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ASSESSMENT OF EXISTING GENETIC VARIABILITY AND DIVERSITY IN SOYBEAN

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ABSTRACT

A study was conducted to assess the extent and pattern of genetic variability of soybean genotypes with respect to ten traits in forty soybean genotypes. The analysis of variances has shown that there was significant variation among the genotypes in all traits. The high heritability (>60%) was recorded for all traits. The multivariate analysis has resulted in formation of twelve clusters. Out of twelve clusters formed, cluster 1 was the largest with twenty genotypes followed by cluster 2 and 4 with five genotypes. The highest genetic distance was recorded between cluster 4 and 6 (361.76), while lowest genetic distances noticed between cluster 8 and 10 (36.72). Cluster 8 included one genotype with highest mean for number of primary branches per plant (4.40), number of pods per plant (118.53), number of seeds per pod (3.40). Cluster 9 highest mean for 100 seed weight (18.40g), protein content (40.93%) and seed yield per plant (23.96g). Thus, on the basis of present finding there is a possibility of simultaneously improving the protein content as well as the oil content with seed yield per plant of the genotypes through inter crossing between genotypes *viz.*, JS-79214, JS-335, EC-457159, IC-15545, EC-457159, DS-228, M-108, EC-457211, EC-457159, and EC-343307. Among ten traits studied number of pods per plant (35.90%) contributed highest towards the genetic divergence followed by plant height (20.13%) and seed yield per plant (20.00%).

Keywords: Genetic Variability, Genetic Diversity, Soybean, D^2 value**.**

INTRODUCTION

Soybean, *Glycine max* (L.) Merrill 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 yields more usable protein per hectare than any other cultivated crop at least three times more than rice, wheat or maize. Soya proteins are higher in lysine, tryptophan than the common cereal grains. The biological value of the soybean protein is as good as a meat and fish protein. Soybean has become a major oilseed crop in India next to groundnut (*Arachis hypogea)* and Indian mustard (*Brassica juncea* (L.) Czern).

Genetic variation among traits is important for breeding and in selecting desirable types. Knowledge of diversity patterns will allow breeders to better understand the evolutionary relationships among accessions, to sample germplasm in a more systematic fashion and to develop strategies to incorporate useful diversity in their breeding programs (Bretting &

Widrlechner, 1995). Introgression of new genetic diversity through hybridization with introduced germplasm is one way to increase genetic variation in breeding populations, the base upon which gain from selection depends (Guedira *et al*., 2000). Sandoval *et al*., (1997) have shown that genetic variation for seed yield and other agronomic traits in soybean populations derived from crosses among elite lines can be limited by a lack of genetic diversity.

Therefore, much need to be done to utilize natural variation that might exist among genotypes for protein content as well as oil content with seed yield per plant. Assessing the genetic diversity and relation among soybean genotypes based on their morphological traits, oil and protein content is thus prerequisite which may help in identifying important genotypes and selection criteria for improvement of soybean. Therefore, this study was executed with the objective of assessing the extent and pattern of genetic variability of soybean genotypes of diverse agro climatic region of the country and some exotic collection.

MATERIAL AND METHOD

The material used for the present investigation comprised of forty genotypes, received from the Soybean Breeder, Agriculture Research Station Digraj, District- Sangli (MPKV, Rahuri). The experiment was carried out using Randomized Block Design with three replication at Botany Section, College of Agriculture, Kolhapur (Maharashtra) during *kharif* 2011. Each genotype was grown in a single row of 5 m length with a spacing of 45 cm between rows and 10 cm within row. All recommended agronomic practices were followed to raise good crop. Ten plants were tagged at random in each replication for find out viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), protein content (%), oil content(%) and seed yield per plant (g). Data were collected on protein content (%) and oil content (%) determined using Nuclear Magnetic Resonance Spectrometry (NMRS).

Analysis of variance was performed following the standard procedures described by Panse and Sukhatme (1995). The phenotypic and genotypic coefficients of variability were computed according to the method suggested by Burton (1952). Heritability (broad sense) and genetic advance were estimated as per Johnson *et al*. (1955a). Multivariate analysis such as clusters and principal components analysis of the genotypes values computed as per Tocher's method (Rao, 1952). Genetic distance between clusters was calculated using the generalized Mahalanobis D^2 statistics.

RESULT AND DISCUSSION

The analysis of variance has shown that there was significant variation among the genotypes in all traits. This indicates that existence of considerable genetic variability for selection and breeding. Means and range of traits of the genotypes are presented in Table 1. The estimates of genetic variability (table 1) exhibited the highest GCV for seed yield per plant (27.68). The GCV was medium for days to 50% flowering (10.54), plant height (15.33), number of primary branches per plant (11.34), number of pods per plant (18.69), number of seeds per pod (13.93), and 100-seed weight (18.36). The differences between GCV and PCV were very low for all characters, was mostly due to genetic factors (Datt Shiv *et al.* 2011). The presence of high genetic variability is an indication of good scope for their improvement through hybridization followed by selection.

High heritability recorded almost all traits. High heritability coupled with high genetic advance as per cent of mean was recorded for days to 50% flowering, plant height, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant revealing the influence of additive gene action for these traits. Hence the improvement of these traits can made through direct phenotypic selection. High heritability coupled with low genetic advance as per cent mean recorded for days to maturity, protein content (%) and oil content (%), indicating the effect of non additive gene action in crop improvement like heterosis breeding may be beneficial.

In any crop improvement venture, genetically distant parents are needed for crossing programs. This is to create the required genetic diversity between genotypes in terms of gene frequencies which may result of heterotic group and transgressive sergeants. Clustering produced clear grouping of the forty genotypes into twelve clusters (Table 2). Kayande and Patil (2009) reported that high divergence between the clusters of 50 genotypes which were grouped in to ten clusters. Similarly, Shadakshari *et al.* (2011) reported that the existence of genetic diversity among 50 soybean genotypes which were grouped into ten clusters.

Table 1. Range and estimates of genetic parameters for different ten traits of soybean

Sr. No.	Characters	Mean	Range	GCV	PCV	h^2 (BS)	GA	GA as % Mean
1	Days to 50% flowering	45.97	37.66-56.33	10.54	11.14	89.61	09.46	20.57
2	Days to maturity	97.30	87.00-106.66	04.80	05.09	88.92	09.08	09.33
3	Plant height (cm)	75.80	51.60-118.67	15.33	15.67	95.74	23.43	30.91
4	No. of primary branches Per plant	03.76	02.63-04.60	11.34	14.13	64.51	00.71	18.78
5	No. of pods per plant	83.71	53.53-118.53	18.69	18.95	97.25	31.79	37.97
6	No. of seeds per pod	02.97	02.00-03.60	13.93	15.88	77.01	00.75	25.20
7	100 seeds weight (g)	13.93	08.03-18.40	18.36	19.51	88.55	04.96	35.59
8	Protein content (%)	36.48	32.74-40.92	05.08	05.70	79.30	03.40	09.32
9	Oil content (%)	19.27	15.97-21.06	05.55	06.88	65.22	01.78	09.25
10	Seed yield per plant (g)	15.03	08.47-23.96	27.68	028.47	94.47	08.33	55.41

GCV: genetic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2 (BS): heritability in broad sense, GA: genetic advance

Table 2. Distribution of forty soybean genotypes in different clusters

Cluster Number	Total no. of genotypes in each cluster	Genotypes included in the cluster
1	20	EC-572009, EC-456660, EC-389154, EC-481518, EC-528628, KB-17, Ge-2263, EC-396068, KS-112, EC-391332, EC-396057, EC-396067, EC-391346, EC-487282, MACS-450, P-205, KS-103, EC-468600, EC-547464, EC-456447
2	5	EC-391012, EC-102612, VP-1147, EC-481515, JS-811625
3	1	EC-457211
4	5	EC-473111, EC-457172, EC-389148, EC481369, MAUS-71
5	1	EC-468597
6	2	IC-15545, EC-343307
7	1	EC-34117
8	1	JS-79214
9	1	EC-457159
10	1	JS-335
11	1	DS-228
12	1	M-108

Table-3. Pair wise generalized squared distance (D^2) among forty genotypes of soybean in twelve clusters based on their morphological traits.

Cluster Distances	C 1	C 2	C 3	C 4	C 5	C 6	C 7	C 8	C 9	C 10	C 11	C 12
C 1	**27.14**	60.22	38.56	77.09	46.51	158.5	82.08	111.09	79.60	107.33	99.80	88.17
C 2		**31.25**	58.37	158.00	139	116.42	85.75	56.55	54.61	83.36	70.56	48.16
C 3			**0**	132.48	59.91	104.45	115.13	80.46	97.81	95.06	57.30	97.02
C 4				**36.24**	76.39	361.76	118.16	251.54	162.56	217.86	265.36	152.77
C 5					**0**	231.34	169.00	177.42	167.44	143.28	139.47	163.07
C 6						**29.38**	186.32	124.32	138.06	205.63	85.75	224.1
C 7							**0**	206.78	83.72	252.81	204.2	153.02
C 8								**0**	86.49	36.72	37.45	71.40
C 9									**0**	108.37	122.1	80.00
C 10										**0**	51.12	52.13
C 11											**0**	112.57
C 12												**0**

Underline figures indicate intra cluster D^2 values, C-Cluster

C1 was the largest with twenty genotypes followed by C2 and C4 with five genotypes, C6 with two genotypes, and C3, C5, C7, C8, C9, C10, C11 and C12 monogenotypic. The individuals within any one cluster are more closely related than are individuals in different clusters. Among twelve clusters studied important traits contributing to the divergence was number of pod per plant (35.90%) followed by plant height (20.13%) and seed yield per plant (20.00%), whereas number of primary branches per plant (0.26%) showed lowest contribution towards the divergence (Table 5). The pair wise generalized D^2 distance among the clusters is presented in Table 3. Genetic distances among most clusters were significant. The highest genetic distance was recorded between C4 and C6 (361.76) followed by C4 and C11 (265.36), C7 and C10 (252.81), C4 and C8 (251.54), C5 and C6 (231.34), C7 and C11 (204.20), C6 and C7 (186.32), C5 and C8 (177.42) were highly significant from which parents may be selected for crossing in order to obtain genetic recombination and transgressive segregants in the subsequent generation. However, it is also valuable considering genotypes with in cluster with respect to a trait of interest as suggested by Chahal and Gosal (2002) and Keneni *et al.* (2005). Genetic distances between C8 and C10 (36.72) followed by C8 and C11 (37.45), C1 and C3 (38.56) and C1 and C5 (46.51) were non-significant, indicating close relationship among the genotypes (Shadakshari *et al.* 2011).

Pattern of distribution of genotypes in different clusters showed no correspondence between genetic diversity and geographic origin. The grouping of genotypes of the same origin in the same cluster may be result of their similar genetic background (KS-103, KS-112, EC-572009 and EC-456660 were same origin group in C1). On the other hand, there are also genotypes with same geographical origin but grouped in different clusters (JS-811625 in C2, JS-79214 in C8, JS-335 in C10 were same origin but group in different cluster) in which differential selection criteria, genetic drift and adaptation to different agro-climatic conditions might be the cause. Paradoxically, genotypes with different geographical origin were grouped in same cluster (EC-468600, MACS-450, KS-103, KB-17, and P-205 were group in C1, EC-391012, VP-1147 and JS-811625 were in C2 and CE-473111 and MAUS-71 were different origin but grouped in cluster 2) in which case

Table 4. Intra class average values for ten traits of the twelve clusters of soybean genotypes.

Cluster no.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight (g)	Protein content (%)	oil content (%)	Seed yield/ plant (g)
C 1	44.50	95.97	77.12	3.84	80.88	2.94	13.62	36.21	19.31	13.50
C 2	52.80	103.47	72.62	3.93	91.84	3.37	15.95	36.19	19.58	19.03
C 3	46.67	100.33	84.23	3.30	92.97	2.17	11.50	35.00	20.20	13.33
C 4	39.93	92.00	62.84	3.56	60.17	2.80	10.51	35.99	18.11	11.25
C 5	37.67	87.00	79.70	3.60	83.60	2.87	10.46	35.83	19.37	08.47
C 6	52.00	103.33	110.80	3.93	104.85	3.08	17.92	35.48	19.12	20.74
C 7	51.67	104.33	83.10	3.67	55.87	3.20	15.18	38.47	19.60	17.51
C 8	49.00	100.33	70.93	4.40	118.53	3.40	12.29	38.69	19.22	23.13
C 9	47.00	96.00	79.20	3.40	83.33	2.17	18.40	40.93	18.97	23.96
C 10	45.33	97.33	59.43	3.60	115.33	2.87	16.27	39.43	20.10	17.19
C 11	50.67	101.67	82.78	3.83	115.00	3.27	15.04	40.29	20.17	15.43
C 12	53.00	101.67	51.60	2.63	96.38	3.17	17.24	34.47	20.23	19.17

synchronization of selection differential for different traits in different areas might have been occurred. The aforementioned phenomena have also reported by Das *et al. (*2001) and Malik *et al.* (2009).

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in intra class average for different traits (Table 4). High seed yield per plant (23.96g) with 100 seed weight (18.40g) and protein content (40.93%) were showed by C9. Other hand C5 had low seed yield per plant (08.47g) with early for days to 50% flowering (37.67g) and days to maturity (87). The highest oil content (20.23%) in their seed was revealed in C12, followed by C3 (20.20%) and C11 (20.17%), lowest showed by C4 (18.11%). The genotype in C8 was recorded highest number of primary branches per plant (4.40), number of pod per plant (118.53) and number of seeds per pod (3.40). The genotypes in C6 were highest plant height (110.80cm).

Clustering of genotypes into groups was mainly attributed by cumulative effects of individual traits. In general, this study indicate that there is a possibility of simultaneously improving the protein content as well as the oil content with seed yield per plant of the genotypes through further breeding endeavor such as inter crossing between genotypes *viz.*, JS-79214, JS-335, EC-457159, IC-15545, EC-457159, DS-228, M-108, EC-457211, EC-457159, and EC-343307 were selected as per the inter-cluster distance, cluster mean and per se performance of genotypes and divergent cluster combination observed in the present study. The present investigation also revealed that diverse geographic origins of the genotypes could not necessarily be an index of variation and the factors other than geographic diversity such as genetic drift, selection pressure and environment may be responsible for discrepancy of genotypes.

Table 5. Per cent contributions of traits into total divergence.

Sr. No.	Characters	Times ranked 1St	Percent contribution
1	Days to 50% flowering	23	2.95
2	Days to maturity	33	4.23
3	Plant height (cm)	157	20.13
4	Number of primary branches per plant	02	0.26
5	Number of pods per plant	280	35.90
6	Number of seeds per pod	34	4.36
7	100 seed weight (g)	48	6.15
8	Protein content (%)	28	3.59
9	Oil content (%)	19	2.44
10	Seed yield per plant (g)	156	20.00
	Total	**780**	**100**

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