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ANALYSIS OF GENETIC DIVERSITY FOR SEED YIELD AND ITS RELATED TRAITS IN SOYBEAN (*GLYCINE MAX* L. MERRILL) GENOTYPES

Abhishek Bairwa*, B.L. Meena, S.C. Sharma, C.B. Meena, K.M. Sharma, Yash Nagar and Govind Tikiani

College of Agriculture, Ummedganj-Kota, Agriculture University, Kota, Rajasthan, India

*Corresponding author E-mail: abhikumarbairwa1234@gmail.com

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ABSTRACT

The present investigation was carried out to assess genetic diversity among 40 soybean genotypes including 3 checks *viz.*, JS 20-34, NRC 138 and JS 20-98 in randomized block design for 14 traits. The genotypes were grouped into eight distinct clusters performing Tocher's method using Mahalanobis D^2 distance. The maximum intra-cluster distance was observed in Cluster IV (62.11), followed by Cluster I (61.19) and Cluster V (59.72), while highest inter-cluster distance was recorded between Cluster IV and Cluster VII (444.35), followed by cluster IV and VIII (362.78). Cluster VIII exhibited highest mean value for plant height, 100-seed weight, biological yield per plant and seed yield per plant. Cluster V had highest mean value for days to 50% flowering and days to maturity. Therefore, selecting these traits and implementing crosses between the identified clusters may enhance genetic diversity, offering valuable potential for the development of superior soybean varieties.

Keyword: Genetic diversity, Tocher's methods, Mahalanobis D^2 , Cluster

Introduction

Soybean [*Glycine max* (L.) Merrill.] is a self-pollinating legume belongs to the family Fabaceae and subfamily Fabioideae, having the chromosome number of $2n = 2x = 40$ (Jain *et al.*, 2017). It is an annual plant that varies in growth habit and height. Soybean also known as the 'Golden Bean' and 'Miracle Crop' of the twenty-first century. It is believed to have originated in North-Eastern China. Soybean oil is the most widely used vegetable oil in the world. It is highly valued protein and oil owing to its use in food, feed, and industrial applications. Soybean contains approx. 40-45% protein and 18-22% oil (Goyal *et al.*, 2012). Soybean oil provides a number of health benefits to the consumers because it contains omega-3 fatty acids as well as it is rich in unsaturated fatty acids. Soybean seeds also contain a good amount of other nutrients like calcium, phosphorus, iron and vitamins like A, B, and E. It is also good source of lysine (6.4%), an essential amino acid that is not provided by most of the cereal-based diets. Soy protein quality is superior to that of animal protein and superior to that of grains and

pulses. Soybean edible oil provides necessary fatty acids and is around 85% unsaturated. Soybean meal and soybean oil make up about 85% of the global soybean edibles such as tempeh tofu, soy milk, soy sauce, soy cheese, soy meat.

Genetic diversity is essential for plant survival in nature and for agricultural enhancement. Due to higher diversity in segregating generations, which may be exploited for improvement, genetic divergence amongst parents plays a critical role in cultivar development. Genetic variability and divergence play a vital role in framing a successful breeding programme. The concept of D^2 statistic developed by Mahalanobis (1928) provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence. D^2 statistic is more reliable in selection of potential parents for hybridization programme. Application of original concept of D^2 statistics of Mahalanobis (1928) for assessment of genetic diversity was suggested by Rao (1952).

Material and Methods

The experiment was conducted at Research Farm, Agricultural Research Station, Ummadganj, Agriculture University, Kota, Rajasthan during *Kharif* 2024. The experimental material consisted of forty diverse genotypes of soybean [*Glycine max* (L.) Merrill]. These genotypes were obtained from AICRP on Soybean, Agricultural Research Station, Ummadganj, Agriculture University, Kota.

The genotypes were evaluated during *Kharif* 2024 in Randomized Block Design (RBD) with three replications. The plot size for each genotype was 3.0 m x 1.35 m with row to row spacing 45cm and plant to plant 10 cm. The observations were recorded on five randomly selected plants per plot for 14 characters *viz.*, plant height (cm), number of primary branches per plant, number of clusters 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 (%) and seed yield per plant (g), except days to 50% flowering and days to maturity which recorded on whole plot basis.

The detailed procedures adopted for taking observation were mentioned below:

Days to 50 % flowering

The number of days taken from the date of sowing to the day on which 50% of the plants in a genotype initiate first flower was recorded as days to 50% flowering.

Days to maturity

The number of days taken from date of sowing to the date when plant reached at physiological maturity was recorded as days to maturity.

Plant height (cm)

Plant height was measured in centimeters of the main stem from the ground level to the top of the main stem at the time of maturity.

Number of primary branches per plant

The total number of branches arising directly from main shoot was counted at the time of maturity from each selected plant.

Number of clusters per plant

The number of clusters per plant was counted at the time of maturity for each selected plant

Number of pods per plant

Total number of seeds bearing pods per plant were harvested at the time of maturity and counted.

Pod length (cm)

It was measured in centimeter from the base of pod to the tip of that pod from each selected plant.

Number of seeds per pod

The pods which were taken for measuring the length of pods were used for counting the number of seeds per pod to obtain average number of seeds per pod.

Seed yield per plant (g)

All the pods of each selected plant were hand threshed and seed yield per plant was recorded in gram (g).

100-seed weight (g)

The weight of 100-seeds from the produce of randomly selected five plants were weighted and recorded in gram (g).

Biological yield per plant (g)

Each selected plant was harvested separately and weight of each plant was taken in gram. Biological yield per plant was recorded when plants were completely dry in the field. Roots and leaves were not counted for dry matter weight.

Harvest index

Harvested index of the selected plants was calculated by following formula:

$$\text{Harvest index} = \frac{\text{Seed yield (g)}}{\text{Biological yield per plant (g)}} \times 100$$

Protein content (%)

The protein content was estimated by using the method described by Lowry *et al.* 1951 at Central Laboratory of Agricultural Research Station, Ummadganj-Kota.

Oil content (%)

Oil content was determined by using the method described by Soxhlet, 1879 at Central Laboratory of Agricultural Research Station, Ummadganj-Kota.

Result and Discussion

Cluster constellation

In culmination to genetic relationship, based on relative magnitude of D^2 , the forty soybean genotypes were grouped into eight distinct, non-overlapping clusters, as presented in Table 1. Among the eight clusters, Cluster I was the largest, comprising 19 genotypes, cluster V included 10 genotypes and cluster IV consisted of 6 genotypes. The remaining cluster II,

cluster III, cluster VI, cluster VII and cluster VIII contained single genotype only.

Intra and inter-cluster distance

The intra-cluster distances (Table 2 with Fig 1) among the soybean genotypes ranged from 59.72 to 62.11. The maximum intra-cluster distance was observed in Cluster IV (62.11), followed by Cluster I (61.19) and Cluster V (59.72). Cluster II, cluster III, cluster VI, cluster VII and cluster VIII recorded an intra-cluster distance of (0.00), as each of these clusters contained only a single genotype. The inter-cluster distances, between genotypes from different clusters, ranged from 76.39 to 444.35. The highest inter-cluster distance was recorded between Cluster IV and Cluster VII (444.35), followed by cluster IV and VIII (362.78), cluster II and VIII (351.68), cluster III and VII (340.15), cluster II and VII (337.99), cluster II and V (246.97), Cluster IV and V (229.65). The lowest inter-

cluster distance was observed between Cluster III and Cluster IV (76.39), followed by cluster VII and VIII (81.63), cluster I and III (93.18), cluster I and VI (103.53), cluster I and II (106.34), cluster I and V (117.4) and cluster VI and VII (118.92). The mean value of 14 characters for 8 clusters are displayed in Table-3. The higher mean value for days to maturity was recorded in Cluster II. The highest mean for days to 50 % flowering, plant height, 100-seed weight, biological yield per plant and seed yield per plant was recorded in Cluster VIII. The highest number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, harvest index and oil content was recorded in Cluster VII. Cluster III had highest mean value for protein content. Similar findings were reported earlier by Neelima *et al.* (2017), Arora (2018), Dubey *et al.* (2018), Mishra *et al.* (2018), Sareo *et al.* (2018), Nag and Sarawgi (2021), Nayak *et al.* (2023).

Table 1 : Distribution of soybean genotypes into different clusters

Cluster	Number of genotypes	Genotypes
Cluster I	19	AUKS 24-1, AUKS 24-2, AUKS 24-3, AUKS 24-5, AUKS 24-7, AUKS 24-8, AUKS 24-13, AUKS 24-14, AUKS 24-15, AUKS 24-18, AUKS 24-20, AUKS 24-25, AUKS 24-26, AUKS 24-28, AUKS 24-29, AUKS 24-32, AUKS 24-35, AUKS 24-36, JS 20-98 (C)
Cluster II	1	AUKS 24-23
Cluster III	1	AUKS 24-19
Cluster IV	6	AUKS 24-16, AUKS 24-17, AUKS 24-21, AUKS 24-22, AUKS 24-27, AUKS 24-34
Cluster V	10	AUKS 24-4, AUKS 24-9, , AUKS 24-10, AUKS 24-11, AUKS 24-12, AUKS 24-30, AUKS 24-31, AUKS 24-33, JS 20-34 (C), NRC 138 (C)
Cluster VI	1	AUKS 24-37
Cluster VII	1	AUKS 24-6
Cluster VIII	1	AUKS 24-24

Table 2 : Average intra and inter-cluster distances based on corresponding D^2 values

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	61.19	106.34	93.18	133.37	117.4	103.53	190.89	156.9
Cluster II		0	158.87	123.55	246.97	124.14	337.99	351.68
Cluster III			0	76.39	129.88	181.44	340.15	200.69
Cluster IV				62.11	229.65	191.94	444.35	362.78
Cluster V					59.72	169	176.07	133.53
Cluster VI						0	118.92	187.91
Cluster VII							0	81.63
Cluster VIII								0

Table 3 : Clusters mean of seed yield and its attributing traits for 40 genotypes of soybean

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. clusters per plant	No. pods per plant	Pod length (cm)	No. 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	45.16	99.75	51.41	7.27	5.59	41.60	3.08	2.64	7.55	26.96	31.87	35.58	16.31	8.59
Cluster II	46.67	102.67	53.38	3.47	2.73	40.20	2.89	2.33	4.65	15.02	29.86	37.57	17.15	4.47
Cluster III	44.67	101.33	51.67	6.60	4.22	36.34	2.91	2.27	12.63	36.98	28.78	37.91	13.70	10.64
Cluster IV	44.22	101.89	54.67	5.38	5.15	36.44	3.13	2.60	8.34	27.33	28.64	36.03	12.27	7.74
Cluster V	36.97	89.97	51.73	7.91	6.97	51.52	3.17	2.48	9.49	31.89	36.19	36.03	16.49	11.42
Cluster VI	46.67	100.67	53.27	6.90	11.95	66.18	2.79	2.60	5.42	27.20	34.55	37.28	16.54	9.33
Cluster VII	46.00	98.33	58.77	10.96	12.05	71.38	3.25	2.67	6.25	29.65	42.07	34.64	19.95	12.30
Cluster VIII	48.33	100.67	59.14	10.37	9.42	40.09	2.97	2.60	12.72	37.69	35.00	34.24	17.64	13.16



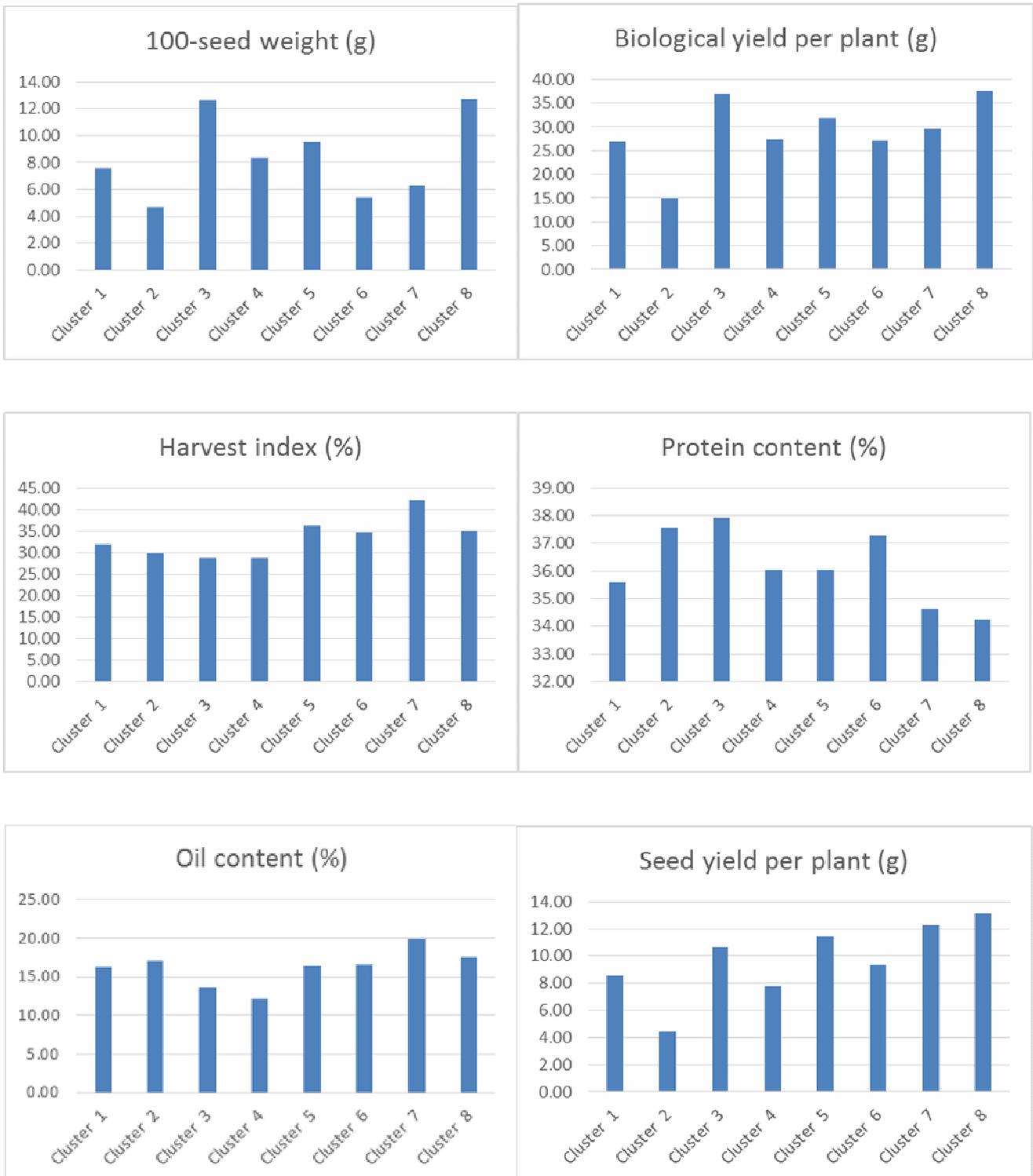


Fig. 1: Cluster Mean Bar Graphs for different traits in forty soybean genotypes

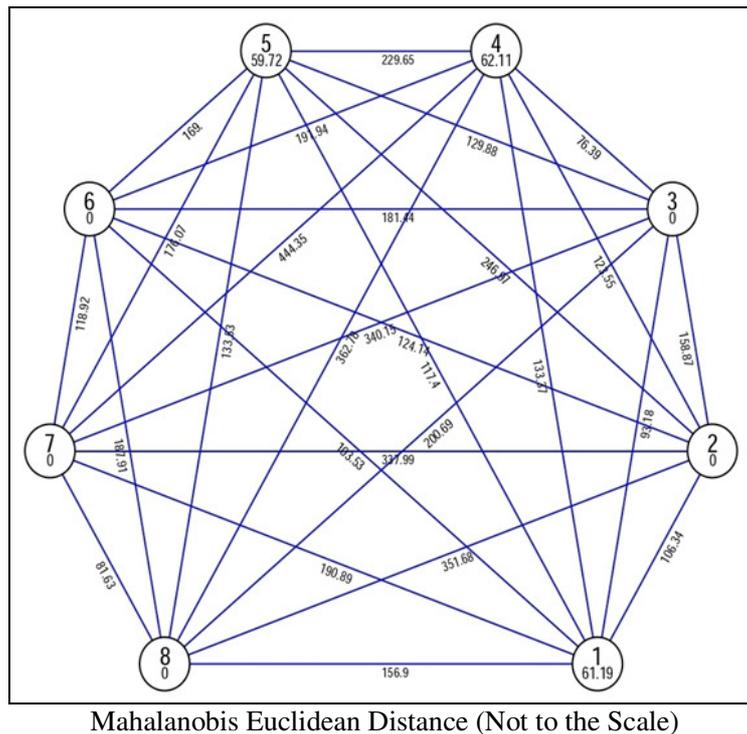


Fig. 2 : Diagrammatic representation of intra and inter-cluster distances

Conclusion

The result of diversity analysis revealed that, clusters VII, cluster VIII and cluster V were the best clusters and in cluster VII the genotype present in it showed highest values of mean for most of the characters such as number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and harvest index. Cluster VIII exhibited highest mean value for plant height, 100-seed weight, biological yield per plant and seed yield per plant. Cluster V had highest mean value for days to 50 per cent flowering and days to maturity. Therefore, selecting these traits and implementing crosses between the identified clusters may enhance genetic diversity, offering valuable potential for the development of superior soybean varieties.

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