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

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ABSTRACT

Fifty one genotypes of soybean (*Glycine max* (L.) Merrill.) collected from different geographic sources were analysed by D^2 analysis. All genotypes were grouped into ten different clusters. Genetic diversity was independent of geographic region.

Key words: Soybean (*Glycine max*), genetic diversity.

The development of new varieties is mainly governed by the magnitude of genetic variability in the base material and extent of variability for the desired characters [1]. Genetic variability and divergence is of greatest interest to the plant breeder as it plays a vital role in framing a successful breeding programme. The genetically diverse parents are likely to produce high heterotic effects and desirable segregates. The multivariate analysis (D^2) is a powerful tool to measure genetic divergence within a set of genotypes [2]. Considerable amount of variability in soybean for yield and its component characters among the 36 genotypes grouped into 12 groups [3] and among 58 genotypes grouped into seven groups [4] has been reported earlier. The present study based on fifty one genotypes is an attempt to ascertain the nature and magnitude of genetic diversity to identify suitable donors having wider genetic distance.

MATERIALS AND METHODS

Fifty one varieties of soybean collected from different sources (Table 1) were grown in four-row plots of 5.0 m length in randomized block design with two replications keeping spacing between and within rows 45 and 10 cm, respectively.

Five plants were randomly taken from the central two rows (excluding borders) from each treatment and replication to record observations on eight morphological and developmental characters (Table 3). The analysis of variance was carried out for all the characters individually. Multivariate analysis was done as per Mahalanobis [5] and clustering was done following the Tocher's Method [6].

RESULTS AND DISCUSSION

Genetic divergence in a population, especially in respect of the characters in which improvement is sought, is an indispensible prerequisite for successful crop improvement programme. The D^2 statistics has found favour as a tool for estimating genetic divergence which is the basis in choosing parents for hybridization in a breeding programme, progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability providing greater scope for isolating high yielding segregates in the succeeding generations.

The analysis of variance for each individual character showed highly significant differences among the genotypes for all the eight characters studied. The pooled divergence for all the characters within the lines, tested by the Wilk's criterion, was significant (χ^2 = 983.9 for 400 d.f.). Hence the analysis of genetic divergence among genotypes used in the study was considered relevant.

The multivariate analysis giving the D^2 values between fifty one varieties revealed that all these varieties can be grouped into ten clusters (Table 1). Among these, cluster II consists of 18 varieties, followed by cluster I (12), V (5), III and IV (4), VI (3), VII (2), and clusters VIII, IX and X with one genotype each. The intracluster distances ranged from 0 (in monogenotypic clusters) to 13.4 (IV). Clusters II, V, VII had more or less similar intracluster distances (Table 2). The clustering pattern obtained in the present study revealed that there was no association between eco-geographical distribution of genotypes as all clusters consisting more than one strain included strains from different eco-geographic regions thus supporting the view [3, 4] that geographic distribution and genetic divergence do not follow the same trend. No correspondence between genetic and geographic diversity was found in rice also [7, 8].

The minimum intercluster distance was between clusters I and III. Both these clusters taken together account for 27.5% of all the genotypes of diverse origin. The maximum distance was recorded between clusters VII and X, which together covered only three varieties. The results of the present investigation indicate that all the genotypes/varieties are genetically diverse. Similar diversity has been reported earlier in rice [7, 9].

The intracluster distances (Table 2) varied from 0.0 (VIII, IX and X) to 13.2 (IV), indicating considerable diversity between different clusters. The intracluster distances for clusters II, V, VII (9.2, 10.0 and 8.9, respectively) indicated close relationship and almost parallel diversity among the genotypes included in respective clusters.

Table 1. Distribution of 51 soybean varieties and strains into different clusters

Cluster	No. of genotypes	Varieties/strains	Source/origin
I	12	EC-34082	Hungary
		EC-34363, EC-34401, EC-39074	West Germany
		EC-36999, EC-39361, EC-95264	U.S.A.
		EC-396698	
		EC-14480	Australia
		EC-37053	U.S.S.R.
		IC-2043, MACS-309	India
II	18	EC-14451	Australia
		EC-30194	U.S.A.
		PLSO-80, MACS-57, MACS-58 MACS-124, MACS-239, MACS-249, MACS-267, MACS-287, MACS-288, MACS-298, MACS-308-A, MACS-311, MACS-321, MACS-329, MACS-330 MACS-346	India
III	4	EC-2581	U.S.A.
		EC-14475, EC-14469	Australia
		EC-18190	Nepal
IV	4	EC-203	U.S.A.
		PK-7355, MACS-13, MACS-308-B	India
V	5	EC-57043	China
		IC-9451, MACS-304, MACS-348, MACS-349	India
VI	3	MACS-227, MACS-294, MACS-359	India
VII	2	EC-39707	Italy
VIII	1	EC-93163	U.S.A.
IX	1	IC-2065	Kalimpong
X	1	Yellow Tur	India

The cluster means (Table 3) showed that the maximum and minimum values, respectively were: days to 50% flowering 50.0 (cluster IX) and 36.8 (VIII), days to maturity 97.0 (IX) and 80.1 (I); plant height 80.9 cm (X) and 25.6 cm (VII); branches/plant 7.8 (IX) and

Table 2. Average intra- (in bold) and intercluster distances in soybean

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**11.4** **3.4**	86.1	63.5	120.4	162.9	131.6	35.6	165.6	300.6	317.2
II	9.3	**9.2** **3.0**	43.8	40.1	6.0	42.0	77.3	120.1	113.0	153.2
III	8.0	6.6	**12.1** **3.5**	59.2	55.5	62.8	88.0	129.2	160.9	90.3
IV	11.0	6.3	7.7	**13.4** **3.7**	83.0	57.0	112.8	196.7	180.3	232.2
V	12.8	6.7	7.4	9.1	**10.0** **3.2**	51.0	158.8	93.9	88.0	101.9
VI	11.5	6.5	7.9	7.6	7.1	**11.1** **3.3**	152.1	145.0	136.0	141.0
VII	6.0	8.8	9.4	10.6	12.6	12.3	**8.9** **2.98**	247.3	277.5	332.2
VIII	12.9	11.0	11.4	14.0	9.7	12.0	15.7	**0.0** **0.0**	177.7	70.4
IX	17.3	10.6	12.7	13.4	9.3	11.7	16.7	10.8	**0.0** **0.0**	65.5
X	17.8	12.4	9.5	15.3	10.1	11.9	18.2	8.4	8.1	**0.0** **0.0**

Note. D values given below and D^2 values above in the diagonal.

3.1 (I); pods/plant 61.7 (IV) and 26.7 (I); grains/plant 135.8 (VI) and 49.2 (VIII); grain yield/plant 15.9 g (III) and 9.9 g (IX); and 100-grain weight 15.1 g (VI) and 6.8 g (VIII). The highest grain yield/plant observed in cluster VI (15.9 g) was due to the highest number of pods/plant (61.7) and grains/plant (135.8).

From Table 3 it appeared that donors for different characters can be taken from the clusters as follows: early flowering and maturity (I and VII); dwarfness (VII); tallness (X); more branches/plant (IX); more number of pods (VI); grains and grain yield/plant (VI); and increased grain weight (I and III). The results obtained in the present study are in conformatory with earlier reports [10, 11].

Table 3. Cluster means for eight characters in soybean

Character	Character means in clusters										Overall
	I	II	III	IV	V	VI	VII	VIII	IX	X	mean
Days to 50% flowering	36.9	45.0	43.1	48.2	47.4	48.0	36.8	41.0	50.0	47.0	43.7
Days to maturity	80.1	92.5	88.1	95.0	96.8	96.7	81.5	90.0	97.0	95.0	91.3
Plant height (cm)	26.5	41.9	43.0	32.5	58.6	46.3	25.6	67.4	76.5	80.9	49.9
Branches/plant	3.1	4.5	5.1	4.0	3.3	5.6	3.8	3.6	7.8	4.8	4.6
Pods/plant	26.7	44.5	36.0	41.7	52.6	61.7	26.5	27.7	53.0	52.8	42.4
Grains/plant	50.7	86.4	56.9	84.9	101.2	135.8	53.6	49.2	97.8	121.5	83.8
Yield/plant (g)	7.9	9.2	10.0	11.4	10.4	15.1	7.5	6.8	9.6	11.2	9.8
100-grain weight (g)	15.3	11.4	15.9	12.8	12.4	12.7	11.4	11.6	9.9	11.3	12.5

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