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Research Note

Assessment of genetic diversity for yield and seedling traits in soybean (*Glycine max* L. Merrill)

Manav* and R.N. Arora
Department of Genetics and Plant Breeding, College of Agriculture, CCS Haryana Agricultural University, Hisar-125 004, Haryana, India
***E-mail:** manavhisar@gmail.com

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Abstract

Forty five germplasm accessions of soybean were selected at CCSHAU, Hisar during *kharif,* 2014 to study genetic diversity utilizing Mahalanobis D^2 statistic. The analysis suggested considerable genetic divergence among the material for all the character studied. Based on Mahalanobis D^2 statistic, the 45 accessions were grouped into 8 cluster, wherein cluster II was the largest one having 11 accessions. The maximum inter-cluster distance was observed between cluster III and VII. Intra-cluster distance was maximum for cluster V, indicating the existence of high variability within the cluster. Cluster mean values for yield and seedling traits revealed considerable differences between the clusters for all characters under study. Among the 15 characters studied, the most important character contributing to the total divergence was number of pods per plant (42.75%) followed by seed yield per plant (22.10%) and root length (19.70). So, these characters should be given due consideration while selecting parents for hybridization.

Key Words

Soybean, genetic diversity, cluster analysis, D^2 statistic

Soybean [*Glycine max* (L.) Merrill] is recognized as the most important grain legume in the world in terms of total production and international trade (Golbitz *et al*., 2007) being an important source of protein and oil. Soybean oil contains about 38 to 42 per cent high quality protein and 18 to 20 per cent oil, which can meet present and future needs of the world for protein and edible oil. Assessment of genetic diversity facilitates classification and identification of diverse genotypes in a germplasm collection. In a breeding programme, progenies derived from crosses involving diverse parents, are selected on the basis of genetic divergence analysis, are expected to 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 [Jain and Ramgiry (2000), Shrivastava *et al.* (2001) and Kayande and Patil (2009)] for the selection of potential parents to be used in a hybridization programme for obtaining desirable segregants. Multivariate analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936) is a powerful tool in identifying the degree of divergence in biological population at genetic level. Therefore, an effort has been made to assess the genetic diversity in 45 genotypes of soybean for fifteen traits.

The experimental material comprised of 45 germplasm accessions of soybean collected from various sources, viz. Pulses Section, Department of Genetics and Plant breeding, CCSHAU, Hisar during *kharif,* 2014. All these accessions were sown in randomized block design having three replications in single row of 3m length, keeping row to row distance of 45 cm and plant to plant distance of 10 cm. In each replication, 3 checks (PS 688, PS 1347 and PK 416) were also sown randomly in order to avoid block effect. Data were recorded on five randomly selected competitive plants for all the quantitative traits. The replicated data were subjected to analysis of variance followed by multivariate analysis of D^2 statistic according to Mahalanobis (1936). The genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952).

The analysis of variance revealed highly significant difference among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Based on D^2 statistic, 45 genotypes studied were grouped in 8 clusters indicating the presence of large amount of diversity among the genotypes (Table 1). Clustering pattern revealed that cluster II was the largest one with 11 genotypes, followed by cluster I with 9 genotypes, cluster IV and VI each with 7 genotypes, cluster III, VII and VIII with 3 genotypes each and cluster V with 2 genotypes (Table 1). It was observed that clusters having more than one genotype included the genotypes originating from different eco-geographical regions and that the genotypes belonging to the same eco-geographical region were included in different clusters suggesting that geographical diversity does not necessarily represent genetic diversity. This was in agreement with the results obtained earlier by Jeethava *et al*. (2000), Jeena and Arora (2002), Reddy *et al*. (2004), Patil *et al*. (2011) and Sharma *et al*. (2012). The average inter- and intra-cluster D^2 values among the 8 clusters are presented in table 2. An analysis of the inter and intra-cluster distances revealed that the inter-cluster distance was maximum between clusters III and VII (9.26) followed by clusters III and VIII (9.20), IV and VII (8.77), IV and VIII (8.46) indicating that genotypes from these clusters were highly divergent meriting their consideration in selection for hybridization. It is true that larger the divergence between genotypes, higher would be the heterosis when hybrid development programme is planned to develop yield superior varieties (Bekele *et al.*, 2012). Minimum inter-cluster distance was observed between clusters I and II (3.33) indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. However, it is also valuable considering genotypes within cluster with respect to a trait of interest as suggested by Chahal and Gosal (2002) and Keneni *et al.* (2005). Cluster VI had the minimum intra-cluster value (2.109) indicating a minimum difference among the genotypes grouped in this cluster whereas, cluster V had the maximum intra-cluster distance of 5.148 followed by cluster VII (3.836) and cluster VIII (3.311). Hence, the genotypes included in cluster III and VII may be selected for more effective crossing programme and would result in wide spectrum of variability to operate selection in segregating population. A perusal of the results on cluster means for yield and seedling traits (Table 3) revealed considerable differences between the clusters for all the characters under study. Genotypes in cluster V, I and III were early in flowering. The genotypes in cluster II, III and IV were early in maturity. Highest plant height was recorded in cluster VII (96.11) while lowest was observed in cluster IV (62.81). Cluster VIII recorded highest mean value for number of branches per plant (6.47), whereas cluster III had the lowest mean value (3.75). The cluster mean for number of pods per plant ranged from 26.61 to 69.54 which were attained by group VII and I, respectively. For pod length, the highest mean value was possessed by cluster VIII (7.57) and the lowest was possessed by cluster I (4.65). More number of seeds per pod was recorded by the individuals in the cluster V (4.05) while less number was seen in cluster I (2.83). With respect to 100-seed weight, Cluster VIII recorded the highest mean value (14.96) while cluster III recorded the lowest (8.31). The highest mean value for seed yield per plant was recorded in cluster VII (84.06) and the lowest in cluster I (39.80). Maximum germination percentage was recorded by the genotypes in Cluster VII (97.44) while minimum was recorded by the genotypes in cluster IV (78.85). The mean value for root length was in the range of 12.74 (cluster III) to 16.89 (cluster VIII). For shoot length, the highest mean value was possessed by cluster VII (20.76). The cluster mean for fresh weight of seedlings ranged from 4.38 to 6.83 which were attained by cluster VI and VII, respectively. Cluster VII (1.66) recorded the highest mean value for seedling dry weight. The highest mean value for seedling vigour index was recorded in cluster VII (35.73). These observations suggested that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Therefore, the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. For bringing improvement in specific traits, genotypes like DS 3101 of cluster VII for plant height, number of branches per plant, number of pods per plant, germination percentage, shoot length, fresh weight of seedlings, seedling vigour index and seed yield per plant; SL 1137 of cluster V for early flowering; SL 1028 of cluster VIII for 100-seed weight; MAUS 76 of cluster VIII for pod length and number of seeds per pod could be considered in soybean improvement programme as shown by their *per se* performance (Table 5). Information on the relative contribution of various plant characters towards divergence has also been reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations (Suneetha *et al.*, 2012). Based on D^2 values, per cent contribution of different characters towards divergence was calculated (Table 4). Among the 15 characters studied, the most important character contributing to the total divergence was number of pods per plant (42.75%) followed by seed yield per plant (22.10%) and root length (19.70). These characters can be given greater importance in selection of potential parents for hybridization. Similar results for one or more characters have been reported by Chandel *et al.* (2013). Contribution of the remaining characters to total divergence was relatively low. Therefore, traits like number of pods per plant, seed yield per plant and root length contributing to 84.55 per cent of the total divergence need to be stressed in selection of parents for hybridization.

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Table 1. Distribution of soybean genotypes into different clusters based on genetic divergence

Cluster No.	Number of genotypes in cluster	Genotypes included in the cluster
I	9	PS 1539, DS 12-5, PS 1543, DS 12-13, PS 1540, PS 1477, DS 2705, DS 2706, DS 3047
II	11	DS 2961, SL 744, DS 3050, SL 525, SL 955, SL 979, SL 958, SL 980, SL 925, SL 982, SL 778
III	3	SL 983, SL 1031, SL 1039
IV	7	SL 1055, SL 1074, SL 1108, SL 1113, SL 1127, SL 1129, SL 1130
V	2	SL 1137, PK 416
VI	7	SL 1172, SL 1175, SH 1, P 1213, P 9712, PS 1347, PS 688
VII	3	JS 20-98, SL 1028, DS 3101
VIII	3	DS 3102, 1VT 13, PS 1556

Table 2. Average intra- and inter-cluster distance (D^2) values among 45 genotypes of soybean

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**2.220**	3.338	4.979	4.966	6.348	5.414	7.071	7.803
II		**2.416**	3.836	3.868	6.198	5.235	8.121	8.002
III			**2.941**	4.472	6.224	5.973	9.263	9.206
IV				**3.211**	6.326	5.185	8.776	8.464
V					**5.148**	4.808	6.845	6.413
VI						**2.109**	6.863	6.843
VII							**3.836**	5.030
VIII								**3.311**

(Bold figures indicate intra-cluster distance)

Table 3. Cluster mean values of 15 characters in 45 genotypes of soybean

Cluster	DTF	DTM	PH	BP	PP	SP	PL	HSW	G	RL	SL	SFW	SDW	SVI	SY/P
I	51.58	120.11	79.70	5.01	**69.54**	**2.83**	**4.65**	10.79	88.59	14.51	18.83	5.47	1.41	29.53	**39.80**
II	54.32	116.45	73.72	4.57	63.41	3.12	5.28	9.47	85.03	16.70	17.95	5.09	1.28	27.57	50.16
III	52.23	**113.66**	68.22	**3.75**	56.64	3.48	5.95	**8.31**	81.33	**12.74**	17.32	4.83	1.22	25.74	58.43
IV	57.21	115.71	**62.81**	5.24	51.86	3.18	5.04	11.74	**78.85**	15.70	17.01	4.66	1.20	**24.01**	62.54
V	**47.95**	126.00	86.33	5.60	36.38	**4.05**	6.76	13.18	93.00	13.10	17.80	5.25	1.15	27.70	71.45
VI	56.16	125.61	85.71	5.50	35.37	3.29	5.03	13.01	93.23	14.31	**14.91**	**4.38**	**1.14**	31.35	71.42
VII	53.32	**131.77**	**96.11**	6.45	**26.61**	3.35	4.93	13.75	**97.44**	13.71	**20.76**	**6.83**	**1.66**	**35.73**	**84.06**
VIII	**63.31**	130.00	92.55	**6.47**	28.73	3.84	**7.57**	**14.96**	96.66	**16.98**	20.10	6.34	1.58	34.23	80.68

DTF = Days to 50% flowering, DTM = Days to maturity, PH = Plant height (cm), BP =Number of branches/plant, PP = Number of pods/plant, SP = Number of seeds/pod, PL = Pod length (cm), HSW = 100-seed weight (g), G =Germination (%), RL = Root length (cm), SL = Shoot length (cm)SFW = Seedling fresh weight (g), SDW = Seedling dry weight (g), SVI = Seedling vigour index (%), SY = Seed yield/plant (g)

Table 4. Relative contribution of characters studied towards total genetic divergence among 45 soybean genotypes

S. No.	Characters	Number of ranked first	Contribution towards divergence (%)
1.	Days to 50% flowering	13	1.31
2.	Days to maturity	1	0.10
3.	Plant height (cm)	5	0.51
4.	Number of branches/plant	2	0.20
5.	Number of pods/plant	421	42.75
6.	Number of seeds/pod	18	1.82
7.	Pod length (cm)	15	1.52
8.	100-seed weight (g)	5	0.51
9.	Germination (%)	6	0.61
10.	Root length (cm)	195	19.70
11.	Shoot length (cm)	32	3.23
12.	Seedling fresh weight (g)	48	4.85
13.	Seedling dry weight (g)	7	0.71
14.	Seedling vigour index (%)	1	0.10
15.	Seed yield/plant (g)	221	22.10

Table 5. List of diverse and promising genotypes selected for various characters in soybean

Genotype	Cluster	Characters
SL 1137	V	Days to 50% flowering
SL 1028	VII	100-seed weight
DS 3101	VII	Plant height, number of branches per plant, number of pods per plant, germination percentage, shoot length, fresh weight of seedlings, seedling vigour index, seed yield per plant
DS 3102	VIII	Shoot length
MAUS 76	VIII	Number of seeds per pod, pod length