering the importance of genetic parameters like GCV, PCV, heritability and genetic advance (% mean) together, it is evident that the number of branches per plant, number of pods per plant and number of seeds per pod are the most important traits in soybean seed yield improvement. Selection for these traits in the segregating generations would be fruitful for further genetic improvement in soybean.

Table 1. Analysis of variance (mean squares) for 15 characters among 45 genotypes in soybean

Sr. No.	Characters	Mean sum of squares			CV (%)
		Replication	Genotype	Error	
		2	44	88	
1.	Days to 50% flowering	176.02	96.89**	29.33	9.92
2.	Days to maturity	14.54	115.19**	18.12	3.53
3.	Plant height (cm)	65.87	310.19**	46.68	8.76
4.	Number of branches/plant	0.01	1.57**	0.22	9.08
5.	Number of pods/plant	5.35	730.09**	5.50	4.50
6.	Number of seeds/pod	0.03	0.47**	0.05	7.12
7.	Pod length (cm)	0.02	2.75**	0.46	12.80
8.	100-seed weight (g)	2.24	12.20**	1.69	11.42
9.	Germination (%)	62.23	137.03**	25.28	5.73
10.	Root length (cm)	2.16	11.36**	0.58	5.02
11.	Shoot length (cm)	1.53	9.16**	0.47	3.84
12.	Seedling fresh weight (g)	0.04	1.54**	0.10	6.06
13.	Seedling dry weight (g)	0.01	0.08**	0.01	6.65
14.	Seedling vigour index (%)	11.00	39.75**	6.02	8.50
15.	Seed yield/plant (g)	113.21	640.36**	86.53	10.73

**Significant at 1% *Significant at 5%

Table 2. Genetic parameters in soybean for different quantitative characters

Characters	Mean±SE(m)	Range	GCV (%)	PCV (%)	GA as % of mean	h^2(%) (bs)
Days to 50% flowering	54.62 ±3.13	43.66-72.00	8.69	13.18	11.79	43.43
Days to maturity	120.66±2.46	109.00-133.33	4.71	5.89	7.78	64.10
Plant height (cm)	78.03 ±3.94	59.33-99.00	12.01	14.86	19.99	65.30
Number of branches/plant	5.16± 0.27	3.16-6.90	13.00	15.86	21.95	67.20
Number of pods/plant	52.06±1.35	23.43-74.07	29.85	30.19	60.81	97.78
Number of seeds/pod	3.23 ±0.13	2.44-4.11	11.59	13.60	20.33	72.56
Pod length (cm)	5.32±0.39	3.88-8.72	16.40	20.80	26.64	62.16
100-seed weight (g)	11.38±0.75	8.23-16.33	16.45	20.02	27.83	67.46
Germination (%)	87.77±2.90	70.66-98.67	6.95	9.01	11.06	59.58

Root length (cm)	15.13±0.44	11.46-18.67	12.53	13.49	23.95	86.18
Shoot length (cm)	17.79±0.40	12.43-21.67	9.57	10.31	18.30	86.12
Seedling fresh weight (g)	5.18 ±0.18	4.20-7.73	13.38	14.69	25.10	82.97
Seedling dry weight (g)	1.31± 0.05	1.10-1.80	11.76	13.51	21.10	75.79
Seedling vigour index (%)	28.88±1.42	21.96-37.33	11.61	14.39	19.31	65.14

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