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Genetic diversity studies in soybean [*Glycine max* (L.) Merrill]

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Abstract

The current investigation was carried out to evaluate genetic diversity analysis among forty genotypes of soybean in RBD with three replications during *khariif*-2022, including three check varieties viz., JS 20-34, JS 95-60 and RKS-113 and thirteen component characters were studied for genetic diversity by using D2 statistics. The genotypes were grouped into ten distinct non-overlapping clusters, Cluster III had the maximum intra-cluster distance followed by cluster II and minimum intra-cluster distance was recorded by cluster I. maximum inter-cluster distance were observed between cluster I and X followed by cluster VI and X, cluster VIII and X, cluster I and V, cluster VIII and V, cluster I and IV. The minimum inter-cluster distance was noticed between cluster IX and VII followed by cluster I and VIII, cluster II and V, cluster II and IV indicating efficient breeding program can be undertaken to improve productivity and other yield attributes by selecting superior genotypes in segregating generation.

Keywords: Soybean [*Glycine max* (L.) Merrill], genetic diversity, cluster, D² statistics

Introduction

Soybean [*Glycine max* (L.) Merrill] is an annual herb, self-pollinated legume crop having 2n=40 chromosomes, belongs to family *Fabaceae* and genus *Glycine*. *Glycine* is divided into two sub-genera namely *Glycine wild* and *Glycine soja*. The cultivated species *Glycine max*, hybridizes easily with its annual wild relative *Glycine soja* (most probable progenitor) where it has low rate of cross ability with perennial wild relatives (Singh and Hymowitz, 1999) [4]. As a potentially high-yielding crop, soy can play an important role in increasing oilseed production in the country. Soybean is greatly valued crop in terms of their contribution to human nutrition. Soybean contains 40-42% protein and 18-20% oil. It is also rich in minerals such as calcium, phosphorus and iron, and provides vitamins such as A, B and E. It is a rich source of many essential amino acids (EAA), including lysine. Soybean oil is also used in industrial paints, varnishes, linoleum, and other products. Lecithin is a natural extract from soybean oil that has emulsifying properties and is also used as a lubricant in many commercial and industrial applications. Soybeans have recently been used to produce biofuels and ethanol. Soybean hulls are rich in carbohydrates and could therefore be used in ethanol production (Mielenz *et al.*, 2009) [5]. For biofuel production, oil is first extracted from the seeds, degummed and converted into biofuel through a process called Trans esterification.

India has occupied an area of 12.4 m ha with the production of 13.97 m tonnes and productivity of 1130 kg/ha in 2021-22. The major soybean producing states in India are Madhya Pradesh, Maharashtra and Rajasthan. In Rajasthan, area under soybean production was 1.03 m ha with the production and productivity of 0.99 m tonnes and 953 kg/ha, respectively during 2021-22. (Anonymous 2022b) [1]. The development of high yielding soybean varieties for variable agro-ecological conditions depends upon the nature and amount of variability present in the germplasm collection.

A method used by Mahalanobis (1936) [3] called the Mahalanobis D2 statistic is widely used to determine the genetic diversity of the available genotypes. Genetic diversity, which is the basis of plant breeding, arises from inherent genetic differences in plant species and is of great interest to the plant breeder. The D2 statistic measures the degree of diversification and determines the relative contribution of each individual character to the total diversity. It aids in measuring differentiation power at the intra-cluster and inter-cluster levels and aids in the selection of genetically distinct parents for use in the hybridization program. Genetic diversity is an important parameter in any crop improvement program, which is an essential requirement

for obtaining desirable segregants. The diversity of plant genetic resources offers plant breeders the opportunity to develop new and improved cultivars that have high yield potential and are resistant to biotic and abiotic factors.

Materials and Methods

The experiment was conducted at Agricultural Research Station, Ummadganj, Kota, Rajasthan during *Kharif-2022* which is situated at 25.10 North latitude and 75.500 East longitude at an altitude of 258 meters above mean sea level. In Rajasthan, this region falls under the Agro-Climatic Zone-V (Humid South Eastern Plain Zone).

The experiment was laid out in Randomized Block Design (RBD) with three replications. Each genotype comprised of 4 rows of 3 m long and spaced at 45 cm between the lines, while plant to plant distance was 10 cm. Appropriate and uniform agronomical operation was carried out during the crop growing period. Plant protection measures were timely applied to raise a good and healthy crop stand.

Traits *viz.*, plant height (cm), pod length (cm), number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%) were recorded on the basis of five randomly selected plants from each genotype in each replication, whereas observation of remaining characters *viz.*, days to 50% flowering, days to maturity, protein content (%) and oil content (%) were documented on plot basis.

Results and Discussion

Analysis of variance exhibited that all the genotypes were found significantly differ for each of the thirteen traits under investigation, demonstrating that research materials contain a broad range of variation among itself. So, this provides a lot of possibilities to select promising lines from the available genotypes for yield and its component attributes in soybean crop improvement programmes. (Table: 1)

Genetic diversity analysis was carried out by calculating D2 values from means of 40 genotypes of soybean for 13 characters. In culmination to genetic relationship, based on relative magnitude of D2 estimates the 40 Soybean genotypes were grouped into ten distinct non-overlapping clusters (Table: 2). The discrimination of genotypes in to discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Among 10 clusters, cluster II was the biggest with 21 genotype AUKS 22-44, AUKS 22-47, AUKS 22-34 AUKS 22-36, AUKS 22-32, AUKS 22-38, AUKS 22-27, DS-1312, AUKS 22-29, AUKS 22-24, AUKS 22-23, AUKS 22-25, JS-20-34, AUKS 22-39, RKS-113, AUKS 22-52, AUKS 22-40, NRC-191, AUKS 22-28, AUKS 22-53, AUKS 22-41, AUKS 22-42 followed by cluster I and cluster III contain in each 7 and 5 genotypes (cluster I AUKS 22-33, AUKS 22-43, AUKS 22-37, AUKS 22-34, AUKS 22-45, AUKS 22-49, RVSM-16-20) and (cluster III genotype AUKS 22-31, AUKS 22-35, JS-95-60, AUKS 22-30, AUKS 22-48) While rest of the cluster IV to X contain in each single genotype only. Cluster IV contained genotype (SL-1282), cluster V (PS-1682), cluster VI (AUKS 22-50), cluster VII (AUKS 22-26), cluster VIII (AUKS 22-51) cluster IX AUKS 22-46 and cluster X (TS-21-2).

The intra cluster distance was range from 41.67 to 59.30. The maximum intra cluster distance was recorded by cluster III (59.30) followed by cluster II (57.59), cluster I (41.67), and cluster IV to X were (0.00) because of these cluster contained single genotype. (Table: 3)

The inter cluster distances ranged from 58.88 to 425.71. Highest inter cluster distance were observed between cluster I and X (425.71) followed by cluster VI and X (333.93), cluster VIII and X (326.47), cluster I and V (268.92), cluster VIII and V (263.13), cluster I and IV (252.08) and cluster I and VI (244.25). The lowest inter cluster distance was noticed between cluster IX and VII (58.88) followed by cluster I and VIII (66.63), cluster II and V (76.15), cluster II and IV (79.42) and cluster II and VII (82.11). (Table: 3)

The cluster means for the 13 characters are given in Table: 4. The lowest cluster mean value was exhibited for days to 50% flowering by cluster VIII, days to maturity was recorded by cluster IX and for plant height by VI. The highest cluster means for number of branches per plant by cluster IX, number of pods per plant by cluster I. The cluster means for pod length was exhibited highest in clusters VII, for number of seeds per pod by biological yield per plant was observed in cluster VIII, highest cluster mean for pod length was observed in cluster II and for number of seeds per pod by cluster I and VIII and seed yield per plant was observed in cluster VIII. The cluster means for 100-seed weight in cluster I, for biological yield per plant by cluster VIII, for harvest index by cluster VIII, for protein content by cluster X and for oil content by cluster VIII. Hence, the genotypes in this cluster were high yielding.

Genetic diversity evaluation helps in interpreting the genetic background and breeding value of the germplasm. The presence of wide diversity among the genotypes helps in selection of parents in hybridization for the character of interest. In addition, inclusion of genetically diverse parents in any breeding programme is useful to generate new variability and superior transgressive recombinants. One of the best techniques of measuring genetic diversity is the D2 statistics proposed by Mahalanobis in 1936 [3]. D2 statistics measure the forces of differentiation at intra and inter cluster levels and determines the relative contribution of each component trait to the total diversity. The present research was planned with the goal of assessing the extent of genetic diversity in the available genotypes.

On the basis of multivariate analysis as per Mahalanobis D2 statistic forty genotypes of soybean for thirteen important quantitative characters were grouped in ten clusters following the Tocher's method explained by Rao (1952) [6]. Similar result was also reported by Kumar *et al.* (2018) [7] for grouped forty soybean genotypes into ten clusters.

The minimum cluster mean value was exhibited for days to 50% flowering by cluster VIII, days to maturity was recorded by cluster IX and for plant height by VI. The maximum cluster means for number of branches per plant by cluster IX, number of pods per plant by cluster I. The cluster means for biological yield per plant was exhibited maximum in cluster VIII, maximum cluster mean for number of seeds per pod by cluster I and VIII and seed yield per plant was observed in cluster VIII. The cluster means for 100-seed weight in cluster I, for biological yield per plant by cluster VIII, for harvest index by cluster VIII, for protein content by cluster X and for oil content by cluster VIII. Hence, the genotypes in this cluster were high yielding.

Similar result was also reported by Kumar *et al.* (2018) [7] for cluster like IV had high values for number of branches per plant, plant height.

Therefore, hybridization between the selected genotypes form divergent clusters is essential to judiciously combine all the targeted traits.

Table 1: Distribution of Soybean genotypes into different clusters

Cluster	Number of genotypes	Genotypes
Cluster I	7	AUKS 22-33, AUKS 22-43, AUKS 22-37, AUKS 22-34, AUKS 22-45, AUKS 22-49, RVSM-16-20
Cluster II	21	AUKS 22-44, AUKS 22-47, AUKS 22-34 AUKS 22-36, AUKS 22-32, AUKS 22-38, AUKS 22-27, DS-1312, AUKS 22-29, AUKS 22-24, AUKS 22-23, AUKS 22-25, JS-20-34, AUKS 22-39, RKS-113, AUKS 22-52, AUKS 22-40, NRC-191, AUKS 22-28, AUKS 22-53, AUKS 22-41, AUKS 22-42
Cluster III	5	AUKS 22-31, AUKS 22-35, JS-95-60, AUKS 22-30, AUKS 22-48
Cluster IV	1	SL-1282
Cluster V	1	PS-1682
Cluster VI	1	AUKS 22-50
Cluster VII	1	AUKS 22-26
Cluster VIII	1	AUKS 22-51
Cluster IX	1	AUKS 22-46
Cluster X	1	TS-21-2

Table 3: Inter and Intra-cluster distance among seed yield and its attributing traits

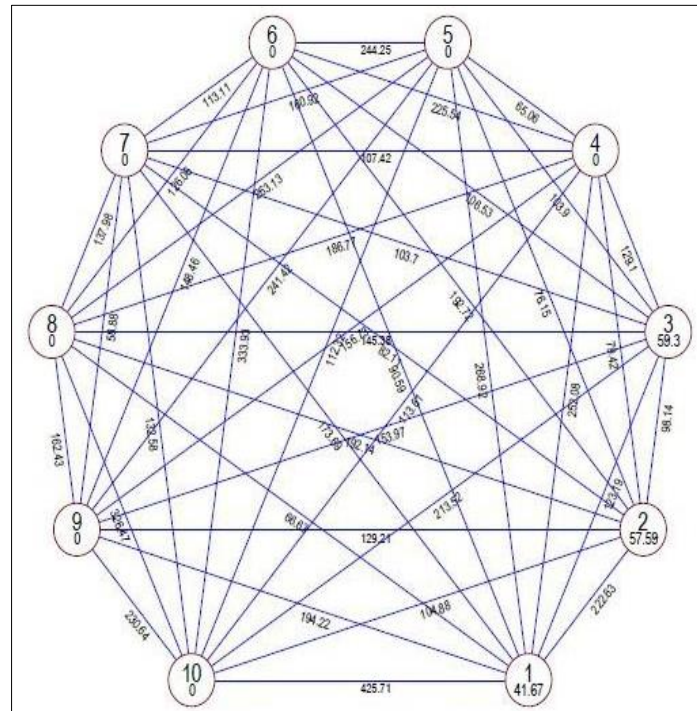
Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	41.67	222.63	123.19	252.08	268.92	90.59	173.69	66.63	194.22	425.71
Cluster II		57.59	98.14	79.42	76.15	192.72	82.11	192.14	129.21	104.88
Cluster III			59.30	129.1	103.9	106.53	103.7	145.38	153.97	213.52
Cluster IV				0.00	65.06	225.54	107.42	186.77	156.73	113.61
Cluster V					0.00	244.25	160.92	263.13	241.42	112.32
Cluster VI						0.00	113.11	126.06	148.46	333.93
Cluster VII							0.00	137.98	58.88	132.58
Cluster VIII								0.00	162.43	326.47
Cluster IX									0.00	230.64
Cluster X										0.00

Table 4: Cluster means of grain yield and its attributing traits

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Protein content (%)	Oil content (%)	Seed yield per plant (g)
Cluster I	36.43	92.29	30.9	5.62	61.03	4.08	3	10.69	12.66	23.7	44.72	34.85	18.19
Cluster II	38.44	97.05	37.16	3.21	37.22	3.36	2.19	5.44	9.82	15.36	36.77	35.37	16.71
Cluster III	37.2	99	40.91	4.11	53.16	3.63	2.43	6.65	11.2	16.03	43.59	35.65	15.29
Cluster IV	41.67	106.67	45.33	4.33	34.7	3.59	2.33	5.12	8.6	18.37	27.87	37.48	16.97
Cluster V	41.67	107.33	41.13	2.5	46.73	3.65	2	4.6	9.5	19.57	25.5	40.43	16.5
Cluster VI	36.67	91.67	25.96	5.5	56.2	4.25	2.93	10.07	11.77	23.8	42.23	34.93	12.73
Cluster VII	33	97.67	26.43	4.57	32.6	4.32	2.13	5.48	11.3	13.69	40.03	31.98	15.5
Cluster VIII	32	92	32.63	5.83	46.93	3.83	3	13	11.37	25.5	50.9	36.45	19.43
Cluster IX	37.67	87	26.6	6.03	38.1	3.37	2	4.07	9.77	9.83	41.37	35.28	15.7
Cluster X	37	100	34.2	2.33	19.57	3.89	2	4.8	8.7	10.63	45.15	41.35	15.33

Table 5: Contribution of characters to genetic divergence in soybean

S. No	Character	Times ranked 1st	Contribution percent
1	Days to 50% flowering	14	1.79
2	Days to maturity	8	1.03
3	Plant height	22	2.82
4	No. of branches per plant	216	27.69
5	No. of pods per plant	222	28.46
6	Pod length(cm)	6	0.77
7	No. of seeds per pod	39	5.00
8	100-seed weight	19	2.44
9	Biological yield per plant	79	10.13
10	Harvest index	2	0.26
11	Protein content	56	7.18
12	Oil content	34	4.36
13	Seed yield per plant	63	8.08

Mahalanobis Euclidean distance**Fig 1:** Tocher's Method**Conclusion**

Among the forty genotypes, AUKS 22-34, AUKS 22-51, AUKS 22-43, AUKS 22-33 and AUKS 22-37 were recorded higher seed yield per plant. AUKS 22-51 was found to be early with respect to days to 50% flowering, while AUKS 22-46 was observed early maturing type with respect to days to maturity. SL-1282 was found dwarf among the all genotypes. AUKS 22-34 showed the maximum mean value for number of branches per plant. while AUKS 22-37 maximum number of pods per plant. AUKS 22-26 reported maximum pod length. AUKS 22- 32 for highest number of seeds per plant. AUKS 22-34, highest mean performance for 100- seed weight. AUKS 22-34 for highest biological yield per plant, AUKS 22-35 for greatest harvest index. TS-21-2 for high protein content and AUKS 22-34 for high oil content were the best performing genotypes in their respective characters.

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