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Genetic divergence in soybean (*Glycine max* (L.) Merrill.)

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Abstract: Mahalanobis D^2 analysis was employed to study the genetic diversity of 50 soybean genotypes. A wide genetic diversity was observed among the 50 genotypes tested. Based on D^2 of Mahalanobis, the genotypes were grouped into ten clusters. The clustering pattern indicated that the geographic diversity need not necessarily be related to the genetic diversity. This could be evidenced from the study that genotypes from the same eco-geographic region did scatter in different clusters. Similarly genotypes from different eco-geographic regions were identified in one cluster. The intercluster distance between clusters VI and VIII was the highest and the lowest was between clusters VII and IX. Among the ten characters, hundred seed weight contributed maximum to the genetic divergence followed by number of pods and plant height. *(Key words: Soybean, Genetic divergence).*

Success of crop improvement programmes in any crop depends on the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. Despite the richness of soybean germplasm, a very narrow spectrum of variability existing among the cultivars limit the improvement programmes. For soybean improvement, breeding methods like intervarietal hybridization and interspecific hybridization have promise to broaden the genetic base either through creation of variability or introgression of desirable genes from wild species (Bhatnagar and Karmakar, 1995). The choice of the parents is an Important step in hybridization programme to create variation for selection of useful recombinants. Variability is an outcome of divergent introgression during natural evolution hence it should be considered in consonance with genetic diversity. Multivariate analysis (D^2 statistic) developed by Mahalanobis in 1936 is found to be a powerful tool to measure genetic divergence among a set of given genotypes (Murthy and Arunachalam, 1966).

Materials and Methods

Fifty eco-geographically different genotypes of soybean *(Glycine max* (L). Merrill.) were taken for study and raised in a randomized block design with four replications at the school of Genetics, Tamil Nadu Agricultural University, Coimbatore. Each genotype was raised in a row of 4m length with a spacing of 30 cm x 10 cm. Observations on days to flowering, days to maturity, plant height, number of branches, number of pods, 100 seed weight, protein content, oil content, dry matter production and seed yield were recorded in five randomly selected plants in each genotype in each replication.

The data were subjected to multivariate analysis (Rao, 1952). The original mean values were transformed to normalised variables and all-possible D^2 values were calculated. For determining group constellations or clusters, a relatively simple criterion suggested by Rao (1952) was followed. After establishing the clusters, the intercluster distance was worked out by taking the average of the component genotypes in that cluster. The average intercluster divergence was arrived at by taken into consideration all the component D^2 values possible among the members of the two clusters considered. The value of the, 'D' the genetic distance between the clusters, was arrived by taking the square root of the average D^2 values (Mahalanobis, 1936).

Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the ten characters studied. The D^2 values for all possible pairs (1225 D^2 values) ranged from 1.59 to 844.09. By application of clustering techniques, 50 genotypes could be grouped into ten clusters. The constituents of different clusters with their source are presented in Table 1. Nineteen genotypes formed the cluster I followed by 12 genotypes in cluster II. Four genotypes constituted the cluster III, while clusters IV, V and VI were constituted by three genotypes each. Clusters VII and VIII

Table 1. Composition of D^2 clusters

Cluster No.	No. of entries	Genotypes	Origin	Genotype	Origin
I	19	Co 1	Tamil Nadu	EC 2043	China
		UGM 34	Tamil Nadu	EC 7025	Australia
		UGM 37	Tamil Nadu	EC 7034	Australia
		Khasb 2	Karnataka	EC 7027	Australia
		Hardee	USA	EC 11796	Japan
		Gibson	USA	EC 14460	Australia
		Jackson	USA	IC 13048	West Bengal
		Nimsoy	Italy	IC 15960	Madhya Pradesh
		Bioloxy	Hungary	IC 15995	Madhya Pradesh
		Callard	USA		
II	12	MACS 58	Maharastra	EC 9311	Japan
		JS 79-411	Madhya Pradesh	EC 11695	Japan
		AVRDC 516	Taiwan	EC 39824	Thailand
		EC 2572	USA	IC 2061	West Bengal
		EC 3439	USA	IC 13006	West Bengal
		EC 2575	USA	IC 15967	Madhya Pradesh
III	4	Dortch	USA	AVRDC 508	Taiwan
		MACS 124	Maharastra	IC 220	Bihar
IV	3	Charlee	USA	EC 2541	China
		UPSS 46	Uttar Pradesh		
V	3	Monetta	USA	PK 257	Uttar Pradesh
		Bragg	USA		
VI	3	UGM 30	Tamil Nadu	EC 6103	USA
		EC 4296	USA		
VII	2	IC 2065	West Bengal	IC 9460	Sikkim
VIII	2	Co 2	Tamil Nadu	JS 87-38	Madhya Pradesh
IX	1	EC 9472	Japan		
X	1	Kalitur	Uttar Pradesh		

were formed by two genotypes each, while clusters IX and X represented by one genotype each.

The clustering pattern in the present study revealed that the tendency of genotypes from diverse eco-geographic locations to group together in one cluster which could be attributed to the free exchange of breeding materials from one place to another (Verma and Mehta, 1976). This may also be due to the fact that the unidirectional selection practised for a particular trait in several places produced similar phenotypes which were aggregated in one cluster irrespective of their distant geographic origin (Timothy, 1963; Arunachalam and Jawahar Ram, 1967; Govil and Murthy, 1973).

Another feature that came to light was that many genotypes originating from one place (USA) were scattered over different clusters (I, II, III, IV, V, VI). Such genetic diversity among the genotypes of common geographic orgin could be due to factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Murthy and Arunachalam, 1966).

Table 2. Inter and intra (diagonal) cluster average of D^2 and D values (within parenthesis) among the clusters.

	I	II	III	IV	V	VI	VII	VII	IX	X
I	31.34	72.20	110.82	85.12	203.06	77.27	122.43	370.55	223.77	91.03
	(5.60)	(8.50)	(10.53)	(9.23)	(14.25)	(8.79)	(11.06)	(19.52)	(14.96)	(9.54)
II		44.73	116.51	121.62	97.87	162.69	84.52	257.86	125.96	64.94
		(6.69)	(10.79)	(11.03)	(9.89)	(12.75)	(9.19)	(16.06)	(11.22)	(8.06)
III			23.85	107.37	83.22	332.36	108.07	116.09	118.23	68.84
			(4.88)	(10.36)	(9.12)	(18.23)	(10.40)	(10.77)	(10.87)	(8.30)
IV				20.23	215.05	189.34	72.25	255.76	162.11	132.62
				(4.50)	(14.66)	(13.76)	(8.50)	(15.99)	(12.73)	(11.52)
V					38.71	391.26	128.75	136.82	99.94	86.46
					(6.22)	(19.78)	(11.35)	(11.70)	(9.10)	(9.30)
VI						46.88	236.96	600.77	368.04	198.91
						(6.85)	(15.36)	(24.49)	(19.18)	(14.08)
VII							34.55	170.25	61.03	1-3.00
							(5.88)	(13.05)	(7.81)	(10.15)
VIII								39.49	73.51	162.06
								(6.28)	(8.57)	(12.73)
IX										101.67
X										10.08

Table 3. Contribution of characters to genetic divergence

S.No	Character	Percentage of Contribution
1.	100 - seed weight	48.54
2.	Number of pods	19.72
3.	Plant height	10.69
4.	Seed yield	5.64
5.	Oil content	4.25
6.	Dry matter. production	4.08
7.	Number of branches	3.31
8.	Protein content	3.18
9.	Days to maturity	0.35
10.	Days to flowering	0.24

The clustering pattern thus failed to indicate any relationship between genetic divergence and geographic distribution. This was in agreement with the findings of Bargale *et al.* (1986); Ghatge and Kadu (1993); Mehetre *et al.* (1994) and Kumar and Nadarajan (1994).

'The intra and intercluster D^2 and D values among ten clusters are presented in Table 2. Based on the range of D values (from 7.81 to 24.49) obtained in the present study, the rating of divergence was clasified as low (below 11.00), moderate (10.01 to 15.00) and high (above 15.01). It is clear from the above rating that all the genotypes within each cluster were genetically closer since sill the cluster had low intra cluster distances. The relative divergence of each cluster from other cluster (intercluster distance) indicated high order of divergence between cluster VI and VIII, followed by cluster V and VI, I and VIII,

VI and IX and III and VI. Thus hybridisation between genotypes from these clusters should result in maximum hybrid vigour and highest number of useful segregants in soybean (Shwe *et al.* 1972).

The relative contribution of different characters to genetic divergence is given in table 3. Among the characters that contributed to genetic divergence, the maximum contribution of 48.54 percent was by 100 seed weight. Number of pods was the second character of importance that contributed substantially to genetic divergence (19.72 per cent) followed by plant height (10.69 per cent).

The importance of 100 seed weight as a contributing factor for genetic divergence has been recorded by Verma *et al.* (1973) and Kumar and Nadarajan (1994). The importance of number of pods and plant height contribution to genetic diviergence has been brought out by Kumar and Nadarajan (1994).

Among the other characters seed yield, oil content, drymatter production, number of branches and protein content, have contributed between three to six per cent to genetic divergence.

Genotypes from the clusters 1, 111, V, VI, VIII and XI with high intercluster distance and diversity can be exploited for recombination breeding in soybean.

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