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Short Communication

GENETIC DIVERSITY IN SOYBEAN

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Three hundred exotic accessions of soybean (*Glycine max* L.) from various countries were evaluated for several quantitative characters. The accessions were grouped into five clusters. There was no correspondance relation between the geographic distribution and their inclusion in a particular cluster. Genetic divergence analysis showed that the maximum distance was between II and V followed by I and IV cluster. Based on cluster means it is concluded that the crosses among the accessions of the cluster I, III and IV might be useful. The accessions viz. EC-2542, EC-9309, EC-11740-A, EC-11741-A, EC-14472, EC-14474, EC-26692, EC-34041, EC-34146-B, EC-37004, EC-37005 and EC-37066 showed desirable characteristics. These accessions can be utilised in hybridization programme to achieve high levels of yield and oil.

Key words : Soybean, genetic diversity, germplasm

The germplasm of soybean were introduced in India at large scale during mid seventies. The area under soybean has increased 1500 folds since 1967-68 and 40 soybean varieties have been released for its commercial cultivation, so far. Broad genetic base is an important aspect for any breeding programme. Genetic diversity among parental lines is also an important factor for developing a variety. Only very meagre information is available for genetic diversity in this crop for Vidarbha region of Maharashtra. Genetic divergence analysis which quantify the differences among the quantitative characters is an efficient method to evaluate genetic diversity. Therefore, the present study was carried out using non hierrarchical euclidean cluster analysis to classify 300 accessions of soybean into group on the basis of quantitative characters.

The experimental material comprised 300 exotic accessions of soybean from China, USA, Brazil, Canada, South Africa, Australia, Japan, Nepal, Italy, UK, Germany, Hungary, Argentina, Taiwan and Russia. These were grown at Experimental Farm, National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Akola during the Kharif, 1996, in augmented block design, using two checks i.e. Bragg and MACS-13. The row length was three meter long and spaced 60 cm apart. Observations were recorded on days to 50 per cent flowering, days to maturity, number of leaflets,plant height, seeds/pod, yield/plant(g), 100-seed weight(g) and oil content. Non hierrarchical euclidean cluster analysis was used for accessing the genetic divergence among the 300 accessions of soybean following method as suggested by Spark (1973). The accessions were grouped into five clusters.

In this present study, 300 accessions of soybean were classified into 5 clusters (Table 1).

Table 1. Grouping of 300 accessions of soybean in different clusters

Cluster	No. of entries	Source country
I	126	China, Australia, Nepal, S. Africa, Canada, Germany, Italy, Hungary, Taiwan, Japan, USSR
II	84	China, USA, Brazil, Australia, Japan, Nepal, Italy, Argentina, Hungary, Germany, Taiwan
III	44	China, USA, Japan, Australia, Germany, Nepal, Italy, UK, Hungary, USSR
IV	45	China, USA, Canada, S. Africa, Australia, Japan, Hungary, USSR
V	1	USA

The clustering pattern in the present study indicated that the genotypes from one source country were distributed in to different clusters. This suggests the lack of distance build up of geographical diversity. The average intra and inter cluster distances have been presented in Table 2. Average inter cluster distance values ranged from 2.57 to 17.70 (Table 2). The maximum distance existed between cluster II and V (17.70), however, cluster V showed much distance with cluster I, II, III and IV. Intracluster distance was 0 for all the clusters indicating similarity within the clusters. Cluster I contained the maximum number of accessions (126). These accessions were early flowering and maturity (28-32 days to flowering and 67-83 days matirity), dwarf to medium plant height, medium seed size and moderate oil content.

Table 2. Inter and intra-cluster values in 300 exotic accessions of soybean

	I	II	III	IV	V
I	0				
II	2.69	0			
III	3.23	3.13	0		
IV	3.17	2.74	2.57	0	
V	17.66	17.70	17.48	17.49	0

$\overline{D} = 5.85$

Table 3. Cluster means for eight characters in 300 exotic accessions of soybean

Character	I	II	III	IV	V
Days to 50% flowering	30.01	39.51	36.82	44.02	39.00
Days to maturity	78.37	93.27	90.61	101.84	97.00
No. of leaflets	3.00	3.00	3.00	3.00	3.00
Plant height(cm)	36.62	61.38	69.83	45.97	58.00
Seeds/pod	2.10	2.10	2.51	2.09	2.80
Yield/plant(g)	3.16	3.72	12.99	6.82	4.70
100-seed weight(g)	9.58	6.87	10.21	10.68	11.80
Oil (%)	18.60	17.30	19.07	19.49	20.00

Cluster II comprised 84 accessions contained late flowering, medium maturity, tall, small seed size, low yielder and low oil content. Cluster III contained 44 accessions showed highest yield/plant (12.99 g) as compared to all clusters. Cluster IV had 45 accessions showed late flowering and maturity, medium plant height,medium seed size and high oil content (19.49%).

The utility of classifying germplasm for selection of diverse parents for hybridization has long been appreciated (Bhatt, 1970). The accessions grouped in cluster I and IV followed by I and III were wide apart for days to flowering, days to maturity, plant height, yield/plant. Cluster III showed highest genetic divergence for yield/plant, however cluster IV showed highest genetic divergence for oil content. High oil can be harvested by obtaining high yield with the condition that a variety must have good oil content. Obviously, the crosses between accessions of cluster I, III and IV might be useful for obtaining the transgressive segregants in segregating generations. Apart from high genetic divergence, the performance of the accessions for characters such as early flowering and maturity, plant height, yield/plant and seed size should be considered prior to their inclusion in breeding programme.

Soybean is believed to be of native of south-east Asian origin. Nagata (1959, 1960) suggested that the soybean originated in China proper, probably in the north and central regions. The soybean germplasm originally desseminated from China to rest of the world. The genetic divergence of the accessions in this study is in no way influenced by geographic distribution. There are various examples of accessions having same origin but falling in different groups. Griffin and Palmer (1995) studied genetic distance among Asian gene centres and North American cultivars based on gene frequencies for all of the *G. max* and the *G. soja* accessions. Distances among *G. max* and *G. soja* groups generally were smaller than between *G. max* and *G. soja* groups. The G. max cultivars developed by selection from plant introductions were closest to the accessions from China, Japan, Korea and the Man Sib region. It indicates no influence on geographic distribution of the soybean germplasm lines.

The accessions EC-2542, EC-9309, EC-11740A, EC-11741A, EC- 14472, EC-14474, EC-26692, EC-34041, EC-34146B, EC-37004, EC-37005 and EC-37066 showed desirable characters including oil content. These accessions can be utilised as parents in the hybridization programme.

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