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GENETIC DIVERGENCE STUDIES IN SOYBEAN (*GLYCINE MAX* (L.) MERRILL)

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ABSTRACT

Genetic divergence study of 64 genotypes of soybean for 11 traits led to their grouping into 11 clusters. Grouping of genotypes in different clusters was not related to their geographic origin, and genotypes from different geographic locations were grouped into one cluster while genotypes of the same geographic origin showed genetic diversity. The diversity among the genotypes, measured by intercluster distances, was adequate for improvement by hybridization and selection. Based on mean performance, genetic distance and clustering pattern, hybridization involving genotypes SDP (L), KB 83, KB 85, IC 16990 and AMSS 52 are likely to give desirable segregates. Based on the differences in cluster means, 100-grain weight, followed by plant height and pods/plant, were the major factors of differentiation among genotypes.

Key words: Soybean, genetic divergence.

MATERIALS AND METHODS

The materials for the present investigation comprised 31 Indian and 33 exotic soybean genotypes grown in randomised block design with three replications, each genotype raised in a single row of 6 m length at spacing 45 x 10 cm spacing. Observations were recorded on 20 random plants of each genotype per replication of 11 traits. Genetic divergence was estimated by Mahalanobis' D^2 statistics and the genotypes were grouped on the basis of minimum generalised distances using Tocher's method as described by Rao [1].

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the 64 genotypes for all the 11 characters. This indicated the existence of significant amount of variability

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among the genotypes for the characters studied. On the basis of D^2 analysis, the 64 genotypes were grouped into 11 clusters (Table 1). The maximum number of genotypes (33), were included in cluster II. Clusters I, III, VII and Vi had 8, 7, 4 and 3 genotypes, respectively, clusters IV, V and VIII had two genotypes each, and the remaining clusters IX, X and XI had one genotype each. The pattern of group constellations proved that geographical diversity need not necessarily be related to the genetic diversity. This was in line with the results obtained earlier in soybean [2, 3]. This means that geographic diversity, though important, may not be the only factor in determining genetic divergence. Genetic diversity is the outcome of several factors, including geographical diversification. Therefore, selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity.

The clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the free exchange of breeding materials from one place to another [4]. This may also be due to the fact that the unidirectional selection practised for a particular trait in several places produced similar

Table 1. Composition of clusters and origin of soybean genotypes

Cluster	Genotypes	Origin
I	EC 1807 (M)	Nepal
	PLSO-3, IC 24058	Madhya Pradesh
	15590	USA
	MACS 201	Maharashtra
	IC 2716	Kalimperi
	CO1, ADT 1	Tamil Nadu
II	UGM 30, EC 3294, EC 109545 (W), EC 100776, EC 95287, 95273, EC 25166, EC 18733, EC 109545-B, 101879	USA
	MACS 125, AMSS 49	Maharashtra
	EC 50084, EC 50082, AVRDC 401, EC 18755	Taiwan
	EC 14434, EC 95681, EC 2541	Australia
	ACC NO. 2004, ANAIKATTI	Tamil Nadu
	IC 15086	Meghalaya
	EC 18226, EC 18596	Nepal
	PBN 104	Parbhani
	EC 99990	New Guinea
	EC 26691	Italy
	PLSO-1	Madhya Pradesh
	KB 80, KB 8	Karnataka
	37656	South America
	IC 13006	West Bengal
	PK 634	Uttar Pradesh
III	JS 81-714, JS 81-303	Madhya Pradesh
	KB 79	Karnataka
	DS 295	New Delhi
	PK 472	Uttar Pradesh
	MACS 180	Maharashtra
	EC 18676	Taiwan
IV	KB 85, KB 83	Karnataka
V	KB 93, KB 78	Karnataka
VI	IC 13007	West Bengal
	EC 109548	USA
	ACC NO 1322	Tamil Nadu
VII	UGM 34	China
	EC 62384	Philippines
	94038	USA
	EC 14426	Australia
VIII	IC 16990	Madhya Pradesh
	AMSS 52	Maharashtra
IX	EC 95258	USA
X	EC 14390	Taiwan
XI	SDP (L)	USA

Table 2. Intra- (in bold) and intercluster D values in soybean

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**26.6**	47.6	73.88	132.91	66.69	43.87	36.12	54.32	32.05	84.91	47.16
II		**28.9**	55.25	101.38	39.67	75.02	45.29	41.20	39.39	55.21	40.59
III			**29.63**	72.33	38.21	93.88	83.31	73.77	55.29	36.71	70.71
IV				**17.24**	72.59	157.76	136.36	113.30	160.18	72.93	172.28
V					**16.24**	94.10	68.52	49.17	41.87	46.81	61.79
VI						**35.26**	57.25	82.79	54.99	110.62	67.59
VII							**28.56**	44.15	43.81	88.72	39.87
VIII								**22.94**	45.76	72.62	49.27
IX									**0**	66.40	49.62
X										**0**	77.44
XI											**0**

phenotypes which were aggregated in one cluster irrespective of their distant geographic origin [5]. On the other hand, many genotypes originating from one place were scattered over different clusters (Table 1). Such genetic diversity among the genotypes of common geographic origin could be due to factors like heterogeneity, genetic architecture of the

Table 3. Cluster mean values for different characters in soybean

Cluster	Days to flowering	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	Yield per plant (g)	100-grain weight (g)	Harvest index (%)	Protein content (%)	Oil content (%)
I	34.63	51.71	4.12	90.98	3.41	2.30	18.15	10.47	0.377	35.91	14.74
II	33.65	50.81	4.44	105.31	3.78	2.29	27.05	13.25	0.415	36.32	13.22
III	30.86	23.31	3.59	55.73	3.94	2.26	15.96	15.33	0.359	40.39	16.51
IV	32.17	23.75	2.52	46.55	4.49	2.19	15.30	20.79	0.329	38.71	15.10
V	34.15	48.87	4.22	65.24	4.03	2.62	23.40	15.52	0.306	40.52	14.92
VI	32.56	40.34	3.92	85.28	3.54	2.34	11.42	8.42	0.302	38.32	15.13
VII	34.75	65.30	4.95	121.52	3.72	2.44	29.59	10.57	0.415	38.89	12.83
VIII	31.84	80.45	6.38	101.70	4.12	2.25	24.80	12.88	0.330	39.34	16.02
IX	31.67	53.47	3.10	59.43	3.47	2.33	15.70	11.93	0.372	39.61	17.17
X	30.67	32.43	3.03	64.23	4.20	2.63	20.43	16.93	0.428	35.63	13.10
XI	34.00	46.03	4.70	161.00	3.87	2.17	31.70	11.53	0.423	45.08	17.00

populations, past history of selection, developmental traits, and degree of general combining ability [6].

The average intra- and intercluster D values are presented in Table 2. The generalised intracluster distances (D) ranged from 16.2 (cluster V) to 35.3 (cluster VI). The generalised intercluster distances ranged from 32.5 (between clusters I and IX) to 172.3 between clusters VI and IX). Based on the range of D values obtained in the present study, the rating of divergence was classified as low (below 50), moderate (50.1 to 100) and high (100). It is clear from the above rating that all the genotypes within each cluster were genetically closer since all the clusters had low (< 50) intracluster distances. The relative divergence of each cluster from other clusters (intercluster distance) indicated high order of divergence between clusters IV and XI, followed by clusters IV, and I, II, VI, VII, VIII and IX. Thus, hybridization between genotypes from these clusters should result in maximum hybrid vigour and highest number of useful segregates [2]. Hybridization between genotypes from highly divergent groups could even produce new and hitherto unknown gene combinations. Hybridization between genetically distant genotypes to generate promising breeding material has been suggested frequently [7].

The average cluster means for different characters (Table 3) show that the genotypes included in clusters X and III were early flowering. The genotype SDP (L), forming a separate cluster (XI), had maximum seed yield, maximum pods/plant, high harvest index, maximum protein, content and high oil content. Thus, this genotype holds great promise as a parent to obtain promising hybrids and create further variability for these characters. The genotypes of cluster IV had maximum pod length and 100-grain weight, and those in cluster VIII had maximum plant height and highest number of primary branches.

In addition to the general features of variation and divergence, this study also provides information on the characters that contributed maximum to the total divergence among genotypes (Table 4). The most

Table 4. Relative contribution of different characters towards genetic diversity

Parameter	Days to flowering	Plant height	Branches per plant	Pods per plant	Pod length	Seed per pod	Yield per plant	100-grain weight	Harvest index	Protein content	Oil content	Total
Frequency of occurence in first rank	2	363	13	368	1	1	50	1116	22	42	38	2016
Percentage	0.10	18.01	0.64	18.25	0.05	0.05	2.48	55.36	1.09	2.08	1.88	100.00

important trait causing maximum genetic divergence was 100-seed weight, and was responsible for differentiating the genotypes studied. Plant height and pods/plant were the next important traits responsible for the divergence recorded. Pod length and seeds/pod contributed minimum to the genetic divergence among the genotypes studied. Low variability for these traits in such a wide variety of genotypes may also suggest high degree of constancy and heritability of these traits.

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