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Genetic diversity analysis among soybean (*Glycine max)* genotypes based on agro morphological characters

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ABSTRACT

The experiment was carried out to study the extent of genetic diversity among the 75 genotypes of soybean [*Glycine max* (L.) Merr.] under rainfed condition of Manipur by employing Mahalanobis D^2 analysis based on 13 morphological characters. The 75 genotypes of soybean were grouped into 9 clusters. Maximum numbers of genotypes were included in the cluster I comprising 28 genotypes followed by cluster II with 13 genotypes, cluster IV with 12 genotypes, cluster III and cluster V with 9 genotypes each and clusters VI, VII, VIII and IX with 1 genotype each. The value of intra-cluster distances ranged from 0.00 to 1181. The highest inter cluster distance (8937) was observed between cluster III and IX. The character plant height (34.13%) contributed highest to the total divergence of the genotypes, followed by pods/plant (29.62%) and days to 80% maturity (14.59%). The highest cluster means values for yield and its component characters were observed in cluster IX. On the basis of inter-cluster distance, cluster mean values, mean per se performance it is advisable to attempt crosses between genotypes from cluster III and cluster IX which may lead to obtaining higher heterotic effect and broad spectrum variability in the segregants.

Key words: Cluster, D^2 statistics, Genetic diversity, Genotypes, Soybean

Manipur is one of the important soybean [*Glycine max* (L.) Merr.] growing states in North-Eastern Hill region. Since time immemorial, farmers of Manipur grew soybean in the vicinity of their dwellings for culinary purposes. The green/matured grains are used for making various fermented and non-fermented foods. Soybean cultivation in Manipur was confined only in kitchen garden and the total area was negligible but by the early part of millennium the area increased up to 3000 ha.

The average yearly yield of soybean is about 820 kg /ha which is below the national average yield of 1000 kg/ ha. The low rate of increase in area is may be due to the limited availability of suitable location specific high yielding varieties. Thus, Development of high yielding varieties with proper plant architecture and duration is of paramount importance. For this purpose selection of genotypes with suitable plant types to be used as parents in hybridization program is the need of the hour. The genetic diversity between the genotypes is important as the genetically diverse parents are able to produce high heterotic effects (Falconer 1960, Arunachalam 1981, Ghaderi *et al*. 1984, Mian and Bahl 1989, Hallauer *et al*. 1989). Effective hybridization programme between genetically diverse parents will lead to considerable amount of heterotic response in F1 hybrids and broad spectrum of variability in segregating generations. Keeping in view of the above information the present study was carried out to study the extent of genetic diversity among the available genotypes of soybean and identification and prediction of potential combinations for further improvement under rainfed condition of Manipur.

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MATERIALS AND METHODS

The present study was carried out, at CAU Research Farm, Andro, Imphal East during *kharif* 2015. Seventy five different genotypes of soybean (comprising several advanced lines and local collection) were evaluated. The experiment was laid out in augmented design in five blocks with five checks. Each genotype was sown in single line of 4 m length with spacing of 45×10 cm. The recommended package of practices was followed to raise a good crop. The observations were recorded from five randomly selected plants in each line on plant height (cm), number of nodes/ plant, number of primary branches/plant, number of pods/ plant, number of seeds/pod, number of pod clusters/plant, number of clusters/plant, seed yield/plant (g), 100 seeds weight (g) and harvest index (%). Data on plant population, days to 50% flowering and days to maturity were recorded by visual observation. Data on oil content (%) was estimated by using AOAC Method (2000). The mean of the 5 plants

were subjected to statistical analysis according to Federer (1956). Wilk's criterion derived by Rao (1952) was used to test the significance of difference in the mean values for all characters. Genetic diversity was estimated as per Mahalanobis D^2 statistics (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters indicating the existence of genetic variability among the experimental material. The 75 genotypes of soybean were grouped into 9 clusters based on the relative magnitude of D^2 values the composition of which is presented in Table 1. Maximum number of genotypes were included in the cluster I comprising 28 genotypes, followed by cluster II with 13 genotypes, cluster IV with 12 genotypes, cluster III and cluster V with 9 genotypes each and clusters VI, VII, VIII and IX with 1 genotype each. The random clustering pattern of genotypes, i.e. grouping of genotypes from different regions in the same cluster (two local genotypes CAU-SLC-2/P and CAU-SLC-7 were grouped together with 7 other genotypes from Indore) indicated that the genetic diversity of the genotypes is not necessarily related to geographical diversity. Support for such a conclusion comes from findings of Patil *et al.* (2011), Shadaksari *et al.* (2011), Shinde *et al.* 2013, Ganesamurthy and Seshadri (2002) and Jency and Kalaimagal (2015). The genetic diversity, among the genotypes in the present study may have resulted from genetic drift and selection that cause greater diversity than geographical distribution as suggested by Murty and Arunachalam (1966).

Average inter and intra-cluster distances are presented in Table 2. The value of intra-cluster distances ranged from 0.00 (clusters VI, VII, VIII and IX) to 1181 (cluster V). The maximum intra-cluster distance was observed for cluster V (1181) followed by cluster IV (602), cluster II (466.49), cluster II (429.86) and cluster I (270.90). As the clusters VI, VII, VIII and IX were mono genotypic, the intra cluster distances were 0.00. Higher intra-cluster also indicated greater heterogeneity of the genotypes (Shwe 1972). Since the intra-cluster distance was found to be highest in cluster V, it is evident that there is considerable amount of heterogeneity among the genotypes in this cluster and hence the genotypes from this cluster (Cat 3476, Cat 6267 A, HARDEE, Cat 3339, Cat 2029 B, Cat 2126 A, CAU-SLC-2/P, CAU-SLC-7 and Cat 1843 A) can also be

Table 1 Grouping of 75 genotypes of soybean into various clusters

Cluster	No. of genotypes	Name of the genotypes
I	28	Cat 2114 A, Cat 2115 B, Cat 1979 B, Cat 2144 B, Cat 2130 B, Cat 96, Cat 1523 A, RKS -18,Cat 3460,Cat 3492,Cat 2125, Cat 3467,Cat 3447,NRC 37,CAT 489, JS 335,Cat 3438,Cat 833, Cat 1341 A, Cat 3502,Cat 1508 B, Cat 3487,Cat 3470,Cat 3446, PS- 1347,CAT 1084 B, Cat 2503,Cat 3443.
II	13	Cat 3401,Cat 2205 B, Cat 1935,Cat 2083 A, Cat 700 A, Cat 2207 A, Cat 3458, Cat 1328,Cat 301 A, Cat 1181 A, Cat 2134 A, Cat 473,Cat 460 B.
III	9	Cat 1921 A, Cat 872 B,JS 95 – 60,Cat 2891,Cat 3441, Cat 3439,Cat 3437,Cat 2119 B, Cat 198
IV	12	Cat 18 A, Cat 3507,Cat 1296 B, Cat 411,Cat 3448,Cat 523, Cat 3442, Cat 492 A, Cat 2237,Cat 2117B, CAU-SLC-6,Cat 2122 A.
V	9	Cat 3406, Cat 6267 A, HARDEE, Cat 3339, Cat 2029 B, Cat 2126 A,CAU-SLC-2/P,CAU-SLC-7,Cat 1843 A
VI	1	Cat 3476
VII	1	Cat 579
VIII	1	CAU-SLC-3
IX	1	CAT 2121 B

Table 2 Average intra and inter cluster distances of 75 soybean genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	270.907	589.049	464.690	1257.182	1976.912	996.104	3330.499	3184.434	7787.723
II		466.499	895.300	896.416	1366.501	986.101	2091.786	2241.042	5816.898
III			429.861	1468.759	2495.522	1541.166	3952.368	3599.901	8937.077
IV				602.602	1937.966	1558.303	1646.823	1846.254	6363.221
V					1181.460	2476.396	2105.396	2132.398	3547.712
VI						0.000	2455.459	4008.322	6803.900
VII							0.000	2563.242	2782.473
VIII								0.000	5434.918
IX									0.000

Table 3 Cluster mean values for 13 different characters of soybean genotypes

Cluster	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	Nodes/ plant	Primary branches/plant	Pod clusters/ plant	Pods/ clusters	Pods/ plant	Seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)	Harvest index (%)	Oil content (%)
I	46.804	96.891	36.759	17.787	2.752	10.762	2.289	26.383	2.228	14.840	6.425	51.937	12.843
II	49.331	102.178	47.697	18.274	3.238	15.276	2.243	34.190	2.121	13.840	8.600	50.684	13.045
III	40.578	100.302	35.548	14.444	2.661	9.949	2.144	21.672	2.164	15.600	5.594	48.562	12.778
IV	51.983	106.807	60.989	21.737	3.278	13.676	2.182	24.588	2.069	11.075	5.004	42.330	11.415
V	52.422	107.884	47.836	30.173	4.325	19.797	2.539	52.974	2.262	14.828	10.575	42.765	12.588
VI	51.100	93.040	53.992	24.960	2.316	7.788	2.612	29.256	2.064	12.492	7.380	73.380	13.188
VII	56.200	106.440	81.552	35.280	6.816	31.148	2.352	39.556	1.764	20.080	13.712	48.904	9.328
VIII	75.800	130.840	55.752	19.320	3.576	19.668	2.792	40.596	1.984	7.900	2.960	33.120	11.908
IX	55.800	111.240	71.832	54.040	5.636	48.088	3.032	83.016	2.604	11.406	20.442	49.108	13.068
	Contribution of each character to the divergence												
No. of times appearing first in ranking	128	405	947	116	0	37	0	822	0	56	2	260	2
Percentage of contribution toward total divergence	4.61	14.59	34.13	4.18	0.00	1.33	0.00	29.62	0.00	2.02	0.07	9.37	0.07

selected for use in hybridization programme for specific breeding objectives.

The average inter-cluster distance ranged from 464.690 (between cluster III and 1) to 8937 (between cluster III and IX). Maximum inter-cluster distance suggested wide diversity between the groups while the minimum inter-cluster distance indicated close relationship (Singh and Chaudhary 1985). Genotypes belonging to the separate clusters separated by a high estimate of statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants (De *et al.* 1992). Further it was also suggested that the magnitude of heterosis largely depended on the degree of genetic diversity in the parental lines (Roy *et al.* 1993).

The contribution of different characters towards the divergence of 75 soybean genotypes is presented in Table 3. The character plant height (34.13%) contributed highest to the total divergence of the genotypes, followed by pods/plant (29.62%), days to 80% maturity (14.59%), harvest index (9.37%), number of days to 50% flowering (4.61%), number of nodes/plant (4.18%), 100 seed weight (2.02%), number of pod clusters/plant (1.33%), and the least contribution towards divergence was recorded for the characters seed yield/plant and oil content with a relative contribution of 0.07% each. The maximum contribution of plant height and number of pods/plant in the present study was in conformity with results reported by Shinde *et al*. (2013).The importance of number of pods/plant and plant height towards divergence in soybean were also reported by Kumar and Nadarajan (1994). However Kachhadia *et al.* (2014) reported that the important traits causing maximum genetic divergence were the number of pod clusters/plant and oil content. The difference in the result reported is may be due to different material or genotypes used. The contribution of the characters like number of primary branches/plant, number of seeds/pod and pods/cluster were found to be negligible. The characters number of seeds/pod and number of primary branches/plant were found to have no contribution towards divergence. Similar results were reported by Jency and Kalaimagal (2015). The data on cluster means summarized in Table 3 revealed that different clusters exhibited marked differences in respect of all 13 characters studied. The highest cluster means values for the characters, viz. plant height, number of nodes/plant, number of pods/cluster/plant, number of pods/cluster, number of seeds/pod, number of pods/plant and seed yield/plant was observed in cluster IX; and for days to 50% flowering and days to 80% maturity was observed in cluster VIII, cluster VII for number of primary branches/plant and 100 seed weight, cluster VI for cluster I for harvest index and oil content. Genotypes belonging to the separate clusters separated by a high estimate of statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants (De *et al.* 1992).

On the basis of inter-cluster distance, cluster mean values, mean per se performance and contribution of individual character towards divergence it is advisable to attempt crosses between genotypes from cluster III and cluster IX which may lead to obtaining higher heterotic effect and broad spectrum variability in the segregants.

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