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# Genetic divergence Analysis in Groundnut (*Arachis hypogaea* L.)

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**ABSTRACT: The present study was conducted to analyze genetic diversity among 45 groundnut genotypes for twenty two characters using Mahalanobis $D^2$ statistics. Based on Tocher's method of clustering, 45 genotypes were grouped into eight clusters of which cluster I was the largest with 31 genotypes followed by cluster II with 8 genotypes. The inter cluster distance was maximum between cluster VII and VIII (22.25) followed by cluster V and VII (21.65) and cluster II and VI (20.68). Considering the cluster distance and cluster means, crossing between the genotypes of cluster VII and cluster VIII, cluster V and VII is suggested in order to get transgressive segregants for yield and yield traits. The character, number of pods plant$^{-1}$ (30%) contributed maximum towards genetic diversity followed by hundred kernel weight (25.25%) and number of pegs plant$^{-1}$ (13.4%).**

**Keywords:** Cluster, $D^2$ statistics, Genetic diversity, Groundnut.

## INTRODUCTION

Groundnut (*Arachis hypogaea* L.), is an annual self pollinated leguminous oilseed crop having genome AABB with a chromosome number of 2n = 4x = 40. It is a segmental allotetraploid, belongs to the family *Fabaceae*. It is the only nut found under the soil and designated as "wonder legume". It is native to South America, grown throughout the tropical and sub-tropical regions of the world between the latitudes of 40° N to 40° S. It is a rich source of high quality oil (44-56%), protein (22-30%) on dry seed basis, carbohydrates (10-25%), vitamins (E, Z and B complex), minerals (Ca, P, Mg, Zn and Fe) and fiber (Gulluoglu *et al*., 2016). Being a legume it adds nitrogen (25-75 lb of nitrogen per acre per year) and organic matter to the soil (Frankow - Lindberg and Dahlin 2013).

In India, groundnut is cultivated in an area of 49.14 lakh hectares with production of 82.54 Mt and productivity of 1676 kg/ha (Directorate of Economics and Statistics, 2021-2022). The reasons for low yield are mainly due to incidence of late leaf spot, rust, stem rot and drought at pod development stage of the crop. To step up groundnut yields per unit area and per unit time, there is need to develop high yielding varieties with resistance to biotic and abiotic stresses. For finding the gene source for the particular trait within the available germplasm, assessment of genetic diversity is an important step in any crop improvement programme as it plays an important role in selection of parents because the hybrids between genetically diverse parents manifest greater heterosis than those between more closely related parents (Arunachalam *et al.*, 1981). Hence, it increases the probability of getting wide range of segregants which increases the scope for selection for the targeted traits. Therefore, in the present study 45 genotypes were evaluated to assess the magnitude of genetic diversity among them.

## MATERIAL AND METHODS

The base material for present study consisted of 45 groundnut genotypes (Table 1) which includes 8 released varieties, 21 advanced breeding lines from RARS, Tirupati and 16 ICRISAT lines. The material was sown during *kharif*, 2021 in a Randomized Block Design (RBD) with three replications in order to study the genetic diversity. In each replication, every genotype was sown in three rows of 3 m length with a spacing of 30 cm between rows and 10 cm between plants within a row. Need based recommended agronomic and cultural practices and plant protection measures were followed. The data was collected from five randomly selected plants of each genotype in each replication for 22 characters *viz.*, days to 50 % flowering, days to maturity, SCMR at 60 DAS, SLA at 60 DAS ($cm^2$ $g^{-1}$), plant height (cm), number of primary branches $plant^{-1}$, number of pods $plant^{-1}$, number of pegs $plant^{-1}$, pods to pegs ratio, hundred pod weight (g), shelling per cent, hundred kernel weight (g), sound mature kernel per cent, dry haulms yield $plant^{-1}$ (g), harvest index (%), protein content (%), oil content (%), oleic acid content, linoleic acid content, O/L ratio, kernel yield $plant^{-1}$(g) and pod yield $plant^{-1}$ (g) except days to 50% flowering and days to maturity which were recorded on plot basis.

In present investigation, analysis of genetic divergence was carried out using Mahalanobis's $D^2$ statistics (1936). Grouping of genotypes into clusters was done by the Tocher's method as described by Rao (1952). The data analysis was carried out with WINDOWSTAT 9.2 software.

## RESULTS AND DISCUSSION

Based on $D^2$ statistic, forty five genotypes of groundnut were grouped into eight clusters by using Tocher's method. The distribution of genotypes into eight clusters is presented in Table 2 and Fig. 1. Cluster I is the largest cluster comprising 31 genotypes followed by Cluster III having eight genotypes and remaining clusters (II, V, VI, VII and VIII) are monogenotypic clusters. The average inter and intra-cluster $D^2$ and D values were furnished in Table 3 and Fig. 2. The inter-cluster distance were larger than the intra-cluster distance which indicated that greater diversity was present among the genotypes of different clusters (Zaman *et al*., 2010, Dolma *et al.,* 2010). The average intra cluster distance ranged from 0 to 10.18. The maximum intra-cluster distance was observed in cluster III (10.18) followed by cluster I (10.16). Intra-cluster distance for other clusters *i.e.*, II, V, VI, VII, and VIII is zero as they are solitary clusters. While, the inter-cluster $D^2$ values varied from 9.73 to 22.25.

Highest inter-cluster distance was observed between cluster VII and VIII (22.25) followed by cluster V and VII (21.65) and cluster II and VI (20.68) as compared to others, indicating greater diversity between genotypes of these clusters.

Hence, elite genotypes from these diversified clusters can be used as parents for hybridization which would result in transgressive segregants for yield and yield related traits in filial generations. Crossing between such genotypes will also be helpful to create variability for desired traits and to select superior recombinants for the improvement of traits. The cluster means for 22 characters are furnished in Table 5.

**Table 1: The list of 45 genotypes studied in the present study.**

| Sr. No. | Genotypes |
|---|---|
| **1** | TCGS-1694 |
| **2** | TCGS-1707 |
| **3** | TCGS-1862 |
| **4** | TCGS-2217 |
| **5** | TCGS-2219 |
| **6** | TCGS-2223 |
| **7** | TCGS-2229 |
| **8** | TCGS-2243 |
| **9** | TCGS-2244 |
| **10** | TCGS-2245 |
| **11** | TCGS-2246 |
| **12** | TCGS-2247 |
| **13** | TCGS-2248 |
| **14** | TCGS-2249 |
| **15** | TCGS-2250 |
| **16** | TCGS-2251 |
| **17** | TCGS-2252 |
| **18** | TCGS-2253 |
| **19** | TCGS-2254 |
| **20** | TCGS-2255 |
| **21** | TCGS-2256 |
| **22** | TCGS-2257 |
| **23** | Tirupati 1 |
| **24** | Dharani |
| **25** | Dheeraj |
| **26** | Narayani |
| **27** | Kadiri-6 |
| **28** | Nithya Haritha |
| **29** | ICGV-08146 |
| **30** | ICGV-86856 |
| **31** | ICGV-86590 |
| **32** | ICGR-161929 |
| **33** | ICGR-161930 |
| **34** | ICGR-161999 |
| **35** | ICGR-162009 |
| **36** | ICGR-162020 |
| **37** | ICGR-162044 |
| **38** | ICGR-162059 |
| **39** | ICGR-162066 |
| **40** | ICGR-162096 |
| **41** | ICGR-162105 |
| **42** | NRCG CS-19 |
| **43** | ICGV-181424 |
| **44** | ICGV-181458 |
| **45** | ICGV-181482 |

**Table 2: Clustering of groundnut genotypes based on Tocher's method.**

| Clusters | Number of Genotypes | Genotypes |
|---|---|---|
| I | 31 | Narayani, Dharani, TCGS-2253, TCGS-2247, TCGS-2229, TCGS-1862, NRCG CS-19, TCGS-2250, TCGS-2248, TCGS-2223, TCGS-2251, TCGS-2254, TCGS-2249, Kadiri-6, Nithya Haritha, TCGS-2246, TCGS-2257, TCGS-2217, TCGS-2252, TCGS-2243, TCGS-2245, TCGS-2255, TCGS-2256, ICGR-162096, ICGR-162059, ICGR-162020, ICGR-162066, ICGR-162044, ICGR-161999, ICGV-181458, Dheeraj |
| II | 1 | ICGR -162009 |
| III | 8 | ICGR-161930, ICGR-161929, ICGV-181424, ICGV-86856, ICGV- 181482, ICGV- 08146, TCGS-2219, TCGS-1707 |
| IV | 1 | TCGS-2244 |
| V | 1 | TCGS-1694 |
| VI | 1 | Tirupati1 |
| VII | 1 | ICGV-86590 |
| VIII | 1 | ICGR- 162105 |

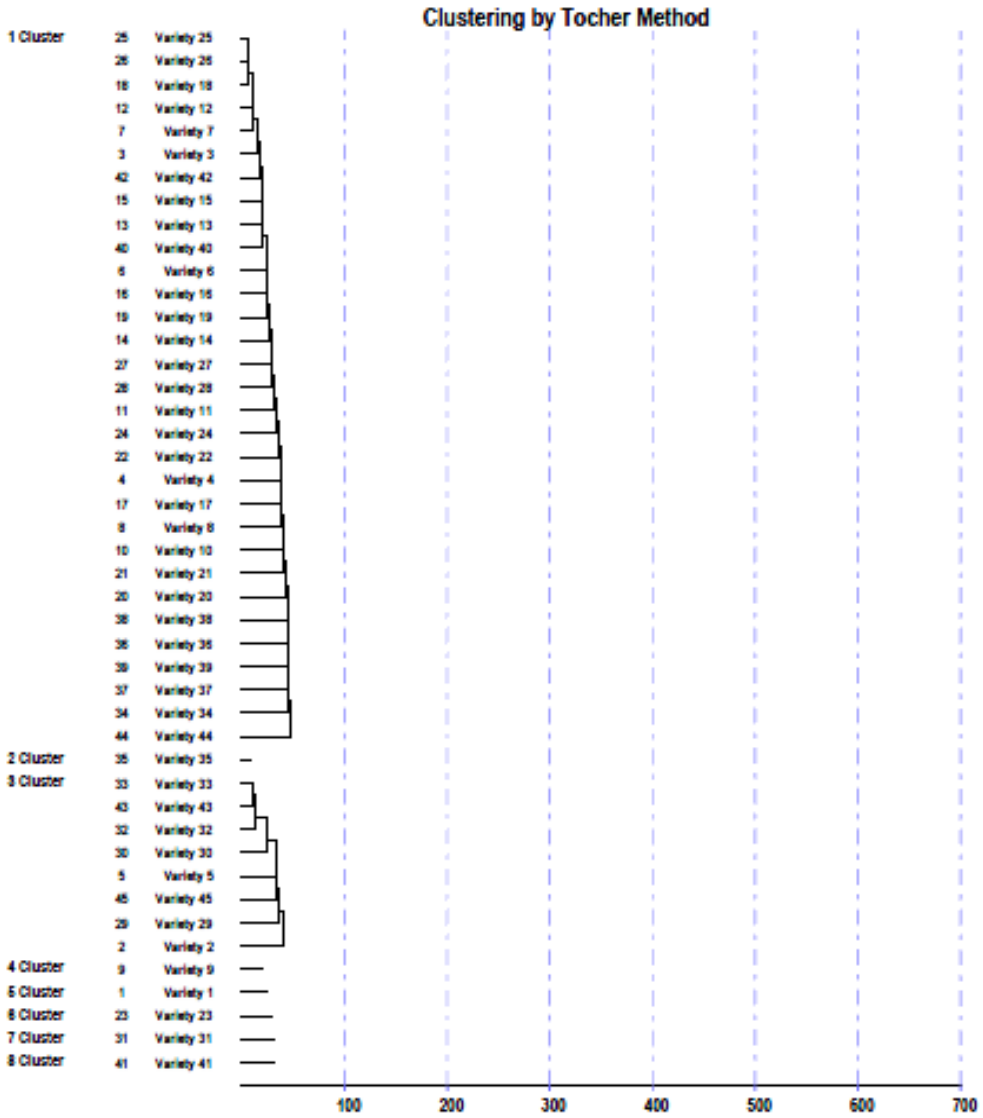


**Fig. 1.** Grouping of genotypes into clusters using Tocher's method.

**Table 3: Inter and Intra cluster (diagonal) average $D^2$ and D values (in parentheses) among 45 genotypes of groundnut.**

| Clusters | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| **I** | **103.21 (10.16)** | 167.89 (13.03) | 177.45 (13.32) | 145.15 (12.05) | 144.29 (12.01) | 172.81 (13.15) | 218.67 (14.79) | 182.28 (13.50) |
| **II** | | **0.00 (0.00)** | 94.71 (9.73) | 205.75 (14.34) | 284.71 (16.87) | 427.77 (20.68) | 166.10 (12.89) | 242.16 (15.56) |
| **III** | | | **103.57 (10.18)** | 219.87 (14.83) | 316.84 (17.80) | 396.74 (19.92) | 190.80 (13.81) | 263.52 (16.23) |
| **IV** | | | | **0.00 (0.00)** | 238.54 (15.44) | 237.15 (15.40) | 110.25 (10.50) | 384.35 (19.60) |
| **V** | | | | | **0.00 (0.00)** | 157.76 (12.56) | 468.5 (21.65) | 140.32 (11.85) |
| **VI** | | | | | | **0.00 (0.00)** | 372.04 (19.29) | 236.54 (15.38) |
| **VII** | | | | | | | **0.00 (0.00)** | 494.97 (22.25) |
| **VIII** | | | | | | | | **0.00 (0.00)** |

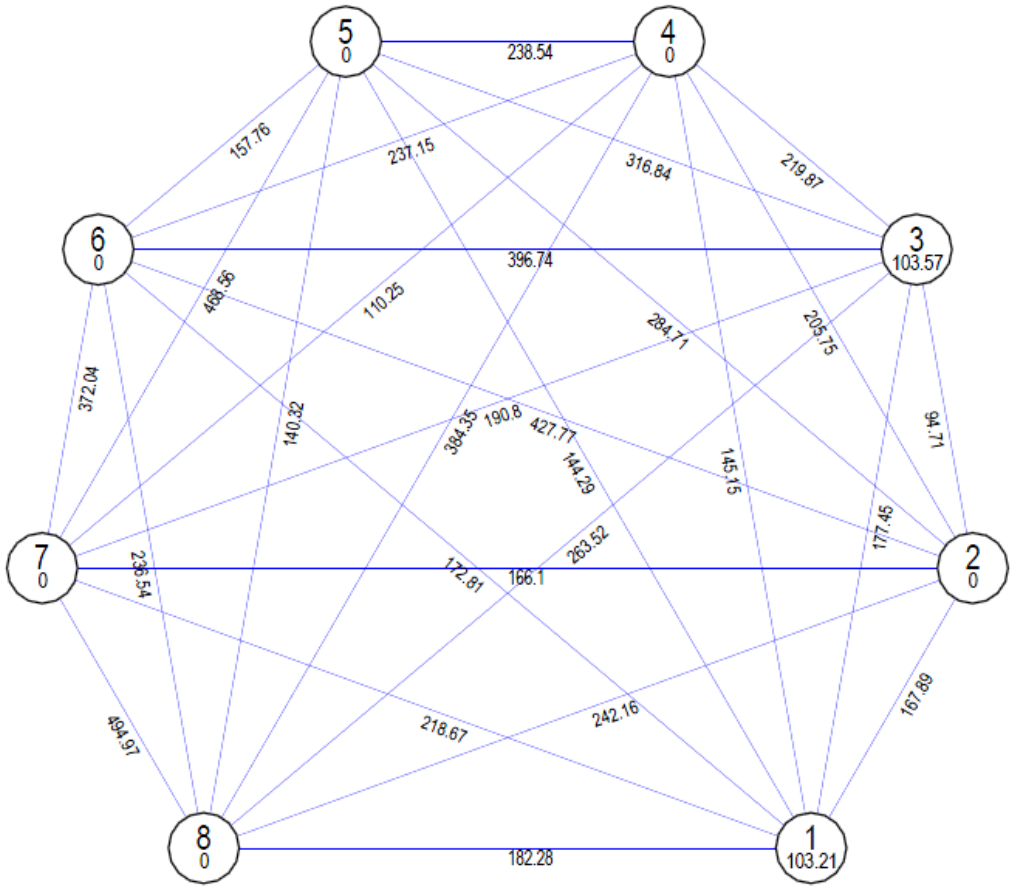


**Fig. 2.** Statistical intra and inter-cluster ($D^2$) distances among eight clusters of groundnut.

**Table 4: Cluster mean analysis of yield and yield attributes with overall character wise score in 45 groundnut genotypes.**

| Cluster | DF | DM | SCMR | SLA | PH | NPB | NPP | NPEGS | PODS: PEGS | 100PW | SP | 100KW | SMK | DHY | HI | PROTEIN | OIL | OA | LLA | O/L | PYP | KYP | Total Score | rank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 26.44 (3) | 109.95 (3) | 45.13 (4) | 159.92 (6) | 44.42 (3) | 5.33 (5) | 18.49 (5) | 26.27 (5) | 71.1 (5) | 113.89 (3) | 69.12 (5) | 46.84 (5) | 64.64 (4) | 17.79 (5) | 47.83 (5) | 24.98 (4) | 50.77 (3) | 48.77 (6) | 32.7 (2) | 1.59 (5) | 18.1 (5) | 12.47 (5) | 96 | 4 |
| II | 28 (6) | 116.67 (7) | 46.67 (2) | 156.16 (5) | 38.33 (6) | 6.33 (2) | 26.33 (2) | 33 (3) | 79.69 (1) | 94.32 (6) | 74.15 (2) | 42.27 (6) | 46 (8) | 20.5 (3) | 53.3 (1) | 22.15 (8) | 52.62 (1) | 52.91 (2) | 29.78 (6) | 1.78 (3) | 25.67 (2) | 19 (1) | 83 | 1 |
| III | 28.29 (7) | 112.67 (4) | 45.21 (3) | 147.38 (3) | 42.42 (4) | 6.17 (3) | 25.79 (3) | 35.96 (2) | 72.04 (3) | 111.78 (4) | 66.71 (7) | 49.18 (4) | 61.48 (5) | 22.97 (2) | 49.73 (2) | 24.46 (5) | 51 (2) | 48.65 (7) | 32.41 (3) | 1.54 (7) | 24.79 (3) | 16.42 (3) | 86 | 2 |
| IV | 26.67 (4) | 109 (2) | 45 (5) | 141.49 (1) | 54.33 (1) | 4.67 (7) | 13.67 (6) | 19 (7) | 71.9 (4) | 87.13 (7) | 63.1 (8) | 57.76 (2) | 56.5 (6) | 17.29 (7) | 42.84 (8) | 28.6 (1) | 46.44 (8) | 49.93 (5) | 31.68 (4) | 1.58 (6) | 14.67 (8) | 9 (8) | 115 | 6 |
| V | 25.33 (2) | 105.33 (1) | 41 (7) | 151.89 (4) | 36.33 (7) | 5 (6) | 12.33 (7) | 17.67 (8) | 69.7 (6) | 72.67 (8) | 73.41 (3) | 35.07 (8) | 69 (3) | 15.08 (8) | 47.71 (6) | 24 (6) | 47.99 (6) | 52.66 (3) | 27.22 (8) | 1.93 (1) | 15 (7) | 11 (7) | 122 | 7 |
| VI | 24 (1) | 105.33 (1) | 49.67 (1) | 173.75 (7) | 38.33 (6) | 6.67 (1) | 12.33 (7) | 20.33 (6) | 60.51 (8) | 138.86 (1) | 77.28 (1) | 50.91 (3) | 75.5 (1) | 17.59 (6) | 44.28 (7) | 25.69 (3) | 47.87 (7) | 51.56 (4) | 30.24 (5) | 1.71 (4) | 15.67 (6) | 12 (6) | 92 | 3 |
| VII | 27.67 (5) | 115 (5) | 43.33 (6) | 144.72 (2) | 45 (2) | 5 (6) | 20 (4) | 27 (4) | 73.98 (2) | 134.3 (2) | 66.86 (6) | 63.29 (1) | 47.13 (7) | 19.93 (4) | 48.05 (4) | 23.82 (7) | 48.33 (5) | 40.29 (8) | 40.81 (1) | 0.99 (8) | 19.67 (4) | 13.33 (4) | 101 | 5 |
| VIII | 30 (8) | 115.67 (6) | 46.67 (2) | 245.85 (8) | 40.67 (5) | 6 (4) | 32.33 (1) | 47 (1) | 68.67 (7) | 104.9 (5) | 70.99 (4) | 31.84 (7) | 74 (2) | 25.04 (1) | 49.31 (3) | 25.75 (2) | 50.34 (4) | 53.58 (1) | 28.58 (7) | 1.88 (2) | 26 (1) | 18.33 (2) | 83 | 1 |

**Note:** Numbers in brackets indicate the given rank based on mean values. Total score is the aggregate of ranks for all traits and final rank is listed accordingly.

DF : Days to 50% flowering; DM : Days to maturity; SCMR : SPAD chlorophyll meter reading at 60 DAS; SLA: Specific leaf area at 60 DAS ($cm^2$ $g^{-1}$);) PH: Plant height (cm); NPB: No of Primary branches $plant^{-1}$; NMP: No of pods $plant^{-1}$; 100-PW: 100 Pod weight (g); SP: Shelling Per cent; 100-KW: 100 Kernel weight (g); SMK: Sound mature kernel (%); DHY: Dry haulms yield per plant (g); HI: Harvest index (%); PRO: Protein content (%); OIL: Oil content (%); OA: Oleic acid (%); LLA: Linoleic acid (%); O/L: Oleic to Linoleic ratio; KYP: Kernel yield $plant^{-1}$ (g); PYP: Pod yield $plant^{-1}$(g).

**Table 5: Relative contribution of various characters towards genetic diversity in groundnut.**

| Sr. No. | Characters | No times ranked first | % Contribution |
|---|---|---|---|
| 1 | Days to 50% flowering | 0.00 | 0.00 |
| 2 | Days to maturity | 58 | 5.86 |
| 3 | SCMR at 60 days after sowing | 0.00 | 0.00 |
| 4 | Specific leaf areaat 60 DAS ($cm^2$ $g^{-1}$ ) | 1 | 0.1 |
| 5 | Plant height (cm) | 0.00 | 0.00 |
| 6 | Number of primary branches $plant^{-1}$ | 0.00 | 0.00 |
| 7 | Number of pods $plant^{-1}$ | 297 | 30.00 |
| 8 | Number of pegs $plant^{-1}$ | 134 | 13.54 |
| 9 | Pods to Pegs ratio | 12 | 1.21 |
| 10 | Hundred Pod weight (g) | 89 | 8.99 |
| 11 | Shelling per cent | 0.00 | 0.00 |
| 12 | Hundred Kernel weight (g) | 250 | 25.25 |
| 13 | Sound mature kernel per cent | 107 | 10.81 |
| 14 | Dry haulms yield $plant^{-1}$(g) | 0.00 | 0.00 |
| 15 | Harvest index (%) | 0.00 | 0.00 |
| 16 | Kernel yield $plant^{-1}$ (g) | 0.00 | 0.00 |
| 17 | Protein content (%) | 3 | 0.03 |
| 18 | Oil content (%) | 31 | 3.13 |
| 19 | Oleic acid content (%) | 4 | 0.4 |
| 20 | Linoleic content (%) | 4 | 0.4 |
| 21 | O/L Ratio | 0.00 | 0.00 |
| 22 | Pod yield $plant^{-1}$ (g) | 0.00 | 0.00 |

Variation among the means of all the attributes indicated the divergent nature of clusters formed. All the mean values are ranked across the clusters for all twenty two traits. The first rank was given to the highest cluster mean and the clusters possessing next higher means were scored second, third and like that up to the eighth rank for all characters except days to 50 % flowering, days to maturity and SLA at 60 DAS to which the first rank was given to the least mean. If the mean values of two clusters are similar, then the same rank was given for both the clusters. Accordingly, cluster VIII (ICGR 162105) and cluster II (ICGR 162009) secured the first rank with an overall score of 83 among the eight clusters followed by cluster III and cluster VI (Tirupati 1) with an overall score of 86 and 92 respectively, indicating the presence of superior genotypes in these clusters which can be widely used for the crop improvement programme.

Tirupati 1 registered minimum values for days to 50 % flowering (24.00) and maturity (105.33) which is desirable and also had highest cluster mean for SCMR at 60 DAS, number of primary branches per plant,100-pod weight, shelling per cent and sound mature kernel per cent. Similarly, monogenotypic cluster VIII (ICGR 162105) recorded highest values for the number of pods $plant^{-1}$, number of pegs $plant^{-1}$, dry haulm yield $plant^{-1}$, oleic acid content and pod yield $plant^{-1}$. The genotype, TCGS-2244 recorded lowest cluster mean value for SLA at 60 DAS and highest cluster mean value for plant height and protein content. ICGR-162009 registered highest cluster mean value for harvest index, oil content, pegs to pods ratio, kernel yield $plant^{-1}$ and ICGV 86590 for 100 kernel weight and linoleic acid content.

The characters contributing maximum to genetic divergence should be given more importance for effective selection and choice of parents for hybridization which is desirable for genetic improvement of groundnut. The number of times that each character appeared first and its relative contribution towards genetic divergence was presented in Table 4. The character number of pods $plant^{-1}$ was ranked first for 297 times and contributed maximum towards genetic divergence (30.00%) followed by characters like hundred kernel weight, number of pegs $plant^{-1}$, sound mature kernel per cent, hundred pods weight, days to maturity, pods: pegs ratio, oleic acid content, linoleic acid content, O/L ratio, oil content and specific leaf area at 60 DAS in descending order. In contrast, other traits attributed less role in cluster formation indicating narrow genetic diversity for those characters.

Similar results were recorded by the Saritha *et al*., (2018) for SLA at 60 DAS and hundred kernel weight. For oil content and days to maturity the results are in accordance by Shruti *et al*., 2019. Modhvadiya *et al.* (2022) reported similar results for number of pods per plant and 100 kernel weight.

## CONCLUSION

Based on inter cluster distances the clusters VII & VIII, V &VII and II &VI were found to be divergent in decreasing order of their magnitude. Hence, genotypes of these clusters could be utilized as parents and crossing among them would result in heterotic expression for yield components. Due to wide diversity between the genotypes, superior recombinants could be obtained by involving such genotypes as parents in hybridization programme.

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