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Research Note

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

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Abstract
Divergence analysis among sixty one soybean (*Glycine max* (L.) Merrill.) genotypes collected from different geographic sources was carried out using Mahalanobis's D^2 statistic. The genotypes were grouped into eleven different clusters. The maximum inter-cluster distance was found between clusters II and IX (D=150.36) followed by that between clusters II and XI (D=129.64), II and VIII (D=124.78), X and XI (D=117.46), IV and IX (D=101.49) and IV and XI (D=100.02) indicated that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters suggesting that the genotypes belonging to cluster II (J-659), cluster IX (PK-986), cluster XI (PK-926) and cluster VIII (NRC-2-R) should be selected as parents in hybridization programme for improvement in soybean. The most important trait causing maximum genetic divergence was the number of cluster per plant (33.61) followed by plant height (23.28) and oil content (10.27). These three characters contributed 67.16% of the total diversity in the material studied. Hence, it is advisable to select divergent parents based on these three characters and attempt crossing between them so as to achieve a broad spectrum of favourable genetic variability for yield improvement in soybean.

Key words:
Soybean, clusters, genetic divergence

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. 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. It permits precise comparison among all the population in given any group before effecting actual crosses.

Sixty one genotypes of soybean were sown in a Randomized Block Design with three replications during *kharif* 2012. Each entry was accommodated in a single row of 4.0 m length with a spacing of 45 cm between rows and 10 cm between plants within the row. All the recommended packages of practices were followed for raising healthy crop. Data were recorded for 15 characters *viz*., days to 50 % flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, 100-seed weight (g), biological yield per plant (g), harvest index (%), protein content (%), oil content (%) and seed yield per plant (g). Observations on days to 50% flowering and days to maturity were recorded on per plot basis. The D^2 analysis was carried out for all the fifteen characters to access genetic divergence using Mahalanobis's D^2 statistics (1936). The genotypes were grouped on the basis of minimum generalized distance using the Torcher's method (Rao, 1952).

Analysis of variance revealed that highly significant differences among the genotypes were observed for all the traits except oil content indicating the presence of good amount of genetic variability. In the present study, 61 genotypes were grouped into 11 clusters using Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller D^2-values among themselves than those from groups belonging to different clusters.

The cluster I was the largest having 29 genotypes. The second largest was the cluster II having 18 genotypes followed by cluster IV having 5 genotypes and cluster XI included 2 genotypes (Table 1). The cluster III, V, VI, VII, VIII, IX and X were remained solitary with a single genotype each. A released variety of the region, *viz.*, G. Soy-3 was grouped in the cluster I indicating the absence of genetic variability between the checks. The grouping of genotypes revealed that there was no perfect relationship between genetic diversity and geographical diversity as genotypes from different geographical origin were included in one cluster.

The maximum inter-cluster distance was found between clusters II and IX (D=150.36) followed by that between clusters II and XI (D=129.64), II and VIII (D=124.78), X and XI (D=117.46), IV and IX (D=101.49) and IV and XI (D=100.02). The

minimum inter-cluster distance was observed between clusters V and VIII (D=21.01). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates (Table 2). In this context, genotypes from cluster II (J-659), cluster IX (PK-986), cluster XI (PK-926) and cluster VIII (NRC-2-R) should be selected as parents in hybridization programme.

The intra-cluster distance indicating poor diversity (Table 2). Gradual increase in D^2 value over the range without any sudden jumps in the values among the genotypes may be result of their evolution with the same ancestral parents or due to evolution under near identical ecological parameters or they might have been subjected to similar natural selection. In earlier studies of Das *et al.* (2000) reported similar results.

A wide range of variation for several characters among single as well as multi-genotypic clusters was observed (Table 3). However, the most important trait causing maximum genetic divergence was the number of cluster per plant (33.61) and was responsible for differentiating the genotypes studied. Plant height (23.28) and oil content (10.27) were also important traits contributing to total genetic divergence. Thus, these three characters contributed 67.16% of the total diversity in the material studied. Hence, it is advisable to select divergent parents based on these three characters and attempt crossing between them so as to achieve a broad spectrum of favourable genetic variability for yield improvement in soybean. Hence, it is advisable to attempt crossing of these genotypes selecting as divergent parents based on these three characters, which may lead to broad spectrum of favourable genetic variability for yield improvement in soybean. Earlier workers also reported higher genetic diversity due to oil content (Bartul *et al.*, 1985) and plant height (Chikhale *et al.*, 1992 and Ramana and Satyanarayana, 2000). On the other hands, number of primary branches per plant (7.32), seed yield per plant (5.85), biological yield per plant (8.14) and harvest index (4.86) were least responsible for contributing towards the total divergence.

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Table 1. Distribution of 61 genotypes of soybean into various clusters on the basis of D^2-statistic using Tocher's method

No. of Clusters	No. of genotypes	Name of the genotypes
I	29	IC-49864, AGS-72, MACA-104, GUJ SOYA-3, JB-5-2, EC-93748, MACS-52, AGS-144, NRC-6, EC-77205, MACS-132, PBN-134, PBN-107, MO-40, EC-14911, AGS-65, DS-84-10, VLS-111, NRC-5, DS-178, EC-7631, IC-41686, EC-95278, DS-83-12-4, ICAR-124A, BB-22244, PK-746, PK-1042, PK-201
II	18	J-659, BR-13, AGS-58, J-645, PK-805, EC-85603A, EC-15991, EC-93741, BR-7B, PK-178, PK-781, PK-416, PK-1026, AGS-60, PK-1038, EC-117635, EC-149343, PK-766
III	1	DS-84-3
IV	5	AGS-112, Ktark, AGS-78, AGS-98, AGS-107
V	1	IS (SH)-8755
VI	1	J-793
VII	1	AGS-13
VIII	1	NRC-2-R
IX	1	PK-986
X	1	BR-7A
XI	2	PK-926, EC-118308

Table 2. Average inter and intra-cluster (diagonal) distances ($D=\sqrt{D^2}$) values of 61 soybean genotypes

luster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	23.00	48.65	35.59	53.96	43.74	35.21	45.20	74.68	99.28	58.84	86.89
II		27.92	73.24	54.98	85.58	66.85	69.31	124.78	150.36	69.65	129.64
III			0.00	67.24	41.91	31.81	71.65	65.89	61.73	94.79	60.34
IV				40.10	61.41	66.19	60.39	68.21	101.49	60.99	100.02
V					0.00	38.34	32.24	21.01	23.97	41.83	45.69
VI						0.00	42.01	70.26	79.36	64.67	53.94
VII							0.00	44.66	74.67	26.90	90.59
VIII								0.00	31.64	51.56	83.92
IX									0.00	90.64	47.88
X										0.00	117.46
XI											31.70

Table 3. Cluster mean for 15 characters of 61 soybean genotypes

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of pods/ plant	No. of clusters/ plant	No. of pods/ cluster	Pod length (cm)	No. of seeds/ pod	Seed yield/ plant (g)	100 seed weight (g)	Biological yield/ plant (g)	Harvest index (%)	Oil content (%)	Protein content (%)
I	39.11	97.49	34.88	4.18	31.11	6.99	3.31	2.84	2.17	8.00	1.62	25.57	30.90	19.91	36.47
II	38.59	95.94	33.18	4.16	31.98	14.38	3.23	2.59	2.17	7.84	1.82	26.78	29.15	19.71	38.91
III	39.33	95.67	32.53	5.13	34.87	6.73	3.40	3.00	3.00	5.31	1.43	16.63	32.01	20.00	36.08
IV	38.87	92.87	38.09	5.43	38.93	12.20	3.65	2.56	2.13	5.06	1.56	21.43	23.17	19.93	39.33
V	39.33	100.67	50.53	5.67	37.33	7.47	3.27	3.00	2.00	7.43	1.43	22.13	33.45	20.00	38.92
VI	37.00	99.33	42.00	4.87	44.33	6.87	3.07	3.00	3.00	10.27	1.88	30.96	33.10	19.00	36.92
VII	39.33	98.67	51.40	4.67	49.27	8.33	3.73	2.00	2.00	10.75	1.37	32.53	33.07	20.01	34.08
VIII	39.00	98.67	52.93	6.47	48.47	7.37	4.27	3.00	2.33	6.21	1.33	21.95	28.19	21.00	37.50
IX	40.00	94.00	55.13	7.00	39.67	7.77	3.07	2.93	2.33	5.11	1.04	15.33	33.07	20.00	34.08
X	39.00	92.33	54.13	4.20	30.93	9.20	3.20	2.67	2.27	7.93	1.99	27.44	28.63	20.67	40.75
XI	40.67	97.33	50.43	6.17	43.17	7.82	3.63	3.00	2.50	5.50	1.35	17.70	30.77	18.00	35.04
Mean	38.97	96.60	36.70	4.48	33.50	9.70	3.33	2.74	2.20	7.58	1.65	25.13	29.83	19.81	37.42
S. Em. ±	0.95	2.80	2.16	0.27	4.18	1.08	0.34	0.20	0.19	1.06	0.19	2.92	1.47	0.23	1.86
C.V.%	4.26	5.02	10.20	10.73	21.61	19.30	17.82	13.20	15.10	24.35	20.07	20.15	8.54	2.02	8.62
Percentage contribution of characters towards total divergence															
No. of times appearing first	31	10	426	134	13	615	4	4	49	107	3	149	89	188	8
% contribution	1.69	0.55	23.28	7.32	0.71	33.61	0.22	0.22	2.68	5.85	0.16	8.14	4.86	10.27	0.44