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To study genetic diversity among different traits in soybean [*Glycine max* (L.) Merrill]

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Abstract

On the basis of D^2 analysis, forty two genotypes of soybean were divided into seven clusters with varying degrees of divergence. D^2 analysis showed that the genotypes were very diverse, with D^2 values ranging from 14.11 to 57.98. Cluster VII and cluster V had the greatest inter-cluster distance (57.98). Cluster III and cluster I had the smallest inter-cluster distance (14.11). The maximum intra cluster distance was found in Cluster VII (13.96). However, just one genotype was present in clusters III, V, VI. The large range of D^2 values confirms the genotypes significant genetic diversity. The cluster V showed least cluster mean for days to maturity i.e. genotypes in cluster V were earlier than that of other clusters. Cluster VI had the highest cluster mean for plant height. Cluster VII genotypes had the highest cluster mean for number of pods per plant, followed by cluster VI. Cluster VII genotypes reported highest cluster mean for seed yield per plant. Seed yield per plant (36.82%) was the trait that contributed the most to divergence among the 10 variables under investigation, followed by 100 seed weight (33.33%), plant height (10.69%), protein content (8.13%), and oil content (5.57%).

Keywords: Genetic divergence, cluster, diversity, characters, D^2 analysis

Introduction

Soybean [*Glycine max* (L.) Merrill] belongs to Fabaceae (Leguminosae) family, subfamily Fabioideae, and genus *Glycine* all contain the soybean. It is a self-pollinating crop ($2n = 40$). For germination, a temperature range of 30°C to 35°C is recommended. It is a widely cultivated legume that works in symbiosis with *Rhizobium japonicum* to increase soil fertility by storing atmospheric nitrogen in the root nodules. The most popular vegetable oil worldwide is soybean oil. It can be used as a raw ingredient to make paint, varnish, lubricants, and other products. For a population to be biologically diverse, genetic variation is essential. Plant breeders will benefit from the research of the correlation between yield and its contributing factors, which will promote the selection of desired features. The study of diversity within a species is genetic diversity. More diversity increases the likelihood of choosing suitable genotypes for hybridization. The ability to estimate parental diversity may be aided by direct chemical examination of genetic material or gene products. However, the usefulness of this strategy in practice has not been sufficiently established. Mahalanobis (1936) found that generalized distance (D^2) analysis is useful in evaluating genetic diversity between two populations under four such conditions.

Materials and Methods

The present investigation entitled, "Correlation and Path analysis in Soybean [*Glycine max* (L.) Merrill] conducted at Post Graduate Research Farm, Botany Section, College of Agriculture, Dhule (Maharashtra) during *Kharif* season 2022. The experimental material used for the study consisted of 42 genotypes of soybean were obtained from Agricultural Research Station (ARS), Kasbe Digraj, Sangali. Five plants per genotype per replication were selected at random for recording observations on quantitative traits and averages were calculated. The mean values of five randomly selected observational plants for ten different characters were used for statistical analysis. D^2 statistics were introduced by Mahalanobis in 1928 and further developed by Rao (1952) [21]. This method is now frequently used in plant breeding and genetics to investigate genetic differences in diverse breeding materials. The generalized distance between two populations was defined by Mahalanobis (1936) as:

$$D^2 = \sum \lambda \text{ i.j.di. dj.}$$

Where i, j = Reciprocal matrix to the common dispersion matrix.

d_i = Difference between the mean values of two populations for i^{th} character.

d_j = Difference between the mean values of two populations for j^{th} character.

In this, estimating D^2 values using the above formula is quite difficult. Because it requires inversion of a thirteenth order determinant and then evaluating $B(BH) / 2$ terms whose total is D^2 . It was discovered that working with a collection of unrelated characters derived from the original measurements was more convenient. With such modified variables, D^2 is reduced to a simple sum of squares evaluation. Singh and Chaudhary (1977) [15] used the pivotal condensation approach to transform the data. The coefficients for the transformation were calculated by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

In all the combination each character is ranked based on $d_i = y_{ij} - y_{ik}$ values. Rank 1 is given to the highest mean difference and rank p to the lowest mean difference, where p is the total number of characters by Singh and Chaudhary (1985) [16].

Cluster combinations were divided into four divergent groups using the approach suggested by Arunachalam and Bandopadhyaya (1984) [24]. The mean (M) and standard deviation (S) of the intra and inter-cluster divergence (D) were computed in order to determine the level of parental divergence. The four divergent classes (DC), DC1, DC2, DC3, and DC4, are used to classify parental divergence as follows,

DC 1: $D > (m + s)$

DC 2: $D < (m + s)$ and $> m$

DC 3: $D < (m - s)$ and $< m$

DC 4: $D < (m - s)$

They suggested that a cross between two parents whose genetic divergence falls between $(m-s)$ and $(m+s)$, or in the classes DC2 or DC3, have a higher probability of creating high frequency and magnitude of heterosis than one whose parents' genetic divergence falls outside of the limits, $(m-s, m+s)$.

Results and Discussion

In the present investigation, "Correlation and Path analysis in Soybean [*Glycine max* (L.) Merrill]" experiments were

undertaken to investigate the variability of 42 genotypes of soybean for 8 different morphological and 2 biochemical traits. The study examined at the relationship between the dependent and independent factors, as well as their direct and indirect effects on seed yield and genetic diversity across all genotypes.

Soybean genetic distance estimations were calculated using the Mahalanobis D_2 statistic, as described by Rao (1952) [21], and applied to a sample of forty two different soybean genotypes. We used Ward's (1963) recommended procedure for group constellation/ clustering.

All the 42 soybean genotypes, were grouped into seven clusters. The clustering pattern of the genotypes has been presented in (Table 1). Wide range of diversity were also reported by earlier workers were Patil *et al.* (2011) [22], Nag *et al.* (2017) [23], Nag and Sarawgi (2021) [18], Thakur *et al.* (2105), and Kachhadiya *et al.* (2014) [10]. Table 2 displays the average inter and intra-cluster D_2 values. The highest inter-cluster distance was observed between cluster VII and cluster V (57.98) followed by cluster VII and II (48.65), cluster VII and III (48.40) and cluster VII and IV (43.64). The the lowest inter cluster distance was observed between cluster IV and III (12.38) followed by cluster III and I (14.11), cluster IV and I (15.10) and cluster V and II (15.90).

The maximum intra-cluster distance was observed within cluster VII (13.96) followed by cluster VII (13.16), cluster IV (12.57), Cluster I (11.90). The cluster III, V, VI, were solitary hence no intra-cluster distance found within them. The distance between two clusters represents the degree of diversity. The greater the distance between two clusters, the bigger the divergence, on the other hand the smaller the distance between two clusters, the lower the divergence. In the present investigation cluster VII and cluster V had showed the highest inter cluster distance indicating substantial amount of divergence between them followed by cluster VII and II. Cluster VII and III and cluster VII and IV. While cluster IV and III showed the lowest inter cluster distance indicating low divergence between them followed by cluster III and I, cluster IV and I and cluster II and I. The genotypes in the same cluster are more closely related than the genotypes in the other cluster. In other terms genotypes gathered together in one cluster are less divergent than genotypes grouped together in distinct clusters. Table No 3 displays the mean performance of cluster values for ten characters. For the ten traits investigated, a significant inter-cluster variation was observed among the various clusters.

Table 1: Distribution of Genotypes according to cluster

Clusters	No. of Genotypes (N)	Intra cluster distance	Genotypes
I	27	11.90	VLS-103, ACS-1735, HIMSO-1694, KDS-344, DS-3124, JS-23-05, NRC128, DLSB-3, AMS-115, DS-228, RVS-13-15, KSS-204, NRC-192, RVSM-16-20, JS-93-05, VLS-102, KDS-726, DSb-39, MAUS-818, JS-335, DLSB-4, KBS-21-1, BAUS-116, HIMSO-1693, PS-1829, JS-20-34, DS-316
II	4	12.57	JS-23-08, NRC-189, DS-3163, RVS-13-20
III	1	0.00	PS-1682
IV	6	13.16	KDS-753, KDS-992, DS-1312, AMS19-01, SL-1230, JS-93-05
V	1	0.00	AS-24
VI	1	0.00	SL-1282
VII	2	13.96	AS-40, RSC-11-42

Table 2: Average inter and intra-cluster distance (D^2 values) in soybean

Groups	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	11.90	15.54	14.11	15.10	24.79	19.48	41.23
Cluster 2		12.57	15.85	21.12	15.90	26.52	48.65
Cluster 3			0.00	12.38	23.72	27.58	48.40
Cluster 4				13.16	30.38	23.76	43.64
Cluster 5					0.00	36.74	57.98
Cluster 6						0.00	25.47
Cluster 7							13.96

Table 3: Mean performance of ten characters according to their cluster

Cluster	50% flowering	Days to maturity	Plant height	Primary branches per plant	No. of pods per plant	No. of seeds per plant	100 seed weight (g)	Protein content	Oil content	Seed yield per plant
1	43.30	101.20	69.84	5.31	65.33	144.37	13.73	39.07	18.69	18.98
2	44.75	103.75	57.35	4.86	47.00	110.25	12.02	39.31	18.20	14.41
3	45.50	103.00	58.65	4.80	34.50	73.50	16.47	39.72	18.29	11.32
4	43.00	99.00	74.14	4.99	61.92	131.67	16.77	39.28	18.79	20.01
5	39.00	97.50	30.95	4.20	29.50	59.00	9.65	39.89	18.95	8.89
6	41.50	101.00	87.00	4.90	98.50	206.50	11.91	39.36	18.32	22.09
7	40.75	98.50	63.60	5.40	140.00	278.50	11.26	39.19	19.17	22.41
Average	42.54	100.56	63.07	4.92	68.10	143.39	13.11	39.40	18.63	16.87

Table 4 displays the relative importance of the various analyzed traits in explaining the observed genetic difference. The table shows that seed yield per plant (g) accounts for nearly 36.82% of the variance, followed by 100 seed weight (g) (33.33%), plant height (cm) (10.69%), protein content (7.02%), oil content (5.57%), number of pods per plant (2.79%), days to 50 percent flowering (1.63%) primary branch number per plant (1.11%), number of seeds per plant (0.81), days to maturity (0.23%).

The relative importance of characters towards divergence is given by variance of cluster means among the ten character studied in experiment, seed yield per plant, 100 seed weight and plant height contributed more to divergence. More contribution to divergence by seed yield given by Bekele *et al.* (2012) [6]. For plant height given by Kachhadiya *et al.* (2014) [10]. Diversity act as a fundamental requirement for crop improvement programme. Any breeding program's success depends on selection of the best parent having significant expression for economically relevant characters. Among the different techniques for selecting parents, diversity based selection has its own importance. As a result, the diversity of different genotypes was examined in the present investigation, which produced helpful data that might be used to identify potent parents for crossing. As per the findings of Hays and Johnson (1939) and East and Hays (1942), crosses among diverse parents produced greater heterosis than that of closely related parents.

In the current investigation, method proposed by Arunachalam and Bandopadhyaya (1984) [24] was used to categorize cluster combinations into four divergent classes.

The genetic distance (D^2) presented in Fig 1 represent the index of genetic diversity in between the clusters. In order to calculate the degree of parental divergence, the mean (M) and standard deviation (S) of the intra and inter cluster divergence (D) were calculated. It divides parental divergence into four divergent classes (DC), namely DC¹, DC², DC³ and DC⁴. The mean of seven cluster and four intra-cluster distances was 25.63 with standard deviation of 13.24. The distances had minimum (X) and maximum (Y) divergence classes values of 11.90 and 57.98 respectively. Considering above all of the aspects, the following genotypes in the current research deserve to be regarded as potential parents for future cross-breeding programmes aimed at improving seed yield and yield-related traits in soybean.

1. RSC 11-42
2. AS-24 3. SL-1282
3. KDS-753
4. JS-9305
5. JS 20-34
6. SL-1230
7. AMS 19-01

Taking into account the inter-cluster distance, cluster means, genotype per se performance, and divergence class, the above genotypes may be used in future breeding programmes to create a broad spectrum of variability for different yield contributing characters, allowing for the development of superior genotypes for multiple characters.

Table 4: Relative contribution of twelve characters for divergence.

Sr. No.	Source	Times ranked 1 st	Contribution %
1.	Days to 50 percent flowering	14	1.63%
2.	Days to maturity	2	0.23%
3.	Plant height(cm)	92	10.69%
4.	Number of primary branches per plant	0	1.11%
5.	Number of pods per plant	24	2.79%
6.	Number of seeds per plant	7	0.81%
7.	100 seed weight (g)	287	33.33%
8.	Protein content (%)	70	7.02%
9.	Oil content (%)	48	5.57%
10.	Seed yield per plant(g)	317	36.82%

Table 5: Character improvement on the basis of source cluster

Sr. No.	Characters	Source Cluster
1	Days to 50 percent flowering (earliness)	V, VII, VI
2	Days to maturity (earliness)	V, VII, IV
3	Plant height(cm) (Tall)	VI, IV
4	Number of primary branches per plant (Highest)	VII, I, IV
5	Number of pods per plant (Highest)	VII, VI, I
6	Number of seeds per plant (Highest)	VII, VI, I
7	100 seed weight (g) (Highest)	IV, III, I
8	Protein content (%) (Highest)	V, III, VI
9	Oil content (%) (Highest)	V, IV, I
10	seed yield per plant (Highest)	VI, VII, IV

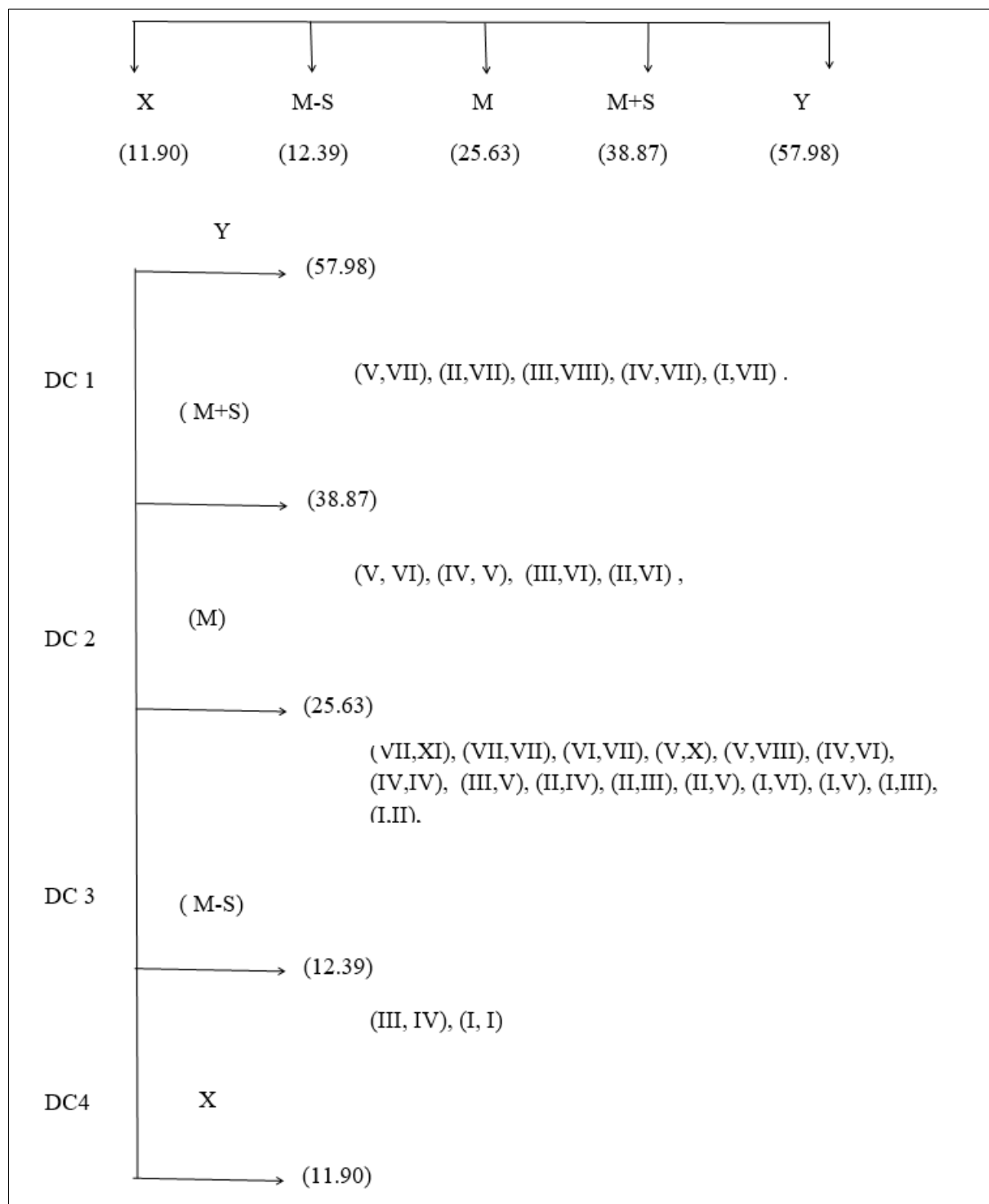


Fig 1: Classification of different cluster into four divergence classes.

Table 6: Tentative suggested crossing programme in future.

Sr. No.	Characters to be improved		Cluster combination with inter-cluster distance	Possible crosses
1.	Earliness	Days to 50 percent flowering	VII X V (57.98)	RSC 11-42 XAS-24 AS-40 X AS-24
		Days to maturity	VII X V (57.98)	RSC 11-42 XAS-24 AS-40 X AS-24
2.	Plant height (cm)		VI X IV (23.76)	SL 1282 X SL1230 SL 1282 XJS 9305
3.	Number of primary branches per plant		VII X IV (43.64)	RSC 11-42 X SL 1230 AS-40 XSL 1230
4.	Number of pods per plant		VII X IV (43.64)	RSC 11-42 X SL 1230 AS-40 XSL 1230
5.	Number of seeds per plant		VII X IV (43.64)	RSC 11-42 X SL 1230 AS-40 XSL 1230
6.	100 seed weight (g)		IV X I (15.10)	JS 93-05 X JS 20-34 SL-1230 X JS 20-34
7.	Protein content (%)		V X VI (36.74)	SL-1282 X AS- 24
8.	Oil content (%)		(V X IV) (30.38)	SL-1230 X AS- 24
10.	Seed yield per plant		VII X IV (43.64)	RSC 11-42 X SL-1230 RSC 11-42 X AMS-1901

Conclusion

On the basis of D^2 analysis, forty two genotypes were divided into seven clusters with varying degrees of divergence. D^2 analysis showed that the genotypes were very diverse, with D^2 values ranging from 14.11 to 57.98. Cluster VII and cluster V had the greatest inter-cluster distance (57.98). Cluster III and cluster I had the smallest inter-cluster distance (14.11). The maximum intra cluster distance was found in Cluster VII (13.96). However, just one genotype was present in clusters III, V, VI. The large range of D^2 values confirms the genotypes significant genetic diversity. The cluster V showed least cluster mean for days to maturity i.e. genotypes in cluster V were earlier than that of other clusters. Cluster VI had the highest cluster mean for plant height. Cluster VII genotypes had the highest cluster mean for number of pods per plant, followed by cluster VI. Cluster VII genotypes reported highest cluster mean for seed yield per plant. Seed yield per plant (36.82%) was the trait that contributed the most to divergence among the 10 variables under investigation, followed by 100 seed weight (33.33%), plant height (10.69%), protein content (8.13%) and oil content (5.57%).

- The broad range of D^2 values reflects a significant level of genetic diversity among the genotypes. In comparison to closely related parents, hybrids of diverse lines generally show higher heterosis thus crossing of clusters having higher inter cluster distances may produced a superior F_1 progeny, which will consist of desirable agronomical and morphological characters.
- Future crop development programs might be effective by selecting AMS19-01, RSC-11-42, AS-24, SL-1282, KDS -753, JS-9305, JS 20-34, and SL-1230 genotypes for crossing programme for obtaining desirable recombinants.

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