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GENETIC DIVERGENS STUDIES IN SOYBEN (*Glycine max* L. MERR.)

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ABSTRACT

The genetic divergence analysis indicated abundant genetic diversity among the 70 genotypes, which were grouped in as many as 11 clusters. Among the 11 clusters, cluster I was the biggest with 50 genotypes followed by cluster II with 8 genotypes and cluster VI with 4 genotypes. Remaining clusters were solitary with single genotype each. The clustering pattern did not show any relationship between geographic distribution and genetic divergence as genotypes from the same area scattered in different clusters and the genotypes of different areas were grouped in the same cluster. It has been observed that number of clusters per plant contributed maximum towards total genetic divergence followed by biological yield per plant and harvest index. The superior cluster with respect to seed yield per plant was cluster X, while for oil content and protein content it was XI and VII. Cluster XI was also superior for number primary branches per plant, number of pods per plant, number of clusters per plant and biological yield per plant. Therefore, the genotype included in this clusters could be utilized in crossing programmes to improve the yield and quality components in soybean.

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. It's considered as one of the important pulses and oilseed crops, because of high nutritional value and 43.2 per cent protein and 18-25 per cent edible oil contains.

The germplasm of soybean were introduced in India at large scale during mid seventies. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse genotypes with possible utility for specific utilization in breeding programme. A logical way to start any breeding programme for crop improvement is to survey the variation present in the germplasm. Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for purposeful hybridization (Mehta 1993). In breeding programme, progenies derived from diverse crosses which is selected based on genetic divergence analysis are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in advance generation (1) and promising heterotic effect may be observed in early generation. Therefore, this study was undertaken to identify suitable soybean parents having diverse characters through genetic divergence analysis.

MATERIALS AND METHODS

The experiment was conducted for genetic divergence on 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 (%) on five randomly selected plants in each entry and replication and their mean values were used for statistical analysis.

The genetic divergence was computed using (2) D^2 statistics among all possible combinations of 70 genotypes. Based on the genetic distance, all the genotypes were grouped into different clusters (3).

RESULTS AND DISCUSSION

The amount of diversity available in the crop decides the success of any crop improvement programme with

Table-1: Distribution of seventy soybean genotypes into different clusters

Sr. No.	Cluster	No. of Genotypes	Name of the genotypes
1	I	50	JS-26-188, MACS-124, MACS-308, J-482, BK-3, Gujarat Junagadh Soybean-3, Himso-1594, J-149, MACS-330, PK-942, JS-79-4-11, JS-79-298, PK-1024, JS-81-20, AGS-174, J-524, JS-84-1, JS-75-10, AGS-61, BR-8, JS(HS)-8612, JS-79-122, DS-531, MACS-229, JS(HS)-8604, JS-4, JS-80-21-R, JS-87-36, PB-1, JS-578, B-16, Cakerstymat, BL-1667, JS-81-12, DS- 7442, JS-81-1615, KDS-6, J-148, PK-1036, PK-764, PK-748, PK-1009, PK-865, PK-805, JS-79-205, IC (SH)-8733, JS-75-19-1, J-609, MACS-72, PK-824
2	II	8	PBN-104, PK-575, PK-743, PK-783, J-167, Himso-1549, JS-75-28-4, MACS-130
3	III	1	PK-805
4	IV	1	PK-771
5	V	1	DS-1
6	VI	4	MACS-321, MACS-66, MACS-34, MACS-311
7	VII	1	J-237
8	VIII	1	BK-12
9	IX	1	PK-960
10	X	1	DS-293
11	XI	1	JS(HS)-8609

Table-2 : Average inter and intra-cluster distance (D=2) values of seventy soybean genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	140.41	469.79	241.23	246.09	635.13	662.26	258.20	277.73	293.67	1364.37	1382.37
II		214.94	480.19	659.20	321.37	600.72	930.70	472.27	947.27	735.70	507.21
III			0.00	62.93	1010.01	955.89	418.05	509.93	601.87	1849.57	1521.67
IV				0.00	1200.26	1015.93	292.93	511.02	451.58	2109.35	1830.69
V					0.00	476.80	1155.81	447.30	959.06	223.62	361.40
VI						176.79	739.96	643.74	896.69	873.31	936.29
VII							0.00	515.35	238.91	2028.44	2158.77
VIII								0.00	199.57	875.16	992.75
IX									0.00	1640.77	1939.88
X										0.00	291.54
XI											0.00

manifold objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. For long term improvement programme, a large and diverse germplasm collection is an invaluable source of parental strains for hybridization and subsequent development of improved varieties. Accurate cultivar evaluation and ability to differentiate between cultivars in respect of genetic parameters associated with adaptedness in cultivated plants and their wild progenitors are critical to any breeding programme.

Improvement of yield, oil and protein content in the soybean attributed with increase in use of genetically diverse parents in the breeding programme. However, in the case of Indian soybean verities, a narrow genetic base has been observed. The use of same parents for evolving varieties has resulted in narrow genetic base. Plant breeders are always interested in assessing the genetic divergence among the varieties or advanced breeding materials available with them, so as to utilize them in directed breeding programmes, because genetically diverse parents are likely to produce high heterotic effects. (4) stated that distantly related parents within species, when utilized in cross breeding programme, are likely to produce a wide spectrum of variability. Hence, knowledge of genetic divergence in

Table-3: Cluster means for fifteen characters of seventeen soybean genotypes

Clusters	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of clusters per plant	Number of pods per cluster	Pod length (cm)
	1	2	3	4	5	6	7	8
I	40.08	66.03	30.63	4.67	27.59	7.93	3.27	2.84
II	39.92	65.79	28.66	4.95	44.78	9.79	3.36	2.74
III	38.00	65.33	23.86	4.13	24.87	7.27	3.60	2.77
IV	40.67	66.33	26.47	4.86	20.30	6.47	3.57	2.73
V	41.00	67.00	40.28	3.90	52.60	12.27	3.27	3.00
VI	40.58	66.67	33.06	5.27	43.18	9.02	3.34	2.81
VII	40.33	65.33	21.67	7.40	17.80	6.60	2.80	2.93
VIII	38.67	66.67	30.02	3.87	31.57	12.43	3.20	3.23
IX	40.00	65.00	33.10	4.93	21.50	10.90	3.67	2.90
X	40.67	67.00	28.61	3.33	63.10	13.33	2.87	2.83
XI	41.67	67.67	31.01	6.83	64.10	14.70	3.50	2.87
Mean	40.09	66.06	30.40	4.76	31.51	8.49	3.28	2.83
S.Em ±	0.84	1.13	1.59	0.41	0.94	0.77	0.22	0.11
C.V.%	3.64	2.98	9.08	15.12	5.18	15.81	12.00	7.11
	Percentage contribution of characters towards total divergence							
Number of times appearing first	2.00	1.00	111.00	56.00	6.00	931.00	42.00	8.00
Per cent contribution	0.08	0.04	4.60	2.32	0.25	38.55	1.74	0.33

Table-3: Contd….

Clusters	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 (%)
	9	10	11	12	13	14	15
I	2.34	28.97	10.37	74.04	39.43	20.30	38.51
II	2.15	31.08	10.01	86.95	35.74	20.32	38.32
III	3.23	28.07	10.49	85.53	32.78	19.89	37.48
IV	2.00	29.83	11.20	87.60	34.06	20.32	37.96
V	2.00	33.60	10.03	78.00	43.06	20.38	38.38
VI	2.17	29.09	10.40	53.67	54.22	20.26	36.46
VII	2.20	26.87	11.90	57.00	47.13	19.85	40.59
VIII	2.33	41.87	9.26	95.33	43.91	20.10	38.35
IX	2.00	40.50	11.51	86.03	47.09	20.05	37.47
X	2.40	43.53	10.71	95.67	45.50	20.56	39.74
I	2.00	40.00	9.18	103.33	38.71	20.63	39.01
Mean	2.29	29.96	10.35	75.72	40.09	20.29	38.38
SEm ±	0.17	1.03	0.51	2.10	0.74	0.32	1.48
C.V.%	13.34	5.95	8.58	4.80	3.22	2.80	6.71
	Percentage contribution of characters towards total divergence						
Number of times appearing first	23.00	55.00	169.00	719.00	288.00	3.00	1.00
Per cent contribution	0.95%	2.28%	7.00%	29.77%	11.93%	0.12%	0.04%

the available cultivars has an immense importance and in tune with immediate need in the selection of parents to be used in hybridization programme for obtaining desirable genetic recombination.

Mahalanobis D^2 statistic is a powerful tool used to quantify the degree of genetic divergence between the genotypes and relate clustering pattern with the geographic origin. The success and usefulness of multivariate technique in quantification of genetic diversity has been demonstrated by (5).

Seventy genotypes used in the present 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 (6).

The absence of relationship between genetic diversity and geographical origin suggests a similarity in their genetic constitution, free exchange of breeding material over places (7) or due to unidirectional selection practiced by breeders of different locations. Similar results have been reported by (7). To a plant breeder, single character is not of much importance, as the combined merit of number of desirable traits becomes more important, when breeder is concerned with a complex trait like seed yield. Thus, for improving the seed yield, selection of parents based on number of characters having quantitative divergence is required, which can be assessed by adopting D^2 statistic concept of generalized distance developed by (2).

In the present investigation, 70 genotypes of soybean were grouped into 11 cluster using Tocher's method (3). Among the 11 clusters, cluster I was the biggest with 50 genotypes followed by cluster II with 8 genotypes and cluster VI with 4 genotypes. Clusters III, IV, V, VII, VIII, IX, X and XI were solitary with single genotype each. The check line Gujarat Junagadh Soybean-3 represented in cluster I.

The intra cluster distances ranged from 0.00 (cluster III, IV, V, VII, VIII, IX, X and XI), which are solitary clusters to 214.94 (cluster II) indicating poor diversity. The inter cluster D^2 values exhibited a highest value of 2158.77 (cluster VIII and XI) and lowest value of 62.93 (cluster III and IV) suggesting only a little diversity among genotypes.

The maximum inter-cluster distance was found between clusters VII and XI (D=2158.77) followed by cluster IV and X (D=2109.35), VII and X (D=2028.44), IX and XI (D=1939.88), III and X (D=1849.57), IV and XI (D=1830.69), IX and X (D=1640.77), III and XI (D=1521.67), I and XI (D=1382.37) and I and X (D=1364.37). The minimum inter-cluster distance was observed between clusters III and IV (D=62.93).

From the present investigation, it was cleared that cluster VII comprising of J-237, cluster IV comprising PK-177, cluster IX comprising PK-960 are the most divergent clusters. Cluster VII showed maximum inter cluster distance with four clusters, whereas cluster IV was farthest with six clusters. Therefore, it can be concluded that the genotypes present in these clusters can be utilized for successful hybridization programme.

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 number of clusters per plant contributed maximum of 38.55 per cent towards total genetic divergence followed by biological yield per plant 29.77 per cent and harvest index 11.93 per cent. Thus, these three characters contributed 80.25 per cent of the total diversity. Hence, selecting divergent parents based on these three characters may be useful. Earlier worker also reported higher genetic diversity due to harvest index (8) and biological yield per plant (9). On the other hand, 100-seed weight (7.00), plant height (4.60), number of primary branches per plant (2.32), seed yield per plant (2.28) and number of pods per plant (1.74) were least responsible for contributing towards the total divergence. The character days to maturity and protein content (0.04) were the least contributor towards total genetic divergence.

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. The variation observed in cluster mean also points to the degree of variability.

The genotypes induced in the cluster III showed early flowering types followed by those in cluster VIII. Genotypes in cluster XI comprised of late flowering types. The genotypes of the cluster IX were early maturing types followed by those of cluster III and VII. The genotypes of cluster XI were late maturity types. The genotypes of cluster V were of tall stature followed by cluster IX and VI, while those of cluster VII were dwarf, while remaining clusters had intermediate height.

Number of primary branches per plant were highest in the cluster VII followed by cluster XI. Cluster X showed the least number of primary branches per plant. The genotypes comprising in the cluster XI showed highest number of pods per plant, whereas those comprising in the cluster VII recorded least number of pods per plant. Number of clusters per plant was maximum for genotypes grouped in the cluster XI and minimum in the cluster IV. Number of pods per cluster was maximum for genotypes grouped in the cluster IX and least for the cluster VII. The genotypes grouped in the cluster VIII possessed highest pod length, while those of cluster IV, recorded the pods shorter in length. Number of seeds per pod was maximum for genotypes in cluster X, but minimum values were observed for the clusters IV, V, IX and XI. The cluster means for seed yield per plant was maximum for the genotypes grouped in the cluster X followed by those of cluster VIII. The means for seed yield was minimum for the genotypes grouped in the cluster VII. The character, 100-seeds weight was maximum for genotypes of cluster VII, but minimum values were observed for the clusters XI and cluster VIII. The cluster means for biological yield per plant was maximum for the genotypes grouped in the cluster XI followed by those of cluster X and VII, while it was minimum for the genotypes grouped in the cluster VI. The genotypes grouped in the cluster VI possessed highest harvest index, while those of cluster III showed the lowest harvest index value.

Oil content was maximum in the cluster XI and minimum in cluster VII grouped of genotypes. Similarly, for protein content the cluster means were maximum for genotypes grouped in cluster VII and minimum in cluster IX.

The cluster XI had least mean values for number of seeds per pod, 100-seed weight and highest mean values for days to 50 per cent flowering, days to maturity, number primary branches per plant, number of pods per plant, number of clusters per plant, biological yield per plant and oil content. The genotype included in this cluster could be utilized in crossing programmes to enhance yield.

In the present study, it was observed that considerable amount of genetic diversity was present among the genotypes with respect to seed yield and yield components and quality traits, oil and protein content. The superior cluster with respect to seed yield per plant was cluster X, while for oil content and protein content it was XI and VII. Cluster XI was also superior for number primary branches per plant, number of pods per plant, number of clusters per plant and biological yield per plant. Therefore, the genotype included in this clusters could be utilized in crossing programmes to improve the yield and quality components in soybean.

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