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

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The genetic distance for 40 genotypes of soybean collected from different soybean growing areas of India and abroad was estimated using D^2 statistics. The results showed adequate genetic diversity for all the traits with D^2 values ranging from 27.14 to 361.76. The results revealed that 40 genotypes were grouped into 12 clusters with substantial divergence between them. Cluster I was very large comprising 20 genotypes followed by cluster II and IV with five genotypes and cluster VI with two genotypes, while clusters III, V and VII to XII were solitary clusters. The maximum inter-cluster distance was obtained between cluster IV and VI (D = 19.02) followed by those between cluster IV and XI (D = 16.29) which may serve as potential parents for hybridization. The genetic divergence had little to do with the geographic factor as noticed by the random distribution of genotypes into various clusters. Number of pods/plant, plant height and seed yield/plant were the major characters contributing to the genetic divergence.

Key words : Genetic divergence, Cluster analysis, D^2 analysis, *Glycine max*

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INTRODUCTION

During the mid seventies, the germplasm of soybean were introduced in India at large scale. Assessment of genetic diversity facilitates classification and identification of diverse genotypes in the germplasm collection. In breeding programme, progenies derived from crosses involving diverse parents that are selected on the basis of genetic divergence analysis expected show broad spectrum of genetic variability, providing greater scope for obtaining heterotic effect in early generation and isolating transgressive segregants in advance generations. Knowledge of genetic diversity is successfully utilized in soybean by several workers (Chauhan, 1983; Singh and Ram, 1985; Chikhale *et al.*, 1992; Karmakar *et al.*, 1998; Jain and Ramgiry, 2000; Shrivastava *et al.*, 2001; Kayande and Patil, 2009) for the selection of potential parents to be used in hybridization programme for obtaining desirable segregants. Mahalanobis D^2 technique is a unique tool for identifying degree of divergence in biological population at genetic level. Therefore, an effort has been made to assess the genetic diversity using ten traits recorded in 40 genotypes of soybean.

RESEARCH METHODOLOGY

The experimental material comprised of 40 diverse genotypes of soybean that were collected from different soybean growing states of India and abroad. The field experiment was laid out in randomized block design with three replications at Post Graduate Research Farm, College of Agriculture, Kolhapur during *Kharif* 2011. Each genotype was planted in a single row plot of 5 m length with inter and intra row spacing of 45 cm and 10 cm, respectively. The recommended agronomic practices and plant protection measures were followed for raising successful crop. Five random plants were selected from each plot for recording the observations on seed yield/plant and its component traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, number of primary branches/plant, number of pods/plant, number of seeds/pod, 100 seed weight, protein content and oil content. The data were subjected to the statistical analysis as suggested by Mahalanobis (1936). The criteria used by Tocher as described by Rao (1952) were followed for making group constellations.

RESEARCH FINDINGS AND ANALYSIS

The Mahalanobis D^2 statistics showed adequate diversity between genotypes with D^2 values ranging from

27.14 to 361.76. Based on D^2 statistics, 40 genotypes were grouped into 12 clusters. The distribution of 40 genotypes in different clusters is given in Table 1. The D^2 values have been used for grouping of genotypes in the clusters in such a way that the genotypes in the cluster had smaller D^2 values than between clusters. Cluster I was very large and comprised of 20 genotypes, out of which 14 genotypes are exotic, two from Kolhapur and one each from Pune, Pantnagar and Karnataka. Cluster II and IV included five genotypes each from different geographic areas. While cluster VI had two genotypes and remaining clusters *viz.,* III, V and VII to XII were solitary clusters comprising single genotype only. The genotypes belonging to same geographic area were grouped into different clusters and the genotypes belonging to different geographic areas were grouped into a same cluster. Hence, the grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Murty and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater genetic diversity than geographic distance. Further, the free exchange of seed materials among the different regions consequently causes character constellations because of human interference and material may lose its individuality. Mehetre *et al.* (1994) and Das *et al.* (2000) also reported that genetic diversity was independent of geographic regions.

The average intra and inter-cluster distance (D) between two populations varied from 0.00 to 6.02 and 6.06 to 19.02, respectively (Table 2). The maximum inter-cluster distance observed between clusters IV and VI (D=19.02) followed by clusters IV and XI (D=16.29) and clusters VII and X (19.90). Clusters III, V and VII to XII had only single genotype, so there intra-cluster distances were zero. It has been well established that if more genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining highly heterotic hybrids and broad spectrum of genetic variability. Therefore, in the present study, based on large cluster distances, it is advisable to attempt crossing of the genotypes from cluster VI and XI with the genotypes of cluster IV which may lead to broad spectrum of genetic variability for seed yield improvement in soybean.

The cluster means (Table 3) for ten characters are presented with their per cent contribution towards the total genetic divergence. The results revealed that number of pods/plant contributed maximum (35.90%) as a first ranker towards the total divergence with its average ranging from 55.87 for cluster VII to 118.53 for cluster VII. The next major contribution towards total divergence came from plant height (20.13%) and seed yield/plant (20.00%). Plant height ranged from 51.60 cm (cluster XII) to 110.80 cm (cluster VI), seed

Table 1: Distribution of 40 soybean genotypes in different clusters on the basis of D^2 statistic			
Clusters	Number of genotypes	Name of the genotypes	Origin/source
I	20	EC-572009, EC-456660, EC-389154, EC-481518, EC-528628, EC-396068, EC-391332,	Exotic collection
		EC-396057, EC-396067, EC-391346, EC-487282, EC-488600, EC-547464, EC-456447.	
		KS-112, KS-103.	
		MACS-450.	Kolhapur (MS)
		KB-17.	Pune (MS)
		P-205.	Karnataka
		Ge-2263.	Pantnagar
		EC-391012, EC-102612, EC-481515.	—
II	5	JS-811625.	Exotic collection
		VP-1147.	Jabalpur (MP)
		EC-457211.	—
III	1	EC-473111, EC-457172, EC-389148, EC-481369.	Exotic collection
IV	5	MAUS-71.	Exotic collection
		EC-468597.	Parbhani (MS)
V	1	IC-15545.	Exotic collection
VI	2	EC-343307.	Indigenous collection
		EC-34117.	Exotic collection
VII	1	JS-79214.	Exotic collection
VIII	1	EC-457159.	Jabalpur (MP)
IX	1	JS-335.	Exotic collection
X	1	DS-228.	Jabalpur (MP)
XI	1	M-108.	Digraj (MS)
XII	1		—

Table 2: Average intra and inter cluster distances (D²) and D values for 40 genotypes in soybean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	27.14	60.22	38.56	77.09	46.51	158.50	82.08	111.09	79.60	107.33	99.80	88.17
	(5.21)	(7.76)	(6.21)	(8.78)	(6.82)	(12.59)	(9.06)	(10.54)	(8.92)	(10.36)	(9.99)	(9.39)
II		31.25	58.37	158.00	139.00	116.42	85.75	56.55	54.61	83.36	70.56	48.16
		(5.59)	(7.64)	(12.57)	(11.79)	(10.79)	(9.26)	(7.52)	(7.39)	(9.13)	(8.40)	(6.94)
III			0.00	132.48	59.90	104.45	115.13	80.46	97.81	95.06	57.30	97.02
				(11.51)	(7.74)	(10.22)	(10.73)	(8.97)	(9.89)	(9.75)	(7.57)	(9.85)
IV				36.24	76.39	361.76	118.16	251.54	162.56	217.86	265.36	152.77
				(6.02)	(8.74)	(19.02)	(10.87)	(15.86)	(12.75)	(14.76)	(16.29)	(12.36)
V					0.00	231.34	169.00	177.42	167.44	143.28	139.47	163.07
						(15.21)	(13.00)	(13.32)	(12.94)	(11.97)	(11.81)	(12.77)
VI						29.38	186.32	124.32	138.06	205.63	85.75	224.10
						(5.42)	(13.65)	(11.15)	(11.75)	(14.34)	(9.26)	(14.97)
VII							0.00	206.78	83.72	252.81	204.20	153.02
							(14.38)	(9.15)	(15.90)	(14.29)	(12.37)
VIII								0.00	86.49	36.72	37.45	71.40
								(9.30)	(6.06)	(6.12)	(8.45)
IX									0.00	108.37	122.10	80.64
									(10.41)	(11.05)	(8.98)
X										0.00	51.12	52.13
										(7.15)	(7.22)
XI											0.00	112.57
											(10.61)
XII												0.00

Table 3: Cluster means for 10 characters in soybean

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches / plant	No. of pods / plant	No. of seeds / pod	100-seed weight (g)	Protein content (%)	Oil content (%)	Seed yield / plant (g)
I	44.50	95.97	77.12	3.84	70.88	2.42	11.62	36.21	19.31	18.20
II	52.80	103.47	72.62	3.93	91.84	3.37	15.95	36.19	19.58	19.03
III	46.67	100.33	84.23	3.30	92.97	2.17	11.50	35.00	20.20	13.33
IV	39.93	92.00	62.84	3.56	60.17	2.80	10.51	35.99	18.11	11.25
V	37.67	87.00	79.70	3.60	57.00	2.20	8.10	35.83	19.37	8.47
VI	52.00	103.33	110.80	3.93	104.85	3.08	17.92	35.48	19.12	20.74
VII	51.67	104.33	83.10	3.67	55.87	3.20	15.18	38.47	19.60	17.51
VIII	49.00	100.33	70.93	4.40	118.53	3.40	12.29	38.69	19.22	23.13
IX	47.00	96.00	79.20	3.40	83.33	2.17	18.40	40.93	18.97	23.96
X	45.33	97.33	59.43	3.60	115.33	2.87	16.27	39.43	20.10	17.19
XI	50.67	101.67	82.78	3.83	115.00	3.27	15.04	40.29	20.17	15.43
XII	53.00	101.67	51.60	2.63	96.38	3.17	17.24	34.47	20.23	19.17
Mean	45.97	97.30	75.81	3.76	76.82	2.64	13.25	36.48	19.27	16.68
S.E.±	0.95	0.95	1.42	0.18	1.52	0.13	0.53	0.55	0.45	0.58
%Contribution	2.95	4.23	20.13	0.26	35.90	4.36	6.15	3.59	2.44	20.00

yield/plant ranged from 8.47 g (cluster V) to 23.96 g (cluster IX). On the other hand, rest of the traits had lower contribution towards the total genetic divergence. A considerable genetic diversity of 76.03% was observed due to these three characters. Hence, selection for divergent parents based on these three characters would be useful for

heterosis breeding in soybean.

The cluster IX is superior with respect to seed yield/plant, 100 seed weight and protein content, while cluster VIII was desirable for number of primary branches/plant, number of pods/plant and number of seeds/pod. Cluster V and IV had desirable values for earliness and cluster XII for oil content. The genotypes with high mean values of character in any cluster as well as high D^2 values between clusters can be used either for direct adoption or for hybridization programme in order to breed for better genotypes of soybean.

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