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GENETIC VARIABILITY ANALYSIS IN SOYBEAN (*Glycine max*L. MERRILL)

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ABSTRACT

The experiment was conducted to estimate the genetic variability in 70 diverse soybean genotypes. 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 15 different characters. Analysis of variance revealed that mean squares due to genotype were found significant for all the traits under study except oil content, indicated 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. The highest genotypic coefficient of variation was observed for number of pods per plant followed by number of primary branches per plant and number of clusters per plant, indicated the presence of wide variation for these characters under study to allow further improvement by selection of the individual traits. The magnitude of heritability was observed to be high for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, seed yield per plant, biological yield per plant and harvest index, indicated that 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. Number of pods per plant and number of primary branches per plant noted high genetic advance. The magnitude of genetic advance as percentage of mean was observed to be high for number of pods per plant, number of primary branches per plant, number of clusters per plant, plant height, biological yield per plant and harvest index. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for number of plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, biological yield per plant and harvest index, 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.

KEY WORDS: Genetic advance, GCV, PCV, Glycine max L. heritability, soybean

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is belonging to genus *Glycine.* The genus *Glycine* wild is divided into two subgenera, *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

43.2 per cent protein and 18-25 per cent edible oil.

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 (Johnson *et al.*, 1955). 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 15 different characters for 70 diverse soybean genotypes.

MATERIALS 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 70 diverse genotypes of soybean. The experiment was laid-out in a Randomized Block Design with three replications at the Instructional Farm, Department of Agronomy, Junagadh Agricultural University, Junagadh during *kharif*2012. The observations were recorded for 15 different characters, *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, seed yield per plant (g), 100-seed weight (g), biological yield per plant (g), harvest index (%), protein content (%) and oil content (%). The genotypic and phenotypic coefficients of variation were computed as per the formula suggested by Burton (1952). Heritability in broad sense was calculated as per the formula suggested by Allard (1960). The expected genetic advance was calculated by the formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Genetic variability is the pre-requisites for genetic improvement in a systematic breeding programme. There is more genetic potentiality in the genetically variable populations; the chances to achieve the desired types are increased. The estimates of genetic parameters are helpful to plant breeders to predict the performance of genotypes in the subsequent generations. So, it is necessary to split the phenotypic variability into heritable and non heritable components.

Analysis of variance revealed that mean squares due to genotype were found significant for all the traits under study except oil content, indicated that enormous phenotypic variability was present among the genetic materials studied (Table 1).

The range for various characters isgiven in Table 2. It is interesting to compare the extent of phenotypic variation observed in present study with that observed in a large number of collections. For instance, NBPGR, Regional Station, Akola (Maharashtra) has evaluated 1120 indigenous collections of soybean. The range reported by them (Anonymous, 1993) as compared to range observed in the present study showed that, for seed yield per plant, days to 50 per cent flowering, plant height, number of seeds per pod and test weight, the ranges of IC collections were on par with the variation observed in present study. But for oil content, the range present in IC collections was more. Therefore, it can be concluded that there is still scope for increasing the oil content of present genotypes.

In the present investigation, 11 genotypes (KDS-6, PK-960, PK-1036, DS-293, BK-12, BL-1667, IC (SH)-8733, DS-1, JS-578, JS (HS)-8609 and JS-75-28-4) gave significantly higher seed yield per plant than population mean (29.96 g) could be utilized for improvement of yield in soybean. All the 70 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. Harerand Deshmukh (1992) also reportedwide range of variation for days to 50 per cent flowering, days to maturity, plant height, number of pods per plant, 100-seed weight and seed yield per plant; Chetti*et al*. (2005) for pods per plant; and Khan *et al*. (2011) for seed yield and most of its attributes in soybean.

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 were obtained by Karnwal and Singh (2009).Number of primary branches per plant, number of clusters per plant and number of pods per plant registered high magnitudes of GCV (>20 %)(Table 2). Moderate magnitudes (10-20 %) of GCV was observed for plant height, number of seeds per pod, seed yield per plant, biological yield per plant and harvest index and low magnitudes (<10%) was observed for days to 50 per cent flowering, days to maturity, number of pods per cluster, pod length, 100-seed weight, oil content and protein content. The high genotypic and phenotypic coefficient of variation was observed for number of primary branches per plant, number of clusters per plant and number of pods per plant, indicated the presence of wide variation for these characters and greater scope of selection to improve these characters. High genotypic and phenotypic coefficient of variation was reported in soybean for number of primary branches per plant by Agrawal *et al.* (2000), Bangar *et al.* (2003), Sirohi*et al.* (2007) and Malik *et al.* (2011); for number of clusters per plant by Sirohi*et al.* (2007) and Khan *et al.* (2011); and for number of pods per plant by Karad *et al.* (2005), Gohil *et al. (*2007), Sirohi *et al.* (2007), Aditya *et al.* (2011), Khan *et al.* (2011), Malik *et al.* (2011) and Ngalamu*et al.* (2012). Moderate magnitudes of genotypic and phenotypic coefficient of variation was observed for seed yield per plant, plant height, number ofseeds per pod, biological yield per plant and harvest index. Bhandarkar (1999) and Bangar*et al.* (2003) also reported moderate magnitude of GCV and PCV for seed yield per plant. Low magnitude of GCV and PCV was observed for days to 50 per cent flowering, days to maturity, number of pods per cluster, pod length, 100-seed weight, oil content and protein content under the present study. Similar kind of results were obtained by Bangar*et al.* (2003) for days to 50 per cent flowering, Harer and Deshmukh (1992), Agarwal*et al.* (2000) and Bangar*et al.* (2003), for days to maturity, Harer and Deshmukh (1992) for protein content and Parameshwar (2006) for oil content. This suggests that there is scope to enrich the variation for these characters.

The genotypic coefficient of variation measures the amount of variation present in a particular character. However, it does not determine the proportion of heritable variation present in the total variation. Therefore heritability, which represents the heritable variation existing in the character, was calculated. 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 (Robinson, 1955).

In the present study, maximum heritability (broad sense) was observed for number of pods per plant (97.60 %) and minimum heritability for oil content (9.20 %)(Table 2). The magnitude of heritability was observed to be high (>30 %) for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, seed yield per plant, biological yield per plant and harvest index. This indicated that 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. Earlier workers also reported high magnitude of heritability for seed yield and its components (Harer and Deshmukh, 1992; Jagtap and Mahetre, 1994; Bhandarkar, 1999; Agawal *et al.,* 2000; Bangar*et al.,* 2003; Karad*et al.,* 2005; Malik *et al.,*2006; and Aditya*et al.,* 2011).

The heritability estimates along with genetic advance are more useful than the former alone in predicting the best individuals. If the heritability estimates, in broad sense, are owing to the non-additive gene effects, the expected gain would be low, but if they are due to additive gene effects, a high genetic advance may be expected. Genetic gain gives an indication of expected genetic progress for a particular trait under suitable selection pressure. In the present study, number of pods per plant (85.50) and number of primary branches per plant (59.41) noted high genetic advance (Table 2). Highest genetic advance for number of pods per plant was observed by Bhadarkar (1999), Agawal *et al.*(2000), Karnwal and Singh (2009), Aditya*et al.* (2011) and Bhat and Basavaraja (2011); and for number of primary branches per plant by Rajarathinam*et al.* (1996) and Bhandarkar (1999). Low genetic advance was observed for oil content (0.71) and protein content (2.28) under the present study. Similar results were reported by Ramteke*et al.* (2010).

The magnitude of genetic advance as per cent of mean was observed to be high (>20%) for number of pods per plant, number of primary branches per plant, number of clusters per plant, plant height, biological yield per plant and harvest index and moderate (10-20%) for seed yield per plant, number of seeds per pod and low (<10%) for 100-seed weight, number of pods per cluster, days to 50% flowering, protein content and oil content (Table 2).Robison *et al.* (1966) suggested that the heritability and genetic advance when considered together would be more reliable and useful in predicting the resultant effects of selection. Rapid progress in selection can be achieved when high heritability is accompanied with high genetic advance, which forms the most reliable index of selection (Burton, 1952). In the present study, high estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for 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 (Panse, 1957).High estimates of heritability with moderate genetic advance were observed for seed yield per plant, which revealed the presence of non-additive gene action and influence of environment in the expression of seed yield and thus, the selection would be less effective. For the characters like, days to 50 per cent flowering, days to maturity, number of pods per cluster, oil content and protein content, low heritability along with low expected genetic advance were recorded, which indicated marked influence of the environment for expression 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 primary branches per plant, number of clusters per plant, number of pods per plant, biological yield per plant and harvest index, 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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Table 1: Analysis of variance for fifteen characters in seventy genotypes of soybean

Source	D. f.	Days to 50 Per Cent Flowering	Days to Maturity	Plant Height (cm)	Number of Primary Branches Per Plant	Number of Clusters Per Plant	Number of Pods Per Plant	Number of Pods Per Cluster	Pod Length (cm)
Replications	2	4.93	8.60	13.13	0.93	4.38	2.52	4.97	1.37
Genotypes	69	4.68**	5.55*	113.74**	5.12**	12.40**	323.08**	0.22*	0.12**
Error	138	2.13	3.88	7.62	0.51	1.80	2.67	0.15	0.04

Source	D. f.	Number of Seeds Per Pod	Seed Yield Per Plant (g)	100-Seed Weight (g)	Biological Yield Per Plant (g)	Harvest Index (%)	Oil Content (%)	Protein Content (%)
Replications	2	0.09	9.34	2.24	38.92	0.37	0.03	18.53
Genotypes	69	0.38**	44.55**	1.44**	394.65**	89.36**	0.42	9.39*
Error	138	0.09	3.18	0.78	13.24	1.67	0.32	6.64

, ** Significant at 5% and 1% levels, respectively

Table 2: Range of variation, mean, Phenotypic (PCV) and genotypic (GCV)coefficient of variation, heritability (h^2) in Broad sense, genetic advance and genetic advance (GA) as percentage of mean for fifteen different characters of Soybean genotypes

Characters	Range of Variation	Mean	Phenotypic Coefficient of Variation (%)	Genotypic Coefficient of Variation (%)	Heritability in Broad Sense h^2 (%)	Genetic Advance	Genetic Advance (GA) as Percentage of Mean
Days to 50 Per Cent Flowering	37.66-44.00	40.09	4.31	2.30	28.50	01.01	2.51
Days to Maturity	63.00-68.66	66.06	3.19	1.12	12.50	00.54	0.81
Plant Height (cm)	18.93-50.53	30.40	21.56	19.56	82.30	11.11	36.54
Number of Primary Branches/Plant	3.13-8.60	4.76	30.10	26.02	74.80	02.20	46.21
Number of Clusters / Plant	5.63-14.70	8.49	27.19	22.11	66.20	03.15	37.10
Number of Pods /Plant	16.10-64.10	31.51	33.19	32.79	97.60	21.02	66.70
Number of Pods / Cluster	2.70-4.23	3.28	12.80	4.46	12.10	00.10	3.04
Pod Length (cm)	2.00-3.23	2.83	9.27	5.93	41.10	00.22	7.77
Number of Seeds / Pod	2.00-3.23	2.29	19.02	13.56	50.80	00.45	19.65
Seed Yield Per Plant (g)	23.37-43.53	29.96	13.74	12.39	81.20	06.80	22.69
100-Seed Weight(g)	8.60-11.89	10.35	9.70	4.53	21.80	00.45	4.34
Biological Yield / Plant (g)	52.66-103.33	75.72	15.64	14.89	90.60	22.10	29.18
Harvest Index (%)	32.53-56.88	40.09	13.86	13.48	94.60	10.83	27.01
Oil Content (%)	19.45-21.50	20.29	2.94	0.89	09.20	00.11	0.54
Protein Content (%)	33.83-42.24	38.38	7.16	2.49	12.10	00.68	1.77

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