

## Assessment of Divergence and Variability in Soybean (*Glycine Max L. Merrill*) Germplasm for Yield Attributing Traits



### Agriculture

**KEYWORDS :** Genetic Divergence, D2 Statistics

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### ABSTRACT

42 soybean genotypes were evaluated for morphological characters to study the diversity pattern among the genotypes. The genotypes were grouped into 7 clusters. Maximum 13 genotypes were grouped in cluster IV followed by 10 in cluster I, 8 in cluster II, 5 in cluster IV, and 4 in cluster V the clusters III and VII are represented by single genotype. The ranges for Intra- cluster D2 values exhibited 0.00 to 774.50 and inter-cluster D2 values 898.25 to 15964.43. Indicating high degree of diversity among the genotypes. The Intra cluster distance is highest in cluster VI (774.50) and lowest by the cluster V (358.03). Highest inter cluster distance was noticed between cluster III and VII (15964.43) and the lowest was between cluster I and II (898.25). Considering all the characters, the genotype MACS 1201, SL 778 and MAUS 449 were identified as the best genotypes for grain yield.

Soybean (*Glycine max* L. Merrill) is known as 'Golden bean' and potential crop of 21st century belongs to family Fabaceae, early domestication traced to the eastern half of North China in the eleventh century B.C. then it was first introduced to U.S.A. in 1804. Migration of this crop to India is believed to have occurred around 1880 A.D (Lance Gibson and Garren 2005). India ranks third after Argentina and Brazil to have registered a phenomenal growth in the production of soybean. Soybean cultivation in India has steadily increased. It was a minor crop during the early 1970s but at present, it occupies third place in the oilseed production in India. The area under soybean in India has rapidly increased from 0.03 million ha in 1970 to 2.6 million ha in 1990 and to 10.8426 million ha in 2012 and production from 1.84 (1970) to 14.68 million tonnes (2012). (Directorate of Economics and Statistics, Government of India 2012-13). Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse heterotic group with possible breeding values in manifestation of breeding potential of genotypes in specific breeding programme. In breeding programme, progenies derived from diverse crosses which is selected based on genetic divergence analysis are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in advance generation (Singh and Mishra 1996) So, for the successful genetic improvement program for yield and yield contributing characters it is important to understand the heterotic group or classification of genetic stocks and choice of genetically divergent parents for hybridization to exploit heterosis is extremely essential. Therefore, this study was undertaken to identify suitable soybean parents having diverse characters through genetic divergence analysis.

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### Materials and methods

The Field Experimentation was conducted with forty-two genotypes of soybean procured from DSR Indore through AICRP, were grown at field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad Agriculture Institute-Deemed University. Allahabad, during kharif season 2010. The experiment was laid out in a randomized complete block design

with three replications. The entries were sown in three rows each of 3 m length with row to row spacing 45 cm and plant to plant 10 cm, ten randomly selected plants from each replication was taken for observation of characters viz., Days to 50 percent flowering, number of pods per plant, pod length (cm), number of branches per plant, plant height (cm), days to maturity, number of grains per pod, grain yield per plant (g), 100 grain weight (g), biological yield per plant (g), harvest index (%) and oil content (%) in each genotypes and replication. D<sup>2</sup> analysis was carried out following Mahalanobis (1936). Clustering of genotypes was done by Tochers's method as detailed by Rao (1952).

### Results and Discussion:

Divergence in the available cultivars is of immense importance for selecting the parents to be used in hybridization programme for obtaining desirable genetic recombination's. Improvement of yield, oil content in soybean is attributed to increased use of genetically diverse parents in breeding programme. Based on D<sup>2</sup> values, 42 genotypes were grouped into seven clusters (Table1). Among the clusters, cluster IV was the biggest (13 genotypes) followed by cluster I (10 genotypes), cluster II (8 genotypes) cluster VI (5 genotypes), cluster V (4 genotypes). Clusters III and VII had single genotype each. The genotypes belonging to diverse ecological regions clustered together, while those of same region entered separate groups. These findings were similar to the reports of Das (2000) and Ramgiry et al. (1999), and Parameshwar (2006).

Average highest intra-cluster distance was observed by cluster VI (774.50) followed by cluster II (493.92), cluster IV (432.79), cluster I (430.36), and cluster V (358.03) presented in (Table3). This suggested that the genotypes in clusters VI were relatively more diverse among themselves, however, in all cases, the inter cluster distances were greater than the intra-cluster distances implying presence of greater degree of genetic diversity between the genotypes of two clusters than the genotypes present within the cluster.

From the inter-cluster distances presented in (Table2) for seven clusters, it can be seen that the highest divergence occurred between Cluster III and VII showed maximum inter cluster distance (15964.43) followed by clusters III and VI (10439.62), cluster III and V (6144.10), cluster I and IV (1002.96). The lowest inter cluster distance was noticed between cluster I and II (898.25). Indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belong-

ing to these clusters may result in high heterosis, which could be exploited in crop improvement. The cluster means from various characters are presented in (Table 3). The cluster VII had the highest mean values for plant height (95.33 cm), 100-grain weight (10.28 g), grain yield per plant (21.79 g), biological yield/plant (15.33 g), and genotypes in cluster VI highest mean values for number of pods per plant (166.75), pod length (3.70), number of branches per plant (7.41) similarly, genotypes includes in cluster III highest mean values for number of seed per pod (2.46), harvest index (56.75 %), and less to number of days for 50 percent flowering (39.00 days), days to maturity (98.25 days) whereas the cluster II recorded highest mean values for oil content was (18.18 %).

Percentage contribution of each character towards genetic divergence had estimated from analysis (Table 3). It has been observed that oil percent (61.67) was highest contributor towards divergence followed by pods per plant (22.65), plant height (6.62), days to 50% flowering (2.67), grain yield per plant (2.44), 100- grain weight (0.35) and the least contributor towards total divergence was grains per pod (0.12). Therefore hence these characters should be given importance during hybridization and selection of segregating populations **Kayande et al., (2009)**.

The genotype MACS 1201, SL 778 and MAUS 449 were identified as the best genotypes for grain yield at Allahabad region. The characters pods per plant, number of branches per plant, grain yield per plant and harvest index with high GCV, The characters number of pods per plant, number of branches per plant,

plant height, 100-grain weight, grain yield per plant and biological yield per plant for high heritability and GA as percent of mean should be given top priority during selection. The cluster III and VII was most diverse to each other. Therefore, crosses could be planned between genotypes of cluster III and II with those of cluster VII and VI, which may yield wide spectrum of variability for these characters.

**Table 1: Distribution of 42 genotypes into different clusters**

So. No.	Cluster No.	No. of Genotypes	Name of the Genotypes
1	I	10	RKS 63, KS 103, HIMSO 1680, JS(SH) 2003-8, AMS-MB-5-19, JS 20-29, NRC 86, AMS 243, SL-525, Dsb 18.
2	II	8	VLS 77, AMS-MB-5-18, DS 15-2, TS 10, PS 1480, VLS 76, NRC 87, KDS 344.
3	III	1	JS 20-34
4	IV	13	PS 1476, PS 1477, NSO 81, NRC 88, KBS 8, CSB 08-08, PS- 1042, Bragg, JS 20-30, MASU 449, SL 871, KSO 245, MASC 1336.
5	V	4	NRC 85, DS 27-11, MASC 1336, MAUS 453.
6	VI	5	SL 778, Dsb 20, MACS 1311, RKS 61, BAUS 40
7	VII	1	CSB 08-09

**Table 2. Average intra (bold) and inter cluster D2 value of 42 soybean genotypes**

Clusters	I	II	III	IV	V	VI	VII
I	<b>430.368</b>	898.25	3045.248	1002.961	1145.613	3134.677	5921.480
II		<b>493.928</b>	1460.974	2476.705	2557.425	5566.582	8952.105
III			<b>0.000</b>	6012.061	6144.107	10439.620	15964.430
IV				<b>432.799</b>	909.257	1919.720	3459.924
V					<b>358.034</b>	1154.804	2941.928
VI						<b>774.502</b>	1852.837
VII							<b>0.000</b>

**Table 3. The cluster mean values, percentage contribution of 12 characters**

Clusters	I	II	III	IV	V	VI	VII	Contribution %
Days to 50% flowering	46.23	48	39	47.74	47.83	47.8	57	2.67
Pods/ plant	90.78	82.04	66	87.26	136.15	166.75	155.23	22.65
Pod Length (cm)	3.68	3.63	3.46	3.64	3.65	3.7	3.64	0
Branches/ plant	5.2	4.2	3.13	5.73	4.48	7.41	6.43	2.32
Plant Height (cm)	57.54	58.47	41.93	61.87	62.83	62.59	95.33	6.62
Days to Maturity	99.53	102.29	90.33	100.43	98.25	99.6	102.66	0.58
Grains/ pod	2.29	2.31	2.46	2.26	2.08	2.46	2.32	0.12
100 Grain Weight (g)	8.18	8.84	8.67	8.71	8.22	8.18	10.28	0.35
Grain Yield/ Plant (g)	12.6	10.86	8.4	17.96	12.67	17.12	21.79	2.44
Biological Yield/plant	34.06	25.2	15.33	45.71	41.83	49.33	58.33	0
harvest Index	37.07	43.5	56.75	39.77	30.81	34.59	37.42	0.58
Oil Content (%)	17.78	18.18	17.99	17.42	17.98	17.76	17.95	61.67

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