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Short communication

Genetic divergence analysis of soybean (*Glycine Max* L.) genotypes using mahalanobis multivariate analysis

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Soybean (*Glycine max* L.*)* is an important oilseed crop of *legumeniaceae* family and also known as 'miracle golden bean' of the 21st century (Agarwal *et al.* 2013). Hermann (1962) divided the genus Glycine into 3 subgenera and the first subgenus Leptocyamus (Benth.) with 6 wild perennial species indigenous to Australia, and the Pacific Islands, the second subgenus Glycine L. with 2 species of African origin and the third subgenus Soja (Moench) containing *G. max* (L.) Merrill and *G. soja* and *G. ussuriensis* (Sherman *et al.,* 2014). But it is seemed that being a largest producer of soybean in the country due to large area coverage, still having low productivity and yield in comparison to other growing countries. This may be due to lack of improved high yielding varieties, narrow genetic base of released varieties, use of poor quality seeds and non-availability of irrigation (Gour, 2018).

Inclusion of genetically diverse parents, which is having good agronomic base in hybridization programme, will serve the purpose of combining desirable genes or obtaining superior recombinations. Among the several methods of multivariate analysis used to the genetic diversity in biological population, D^2 analysis has been a perfect test in the quantitative estimation of genetic diversity. D^2 statististics provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence (Maurya and Singh, 1977). Considering the importance of soybean as a economic value in the agriculture throughout the world and contributing their role in the high yield and quality, this crop require more diversification regarding genetic broadening and systemic study. The present investigation of the genetic component responding yield and quality attributing traits included for evaluation of different accessions/ land races and released variety.The field studies were carried out at Research Farm, under Mandsaur University, Mandsaur (Madhya Pradesh). Mandsaur situated in North Eastern part of Madhya Pradesh state, is located at an elevation of 379.50 meter above mean sea level on latitude of 24.0734° North and longitude of 75.0679° East. The climate of the region is sub-humid type with an average rainfall of about 883 mm and soil of area is sandy-loam in nature. Crop was raised during *Kharif* 2022-23. The area of the experimental field was black soil, clayey in its texture, moderate fertility, uniform in topography and free from water logged condition. The experimental area occupied was quite uniform in respect to topography. The soil's physical and chemical composition is as followed by pH 7.4, EC 0.55, clay 20% and silt 25% etc.

During the present investigation seeds of twenty five diverse genotypes were procured from different geographical sources and collected from Indian Institute of Soybean research, Indore. The field experiments were laid out in randomized block design with three replications. Twenty five entries were planted each in three rows with row to row distance 45 cm and plant to plant distance 5 cm. Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. D^2 analysis was carried out using the data recorded on germplasms. Mahalanobis generalized distance (D^2) between any two populations is given by the formula $D^2 = \sum \lambda^{ij} \sigma^i \sigma^j$. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

Population clusters were determined by Tocher's method using the formula $n(n-1)/2D^2$ given by Rao (1952). Rao (1952) suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2 value be added to this group such that

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it did not increase the average D^2 value appreciably. This process is continued. Any population, which sharply increases the average D^2 value, should not be included in that group. After formation of first cluster, the process is repeated to form second, third etc., clusters using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

Table 1: Clustering pattern of 25 genotypes on the basis of genetic divergence in soybean

Cluster	Name of Genotypes	Number of Genotypes
I	SQL-113, AMSS-44, SQL-110, JS-2034, JS-9560, SQL-97	6
II	TGX-86-24-2F, AURDC-5, AMUS-542, AGS-25, UPSL-742, AURDC-508, JS-335, SL-432	8
III	AGS-205, NALIYAS, UPSL-63, TGX-860-11D, B-327, AGS-156, NP-4, AGS-218, TGX-93-36E, TGX-293-65E, AMUS-76	11

The analysis of variance revealed highly significant differences among genotypes for all the eight characters under investigation. From the estimates of variances and co–variances, D^2 – statistic, which utilizes Wilk's criterion, a simultaneous test for all the eight characters was done, which also showed highly significant differences among genotypes of soybean. These differences suggest the existence of considerable divergence among the experimental material under study. A method suggested by Tocher (Rao, 1952) was used to group the 25 genotypes into three different clusters based on the D2 values. Among three clusters, cluster III were the biggest with 11 genotypes (AGS-205, NALIYAS, UPSL-63, TGX-860-11D, B-327, AGS-156, NP-4, AGS-218, TGX-93-36E, TGX-293-65E, AMUS-76) followed by cluster II with 8 genotypes (TGX-86-24-2F, AURDC-5, AMUS-542, AGS-25, UPSL-742, AURDC-508, JS-335, SL-432) and cluster I with 6 genotypes (SQL-113, AMSS-44, SQL-110, JS-2034, JS-9560, SQL-97). Previously, similar findings were also observed by Kachhadia *et al.*, 2014 among sixty one soybean genotypes.

Clusters means of all the 8 characters have been studied (Table 2). Cluster mean was the highest for days to maturity in cluster II (92.96) and lowest for number of primary branches/ plant in cluster III (3.45). Using cluster means genetic diversity analysis reveals genetic backgrounds and interactions of germplasm and manages crop primary pools. The highest (D= 4.440) inter cluster distance was observed between cluster II and I, followed by, cluster III and II (3.142), cluster III and I (2.913), indicating wide diversity between genotypes in these clusters (Table 3). Moreover we know that heterosis can be best exploited and chances of getting transgressive segregants are maximum, when generating diverse lines are crossed. Because the genotypes from diverge cluster may be advised for inclusion in hybridization program as they are expected to develop excellent segregants (Khumukcham *et al.,* 2022).

Table 2: Cluster means for 8 characters under study in soybean

Traits	Cluster means		
	I	II	III
DFF	43.06	53.04	52.45
DFPI	50.17	60.08	60.06
PH	29.83	52.92	36.33
NPPP	52.06	77.62	63.61
NPBPP	3.76	4.38	3.45
DM	88.61	92.96	89.27
HSW	8.86	8.15	8.74
GYPP	12.85	14.43	12.86

DFF- Days to fifty percent flowering, DFPI- Days to 50% pod initiation, PH- Plant height (cm), NPPP- No. of pods per plants, NPBPP- No. of primary branches/ plant, DM- Days to maturity, HSW- 100 Seed weight (gm), GYPP- Grain yield/plant (gm)

The highest (D = 2.081) intra-cluster distance was found for cluster I, followed by, cluster II (1.961), cluster III (1.913). It is suggested that the genetic materials belonging to these clusters may be used as parents for hybridization programme to develop desirable variety because crosses between genetically divergent lines will generate heterotic segregants (Chandel *et al.*, (2013); Ghodrati (2013); Mahbub *et al.,* (2015); Neelima *et al.*, (2018); Koraddi and Baswaraja, (2019).

Table 3: Average intra and inter cluster D^2 values between the clusters

Clusters	I	II	III
I	2.081	-	-
II	4.440	1.961	-
III	2.913	3.142	1.913

Wilk's criterion was used to group the 25 genotypes into three different clusters based on the D2 values. Cluster III was the biggest with 11 genotypes, followed by cluster II with 8 genotypes and cluster I with 6 genotypes. Cluster mean was the highest for days to maturity in cluster II (92.96) and lowest for number of primary branches/plant in cluster III (3.45). Using cluster means genetic diversity analysis reveals genetic backgrounds and interactions of germplasm and manages crop primary pools. The highest inter-cluster distance was observed between cluster II and I, followed by cluster III and II (3.142), and cluster III and I (2.913). This indicates wide diversity between genotypes in these clusters, which can be exploited to generate transgressive segregants. The highest intra-cluster distance was found for cluster I, followed by cluster II (1.961), and cluster III (1.913). It is suggested that genetic materials belonging to these clusters may be used as parents for hybridization programmes to develop desirable variety.

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