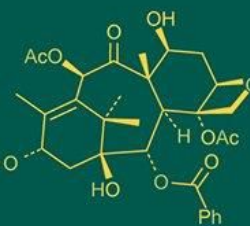


## International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693  
ISSN Online: 2617-4707  
NAAS Rating (2026): 5.29  
IJABR 2026; SP-10(1): 1325-1330  
[www.biochemjournal.com](http://www.biochemjournal.com)  
Received: 10-11-2025  
Accepted: 15-12-2025

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## Multivariate analysis of genetic divergence and selection indices for yield enhancement in soybean [*Glycine max* (L.) Merrill]

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i1Sp.7307>

**Abstract**

In the present study, 45 soybean genotypes [*Glycine max* (L.) Merrill] were evaluated for morphophysiological diversity through Mahalanobis  $D^2$  statistics and selection indices. The experiment was executed at the Main Oilseeds Research Station, JAU, Junagadh during *Kharif*-2024 using a Randomized Block Design with three replications and data were collected on 14 quantitative traits. The genotypes of soybean were grouped into 11 clusters from 45 genotypes. The cluster IV was the largest with 14 genotypes followed by cluster I which contained 12 and cluster V which have 11 genotypes. The remaining cluster i.e. cluster II, III, VI, VII, VIII, IX, X and XI are solitary cluster. The maximum inter-cluster distance was found between clusters XI and X ( $D = 22.66$ ) and intra-cluster distance maximum being in cluster V ( $D = 12.08$ ). the expected genetic advance and relative efficiency assessed for different indices increased considerably when selection was based on two or more characters. seed yield per plant ( $X_1$ ) along with four components viz., number of pods per plant ( $X_2$ ), number of pods per cluster ( $X_3$ ), biological yield per plant ( $X_4$ ) and harvest index ( $X_5$ ) were identified and considered. Thirty-one selection indices were constructed in all possible combinations of the four yield contributing characters and seed yield per plant. relative efficiency of single character index was measured, it was noted that the maximum efficiency of (520.29%) was exhibited by harvest index, Among the combination involving two component characters; number of pods per plant and harvest index ( $X_2+X_5$ ) exhibited maximum relative efficiency of 621.72%, The selection index based on three-character combinations indicated that a discriminant function with number of pods per plant, biological yield per plant and harvest index ( $X_2+X_4+X_5$ ) possessed maximum relative efficiency of 654.74%. In four-character selection index, a function involving seed yield per plant, number of pods per plant, biological yield per plant and harvest index ( $X_1+X_2+X_4+X_5$ ) exerted maximum relative efficiency of 669.50%.

**Keywords:** Genetic divergence, selection indices, soybean

**1. Introduction**

Soybean is a native of Manchuria and is considered to be one of the most ancient crops known to mankind. The utility of this crop has been mentioned in the Chinese medical compilations dating back to 6000 years (Agarwal *et al.* 2013) [1]. In nutritive value, soybean seems to have no equal in supplying protein, fat, carbohydrates, mineral salts like calcium, sodium, manganese, phosphorus and vitamin A, B, C and D. Soybean contain 40% protein of high biological value, resembling that of fish and egg protein. An important characteristic of soybean is that it is a legume and forms a symbiotic relationship with *Bradyrhizobium japonicum* (commonly referred to as rhizobia) bacteria that results in nodules forming on the roots. These nodules reduce atmospheric nitrogen gas to a form that the plant can utilize. A major advantage of soybean is that because of nitrogen fixation, it does not require any nitrogen fertilizer. Soybean contains 35-40% protein on a dry-weight basis, of which, 90% is comprised of two storage globulins, 11S glycinin and 7S  $\beta$ -conglycinin. Soybean contains roughly ~19% oil, of which the triglycerides are the major component. Soy oil is characterized by relatively large amounts of the polyunsaturated fatty acids (PUFA), i.e., ~55% linoleic acid and ~8%  $\alpha$ -linolenic acid, of total fatty acids. The use of soybean in food form for several centuries assures us of its safety and nutritive value for human health (Pratap *et al.* 2011) [11].

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Genetic divergence plays a pivotal role in survival and adaptability of a species. When a specific environment changes, slight genetic variation is necessary for it to adopt and survive. The genetic divergence is a crucial factor in determining the success of hybridization programme and its importance has long been recognized by breeders.

Genetic divergence exerts key influence on the survival and adaptation of any species over the varying environmental condition. The genetic divergence also has notable importance in the success of heterosis breeding programme. Mahalanobis's  $D^2$  statistics is the most potential tool for obtaining quantitative estimates of genetic divergence among biological population and has extensively been applied to assess genetic diversity.

Breeder can practice selection using this information for the isolation of superior accession from available material. The selection indices provide selection criteria for efficient selection strategies among soybean genotypes. Quantitative estimate of genetic divergence among biological populations helps in selection of diverse parents in further breeding programme.

## 2. Materials and Methods

The experiment was carried out during *Kharif 2024*. Forty-five genotypes of soybean were sown in a randomized block design with three replications at the experimental farm of "Main Oilseeds Research Station" Junagadh Agricultural University, Junagadh. The list of accessions taken for study is appended in Table 1. The entire experimental material was divided into three replications with Randomized Block Design (RBD), in which each plot consisted of 2 rows of 3 meters. Each row comprised of 32 plants of single genotype with 45 cm and 15 cm row to row and plant to plant spacing, respectively. Morphological characters *viz.*, days to 50% flowering, days to maturity, number of primary branches per plant, plant height, number of pods per plant, number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod, seed yield per plant, 100-seed weight, oil content, biological yield per plant and harvest index were recorded on five randomly selected plants for different characters on each genotype in all the three replications. Genetic divergence analysis was worked out as per the procedure of Mahalanobis  $D^2$  statistics (Mahalanobis 1936) [9] and grouping of clusters as per Tocher method as described by Rao (1952) Fig 1. Construction of selection indices was done by using the discriminant function technique developed by Fisher (1936) [15].

## 3. Results and Discussion

$D^2$  analysis was carried out using all the twelve characters and generalized distances ( $D^2$ ) was calculated for each pair of genotypes among 45 possible combinations. Grouping of the genotypes was carried-out by following Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller  $D^2$ -values, 11 clusters were formed from 45 genotypes. The cluster IV was the largest with 14 genotypes followed by cluster I which contained 12 and cluster V which have 11 genotypes. The remaining cluster i.e. cluster II, III, VI, VII, VIII, IX, X and XI are solitary cluster Table 2.

$D^2$  values of intra and inter cluster were given in Table 3. Maximum difference among the genotypes within the same cluster (intra cluster) was shown by cluster V (145.92) followed by cluster IV (116.85), cluster I (94.09) and

remaining clusters were solitary. Diversity among the clusters varied with inter cluster distance 513.47 to 54.31. The cluster IX and X (513.47) showed maximum inter cluster distance followed by clusters VII and VI (484.44), clusters X and IX (463.97), clusters IX and VII (423.53), clusters XI and VI (396.01), clusters XI and VII (355.32)). The minimum inter-cluster distance was observed between clusters III and II (54.31). The high intra cluster distance values revealed the presence of genetic diversity between the genotypes which were grouped together in those clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters.

The per cent contribution of each character towards divergence is presented in Table 5. This revealed that the number of pods per plant contributed maximum (17.87 %) as the first ranker towards the total divergence in yield. The next major contribution came from the oil content achieving the second rank 14.75 % towards genetic divergence followed by days to maturity with 12.72 %, number of primary branches per plant with 12.32 % and biological yield per plant with 8.99 %. Apart from above five characters, other characters *viz.*, seed yield per plant 8.08 %, number of seeds per pod 7.37 %, plant height 7.17 %, 100 seed weight 4.65 %, number of clusters per plant 2.63 %, days to 50% flowering 1.31 %, harvest index 1.21, pod length 0.71 % and number of pods per cluster 0.20 % also contributed negligible genetic divergence towards the total divergence. Similar results have been reported by Dubey *et al.* (2018) [4]; Banerjee *et al.* (2023) [2], Zafar *et al.* (2023) [3] and Paikra and NAG (2025) [10].

Hierarchical cluster analysis of quantitative traits among 45 accessions formed eleven clusters, indicating a high level of genetic diversity. Cluster IV included 14 genotypes and Cluster I included 12 genotypes, both from different geographical origins. It was observed that the genotypes of different geographical origin were grouped together and the genotypes with same origin were included in different clusters. The clustering pattern of the accessions showed that geographical diversity was not related with genetic diversity. Similar observations were reported by Gawande *et al.* (2002) [6] and Sharma (2000) [12].

High intra-cluster distances indicated the presence of considerable genetic diversity among genotypes within the same clusters, suggesting lot of scope for gene exchange. Inter crossing between these genotypes could therefore produce superior recombinants. Several authors have reported that crosses between genotypes from clusters with high inter-cluster distances yield better segregants for selection.

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption as improved varieties or as a parent in hybridization to exploit heterosis breeding.

Plant breeders select genotypes based on desired traits. This necessitates the use of selection indices, which assign appropriate weight to two or more traits simultaneously. Hazel and Lush (1943) [8] demonstrated that selection based on such indices is more efficient than selecting traits individually.

Selection indices were constructed using characters that showed a highly significant correlation with seed yield per

plant. Accordingly, seed yield per plant ( $X_1$ ) and four yield components viz., number of pods per plant ( $X_2$ ), number of pods per cluster ( $X_3$ ), biological yield per plant ( $X_4$ ) and harvest index ( $X_5$ ) were considered. A total of thirty-one selection indices were developed using all possible combinations of these traits. Genetic advance and relative efficiency of each discriminant function were calculated and compared with straight selection for seed yield. Details of the selection indices, discriminant functions, genetic advance, and relative efficiency per character are presented in Table 6 with efficiency for seed yield per plant assumed as 100%.

When the relative efficiency of single character index was measured, it was noted that the maximum efficiency of (520.29%) was exhibited by harvest index followed by number of pods per plant (337.08%) and biological yield per plant (206.55%). Among the combination involving two component characters, number of pods per plant and harvest index ( $X_2+X_5$ ) exhibited maximum relative efficiency of 621.72% followed by biological yield per plant and harvest index ( $X_4+X_5$ ) 557.92%. in case of on three-character combinations indicated that a discriminant function with number of pods per plant, biological yield per plant and harvest index ( $X_2+X_4+X_5$ ) possessed maximum relative efficiency of 654.74% followed by seed yield per plant, number of pods per plant and harvest index ( $X_1+X_2+X_5$ ) 635.48%. Among four-character selection index involves seed yield per plant, number of pods per plant, biological yield per plant and harvest index ( $X_1+X_2+X_4+X_5$ ) exerted maximum relative efficiency of 669.50% followed by number of pods per plant, number of pods per cluster, biological yield per plant and harvest index ( $X_2+X_3+X_4+X_5$ ) 659.24 %.

Among all the 31 selection indices, the index based on five characters viz., seed yield per plant, number of pods per plant, number of pods per cluster, biological yield per plant and harvest index ( $X_1+X_2+X_3+X_4+X_5$ ) possessed the highest genetic gain and relative efficiency (26.99 g and 675.26%) as compared to straight selection for seed yield. Gupta *et al.* (2015) [7] and Bhuvu *et al.* (2020) [3] were also with the same opinion that an increase in characters resulted in an increase

in genetic gain and that the selection indices improve the efficiency than the straight selection for seed yield alone. Further, it was observed that the straight selection for seed yield was not that much rewarding (GA = 3.99 g, RI = 100%) as it was through its components like number of pods per plant (GA = 13.47 g, RI = 337.07%), number of pods per cluster (GA = 0.90 g, RI = 22.682), biological yield per plant (GA = 5.17 g, RI = 206.55%) and harvest index (GA = 20.79 g, RI = 520.28%).

#### 4. Tables and Figures

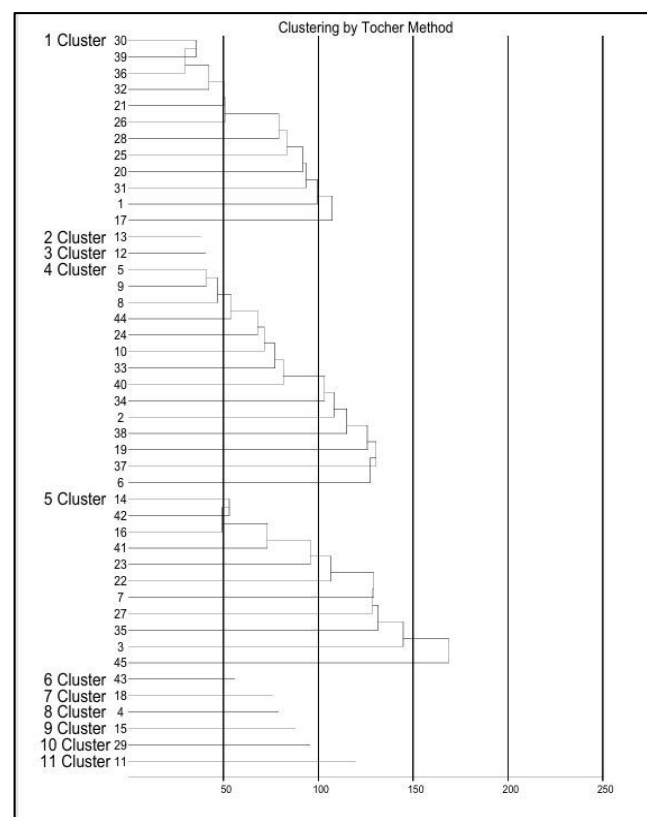


**Fig 1:** Dendrogram showing distribution of soybean genotype in to different clusters

**Table 1:** List of 45 genotypes used in experimental study.

| Sr. No. | Name of Genotypes | Sr. No. | Name of Genotypes |
|---------|-------------------|---------|-------------------|
| 1.      | AS-27             | 24.     | AS-147            |
| 2.      | AS-30             | 25.     | AS-148            |
| 3.      | AS-47             | 26.     | AS-149            |
| 4.      | AS-48             | 27.     | AS-150            |
| 5.      | AS-84             | 28.     | AS-151            |
| 6.      | AS-89             | 29.     | AS-152            |
| 7.      | AS-90             | 30.     | AS-153            |
| 8.      | AS-95             | 31.     | AS-154            |
| 9.      | AS-98             | 32.     | AS-155            |
| 10.     | AS-101            | 33.     | AS-156            |
| 11.     | AS-116            | 34.     | AS-157            |
| 12.     | AS-124            | 35.     | AS-158            |
| 13.     | AS-132            | 36.     | AS-159            |
| 14.     | AS-133            | 37.     | AS-160            |
| 15.     | AS-134            | 38.     | AS-161            |
| 16.     | AS-138            | 39.     | AS-162            |
| 17.     | AS-140            | 40.     | AS-163            |
| 18.     | AS-141            | 41.     | AS-164            |
| 19.     | AS-142            | 42.     | AS-165            |
| 20.     | AS-143            | 43.     | AS-166            |
| 21.     | AS-144            | 44.     | G Soy-4           |
| 22.     | AS-145            | 45.     | JS 20-34          |
| 23.     | AS-146            |         | -                 |

**Table 2:** Grouping of 45 genotypes of soybean using cluster analysis

| Cluster number | Number of genotypes | Name of genotypes                                                                                             |
|----------------|---------------------|---------------------------------------------------------------------------------------------------------------|
| I              | 12                  | AS-153, AS-162, AS-159, AS-155, AS-144, AS-149, AS-151, AS-148, AS-143, AS-154, AS-27 and AS-140              |
| II             | 1                   | AS-132                                                                                                        |
| III            | 1                   | AS-124                                                                                                        |
| IV             | 14                  | AS-84, AS-98, AS-95, G Soy 4, AS-147, AS-101, AS-156, AS-163, AS-157, AS-30, AS-161, AS-142, AS-160 and AS-89 |
| V              | 11                  | AS-133, AS-165, AS-138, AS-164, AS-146, AS-145, AS-90, AS-150, AS-158, AS-47 and JS 20-34                     |
| VI             | 1                   | AS-166                                                                                                        |
| VII            | 1                   | AS-141                                                                                                        |
| VIII           | 1                   | AS-48                                                                                                         |
| IX             | 1                   | AS-134                                                                                                        |
| X              | 1                   | AS-152                                                                                                        |
| XI             | 1                   | AS-116                                                                                                        |

**Table 3:** Average intra (diagonal and bold) and inter-cluster distance values ( $D^2$ ) among 45 genotypes of soybean

| Cluster No. | I       | II       | III      | IV       | V        | VI       | VII      | VIII     | IX       | X        | XI       |
|-------------|---------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| I           | (94.09) | (136.89) | (127.23) | (166.92) | (166.66) | (207.36) | (202.20) | (127.46) | (331.60) | (177.68) | (326.16) |
|             | 9.70    | 11.70    | 11.28    | 12.92    | 12.91    | 14.40    | 14.22    | 11.29    | 18.21    | 13.33    | 18.06    |
| II          |         | 0.00     | (54.31)  | (176.89) | (126.56) | (330.87) | (75.86)  | (240.25) | (286.28) | (247.11) | (322.56) |
|             |         |          | 7.37     | 13.30    | 11.25    | 18.19    | 8.71     | 15.50    | 16.92    | 15.72    | 17.96    |
| III         |         |          | 0.00     | (179.82) | (160.27) | (278.22) | (96.04)  | (188.23) | (257.28) | (249.64) | (297.56) |
|             |         |          |          | 13.41    | 12.66    | 16.68    | 9.80     | 13.72    | 16.04    | 15.80    | 17.25    |
| IV          |         |          |          | (116.85) | (201.92) | (152.52) | (305.20) | (168.22) | (257.28) | (220.22) | (219.63) |
|             |         |          |          | 10.81    | 14.21    | 12.35    | 17.47    | 12.97    | 13.56    | 14.84    | 14.82    |
| V           |         |          |          |          | (145.92) | (284.93) | (209.67) | (242.11) | (317.90) | (261.79) | (318.26) |
|             |         |          |          |          | 12.08    | 16.88    | 14.48    | 15.56    | 17.83    | 16.18    | 17.84    |
| VI          |         |          |          |          |          | 0.00     | (484.44) | (242.11) | (305.55) | (115.77) | (396.01) |
|             |         |          |          |          |          |          | 22.01    | 10.71    | 17.48    | 10.76    | 19.90    |
| VII         |         |          |          |          |          |          | 0.00     | (316.84) | (423.53) | (336.35) | (355.32) |
|             |         |          |          |          |          |          |          | 17.80    | 20.58    | 18.34    | 18.85    |
| VIII        |         |          |          |          |          |          |          | 0.00     | (324)    | (167.70) | (315.41) |
|             |         |          |          |          |          |          |          |          | 18.00    | 12.95    | 17.76    |
| IX          |         |          |          |          |          |          |          |          | 0.00     | (463.97) | (174.50) |
|             |         |          |          |          |          |          |          |          |          | 21.54    | 13.21    |
| X           |         |          |          |          |          |          |          |          |          | 0.00     | (513.47) |
|             |         |          |          |          |          |          |          |          |          |          | 22.66    |
| XI          |         |          |          |          |          |          |          |          |          |          | 0.00     |

**Table 5:** Contribution of various traits towards total genetic divergence in soybean

| Sr. No | Characters                     | Time ranked First | Contribution (%) |
|--------|--------------------------------|-------------------|------------------|
| 1.     | Days to 50% flowering          | 13                | 1.31 %           |
| 2.     | Days to maturity               | 126               | 12.72 %          |
| 3.     | No. of branches per plant      | 122               | 12.32 %          |
| 4.     | Plant height (cm)              | 71                | 7.17 %           |
| 5.     | No. of pods per plant          | 177               | 17.87 %          |
| 6.     | No. of clusters per plant      | 26                | 2.63 %           |
| 7.     | No. of pods per cluster        | 2                 | 0.20 %           |
| 8.     | Pod length (cm)                | 7                 | 0.71 %           |
| 9.     | Number of seeds per pod        | 73                | 7.37 %           |
| 10.    | Seed yield per plant (g)       | 80                | 8.08 %           |
| 11.    | 100-seed weight (g)            | 46                | 4.65 %           |
| 12.    | Biological yield per plant (g) | 89                | 8.99 %           |
| 13.    | Harvest index (%)              | 12                | 1.21 %           |
| 14.    | Oil content (%)                | 146               | 14.75 %          |

**Table 6:** Selection index, discriminate function, expected genetic advance in seed yield and relative efficiency from the use of different selection indices in soybean

| Sr. No. | Selection index                                                                    | Discriminant function                                                                                       | Expected genetic advance | Relative efficiency (%) | Relative efficiency per character (%) |
|---------|------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------|--------------------------|-------------------------|---------------------------------------|
| 1       | X <sub>1</sub> Seed yield per plant                                                | 0.952X <sub>1</sub>                                                                                         | 3.99                     | 100.00                  | 100.00                                |
| 2       | X <sub>2</sub> Number of pods per plant                                            | 0.960X <sub>2</sub>                                                                                         | 13.47                    | 337.08                  | 337.59                                |
| 3       | X <sub>3</sub> Number of pods per cluster                                          | 0.881X <sub>3</sub>                                                                                         | 0.90                     | 22.65                   | 22.68                                 |
| 4       | X <sub>4</sub> Biological yield per plant                                          | 0.934X <sub>4</sub>                                                                                         | 5.17                     | 206.55                  | 206.55                                |
| 5       | X <sub>5</sub> Harvest index                                                       | 0.944X <sub>5</sub>                                                                                         | 20.79                    | 520.29                  | 520.29                                |
| 6       | X <sub>1</sub> + X <sub>2</sub>                                                    | 0.966X <sub>1</sub> + 0.961X <sub>2</sub>                                                                   | 14.28                    | 357.27                  | 178.63                                |
| 7       | X <sub>1</sub> + X <sub>3</sub>                                                    | 0.956X <sub>1</sub> + 1.001X <sub>3</sub>                                                                   | 4.46                     | 111.58                  | 55.79                                 |
| 8       | X <sub>1</sub> + X <sub>4</sub>                                                    | 0.958X <sub>1</sub> + 0.935X <sub>4</sub>                                                                   | 9.38                     | 234.67                  | 117.34                                |
| 9       | X <sub>1</sub> + X <sub>5</sub>                                                    | 0.962X <sub>1</sub> + 0.945X <sub>5</sub>                                                                   | 21.29                    | 532.65                  | 266.32                                |
| 10      | X <sub>2</sub> + X <sub>3</sub>                                                    | 0.959X <sub>2</sub> + 1.059X <sub>3</sub>                                                                   | 13.70                    | 342.76                  | 162.38                                |
| 11      | X <sub>2</sub> + X <sub>4</sub>                                                    | 0.960X <sub>2</sub> + 0.935X <sub>4</sub>                                                                   | 15.89                    | 397.55                  | 198.77                                |
| 12      | X <sub>2</sub> + X <sub>5</sub>                                                    | 0.961X <sub>2</sub> + 0.940X <sub>5</sub>                                                                   | 24.85                    | 621.72                  | 310.86                                |
| 13      | X <sub>3</sub> + X <sub>4</sub>                                                    | 0.898X <sub>3</sub> + 0.936X <sub>4</sub>                                                                   | 8.38                     | 209.66                  | 104.83                                |
| 14      | X <sub>3</sub> + X <sub>5</sub>                                                    | 0.997X <sub>3</sub> + 0.944X <sub>5</sub>                                                                   | 20.86                    | 521.89                  | 260.94                                |
| 15      | X <sub>4</sub> + X <sub>5</sub>                                                    | 0.933X <sub>4</sub> + 0.942X <sub>5</sub>                                                                   | 22.30                    | 557.99                  | 278.96                                |
| 16      | X <sub>1</sub> + X <sub>2</sub> + X <sub>3</sub>                                   | 0.955X <sub>1</sub> + 0.959X <sub>2</sub> + 1.184X <sub>3</sub>                                             | 14.60                    | 365.27                  | 121.76                                |
| 17      | X <sub>1</sub> + X <sub>2</sub> + X <sub>4</sub>                                   | 0.971X <sub>1</sub> + 0.961X <sub>2</sub> + 0.936X <sub>4</sub>                                             | 16.68                    | 417.31                  | 139.10                                |
| 18      | X <sub>1</sub> + X <sub>2</sub> + X <sub>5</sub>                                   | 0.976X <sub>1</sub> + 0.962X <sub>2</sub> + 0.947X <sub>5</sub>                                             | 25.40                    | 635.48                  | 211.82                                |
| 19      | X <sub>1</sub> + X <sub>3</sub> + X <sub>4</sub>                                   | 0.962X <sub>1</sub> + 1.014X <sub>3</sub> + 0.934X <sub>4</sub>                                             | 9.63                     | 240.93                  | 80.31                                 |
| 20      | X <sub>1</sub> + X <sub>3</sub> + X <sub>5</sub>                                   | 0.957X <sub>1</sub> + 1.130X <sub>3</sub> + 0.944X <sub>5</sub>                                             | 21.44                    | 536.40                  | 178.80                                |
| 21      | X <sub>1</sub> + X <sub>4</sub> + X <sub>5</sub>                                   | 0.967X <sub>1</sub> + 0.933X <sub>4</sub> + 0.948X <sub>5</sub>                                             | 22.84                    | 571.43                  | 190.47                                |
| 22      | X <sub>2</sub> + X <sub>3</sub> + X <sub>4</sub>                                   | 0.960X <sub>2</sub> + 1.074X <sub>3</sub> + 0.939X <sub>4</sub>                                             | 16.11                    | 403.05                  | 134.35                                |
| 23      | X <sub>2</sub> + X <sub>3</sub> + X <sub>5</sub>                                   | 0.959X <sub>2</sub> + 1.188X <sub>3</sub> + 0.943X <sub>5</sub>                                             | 25.02                    | 625.97                  | 208.66                                |
| 24      | X <sub>2</sub> + X <sub>4</sub> + X <sub>5</sub>                                   | 0.961X <sub>2</sub> + 0.934X <sub>4</sub> + 0.941X <sub>5</sub>                                             | 26.17                    | 654.74                  | 218.25                                |
| 25      | X <sub>3</sub> + X <sub>4</sub> + X <sub>5</sub>                                   | 1.010X <sub>3</sub> + 0.932X <sub>4</sub> + 0.944X <sub>5</sub>                                             | 22.38                    | 559.92                  | 186.64                                |
| 26      | X <sub>1</sub> + X <sub>2</sub> + X <sub>3</sub> + X <sub>4</sub>                  | 0.959X <sub>1</sub> + 0.960X <sub>2</sub> + 1.193X <sub>3</sub> + 0.935X <sub>4</sub>                       | 16.99                    | 425.07                  | 106.27                                |
| 27      | X <sub>1</sub> + X <sub>2</sub> + X <sub>3</sub> + X <sub>5</sub>                  | 0.956X <sub>1</sub> + 0.958X <sub>2</sub> + 1.295X <sub>3</sub> + 0.943X <sub>5</sub>                       | 25.63                    | 641.23                  | 160.31                                |
| 28      | X <sub>1</sub> + X <sub>2</sub> + X <sub>4</sub> + X <sub>5</sub>                  | 0.981X <sub>1</sub> + 0.962X <sub>2</sub> + 0.934X <sub>4</sub> + 0.942X <sub>5</sub>                       | 26.76                    | 669.502                 | 167.37                                |
| 29      | X <sub>1</sub> + X <sub>3</sub> + X <sub>4</sub> + X <sub>5</sub>                  | 0.961X <sub>1</sub> + 1.125X <sub>3</sub> + 0.932X <sub>4</sub> + 0.941X <sub>5</sub>                       | 22.99                    | 575.18                  | 143.79                                |
| 30      | X <sub>2</sub> + X <sub>3</sub> + X <sub>4</sub> + X <sub>5</sub>                  | 0.963X <sub>2</sub> + 1.189X <sub>3</sub> + 0.933X <sub>4</sub> + 0.947X <sub>5</sub>                       | 26.35                    | 659.24                  | 164.81                                |
| 31      | X <sub>1</sub> + X <sub>2</sub> + X <sub>3</sub> + X <sub>4</sub> + X <sub>5</sub> | 0.962X <sub>1</sub> + 0.959X <sub>2</sub> + 1.036X <sub>3</sub> + 0.933X <sub>4</sub> + 0.945X <sub>5</sub> | 26.99                    | 675.26                  | 135.05                                |

## 5. Conclusion

The present investigation revealed substantial genetic divergence among the soybean genotypes, as evidenced by the formation of eleven distinct clusters based on Mahalanobis D<sup>2</sup> statistics. Where cluster IV was the largest and maximum inter-cluster distance occurred between clusters XI and X indicating wide genetic divergence. Genotypes belonging to these clusters are therefore promising candidates for use as parents in hybridization programmes to exploit heterosis and generate broad variability. Key traits contributing to divergence included number of pods per plant, oil content and days to maturity highlighting their importance in selection strategies. The clustering pattern revealed that there existed no correlation between the geographical diversity and genetic diversity. Selection index analysis demonstrated the superiority of multi-trait selection over straight selection for seed yield alone. Selection Indices thirty-one multi-trait selection indices were constructed using seed yield per plant and components like number of pods per plant, biological yield, and harvest index. The highest relative efficiency (675.26%) was achieved with the five-trait index (X<sub>1</sub>+X<sub>2</sub>+X<sub>3</sub>+X<sub>4</sub>+X<sub>5</sub>) far surpassing straight selection for seed yield alone. Combinations like (X<sub>2</sub>+X<sub>4</sub>+X<sub>5</sub>) and (X<sub>1</sub>+X<sub>2</sub>+X<sub>4</sub>+X<sub>5</sub>) also showed superior genetic advance. These findings indicate high potential for heterosis breeding by selecting parents from distant clusters, such as XI and X, to maximize variability and yield improvement in soybean.

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