The Pharma Innovation Journal 2021; 10(11): 1589-1594

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(11): 1589-1594

www.thepharmajournal.com
Received: 07-08-2021
Accepted: 16-09-2021

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# Study of genetic diversity in groundnut (*Arachis hypogaea* L.) genotypes

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**Abstract**
Thirty genotypes of groundnut were evaluated for analysis of variance that indicated existence of significant differences among the genotypes for majority of the characters. High GCV and PCV values were observed for number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant, dry pod yield per plant, protein content. High heritability coupled with high genetic advance was observed for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant, dry pod yield per plant and protein content. $D^2$analysis demonstrated oil content as the single largest contributor towards total divergence and the large inter-cluster distance between cluster IV and V suggest selection of genotypes between these two clusters would be rewarding for future hybridization programme.

**Keywords:** Cluster, GCV, genetic advance as mean, heritability, PCV

## 1. Introduction
Groundnut (*Arachis hypogaea* L.) is a member of the sub-family Papilionaceae and family Leguminosae. Groundnut is the sixth most important oilseed crop in the world (Peanut, 2008) [15]. Nowadays groundnut is considered to be a high energy food crop due to rich in rich nutrients and vitamins. Groundnuts contain 48-50 per cent of fats consisting mostly of mono- and polyunsaturated fatty acids. A large percentage of the crop is used for edible oil extraction. Groundnut is an important source of plant-based proteins that constitutes around 25-28 per cent of total calories whereas it contains low carbohydrates of 13-16 per cent. Due to low carbohydrate and a rich source of fat, proteins and dietary fibre groundnut has a low glycaemic index (GI), 564 kcal of energy is produced from 100 g of kernels (Jambunathan,1991). It also contains vitamins and mineral such as biotin, copper, niacin, folate, manganese, vitamin E, thiamine, phosphorus and magnesium.
Despite its importance, there are some constraints for the low production due to some environmental challenges. Genetic diversity serves as an indispensable aid to study how these genotypes possess variations and adoption to changing environments. This can be achieved by estimating various parameters that affect growth and yield of the crop in a particular environment. Thus the overall study is to investigate genetic variability and identify the superior groundnut genotypes for further exploitation in breeding programs. The study was generally conducted by recording yield contributing parameters in an isolated environment. Therefore the overall study is to investigate genetic variability and identify the superior groundnut genotypes for further exploitation in breeding programmes.

## 2. Materials and Methods
The experimental material for the genetic divergence studies comprised of 30 diverse genotypes of Groundnut derived from various breeding programmes. The material was made available for study by Agricultural Research Station, Kadiri (Andhra Pradesh). Field study was conducted at Centurion University Agricultural College Farm, Bhagusala, Paralakhemundi, Odisha. The experiment was laid out in a randomized block design replicated thrice. Each genotype was sown in three rows, each with three meter length and a spacing of 22.5cm between the rows and 10cm within the row. Observations were recorded on ten randomly selected plants in each treatment and in each replication. The plants were selected from the middle of the row excluding the border plants.

The crop was harvested at maturity stage on plot basis. Data was collected for characters like days to 50% flowering, days to maturity, plant height (cm), Number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant (g), dry pod yield per plant (g), 100 pods weight (g), 100 seeds weight (g), oil content (%) and protein content (%). The analysis of variance for each character was done as per the standard statistical procedure, given by Cochran and Cox (1950) in randomized block design. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Heritability in broad sense was estimated as per Allard (1930). Genetic advance was estimated as per the formula proposed by Lush (1949) and Johnson *et al.*, (1955) [9]. Genetic divergence studies were estimated by using $D^2$ analysis, Mahalanobis's $D^2$ analysis (Mahalanobis, 1936).

## 3. Results and Discussion

The mean sum of squares for dry pod yield, which is a dependant trait, and their component characters in 30 groundnut genotypes are computed in Table: 1. There is a significant difference between genotypes for all the traits studied except number of secondary branches per plant and protein content that can be attributed to the differential breeding procedures and also to the geo-ecological differences from which they are originated. By the variation among the genotypes for the yield and its attributing characters, these genotypes can be selected as parental breeding material for further improvement. These significant differences among varieties suggested that they are genetically diverse. Similarly Mahesh *et al*., (2018) reported significant differences among the groundnut genotypes for the traits namely, days to 50% flowering, plant height, number of primary branches, number of filled pods per plant, number of unfilled pods per plant, dry pod yield per plant, hundred kernels weight and oil content.

Mean performances of genotypes for yield and its contributing characters presented in table 2. A perusal on data revealed that the 30 groundnut genotypes exhibited a wide range of variability with significant differences among them. Significant differences were chronicled among the genotypes for the traits *viz*., days to 50% flowering, plant height, days to maturity, number of pegs per plant, number of primary branches per plant, number of secondary branches per plant, number of filled pods per plant, number of unfilled pods per plant, number of pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred pods weight, hundred kernel weight and oil content that are useful for selection of genotypes for breeding programme. These results were in accordance with Nayak *et al*., (2018) [5], Zaman *et al*., (2010) [22] and Chavadhari *et al*., (2017).

The results regarding the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), Heritability and Genetic Advance as percent of mean for all the traits were estimated and computed in the Table: 2. GCV and PCV values are high for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant, dry pod yield per plant and protein content. Lower values of GCV and PCV were observed for days to 50% flowering and days to maturity. These observations are in confirmation with the findings of Vasanthi *et al*., (2005) [8] and Zaman *et al.*, (2010) [22]. Hundred seed weight recorded moderate values of GCV and PCV while hundred pod weight chronicled lower values of both GCV and PCV. Nayak *et al.*, (2018) [5] reported similar findings in groundnut. Higher values of both GCV and PCV was observed for number of filled pods per plant and number of unfilled pods per plant and these results were in concurrence with the findings of Kalyani Kumari and Sasidharan (2020) [10]. In the same way Yadav *et al*., (2014) [21] reported higher GCV and PCV values for protein content.

In the present investigation high heritability was observed for the traits namely, days to 50% flowering, plant height, days to maturity, number of pegs per plant, number of primary branches per plant, number of secondary branches per plant, number of filled pods per plant, number of unfilled pods per plant, number of pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred pods weight, hundred kernel weight, oil content and protein content. Moderate heritability was recorded for number of pegs per plant. Hampannavar *et al*., (2018) [7], Savaliya *et al*., (2008) [18], Sudhir *et al*., (2008) [20], Choudhary *et al*., (2013) [3], Patil *et al*., (2020) [14], Vasanthi *et al*., (2012) [8] and Nath and Alam (2002) [11] reported high heritability for the traits days to 50% flowering, number of primary branches per plant, number of filled pods per plant, number of unfilled pods per plant, hundred kernels weight, dry pod yield per plant and oil content. In the same way Rao *et al*., (2014) [16] reported high heritability for traits such as number of mature pods per plant, hundred pods weight and hundred kernels weight. Yadav *et al*., (2014) [21] also observed high heritability for protein content.

High genetic advance was recorded for the traits *viz*., number of primary branches per plant, number of secondary branches per plant, number of filled pods per plant, number of unfilled pods per plant, number of pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred kernel weight, oil content and protein content. Similar observations were noted by Hampannavar *et al*., (2018) [7], Kumari and Sasidharan (2020) [10], Nayak *et al.*, (2018) [5], Kumar *et al.*, (2019), Kalyani Kumari and Sasidharan (2020) [10], Mahesh *et al.*, (2018) and Sonone *et al.*, (2011) [19]. Moderate genetic advance was observed for the traits days to 50% flowering and days to maturity and is in consonance with Vasanthi *et al*., (2012) [8]. Johnson *et al.* (1955) [9] suggested heritability coupled with genetic advance was more efficient and consistent in the forecast of consequential effect of selection than heritability alone. In this study high heritability was associated with high genetic advance for the traits *viz*., number of primary branches per plant, number of secondary branches, number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred seeds weight, oil and protein content.

The $D^2$ values between the genotypes were calculated as the sum of squares of the differences between the mean values of all the characters studied and is used for clustering of the genotypes. The procedure followed was Tocher's method (Rao, 1952) [16] which partitioned all the 30 groundnut genotypes into six clusters by estimating $D^2$ values as the square of the distances. The clustering pattern presented in Fig: 1 and the grouped clusters along with the genotypes were represented in the Table: 3. Among the six clusters, cluster I is the largest one comprising of 22 genotypes followed by cluster II comprising 4 genotypes and Clusters III, IV, V and VI comprises 1 genotype each. Girish *et al*., (2012) in his

report concluded that Cluster I had maximum number of genotypes.

The average intra and inter cluster distances among the six clusters were presented in the Table 4. The intra cluster values ranged from (0.00-128.98). The cluster II had the maximum D value (128.98) followed by cluster I (102.81). The inter cluster D values of the six clusters revealed the highest inter cluster distance between cluster IV and cluster V (665.41) and the least inter cluster distance between cluster III and cluster IV (89.94).

The mean performance of all the characters studied for all the six clusters had displayed in the table 5.The genotypes in cluster V recorded maximum mean value for fresh pod yield (20.2g) whereas; genotypes of cluster IV had minimum mean value for fresh pod yield (6.3g). The mean performance for the trait dry pod yield is maximum (18.18g) for the genotypes in cluster V and minimum dry pod yield (5.6g) for the genotypes in cluster IV. The genotypes of cluster I exhibited maximum hundred seed weight (54.67g) and in cluster IV the genotypes had minimum hundred seed weight (39.41g). Groundnut genotypes grouped under cluster IV recorded maximum percentage of oil (50.66%) and genotypes of cluster V had minimum percentage of oil (30.49%). The genotypes of cluster IV had maximum protein content (0.04%) whereas, genotypes of cluster III had minimum protein content (0.02%).The genotypes in cluster III are early maturing (97 days), whereas late maturing genotypes were included in cluster V (119 days). Late flowering (42 days) genotypes were grouped under cluster VI whereas, early flowering genotypes were included in cluster III (31 days). The genotypes of cluster I had minimum plant height (75.72cm) and the genotypes with maximum plant height (84.8cm) are in cluster IV. Cluster VI contained genotypes with maximum number of primary branches (8 branches) and genotypes with minimum number of primary branches (5 branches) were recorded in cluster V. The genotypes in both the clusters (cluster IV and VI) recorded maximum secondary branches (3 branches) and genotypes with reduced secondary branching are in cluster V (0.67). The genotypes in cluster VI had maximum number of pegs/plant (37.67) and the genotypes of cluster III had minimum number of pegs/plant (31 pegs). The genotypes in cluster V had maximum number of pods (24 pods) and the genotypes in cluster IV had minimum number of pods (15 pods). The genotypes with maximum filled pods (17) were classified under cluster V, whereas cluster IV had genotypes with minimum number of filled pods (5 pods). Cluster V contained genotypes with minimum unfilled pods (6 pods) and genotypes with maximum unfilled pod were noted in both cluster IV and cluster VI (10 pods). Girish *et al*., (2012) reported that hundred seed weight had maximum mean values in cluster I. Muthuselvi and Shanthi (2013) had reported that cluster IV recorded maximum protein content.

The percent contribution of each character towards divergence among the genotypes was presented in Table 6. The results showed that the oil content is the single largest contributor (37.01%) for divergence followed by days to maturity (23.45%), hundred seed weight (14.71%), number of secondary branches (11.49%), protein content (4.83%), number of pods (4.37%), days to 50% flowering (3.22%), number of primary branches (0.69%) and number of filled pods (0.23%) while, the remaining characters had no contribution towards the total divergence. Similar results were observed by Reddy *et al.*, (2017) [17] wherein the oil content and hundred kernels weight contributed for divergence.

Hence it is worthy to note that while calculating cluster means the superiority of particular genotype for a given character gets dilgted by other related but inferior genotypes present in the same cluster. In order to consider the genetically diverse genotypes for hybridization, the material should be initially screened for the important traits contributing for the divergence.

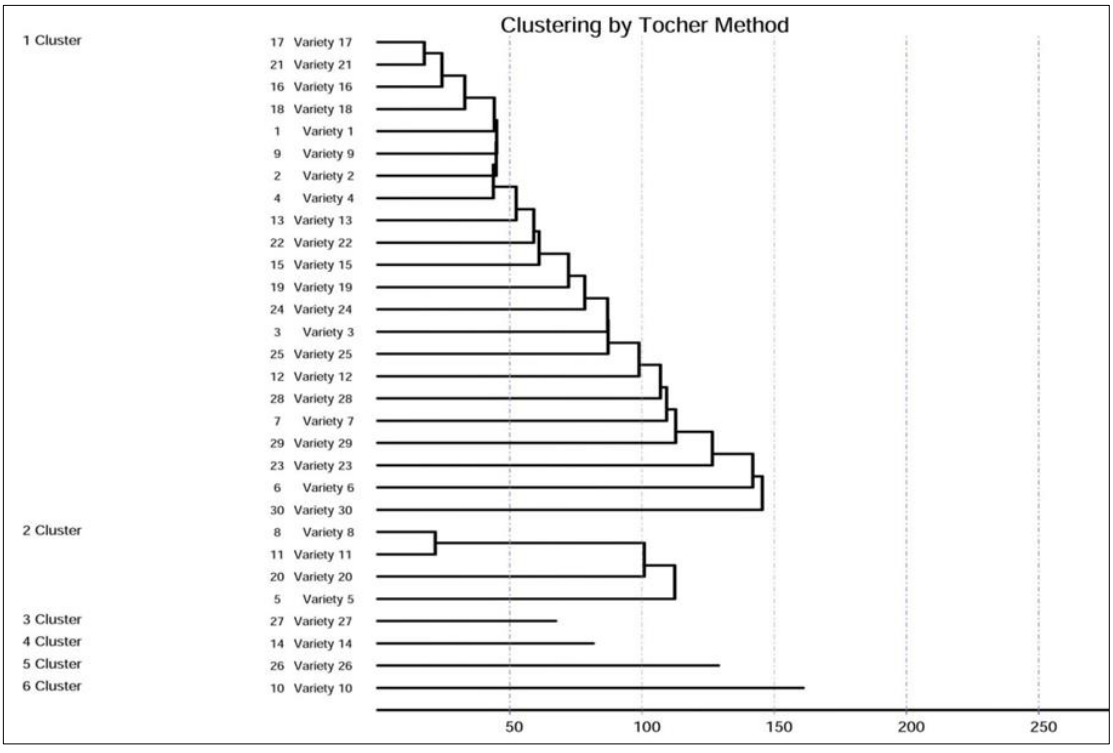


**Fig 1:** Grouping of the clusters by Tocher's method for 30 groundnut genotypes.

**Table 1:** Analysis of variance for fifteen morphological and maturity parameters in thirty groundnut genotypes

| Characters | Mean sum of squares | | | C.V. (1%) | C D (5%) |
|---|---|---|---|---|---|
| Source of variation | Replication | Genotype | Error | | |
| Degree of Freedom | 2 | 29 | 58 | | |
| Day to 50% flowering | 0.077 | 28.369** | 1.778 | 3.84 | 2.17 |
| Plant height(cm) | 2.044 | 44.687** | 21.608 | 6.07 | 7.59 |
| Days to maturity | 0.844 | 230.034** | 3.235 | 1.64 | 2.93 |
| Number of pegs/plant | 0.833 | 147.350** | 32.166 | 16.76 | 9.26 |
| Number of primary branches/plant | 0.3 | 6.537** | 0.782 | 13.82 | 1.44 |
| Number of secondary branches/plant | 0.033 | 2.467 | 0.056 | 17.36 | 0.38 |
| Number of filled pods/plant | 0.844 | 40.752** | 3.936 | 16.75 | 3.24 |
| Number of unfilled pods/plant | 0.677 | 18.729** | 1.321 | 12.52 | 1.87 |
| Number of pods per plant | 2.344 | 75.377** | 3.953 | 9.45 | 3.24 |
| Fresh pod yield/plant(gm) | 0.958 | 44.008** | 4.775 | 15.35 | 3.57 |
| Dry pod yield/plant(gm) | 0.841 | 35.665** | 3.846 | 15.30 | 3.20 |
| 100 pod weight(gm) | 10.145** | 368.760** | 10.835 | 2.72 | 5.37 |
| 100 seed weight(gm) | 1.885 | 95.860** | 2.199 | 2.73 | 3.57 |
| Oil content (%) | 3.124 | 77.161** | 0.404 | 1.35 | 1.03 |
| Protein content (%) | 0 | 0.0001 | 0 | 10.01 | 0.004 |

**Table 2:** Estimation of variability (GCV and PCV), Heritability and Genetic Advance of 30 genotypes of groundnut

| Parameters | Range | | GCV (%) | PCV (%) | Heritability | GA as % of Mean (5%) |
|---|---|---|---|---|---|---|
| | Minimum | Maximum | | | | |
| Day to 50% flowering | 31.00 | 43.66 | 8.57 | 9.40 | 83.28 | 16.11 |
| Plant height(cm) | 69.10 | 84.8 | 3.62 | 7.07 | 26.25 | 3.82 |
| Days to maturity | 94.33 | 127.66 | 7.95 | 8.12 | 95.90 | 16.04 |
| Number of pegs/plant | 22.66 | 50.66 | 18.31 | 24.83 | 54.41 | 27.82 |
| Number of primary branches/plant | 4.33 | 9.66 | 21.64 | 25.68 | 71.02 | 37.57 |
| Number of secondary branches/plant | 0.00 | 3.00 | 65.60 | 67.86 | 93.45 | 130.64 |
| Number of filled pods/plant | 5.00 | 20.00 | 29.58 | 33.99 | 75.71 | 53.01 |
| Number of unfilled pods/plant | 5.66 | 16.33 | 26.25 | 29.08 | 81.45 | 48.79 |
| Number of pods per plant | 13.33 | 31.33 | 23.21 | 25.06 | 85.76 | 44.27 |
| Fresh pod yield/plant(gm) | 6.30 | 23.24 | 25.40 | 29.68 | 73.25 | 44.78 |
| Dry pod yield/plant(gm) | 5.66 | 20.91 | 25.41 | 29.66 | 73.39 | 44.83 |
| 100 pod weight(gm) | 102.60 | 147.30 | 9.05 | 9.19 | 97.06 | 18.38 |
| 100 seed weight(gm) | 39.41 | 68.73 | 10.54 | 10.91 | 93.42 | 20.99 |
| Oil content (%) | 30.48 | 51.60 | 10.77 | 10.86 | 98.44 | 22.02 |
| Protein content (%) | 0.020 | 0.040 | 23.17 | 25.24 | 84.27 | 43.81 |

**Table 3:** Compositions of Clusters Based on $D^2$ Statistics for 30 Groundnut Genotypes

| Clusters | No. of Genotypes | Genotypes |
|---|---|---|
| I | 22 | ICGV-91114, ICGV-00350, K-13,19, Dharani, Chitravathi, Tag-24, Tirupati-4, Vemana, Harithandra, Kadiri-2, Kadiri-3, Kadiri-4, Kadiri-5, Dheeraj, Kadiri-6, Kadiri-7, Kadiri-9, Rohini, Narayani, Prasuna, Karnataka local-2, Amaravathi |
| II | 4 | Anantha, Tirupati-2, Kalahasti, Rajahmundry local |
| III | 1 | Karnataka local-1 |
| IV | 1 | Kadiri-1 |
| V | 1 | Harichandra |
| VI | 1 | Nityaharitha |

**Table 4:** Average of intra and inter cluster distances in 30 Groundnut Genotypes

| Clusters | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | 102.81 | 197.9 | 175.75 | 173.07 | 479.21 | 337.71 |
| II | | 128.98 | 422.52 | 335.87 | 322.62 | 298.32 |
| III | | | 0 | 89.94 | 656.03 | 322.53 |
| IV | | | | 0 | 665.41 | 351.65 |
| V | | | | | 0 | 160.9 |
| VI | | | | | | 0 |

**Table 5:** Mean values of six clusters for 14 morphological characters in 30 Groundnut Genotypes

| Parameters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI |
|---|---|---|---|---|---|---|
| Days to maturity | 109.7 | 110.08 | 97 | 109.67 | 119.33 | 100.67 |
| Days to 50% flowering | 34.24 | 35.42 | 31.67 | 34.33 | 38.33 | 42.33 |
| Plant height | 75.72 | 76.6 | 81.8 | 84.8 | 79.37 | 77.67 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Number of primary branches/plant | 6.52 | 6.08 | 4.67 | 6.33 | 5 | 8.33 |
| Number of secondary branches/plant | 1.2 | 1.5 | 2 | 3 | 0.67 | 3 |
| Number of pegs/plant | 33.27 | 37.08 | 31.67 | 33.33 | 32 | 37.67 |
| Number of pods/plant | 20.71 | 23.17 | 21.33 | 15.33 | 24 | 21.67 |
| Number of filled pods/plant | 11.53 | 14 | 11.67 | 5 | 17.33 | 11.67 |
| Number of unfilled pods/plant | 9.18 | 9.17 | 9.67 | 10.33 | 6.67 | 10 |
| Fresh pod yield/plant | 13.98 | 16.46 | 13.55 | 6.3 | 20.2 | 13.6 |
| Dry pod yield/plant | 12.59 | 14.82 | 12.19 | 5.67 | 18.18 | 12.24 |
| Hundred seed weight | 54.67 | 51.37 | 48.46 | 39.41 | 48.67 | 45.12 |
| Oil content | 48.3 | 45.46 | 47.63 | 50.66 | 30.49 | 35.34 |
| Protein content | 0.03 | 0.03 | 0.02 | 0.04 | 0.03 | 0.03 |

**Table 6:** Percent contribution of characters towards diversity in Groundnut genotypes

| S. No. | Characters | Times Ranked 1st | Percent Contribution |
|---|---|---|---|
| 1 | Days to maturity | 102 | 23.45% |
| 2 | Days to 50% flowering | 14 | 3.22% |
| 3 | Plant height | 0 | 0.00% |
| 4 | Number of primary branches/plant | 3 | 0.69% |
| 5 | Number of secondary branches/plant | 50 | 11.49% |
| 6 | Number of pegs/plant | 0 | 0.00% |
| 7 | Number of pods/plant | 19 | 4.37% |
| 8 | Number of filled pods/plant | 1 | 0.23% |
| 9 | Number of unfilled pods/plant | 0 | 0.00% |
| 10 | Fresh pod yield/plant | 0 | 0.00% |
| 11 | Dry pod yield/plant | 0 | 0.00% |
| 12 | Hundred seed weight | 64 | 14.71% |
| 13 | Oil content | 161 | 37.01% |
| 14 | Protein content | 21 | 4.83% |

## 4. Conclusion

From the present investigation, the results of the analysis of variance revealed significant differences among the genotypes for traits like days to 50% flowering, plant height, days to maturity, number of pegs per plant, number of primary branches per plant, number of filled pods per plant, number of unfilled pods per plant, number of pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred kernel weight and oil content. The GCV and PCV values are high for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant, dry pod yield per plant and protein content. High heritability coupled with high genetic advance were recorded for traits *viz*., number of primary branches per plant, number of secondary branches, number of pods per plant, number of filled pods per plant, number of unfilled pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred seeds weight, oil and protein content suggesting additive gene action and these traits can easily be fixed in the genotypes by selection in the early generations.. The genotypes from cluster IV and cluster V had showed maximum divergence. So, selection of genotypes from these clusters would be effective for hybridization programmes.

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