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Genetic Divergence in Soybean (Glycine max L. Merrill)

G. Neelima, S P Mehtre and G W Narkhede

Department of Agricultural Botany
(Genetics and Plant Breeding)
Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani – 431402 (M.S)

ABSTRACT

An investigation was conducted during the year 2015-2016 with 124 germplasm accessions of soybean (Glycine max (L.) Merrill.) at All India Coordinated Research Project on Soybean, at the experiment fields of Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani to identify the diverse genetic stocks for the use in hybridization programme through genetic diversity based on Mahalanobis D² statistics. The data was recorded on eleven yield contributing characters on accessions raised in Randomized Block Design in two replications. The germplasm accessions were grouped into five different clusters. The maximum inter-cluster distance was found between clusters IV and V (D=66.15) followed by clusters II and V (D=58.81), clusters III and IV (D=57.05), cluster I and V (D=47.12) and clusters I and IV (D=47.00) indicated that these groups of genotypes were highly divergent from each other. Among the five clusters, the Cluster I recorded high mean performance for five characters viz., Days to initial flowering, Days to 50% flowering, Days to maturity, Plant height and 100 seed weight. Regarding the grouping of clusters, cluster I has maximum number of entries i.e., 76 genotypes followed by Cluster II with 46 genotypes, Cluster III with 8 genotypes and Cluster IV and Cluster V with one each respectively.
Key words: *Soybean, divergence, cluster*

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill.) is an important and well recognized oil and protein containing crop of the world. The area under soybean cultivation is increasing as it is short duration crop and higher productivity compared to other legumes family such as blackgram and greengram. The area, production and productivity of soybean in India during 2015-2016 was recorded as 116.5 lakh ha, 80 lakh MT and 687 kg/ha respectively. In Maharashtra the area, production and productivity of soybean during 2015-2016 was recorded as 35.9 lakh ha, 27.8 lakh MT and 776 kg/ha respectively (SOPA, Indore). For creating desirable variability, parents should be selected carefully and some biometrical tools can be used. For assessing the genetic diversity in the germplasm collections, D² statistics is used which measures the forces of differentiation at intra and inter cluster levels. Above all, the greatest potential of soybean lies in increasing the available food supply for the rapidly increasing population in the 21st century (Wilmot, 2001). Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for hybridization program. The development of new varieties is mainly governed by the magnitude of genetic variability present in the base material. Therefore, in the present investigation, an effort was made to understand the quantum and nature of genetic variability present in a set of 124 elite soybean accessions using Mahalanobis D² statistics.

METHODOLOGY

The experiment was conducted using 124 germplasm accessions of soybean in a randomized block design with two replications during *Kharif* 2015-16 at All India Coordinated Research Project on Soybean, at the experiment fields of Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The D² analysis was carried out for all the eleven characters to access genetic divergence using Mahalanobis D² statistics (1936). The traits included under study were days to initial flowering, days to 50% flowering, plant height, number of nodes per plant, number of branches per plant, number of pod clusters per plant, number of pods per plant, 100 seed weight, seed yield per row, oil and protein content. The genotypes

were grouped on the basis of minimum generalized distance using the Tocher's method (Rao, 1952) (Table 1). In the present study, 124 genotypes were grouped into five clusters with the assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from groups belonging to different clusters (Table 2).

RESULTS AND DISCUSSION

Based on D^2 statistics and Tocher's method, the 124 germplasm accessions were grouped into five clusters with variable number of entries revealing the presence of variable amount of diversity in the material (Table 1). The cluster I has maximum number of genotypes i.e.,76 followed by cluster II with 46, cluster III with 8 and clusters IV and V with one each respectively (Table 1). The maximum inter cluster distance was found between cluster IV and V (D=66.15) followed by cluster II and V (D=58.81) and cluster III and IV (D=57.05). The minimum inter cluster distance was observed for clusters I and III (D=33.73) and cluster III and V (D=33.82). 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). Similar results were found by Sharma S.S. (2005), Agdew *et al.*, (2012), Chandel *et al.,* (2013), Shinde *et al.,* (2013)Anupam Barh *et al.,* (2014).

Table No.1 Distribution of soybean genotypes in five clusters.

Cluster No.	No. of Breeding lines included	Breeding Lines
I	76	CAT 1328, CAT 492A, CAT 2197B, HARDER, CAT 833, CAT 2070B, CAT 2134A, CAT 96, G-620, CAT 2207A, CAT 411, CAT 1935B, CAT 489A, CAT 2205B, CAT 1508B, CAT 2122A, CAT 2119B, GP P15, H2P2, PP6, CAT 872A, CAT 3507, CAT 3470, GP 15A, CAT 3453, CAT 2126B, CAT 2114A, VGM-70, CAT 1341B, CAT 3502, CAT 3465, CAT 1267A, CAT 1979B, CAT 2144B, JS 95-60, CAT 2130B, RKS-18, CAT 3401, CAT 3499, CAT 2097B, CAT 3466, AGS-25, CAT 2126A, CAT 1341A, CAT 3293, CAT 2083A, CAT 1979A, CAT 2197A, CAT 1641A, CAT 3492, CAT 449A, G-828, CAT 2891, CAT 2125B, CAT 3439, CAT 676B, CAT 1641B, CAT 3262, CAT 3467, G-688, CAT 2237B, LEE-54, CAT 489A, G4-P17, LEE-95, CAT 3476, JS-335, CAT 700A, CAT 3459, CAT 97B, CAT 2120A, CAT 3438, CAT 3442, CAT 3487, CAT 3284, CAT 412.
II	46	CAT 3447, CAT 3461,CAT 3446, CAT 473, CAT 1921A, CAT 3458, CAT 3406, CAT 3443, CAT 523, CAT 2115B, CAT 1523A, CAT 3442, CAT 1987B, CAT 3441, EC-538828, CAT 2503, CAT 872B, CAT 91B, CAT 3460, G5 P22, CAT 2121B, PS-1347, CAT 1843A, CAT 1533, CAT 610, CAT 3437, CAT 365, CAT 301A, CAT 3198, CAT 3483, CAT 1181A, CAT 3454, CAT 3448, CAT 2117B, CAT 1084B, CAT 3457, CAT 3452, CAT 1921B, CAT 18A, CAT 3440, CAT 460B, CAT 3456, CAT 140A, CAT 3480, CAT 3506, CAT 579
III	8	CAT 411A, MAUS-71, VLS-75, MAUS-162, F4 D92P20, F4 P21, MAUS-158, NRC-37
IV	1	CAT 3339
V	1	G-11

The cluster means of all the 11 characters had presented in theTable 3. For days to initial flowering the cluster mean was high for the cluster I (38.27) followed by cluster III (37.82) and least for cluster II

(32.50) followed by cluster IV (34.19). For days to 50% flowering, least cluster mean was recorded by cluster II (34.83) followed by cluster IV (36.56)) and cluster V (39.18) and high for cluster I (40.55). For days to maturity cluster II (90.58) and cluster IV (92.5) showed least cluster mean and cluster I (96.09) showed high mean performance. For number of branches per plant higher cluster mean was recorded for Cluster I (1.90) followed by Cluster III (1.62) and cluster V (1.52) and minimum for cluster II (1.02). For plant height highest mean performance was recorded for cluster I (46.18) followed by cluster III (43.24) and least for cluster II (34.23). For number of nodes per plant cluster III (8.30) showed highest cluster mean followed by cluster V (8.28) and cluster IV (8.26) and low mean performance for cluster II (7.55). High mean performance for number of pods per plant was recorded for the cluster III (27.34) followed by cluster V (26.79) and lowest for cluster II (25.57).

Table:2 Average Inter and Intra Cluster distances

Cluster	Average Inter and Intra cluster D square values for five clusters
Cluster	**1**	**2**	**3**	**4**	**5**
1	484.48 (22.01)	1345.68 (36.68)	1137.81 (33.73)	2209.45 (47.00)	2220.64 (47.12)
2		551 (23.47)	2351 (48.48)	1017.22 (31.89)	3458.92 (58.81)
3			299.53 (17.30)	3255.53 (57.05)	1144.23 (33.82)
4				0 (0.00)	4375.53 (66.15)
5					0 (0.00)

Table 3: Cluster mean of 11 characters studied for genetic divergence.

Cluster	Days to initial flowering	Days to 50% flowering	Plant Height (cm)	Number of Branches/plant	No. of Nodes/plant	No. of pod clusters/plant
I	38.27	40.55	46.18	1.9	8.12	6.73
II	32.5	34.83	34.23	1.02	7.55	6.33
III	37.82	40.11	43.24	1.62	8.3	6.96
IV	34.19	36.56	40.46	1.36	8.26	6.71
V	36.74	39.18	42.84	1.52	8.28	6.77

Table No. 3 Contd.

Cluster	No. of pods/plant	100-Seed weight	Oil (%)	Protein (%)	Seed Yield/Row (gm)
I	26.59	10.34	17.99	39.33	133.83
II	25.57	10.15	21.97	39.51	120.71
III	27.34	9.65	18.74	39.52	143.92
IV	26.97	10.35	20.14	39.88	140.26
V	26.79	9.7	19.14	39.84	132.41

The trait number of pod clusters per plant has recorded maximum cluster mean performance for the cluster III (6.96) followed by cluster V (6.77) and minimum for cluster II (6.33). In case of 100 seed weight, the highest cluster mean was observed in IV (10.35) followed by cluster I (10.34) while least for cluster III (9.65). For oil content least cluster mean was recorded by cluster I (17.99) followed by cluster III (18.74) and cluster V (19.14) and high for cluster III (27.34). For protein content the highest cluster mean was for cluster IV (39.88)) followed by cluster V (39.84) and cluster III (39.52). For seed yield per

row (g) highest cluster mean as cluster III (143.92) followed by cluster IV (140.26) and cluster I (133.83). Similar results were the findings of Shinde *et al.,* (2013), Ahmad *et al.,* (2014), Vidhya *et al.,* (2014) and Mahbub *et al.,* (2016).

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