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DIVERSITY IN SOYBEAN (*Glycine max*) ACCESSIONS BASED ON MORPHOLOGICAL CHARACTERIZATION AND SEED LONGEVITY CHARACTERISTICS

S.M. Naik[1], K. Madhusudan[2], B.N. Motagi[1,3], H.L. Nadaf[1], Thimmaraju[1]
[1]Uni versity of Agri cul ture Sciences, Dharwad 580005, [2]Col lege of Ag ricul ture ZARS, VC Farm Mandya 571405 [3]ICRISAT, Kano, PMB 3491, Nigeria. Correspondent author : shilpa0643@gmail.com

ABSTRACT

Soybean (*Glycine max* (L.) Merrill) is a significant and cheap source of protein (40%) and soy vegetable oil (20%) is another important product of processing the soybean crop for both human consumption and industrial application. Present study was conducted with the objectives to study the genetic diversity for various morphological traits and seed longevity in 225 accessions of soybean. Clustering pattern of 225 genotypes was grouped into 8 clusters and 6 clusters with 62 genotypes in concern to seed longevity. High range of intra clusters (0-314.62) and inter clusters (324.61-3514.91) distances showed high diversity among the genotypes for various characters. Seed yield per hectare contributed maximum of (23.6%) towards total genetic divergence. Cluster V showed minimum days to maturity with high test weight (13.98g) and cluster VI found to be included genotypes with high oil (19.20%) and seed yield per hectare (4294.44kg). The cluster VIII involved highest number of pods per plant (71.52) with high seed yield per hectare with less reduction in germination (24.19%) in other words with high seed longevity.

Key words : *Di versity, germination, soybean, seed longevity.*

Soybean [*Glycine max* (L.) Merr.]have long been recognized as a plant food product that is relatively high in protein, when compared with other crop plants, hence called as 'meat of the field'. Soybean protein supplies all the essential amino acids, having cardio friendly oil which fulfills 30 percent of world vegetable oil requirement and also has many therapeutic components, like lactose-free fatty acids, antioxidants and folic acid, vitamin B complex (1). Due to the multipurpose nature of this crop, its contribution to industrial, agricultural and medicinal sectors is significantly increasing. Rapid increase of population together with gradual reduction of cultivable land has posed greater challenges to human health in India and other Asian countries.

Quality seed is the prime factor for crop productivity. Seed quality, as measured by its vigour and viability, plays a vital role in establishment of seedling as well as higher crop yields. A major cause of low vigour has been identified as seed ageing. In recent years, soybean has become an important oilseed crop in the world. However, non-availability of good quality seed remains one of the major constraints of soybean cultivation. Soybean seed germination and vigour potential is short lived as compared to other grain crops and it is often reduced prior to planting time (2). Its seed is rapidly deteriorated by high temperature and high relative humidity during storage.

There are thousands of breeding lines and hundreds of elite cultivars developed yearly in the soybean hybridization programme over the world. Development of these breeding lines increased genetic uniformity in the frame of species. Therefore, the genetic basis of these released varietiesis rather narrow. Generation of new and improved varieties can be enhanced by new sources of genetic variation; therefore criteria for parental stock selection need to be considered not only by agronomic value, but also from the point of view of their genetic dissimilarity. That is why the estimation of genetic variation is a very important task not only for population genetics but also for plant breeders.

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. 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 (3).

Keeping these aspects in view, the present study in soybean was conducted with the objectives to study the genetic diversity for various morphological traits and seed longevity in 225 experimental materials which include varieties and accessions of soybean.

MATERIALS AND METHODS

The experimental material used comprised of two hundred and twenty five genotypes ofsoybean including indigenous and exotic collections, released varieties in India and mutant lines of varieties JS-335 and KHSb-2, collected from Nucleus Seed Production/Breeder Seed Production Unit, UAS Dharwad, which are presently being maintained at All India Co-ordinated Research Project on Soybean, University of Agricultural Sciences, Dharwad.

The ex per iment was laid out in Lattice Design (15×15) with two replications. The recommended package of practices was followed for raising ahealthy crop.

The seed longevity was measured in terms of percent reduction in germination before and after accelerated ageing. Germination test was conducted by adopting between paper method. Seeds were incubated in Walk-in germination room in growth cabinets. The temperature of 25 ± 1°C and relative humidity (RH) of 95% was maintained. Germination (%) was recorded on the basis of normal seedlings (ISTA 1993).The seed material was subjected to accelerated ageing by controlled deterioration (CD) test. The chamber was sterilized with alcohol to prevent the fungal contamination. Individual genotypes were taken in separate petri plates, incubated in temperature and relative humidity (RH) control chamber at 40°C temperature and 94 to 100% RH for 72 hours continuously (4).

Seed coat permeability and electric conductivity of seed leachates were used as attributing traits for the seed longevity as they are negatively correlated (5). The permeability of seed coat was measured as amount of water absorbed per unit of seed weight and expressed as percent water absorbed. For this purpose, two replicates of 25 seeds were weighed and then soaked in 50 ml distilled water for 1hr. Excess of water was drained out and thoroughly cleaned with blotting paper and weighed immediately. The rate of seed coat permeability was calculated as per cent water absorbed (4). Five grams of seeds were weighed in two replications from each selected genotypes and soaked in 50 ml distilled water in a beaker and kept at 25±1ºC temperature. 50 ml of distilled water was used as control. After 24 hours of soaking, the leachates were stirred using a glass rod, poured into another beaker and the volume was made up to 25 ml by adding distilled water. The electrical conductivity of the leachates was measured using digital conductivity meter and the mean of two replicates were expressed in dS/m
(4).

The characters studied were days to 50 per cent flowering, plant height, number of branches per plant, days to maturity, number of pods per plant, number of seeds per pod, seed test weight, protein content, oil content, seed yield per plant and seed yield per hectare. For seed longevity study, seed germination test was carried out before and after the accelerated ageing test and per cent reduction in germination was recorded as a measure of seed longevity along with seed coat permeability and electrical conductivity. (6) D^2-statisticsa multivariate analysis was used for assessing of the genetic divergence between genotypes.

RESULTS AND DISCUSSION

Improvement of yield, oil and protein content in soybean is attributed to increased use of genetically diverse parents in breeding programme. However, in case of Indian soybean varieties, a narrow genetic base has been observed perhaps due to use of same parents for evolving new varieties. Likely since seed longevity is a major problem encountered by soybean growers in tropical and sub-tropical countries like India. Thus development of varieties and hybrids with high seed longevity is very much necessary. Hence, knowledge of genetic divergence in the available cultivars is of immense importance for selecting the parents to be used in hybridization programme for obtaining desirable genetic recombination for yield as well as seed longevity.

A clear understanding of the extent of variability prevalent for each of the character in the germplasm collection would just imply the scope for improving the characters studied through selection. But, the success of any crop improvement programmes mainly depends on amount of diversity available in the crop. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity.In the present investigation, 225 soybean genotypes including varieties released for cultivation in different parts of India, some exotic lines and mutants were considered for the assessment of nature of genetic diversity considering 12 quantitative traits by adopting (6) concept of generalized distance (D^2) also genetic diversity analysis was carried out for some selected 62 genotypes for the study of seed longevity by adopting the same method.

The genotypes used in the study representing diverse agro-climatic conditions were distributed at random among the clusters formed based on their genetic distance. The genotypes belonging to diverse ecological regions clustered together, while those of same region entered separate groups. These findings are similar to the reports of (7). The absence of relationship between genetic diversity and geographical origin suggests a similarity in their genetic constitution, free exchange of breeding material over places (8) or due to unidirectional selection practiced by breeders of different locations. Similar results have been reported by (8).

Clustering pattern of entries : Clustering pattern of two twenty five genotypes were grouped into 8 clusters. Among 8 clusters, cluster III was biggest with 74 genotypes followed by cluster I with 56 genotypes, cluster IV comprises 35 genotypes, cluster V contains 25 genotypes, cluster II contains 22 genotypes, cluster VII contains 7 genotypes and cluster VIII contains 5 genotypes. Cluster IV was solitary containing single

Table-1 : Average intra and inter cluster D^2 values of 225 soybean genotypes for agronomic character.

	I	II	III	IV	V	VI	VII	VIII
I	220.06	1007.14	564.93	1112.07	514.1	1326.46	1939.64	1600.03
II		203.58	1519.01	2085.41	532.81	360.79	2918.38	640.97
III			232.51	616.08	1016.94	1843.07	1428.61	2114.46
IV				238.02	1581.16	2411.94	874.95	2681.86
V					139.92	842.42	2413.96	1120.84
VI						0.00	3246.41	324.61
VII							314.62	3514.91
VIII								296.7

Table-2 : The mean values of twelve characters in 8 clusters of 225 soybean genotypes.

Clusters	Days to 50%f lowering	Plant height (cm)	No. of branches	Days to maturity	No. of pod per plant	No. of seed per pod	Test weight (g)	Protein content (%)	Oil content (%)	Seed yield per plant (g)	Seed yield (kg/ha)	Reduction in germination (%)
I	42.25	45.16	3.82	88.28	56.19	2.44	12.72	39.52	17.74	16.02	2977.08	45.81
II	43.25	45.57	4.44	88.80	70.3	2.47	12.39	39.76	17.26	20.91	3962.25	47.00
III	42.22	44.49	3.56	87.78	49.11	2.45	12.84	39.08	18.01	13.26	2458.78	42.93
IV	42.56	42.65	3.46	88.27	44.74	2.48	11.70	39.59	17.57	9.97	1888.41	40.22
V	42.08	43.15	4.02	87.22	58.18	2.52	13.98	39.18	17.89	18.22	3457.78	39.80
VI	42.50	48.79	3.90	89.00	70.50	2.45	13.00	37.30	19.20	24.40	4294.44	46.15
VII	45.93	66.58	3.71	90.64	44.79	2.54	9.93	40.91	16.64	8.86	1054.76	45.36
VIII	42.20	43.42	4.02	87.90	71.52	2.38	13.60	39.20	17.75	23.56	3116.11	24.19

*Values with bold letters indicate intra cluster distance.

Table-3 : The mean values of twelve characters in 8 clusters in soybean genotypes.

Clusters	Protein (%)	Oil (%)	Moisture (%)	Test weight (g)	Initial germination (%)	SCP (% water absorbed)	Electrical conductivity d/Sm)	Reduction in germination (%)	Seed yield (kg/ha)
I	39.22	18.03	8.99	12.48	88.29	56.22	1.47	27.82	2134.26
II	39.32	18.02	8.82	12.16	83.68	47.08	1.37	28.01	1422.96
III	39.03	18.11	8.92	11.93	88.79	50.05	1.38	35.85	2755.75
IV	40.02	17.72	8.72	11.67	85	52.41	1.66	24.19	4081.48
V	39.3	17.8	8.55	6.00	98	9.96	0.42	9.18	1005.56
VI	38.1	17.25	8.8	12.00	87	28.93	0.73	11.54	3344.44

genotype. The check JS-335 and Birsa soy 1 represented cluster III and check JS 93-05 represented cluster IV.

Intra and inter cluster D^2 values : The intra cluster distances ranged from 0 (cluster VI), which is solitary cluster to 314.62 (cluster VII) indicating high diversity. The inter cluster D^2 values exhibited a highest value of 3514.91 (cluster VII and VIII) and lowest value of 324.61 (cluster VI and VIII) suggesting large amount of diversity among genotypes (Table-1). Thus considerable variability prevailed among the genotypes within these clusters may be helpful to realize heterosis or improvement of traits through simple selection.

Based on inter cluster D^2 values, the genotypes belonging to cluster VII and VIII appeared to be more diverse (3514.91) followed by cluster VII and II (2918.38), suggesting that selection of genotypes from these divergent groups would yield higher magnitude of heterosis for the characters concerned. Among the clusters, Cluster VIII has been the most diverse as measured from its inter cluster distances with other clusters which was maximum, while, the cluster VII found to be the nearest with number of other clusters. Selection of genotypes with short inter cluster distance would not be desirable to reap higher yield benefits and this is attributed to smaller allelic frequency difference between these genotypes, which results in lower heterotic progenies.

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank. It has been observed that yield per hectare contributed maximum of 23.6 per cent towards total genetic divergence followed by per cent reduction in germination (seed longevity) and plant height. The character Days to 50 per cent flowering

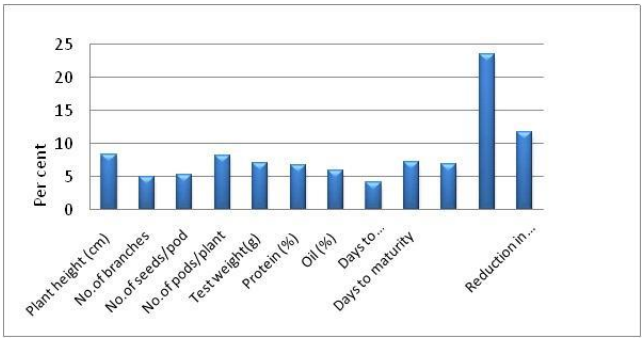

Fig.-1 : Percent contribution of agronomic characters to the total divergence.

(4.12%) was the least contributor towards total divergence (Fig.-1).

Cluster mean analysis : Analysis of cluster means indicates diversity demonstrated by different clusters for a character. Based on the means, it is possible to know the character influencing divergence and the variation observed in cluster mean also points to the degree of variability (Table-2).

There was no much difference for the mean value of character days to 50 per cent flowering. However, genotypes included in the cluster V showed minimum days to maturity (87.22) followed by VIII. Genotypes in cluster VII comprised of late flowering types. The genotypes of cluster VII were tall followed by cluster VI, while those of cluster IV were dwarf, while remaining clusters had intermediate height. Number of branches per plant was highest for the cluster II (4.44) followed by cluster III. The cluster V included genotypes required lesser days to maturity as well as genotypes with high test weight (13.98g). The cluster VII includes late maturing genotypes with highest number of seed per pod and high protein containing genotypes. The cluster VII also include genotypes having low test weight, low oil content and low yielding ability. And the remaining clusters showed more or less intermediate mean value for the above said characters.

Cluster VI include the genotypes having low protein content but with high oil content (19.20%) as well as high seed yielding genotypes (24.4g). The cluster VIII involved genotypes with less number of seed per pod, highest number of pods per plant (71.52). This cluster also comprised genotypes with high seed yield per hectare with less reduction in germination (24.19%) in other words with high seed longevity. But when considering individual genotypic mean value, the genotypes EC 4435 and EC 309552 having high yield and low seed longevity whereas genotype TGX 512-4E low yielding but having high seed longevity, hence these genotypes can be utilized in hybridization programme.

Genetic diversity for seed longevity and component traits : Sixty two genotypes were grouped into 6 clusters among these clusters, cluster I was biggest with 24 genotypes followed by cluster II with 19 genotypes, cluster III contains 14 genotypes and the cluster IV contains 3 genotypes. Cluster V and VI was solitary with single genotypes. The check JS 93-05 included in cluster I, whereas JS-335 and Birsa soy 1 represented cluster II.

Intra and inter cluster D^2 values : The intra cluster distances ranged from 0 (cluster V and VI), which is solitary clusters to 364.42 (cluster IV), followed by 320.63 (cluster II) indicating high diversity. The inter cluster D2 values exhibited a highest value of 3083.96 (cluster IV and V) and lowest value of 474.23 (cluster II and V) suggesting large amount of diversity among genotypes. Thus considerable variability prevailed among the genotypes within these clusters.

From the present investigation, it was clear that a highest difference among the genotypes within the same cluster was shown by cluster IV (3083.47) and V, followed by II and IV clusters (2675.96) comprising the most divergent genotypes. Cluster IV showed maximum inter cluster distance with six clusters. Therefore, it can be concluded that the genotypes present in these clusters can be utilized for successful hybridization programme in future. It has been observed that yield per hectare contributed maximum of 45.8 per cent towards total genetic divergence followed by per cent reduction in germination (seed longevity), seed coat permeability, electrical conductivity, initial germination and test weight. Protein content (2.04%) was the lowest contributor towards divergence.

Cluster mean analysis : Analysis of cluster means indicated substantial variation among clusters grouped according to D^2 analysis. Based on the range of means it is possible to know the characters influencing divergence (Table-3).The genotypes having highest protein content, low initial germination, high electrical conductivity and high yield per hectare was included in the cluster IV. The cluster V includes genotype with desirable characters like low moisture content, low test weight, high initial germination, low seed coat permeability, low electrical conductivity and most importantly with low per cent reduction in germination.

The cluster I included genotypes with highest moisture content, test weight and seed coat permeability. Whereas, the cluster III having genotypes with high oil content as well as genotypes with more per cent reduction in germination. The cluster VII involved genotypes with

low protein and oil content and also with genotypes good yielding ability.

CONCLUSION

Using Mahalanobis D^2 statistics, 225 genotypes were grouped into 8 clusters.Cluster VI was solitary containing single genotype1-28 formed a solitary cluster having high seed longevity with low yield, can be used as a donor parent in hybridization programme and some genotypes were genetically diverse and possess potential variation for economic traits and hence could be extensively evaluated for further exploitation in breeding programmes. The intra and inter cluster distance was maximum in the clusters formed the experimental genotypes. It is desirable to select accessions from clusters having high intercluster distance and also high seed yield as parents in the recombination breeding programmes.Similarly, for seed longevity sixty two genotypes were grouped into 6 clusters. Two clusters were solitary with single genotypes can be used as donor in the hybridization programme.

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