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# ASSESSMENT OF GENETIC DIVERSITY IN 35 SOYBEAN GENOTYPES (*GLYCINE MAX* (L.) MERRIL)

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**ABSTRACT**

In the present investigation, thirty-five soybean (*Glycine max* (L.) Merril) genotypes were evaluated to study genetic diversity using Mahalanobis $D^2$ statistics. The experiment was conducted at Research Farm, Agricultural research station, Kasbe Digraj (Sangli) during rabi 2022. Data were recorded on ten quantitative characters. The thirty-five genotypes of soybean were grouped into six clusters using the Tocher method. Of the six clusters formed, clusters I and IV were the largest groups, comprising ten and nine genotypes, respectively, followed by cluster II with seven genotypes, and clusters III, V, and VI with three genotypes each. Clusters IV and VI had the greatest inter-cluster distance (D=11.86). Intra-cluster distance ranged between 3.43 to 5.63. The biggest contribution to total divergence came from character Trypsin inhibitor activity (77.65 %). Based on cluster mean values for a given character, we can select highly divergent genotypes from the respective clusters for crossing work.
***Keywords*** **:** Soybean, Genetic, Diversity, Divergence, Tocher, Mahalanobis $D^2$.

## Introduction

Soybean (*Glycine max* (L.) Merrill) is a self-pollinating legume that originated in northeastern China. Its importance has surged due to the increasing demand for soybeans and their products. In the 2023-24 period, the global soybean cultivation area was about 139.47 million hectares, producing approximately 396.73 million metric tons with an average yield of 2.84 tons per hectare (Anonymous, 2024). Soybean is a vital oilseed crop, accounting for 25% of global vegetable oil production and is highly valued in oilseed cultivation for its high productivity and profitability (Bhuva *et al*., 2020). About 70-75% of the global soybean production is used for animal feed. Known by various names such as miracle crop, golden bean, crop of the century, meat that grows on plants, protein hope of the future, and functional food of the century, soybean is recognised for its diverse nutrient profile, high-quality protein, essential amino acids, and beneficial unsaturated fatty acids. It also contains several bioactive compounds that provide numerous health benefits (Hassan, 2013). In developing countries, protein-energy malnutrition is a significant issue, making soybeans a promising alternative to expensive animal-based food products due to their rich nutritional content, including protein, essential amino acids, polyunsaturated fatty acids, minerals, and vitamins (Boland *et al*., 2013).

In plant breeding, genetic diversity plays an important role because hybrids between lines of diverse genetic origin generally display greater heterosis than those between closely related parents (Falconer, 1960; Arunachalam, 1981; Ghaderi *et al*., 1984; Mian and Bahl, 1989). The concept of $D^2$ statistics was developed by P.C. Mahalanobis in 1928, and Rao (1952) suggested its use for the assessment of genetic diversity in plant breeding. $D^2$ analysis helps in the selection of genetically divergent parents for their

exploitation in a hybridization program. It measures the degree of diversification and determines the relative proportion of each component character to total divergence. The $D^2$ analysis has been successfully utilized in soybean to classify genotypes and determine their interrelationship by many workers (Mounika *et al*. 2022 and Upadhyay *et al*. 2022). To evaluate their usefulness as parents in a hybridization program, $D^2$ analysis is essential.

## Materials and Methods

Thirty-five germplasm accessions were collected from Agricultural Research Station Kasbe Digraj, Sangli, Maharashtra, India which included 30 soybean germplasms accessions and five checks (JS 335, JS 9305, Phule Sangam, Phule Kimaya, Phule Durva) which are shown in table 1. The field experiment was carried out at the Agricultural Research Station Kasbe Digraj Sangli. Maharashtra, India. All the accessions were evaluated during kharif seasons of 2022 in a Randomized Block Design (RBD) with two replications, spaced planted at 45 × 5 cm in a plot size of 4m × 0.45m. The experimental material was subjected to standard agronomic practices. The following ten characters were observed for statistical analysis namely, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, 100 seed weight, oil content, protein content, trypsin inhibitor content, seed yield per plant. To record observations, five plants were picked at random from each plot and five plants from the check in each replication. Separate observations were conducted on each plant. For each genotype of these plants, the average value for each character was determined individually.

**Table 1 :** List of Genotypes

| Sr.No. | Genotype | Sr.No. | Genotype |
|---|---|---|---|
| 1 | KDS 1096 | 19 | KDS 1276 |
| 2 | KDS 1115 | 20 | KDS 1278 |
| 3 | KDS 1132 | 21 | KDS 1281 |
| 4 | KDS 1149 | 22 | KDS 1283 |
| 5 | KDS 1172 | 23 | KDS 1334 |
| 6 | KDS 1180 | 24 | KDS 1369 |
| 7 | KDS 1181 | 25 | KDS 1371 |
| 8 | KDS 1185 | 26 | KDS 1372 |
| 9 | KDS 1195 | 27 | KDS 1374 |
| 10 | KDS 1197 | 28 | KDS 1376 |
| 11 | KDS 1204-1 | 29 | KDS 1377 |
| 12 | KDS 1209 | 30 | KDS 1378 |
| 13 | KDS 1219 | 31 | JS 335 [c] |
| 14 | KDS 1221 | 32 | JS 9305 [c] |
| 15 | KDS 1233 | 33 | Phule Kimaya (KDS 753) [c] |
| 16 | KDS 1254 | 34 | Phule Sangam (KDS-726) [c] |
| 17 | KDS 1258 | 35 | Phule Durva (KDS-992) [c] |
| 18 | KDS 1259 | | |

## Result and Discussion

The genotypes were categorised into various clusters according to their genetic distances. The distribution pattern of genotypes, intra- and inter-cluster divergence ($D^2$ values), the mean values for each cluster and the contribution percentages of different traits to genetic divergence are presented below.

### Intra and inter-cluster Distance

The average intra-cluster and inter-cluster D values were worked out using $D^2$ values from divergence analysis and are presented in table 2 (Fig.1). The aim of cluster formation and finding out intra and inter-cluster divergence is to provide the basis for the selection of parents for further hybridization programme.

The maximum intra-cluster distance was observed in cluster V (D=5.63) followed by cluster II (D=4.76), cluster IV (D=4.73), cluster VI (D=4.63), cluster I (D=4.19) and cluster III (D=3.43). Soniasabanam *et al.* (2018) found identical results for intra-cluster distances.

The maximum inter-cluster distance was recorded between cluster IV and VI (D=11.868), followed by cluster I and VI (D=10.367), cluster IV and V

(D=10.194), cluster III and IV (D=9.970), cluster II and VI (D=8.927), cluster I and V (D=8.456), cluster I and III (D=8.374), cluster II and IV (D=8.110) and cluster III and VI (D=8.089). Long distance between the clusters i.e. higher D or $D^2$ value suggested that genotypes included in these clusters might had entirely different genetic architecture. The minimum inter-cluster distance was reported between cluster I and II (D=5.89), cluster III and V (D=6.18), cluster I and IV (D=6.21), cluster V and VI (D=6.80), cluster II and V (D=6.84) and cluster II and III (D=7.22). The short distance between the clusters i.e. A lower value of D or $D^2$ suggests that the genetic constitution of the genotypes in one cluster is similar to the genotypes in the other clusters of the pair.

**Table 2 :** Average intra and inter-cluster distances (D Values and $D^2$ values) of 6 clusters for 35 soybean genotypes.

| Cluster | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| **I** | 17.60 (4.19) | 34.71 (5.89) | 70.13 (8.37) | 38.59 (6.21) | 71.50 (8.45) | 107.47 (10.36) |
| **II** | | 22.71 (4.76) | 52.13 (7.22) | 65.77 (8.11) | 46.81 (6.84) | 79.69 (8.92) |
| **III** | | | 11.79 (3.43) | 99.41 (9.97) | 38.29 (6.18) | 65.44 (8.08) |
| **IV** | | | | 22.39 (4.73) | 103.92 (10.19) | 140.85 (11.86) |
| **V** | | | | | 31.76 (5.63) | 46.25 (6.80) |
| **VI** | | | | | | 21.52 (4.63) |

The values in the parenthesis are D= $\sqrt{D^2}$ values

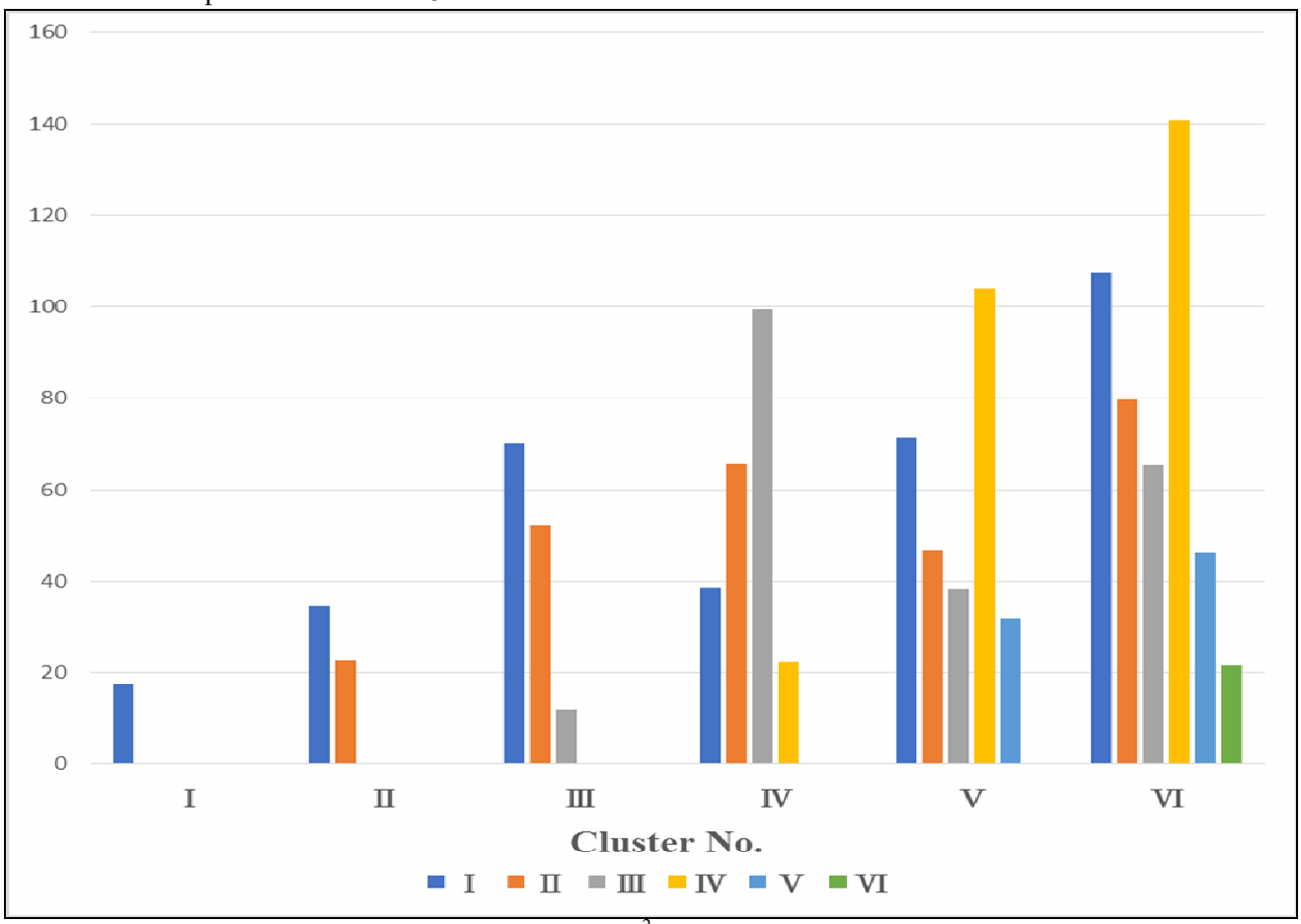


**Fig. 1 :** Average intra and inter-cluster distances ($D^2$ values) between 6 clusters of 35 soybean genotypes

**Clustering pattern**

In this study, all thirty-five genotypes analysed for genetic divergence showed significant differences in the traits examined and exhibited notable divergence. Cluster formation was done by following Tocher's method as described by Rao (1952) by utilizing $D^2$

values. The details about clusters are given in table 3 (Fig. 2). Thirty-five genotypes included in the present investigation were grouped into six clusters. Cluster I is found to be the largest and consists 10 genotypes followed by Cluster IV which consists of 9 genotypes. 7 genotypes were included in cluster II. Cluster III, Cluster V and cluster VI consists of 3 genotypes each. Similar clustering pattern was observed by JENCY and Kalaimagal (2014) and Khedkar *et al.* (2018).

**Table 3 :** Distribution of 35 genotypes of soybean into 6 different clusters

| Cluster No. | No. of genotypes included | Name of genotypes |
|---|---|---|
| **I** | 10 | KDS 1372, KDS 1376, KDS 1185, KDS 1254, KDS 1204-1, KDS 1180, KDS 1374, KDS 1197, KDS 1209, KDS 1378 |
| **II** | 7 | KDS 1281, KDS 1369, KDS 1149, KDS 1181, KDS 1115, KDS 1258, KDS 1377 |
| **III** | 3 | Phule Sangam (KDS-726), Phule Durva (KDS 992), JS 9305 |
| **IV** | 9 | KDS 1276, KDS 1334, KDS 1195, KDS 1278, KDS 1371, KDS 1219, KDS 1259, KDS 1233, KDS 1172 |
| **V** | 3 | KDS 1221, KDS 1283, Phule Kimaya (KDS-753) |
| **VI** | 3 | KDS 1096, KDS 1132, JS 335 |

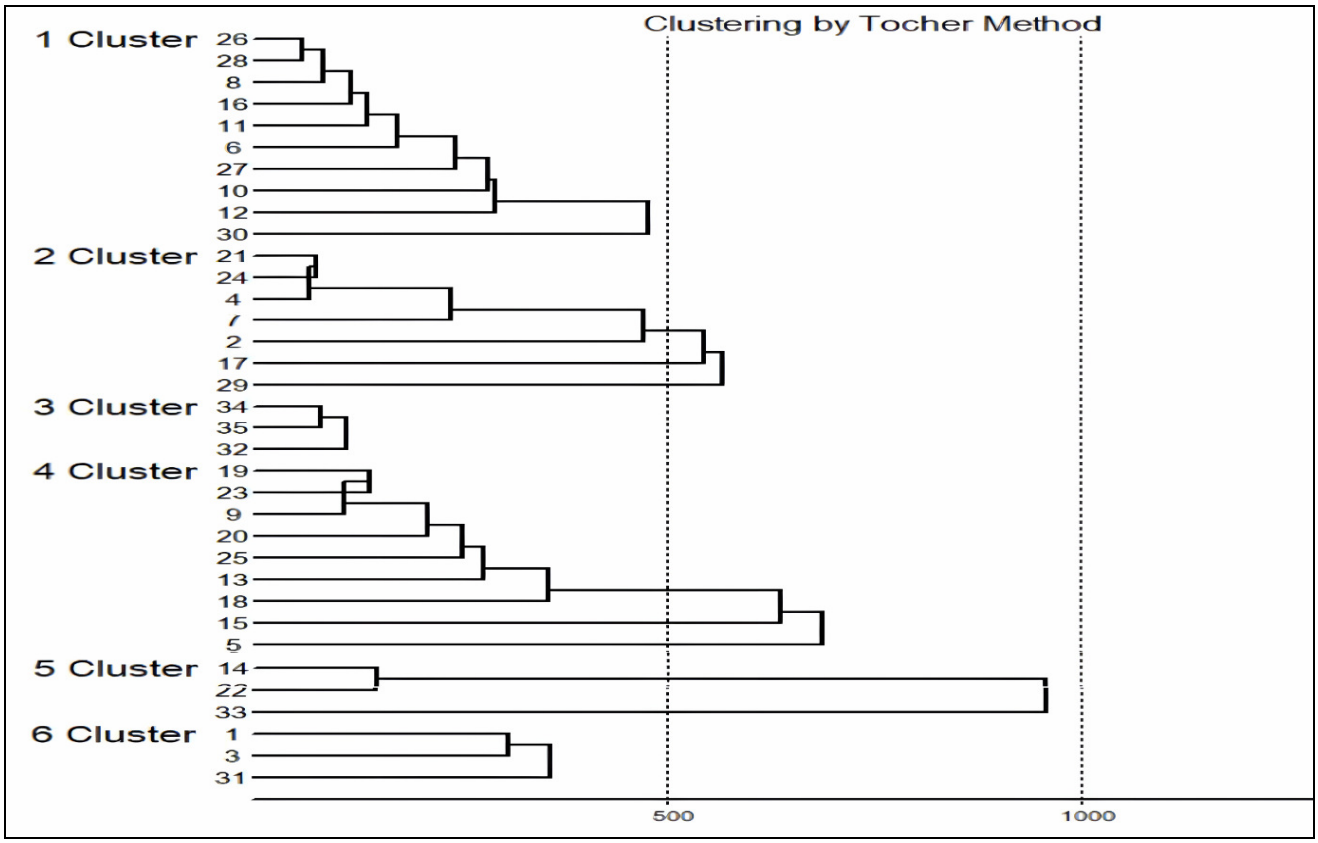


**Fig. 2:** Cluster diagram

**Cluster means of characters in soybean:**

The cluster means of ten characters are presented in table 4 (fig. 3). Cluster I recorded the minimum days to 50% flowering (36.30) and maximum protein content (38.11) among all clusters. Lowest value for days to maturity (98.66) was displayed by cluster III and highest value for number of pods per plant (40.33), oil content (19.92) and seed yield per plant (26.06). Genotypes in cluster IV showed the highest average plant height (43.11) and number of primary branches per plant (5.80) and lowest value for trypsin inhibitor content (30.79). Cluster V included the genotypes with highest average 100 seed weight (13.66).

**Table 4. Cluster means of 6 clusters for 10 characters in soybean.**

| Clusters | Characters | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | DFF | DTM | PH | PBP | PPP | HSW | OC | PC | TIA | SYPP |
| I | 36.30 | 100.70 | 40.58 | 5.66 | 35.58 | 11.88 | 17.46 | 38.11 | 54.90 | 6.17 |
| II | 37.71 | 102.57 | 40.48 | 5.40 | 32.60 | 10.70 | 17.35 | 36.22 | 76.67 | 6.03 |
| III | 38.66 | 98.66 | 35.06 | 5.66 | 40.33 | 12.94 | 19.92 | 35.08 | 88.30 | 26.06 |
| IV | 37.66 | 102.55 | 43.11 | 5.80 | 34.40 | 11.62 | 17.30 | 36.56 | 30.79 | 5.89 |
| V | 40.33 | 105.33 | 35.90 | 4.66 | 30.93 | 13.66 | 18.61 | 35.15 | 100.86 | 10.05 |
| VI | 37.33 | 102.00 | 29.60 | 3.86 | 29.13 | 9.91 | 17.80 | 36.29 | 132.83 | 7.43 |

DFF- Days to 50 percent flowering
DTM- Days to maturity
PH- Plant height
PBP- Number of Primary branches per plant
PPP- Number of Pods per plant
HSW- 100 seed weight
OC- Oil content
PC- Protein content
TIA- Trypsin inhibitor activity
SYPP- Seed yield per plant

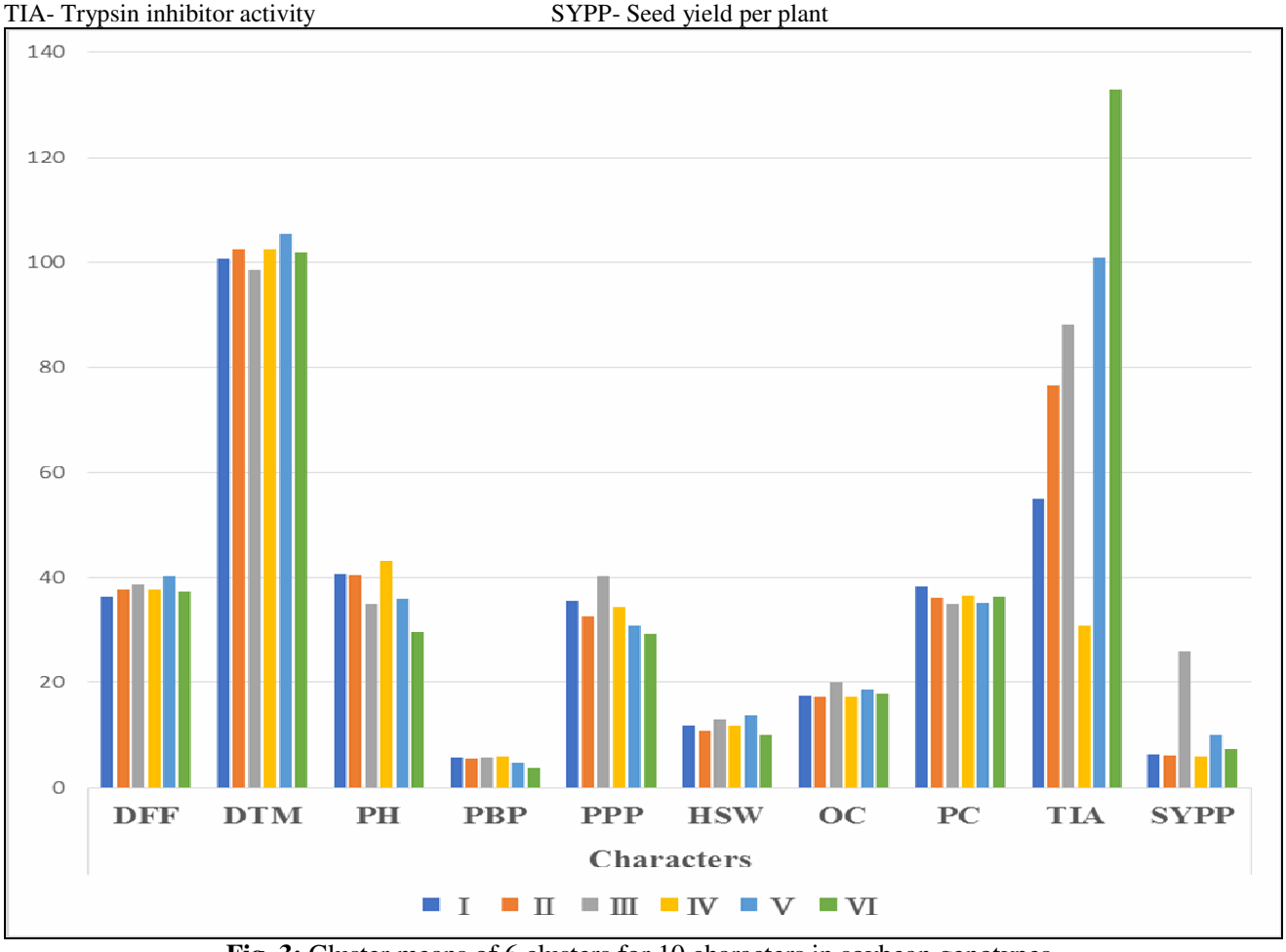


**Fig. 3:** Cluster means of 6 clusters for 10 characters in soybean genotypes.

**Percent contribution of ten characters for divergence in soybean**

The details of the percent contribution of 10 characters for divergence is given in table 5 (Fig. 4). Out of ten characters studied, the character trypsin inhibitor activity (77.65 %) contributed the maximum for divergence and was followed by seed yield per plant (12.10 %), oil content (6.05 %) and 100-seed weight (3.19 %). The minimum contribution to genetic divergence was made by the character's number of primary branches per plant (0.67 %) followed by days to maturity (0.17 %) and the number of pods per plant (0.17). There was no contribution by days to 50 per cent flowering, plant height and protein content in genetic divergence. Similar results were reported by Upadhyay *et al.* (2022), Shadakshari *et al.* (2011), Kachhadia *et al.* (2014), JENCY and Kalaimagal (2014), Promin *et al.* (2014), Dubey *et al.* (2018) and Khedkar *et al.* (2018). It is advisable to select divergent

parents based on the characters that contributed most to the divergence i.e. trypsin inhibitor activity and seed yield per plant to attempt crossing between them for achieving a broad spectrum of favourable genetic variability for yield improvement in soybean.

**Table 5 :** Percent contribution of ten characters for divergence in soybean

| Sr.No | Source | Times Ranked 1st | Contribution (%) |
|---|---|---|---|
| 1 | Days to 50 % flowering | 0 | 0.00 |
| 2 | Days to maturity | 1 | 0.17 |
| 3 | Plant height (cm) | 0 | 0.00 |
| 4 | Number of primary branches per plant | 4 | 0.67 |
| 5 | Number of pods per plant | 1 | 0.17 |
| 6 | 100-seed weight (g) | 19 | 3.19 |
| 7 | Oil content (%) | 36 | 6.05 |
| 8 | Protein content (%) | 0 | 0.00 |
| 9 | Trypsin inhibitor activity (µg/g) | 462 | 77.65 |
| 10 | Seed yield per plant (g) | 72 | 12.10 |

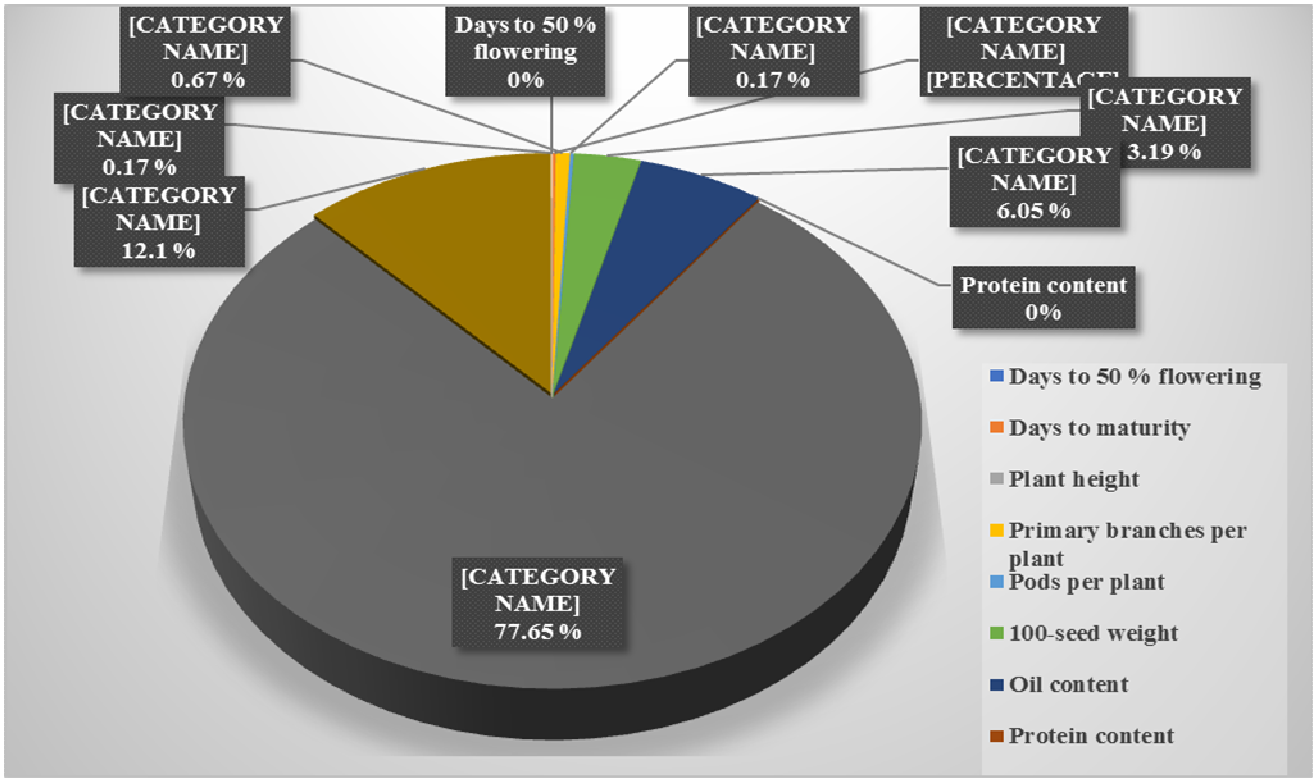


**Fig. 4 :** Percent contribution of 10 characters for divergence

## Conclusion

It can be concluded from the present study that moderate diversity exists in the experimental material. Superior genotypes from clusters IV and VI can be selected due to their maximum inter-cluster distance, which increases the likelihood of obtaining transgressive segregants in later generations. Additionally, cluster III has shown desirable cluster means for days to maturity, oil content, and seed yield per plant. Therefore, superior genotypes from cluster III can be crossed with those from cluster IV, which is at the maximum distance from cluster III and has the lowest cluster mean for trypsin inhibitor content and second highest protein content among all clusters. In this way, information obtained from this study can be used to plan crosses and maximize the use of genetic diversity and expression of heterosis.

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