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**Research Article**

# Genetic divergence analysis in groundnut (*Arachishypogaea*L.)

**K. Saritha[1*], R. P. Vasanthi[2], M. Shanthi Priya[3]and P. Latha[4]**
[1]Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati- 517502, Andhra Pradesh, India.
[2] Principal Scientist,Department of Genetics and Plant Breeding, Regional Agricultural Research Station, Tirupati- 517502, Andhra Pradesh, India.
[3]Senior Scientist, Department of Genetics and Plant Breeding, Agricultural Research Station, Perumalapalli- 51750 , Andhra Pradesh, India.
[4] Senior Scientist, Department of Crop Physiology, Regional Agricultural Research Station, Tirupati- 517502, Andhra Pradesh, India.
* **E-Mail:**sarithakovvuri@gmail.com

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**Abstract**
Genetic diversity among 32 genotypes of groundnut was estimated for six characters using Mahalanobis $D^2$ statistic. The analysis of variance revealed significant differences among the genotypes for all characters. The characters, pod yield per plant, 100 seed weight and SLA at 60 DAS recorded moderate to high GCV, high heritability coupled with high genetic advance as percent of mean indicating that these traits were mainly under the influence of additive gene action and simple selection may be effective for improvement of these traits. Based on Tocher's method of clustering, 32 genotypes were grouped into eight clusters, of which cluster II was the largest containing 10 genotypes followed by cluster I with seven genotypes. The inter-cluster distance was maximum between cluster II and cluster VIII (2031.75) followed by cluster V and cluster VIII (1768.25) and cluster VII and VIII (1702.17). Considering the cluster distances and cluster means, crossing between the genotypes of cluster II and cluster VIII, and cluster VIII and cluster V is suggested in order to get transgressive segregants for yield and yield parameters.

**Keywords**
Groundnut, $D^2$, genetic divergence.

## Introduction

Groundnut is not only a major oilseed crop but also an important food and feed crop across the World. In India, it occupies an area of 40.68 lakh ha with production of 66.15 lakh tonnes and an average productivity of 1626 kg $ha^{-1}$ in *Kharif* season (2017-18) (AICRP on Groundnut, Annual Report, 2017).In *rabi-summer*, it is being grown in 8.39 lakh ha with production of 16 lakh tonnes with productivity of 1909 kg $ha^{-1}$ (2017-18) (AICRP on Groundnut, Annual Report, 2017). In Andhra Pradesh, it is cultivated in an area of 6.48 lakh ha with production of 8 lakh tonnes and productivity of 1238 kg $ha^{-1}$ during *Kharif* season whereas it is cultivated in 0.90 lakh ha area with production of 2.07 lakh tonnes and productivity of 2300 kg $ha^{-1}$ during *rabi* season (AICRP on Groundnut, Annual Report, 2017).

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. Passioura (1977) proposed the physiological framework of Pod Yield = T × TE × HI where T = total water transpired, TE = Transpiration Efficiency and HI = Harvest Index under a given set of environmental conditions. The study of diversity involving the lines from diverse population with observations on targeted traits i.e. traits that confer water use efficiency (WUE) and drought resistance helps in identification of diverse parents for these traits. In groundnut, SCMR, SLA and RWC are the surrogate traits for WUE (Wright and Nageswara Rao, 1994; Nigam *et al.* 2005). Thus, present experiment was carried out to assess the nature and magnitude of genetic diversity present in 32 groundnut genotypes for the targeted that contribute for drought resistance and water-use efficiency.

## Material and Methods

Thirty two groundnut genotypes were studied in a randomized complete block design with two replications at Regional Agricultural Research Station, Tirupati during *rabi*, 2017-18. Among thirty two genotypes included in the study, all the genotypes belong to Spanish bunch (subspecies *fastigata* botanical group *vulgaris*) expect three

genotypes, ICGS 76, ICGV 86325 and GG 20 which belong to Virginia bunch (subspecies *hypogaea* var. *hypogaea*). Though they are classified as Spanish bunch or Virginia bunch. some genotypes have overlapping traits from both the species (Table 1).

The soil of the experimental site is sandy loam and the crop was raised under irrigated situation. Recommended package of practices were followed in raising of the crop. Each genotype was raised in single row of five meter length spaced at 22.5 cm between rows and 10 cm within the row. Five plants were randomly selected from each plot and data were recorded for six characters *viz.,* SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA), relative water content (RWC), shelling percentage, 100-seed weight and pod yield per plant. Genetic parameters, genotypic co-efficient of variation, heritability($h^2$) and genetic advance as per cent of mean were estimated as per Lush (1940), Burton (1952), Allard (1960) and Johnson *et al.* (1955). The 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).Canonical analysis was used to verify the clustering pattern obtained by Mahalanobis's $D^2$ statistic. The canonical vectors or roots were calculated to represent the genotypes in the graphical form (Rao, 1952).

**Results and Discussion**

Analysis of variance for all the characters studied revealed significant differences among the cultivars indicating variation in the material studied for most of the traits (Table 2). Phenotypic coefficient of variation was found to be higher than genotypic coefficient of variation for all the traits indicating the role of environment in the expression of characters.GCV was found to be high for pod yield per plant( 29.24%) and was moderate for 100-seed weight(16.66%) and SLA at 60 DAS (12.37%). Heritability was high for all the characters except for shelling percentage (52.40%). GAM was high for SLA at 60 DAS (25.40%), 100-seed weight (34.11%) and pod yield per plant (50.83%). GAM was moderate for RWC at 80 DAS (25.40%) and it was low for SCMR at 60 DAS (9.06%) and shelling percentage (5.17%)(Table 3).

Bhavya *et al.* (2017) reported low to moderate PCV, GCV, high heritability and low to moderate GAM for SLA and SCMR, low PCV, GCV moderate heritability and GAM for shelling percentage and high PCV, GCV, heritability and GAM for pod yield per plant. Srivalli and Nadaf (2016) observed low to moderate PCV, GCV, high heritability coupled with low genetic advance as percent of mean for SLA, SCMR and RWC. Vasanthi *et al.* (2015) reported low GCV, heritability and GAM for shelling percentage and moderate GCV, high heritability and GAM for 100-seed weight. From the results, it can be concluded that phenotypic selection would be more effective for improvement of SLA at 60 DAS, 100-seed weight and pod yield per plant in early generations.

Thirty two genotypes of groundnut were grouped into eight clusters based on $D^2$ value (Table 4). Among the clusters, cluster II contained maximum number of genotypes (10 genotypes), whereas cluster I comprised seven genotypes, cluster V six genotypes, cluster IV five genotypes, while the cluster III, VI, VII and VIII had one genotype each. Kumar (2004) observed relationship between clustering pattern and place of breeding of genotypes when clustering was carried out based on physiological attributes. In the present study, there was no correspondence with respect to place of breeding or pedigree in grouping of genotypes.

The inter-cluster distance (Table 5) were larger than the intra-cluster distance which indicated that greater diversity was present among the genotypes of different clusters (Zaman *et al.,* 2010). Maximum intra-cluster distance (190.85) was recorded by cluster V while minimum was noticed in clusters III, VI, VII and VIII as they included single genotype each. Average inter-cluster distance was ranged from 164.21 to 2031.75. Maximum inter-cluster distance was observed between cluster II and VIII (2031.75) indicating the greater diversity between individuals of these two clusters. Hence, elite genotypes from these diversitied clusters can be used as parents for hybridization which would result in getting transgressive segregants for yield and yield related traits in filial generations. Crossing between such genotypes will be helpful to create variability for desired traits and to select superior recombinants for the improvement of traits. Similar results were earlier reported by Choudhary *et al.,* (1998) and, John and Mylaswamy (1998). In contrast, the minimum inter-cluster distance was found between III and VII (164.21) indicating the close relationship between the genotypes in these clusters.

The cluster mean value for SCMR at 60 DAS was maximum in cluster III (54.10) and minimum in clusters VI (45.10) (Table 6). Cluster VIII had maximum SLA at 60 DAS (171.00 $cm^2$ $g^{-1}$)while cluster II had minimum SLA at 60 DAS (120.57$cm^2$ $g^{-1}$). Mean values of RWC at 80 DAS ranged from 84.65 % (cluster V) to 97.20 % (cluster VI). Shelling percentage ranged from 61.00 % (cluster VII and VIII) to 72.00 % (cluster III).

Cluster V had maximum mean (47.08 g) for 100-seed weight whereas cluster VII had minimum cluster mean for 100-seed weight (27.00 g). Mean values of pod yield per plant ranged from 3.78 g (cluster VIII) to 10.16 g (cluster V). Intercrossing the elite genotypes from these clusters could be suggested to generate wide range of variability.

The percent contribution of different characters towards total genetic divergence is presented in Table 7. The maximum contribution towards divergence was recorded by SLA at 60 DAS (33.67%) followed by 100-seed weight (33.06%) and RWC at 80 DAS (32.26%). These three characters contributed almost equally toward total genetic divergence in the population. The characters such as pod yield per plant, shelling percentage and SCMR at 60 DAS contributed 0.6, 0.2 and 0.2 %, respectively towards the total genetic divergence. Less variability in population for pod yield could be due to that all the genotypes involved are the best performing lines and released varieties. Maximum contribution of SLA to genetic diversity was in accordance to the reports of Venkataravana (2010). Least contribution of pod yield per plant towards diversity was reported earlier by Venkateswarulu *et al.* (2011).

The group constellations formulated on the basis of Mahalanobis's $D^2$ statistic were confirmed by canonical root analysis. The three canonical roots were responsible for 92.05 per cent of total variance of uncorrelated (Y) variables, which indicated that the differentiation of these traits was nearly complete in these genotypes in five phases (Table 8). The relative distribution of genotypes reflected existence of parallelism between grouping obtained by $D^2$ analysis and canonical root analysis.

The traits that contributed maximum towards divergence i.e. SLA and 100-seed weight showed moderate variability and high heritability accompanied by high genetic advance as percent of mean. The trait , RWC though showed moderate GAM contribution to overall divergence was almost equal to SLS and 100-seed weight. Pod yield per plant had shown higher GAM it does not significant contribution towards divergence which could be due to lower mean values. Absolute GA values were low for pod yield per plant and SCMR.(Table 3)

Considering the cluster distances and cluster means in the present investigation, emphasis should be given to make crosses between promising genotypes of cluster II and cluster VIII; cluster VIII and cluster V in order to get transgressive segregants for yield and yield parameters. Similarly, the crosses between genotypes in cluster VIII and cluster III and, cluster VIII and cluster II could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance. The information on cluster distance and clusters means for different target traits will be useful to breeders in selection of genotypes for hybridization program.

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**Table1.Pedigree and habit group of 32 groundnut genotypes included in the present study**

| S. No | Genotype | Pedigree | Botanical Group |
|---|---|---|---|
| 1 | TCGS-1694 | K 6 × ICG (FDRS) 79 | Spanish bunch |
| 2 | TCGS-1696 | ICG (FDRS) 79 × Tirupati-4 | Spanish bunch |
| 3 | TCGS-1630 | Tirupati-1 × ICG (FDRS) 79 | Spanish bunch |
| 4 | TCGS-1653 | TCGS-45 × TCGS-876 | Spanish bunch |
| 5 | TCGS-1616 | K 6 × Dharani | Spanish bunch |
| 6 | TCGS-1622 | K 6 × Dharani | Spanish bunch |
| 7 | TCGS-1073 | TCGS-29 × JAL-30 | Spanish bunch |
| 8 | TCGS-1157 | TAG-24 × Jyothi | Spanish bunch |
| 9 | R-2001-2-1 | ICGS 11 x ICG 4728 | Spanish bunch |
| 10 | GPBD-4 | KRG-1 × ICGV 86855 | Spanish bunch |
| 11 | R-2001-3-1 | ICGS 11 x ICG 4728 | Spanish bunch |
| 12 | J 89 | ALR-3 × TG 26 | Spanish bunch |
| 13 | R 2001-3 | ICGS 11 x ICG 4728 | Spanish bunch |
| 14 | SG 99 | ICGV 86529 x ICGV 87160 | Spanish bunch |
| 15 | R 2001-2 | ICGS 11 x ICG 4728 | Spanish bunch |
| 16 | ALG-06-320 | (J 11 x CG 52) x ICGV 86015 | Spanish bunch |
| 17 | K 1805 | (ICGV92069 X ICGV93184) X (ICGS44 X ICGS76) | Spanish bunch |
| 18 | K 1725 | Kadiri 7 bold x TAG24 | Spanish bunch |
| 19 | K 9 | Kadiri 4 x Vemana | Spanish bunch |
| 20 | K. Harithandra | 9157-2xPI476177 | Spanish bunch |
| 21 | K. Anantha | Vemana x Girnar | Spanish bunch |
| 22 | TCGS-1097 | TAG-24 × TCGS-522 | Spanish bunch |
| 23 | GG 16 | JSP-14 × JSSP-4 | Spanish bunch |
| 24 | K 1847 | Kadiri 8 bold x TAG24 | Spanish bunch |
| 25 | K 1789 | (ICGV92069 X ICGV93184) X[(ICGV87121XICGV87853)X ICGV92093] | Spanish bunch |
| 26 | K 1811 | (ICGV92069XICGV93184) SIL4 X ICGV98300 | Spanish bunch |
| 27 | ICGS 76 | TMV 10 x Chico | Virginia bunch |
| 28 | ICG 86325 | ICGS 20 x G 201 | Virginia bunch |
| 29 | Dharani | VRI-2 × TCGP-6 | Spanish bunch |
| 30 | Narayani | JL 24 × Ah 316/s | Spanish bunch |
| 31 | GG 20 | GAUG 10 × Robut 33-1 | Virginia bunch |
| 32 | K 6 | JL 24 × Ah 316/s | Spanish bunch |

**Table 2. Analysis of variance for physiological, yield and yieldattributes in 32 genotypes of groundnut**

| Sl. No. | Character | Replications | Treatments | Error |
|---|---|---|---|---|
| | | (df = 1) | (df = 31) | (df = 31) |
| 1 | SCMR at 60 DAS | 4.42 | 18.18** | 3.9 |
| 2 | SLA at 60 DAS ($cm^2$ $g^{-1}$) | 7.76 | 559.12** | 1.89 |
| 3 | RWC at 80DAS (%) | 0.54 | 49.06** | 0.25 |
| 4 | Shelling percentage (%) | 1.26 | 82.13** | 0.49 |
| 5 | 100-seed weight (g) | 12.59 | 10.23** | 3.19 |
| 6 | Pod yield per plant (g) | 0.25 | 13.85** | 2.33 |

* Significant at 5% level;** Significant at 1% level

**Table 3. Genetic parameters for physiological, yield and yield attributes of 32 groundnut genotypes**

| Sl. No. | Character | Mean | Range | | Variance | | Co-efficient of variation | | Heritability (Broad sense %) | Genetic Advance | Genetic Advance as per cent of mean(%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Min. | Max. | Geno-typic | Pheno-typic | Geno-typic (%) | Pheno-typic (%) | | | |
| 1 | SCMR at 60 DAS | 48.85 | 43.20 | 54.10 | 7.14 | 11.04 | 5.47 | 6.80 | 64.63 | 4.42 | 9.06 |
| 2 | SLA at 60 DAS($cm^2g^-$) | 134.91 | 108.22 | 171.00 | 278.61 | 280.51 | 12.37 | 12.42 | 99.33 | 34.27 | 25.40 |
| 3 | RWC at 80DAS (%) | 88.98 | 79.90 | 97.20 | 24.40 | 24.65 | 5.55 | 5.58 | 98.88 | 10.12 | 11.37 |
| 4 | Shelling percentage(%) | 65.59 | 57.00 | 72.00 | 3.52 | 6.71 | 3.47 | 4.79 | 52.40 | 2.80 | 5.17 |
| 5 | 100- seed weight (g) | 38.36 | 27.00 | 52.00 | 40.82 | 41.31 | 16.66 | 16.76 | 98.81 | 13.08 | 34.11 |
| 6 | Pod yield per plant (g) | 8.21 | 3.78 | 13.05 | 5.76 | 8.09 | 29.24 | 34.66 | 71.20 | 4.17 | 50.83 |

**Table 4. Distribution of 32 Genotypes of groundnut in different clusters (Tocher's method)**

| Cluster | Number of Genotypes | Genotypes |
|---|---|---|
| I | 7 | J 89, ICGS 76, ALG-06-320, GG 20, K 6, K. Anantha, R 2001-2 |
| II | 10 | TCGS-1653, Dharani, TCGS-1097, R 2001-3, R-2001-2-1, Narayani, GPBD-4, R-2001-3-1, SG 99, TCGS-1630 |
| III | 1 | K 9 |
| IV | 5 | K 1805, K 1811, ICG 86325, K. Harithandra, TCGS-1616 |
| V | 6 | TCGS-1157, K 1725, TCGS-1694, TCGS-1073, TCGS-1696, TCGS-1622 |
| VI | 1 | K 1789 |
| VII | 1 | K 1847 |
| VIII | 1 | GG 16 |

**Table 5.Average intra and inter cluster $D^2$ values in 32 genotypes of groundnut**

| | Cluster 1 | Cluster 2 | Cluster 3 | Cluster 4 | Cluster 5 | Cluster 6 | Cluster 7 | Cluster 8 |
|---|---|---|---|---|---|---|---|---|
| **Cluster 1** | **125.92** | 381.99 | 221.46 | 288.38 | 542.52 | 308.47 | 532.63 | 826.97 |
| **Cluster 2** | | **121.42** | 225.89 | 966.59 | 461.68 | 749.38 | 585.51 | 2031.75 |
| **Cluster 3** | | | **0.00** | 679.61 | 721.53 | 253 | 164.21 | 1415.41 |
| **Cluster 4** | | | | **158.54** | 925.68 | 449.17 | 1003.56 | 335.88 |
| **Cluster 5** | | | | | **190.85** | 1351.43 | 1494 | 1768.25 |
| **Cluster 6** | | | | | | **0.00** | 181.5 | 813.19 |
| **Cluster 7** | | | | | | | **0.00** | 1702.17 |
| **Cluster 8** | | | | | | | | **0.00** |

Figures in bold indicate intra-cluster $D^2$ values

**Table 6.Cluster means for physiological, yield and yield attributes in 32 groundnut genotypes (Mahalanobis's $D^2$ method)**

| Cluster No. | SCMR at 60 DAS | SLA at 60 DAS | RWC at 80 DAS | Shelling percentage | 100 seed weight | Pod yield per plant |
|---|---|---|---|---|---|---|
| I | 48.73 | 140.65 | 90.57 | 64.57 | 37.93 | 7.71 |
| II | 47.29 | 120.57 | 86.80 | 65.20 | 34.00 | 8.48 |
| III | 54.10 | 123.99 | 94.05 | 72.00 | 35.50 | 9.38 |
| IV | 48.72 | 160.71 | 90.48 | 65.60 | 39.80 | 7.18 |
| V | 50.12 | 126.56 | 84.65 | 68.33 | 47.08 | 10.16 |
| VI | 45.10 | 143.32 | 97.20 | 63.00 | 31.00 | 6.18 |
| VII | 52.70 | 125.54 | 96.85 | 61.00 | 27.00 | 7.59 |
| VIII | 52.90 | 171.00 | 97.00 | 61.00 | 47.00 | 3.78 |

**Table 7. Relative contribution of physiological, yield and yield attributes to genetic diversity in 32 groundnut genotypes**

| Sl. No. | Characters | Number of times ranked first | Contribution (%) |
|---|---|---|---|
| 1. | SCMR at 60 DAS | 1 | 0.20 |
| 2. | SLA at 60 DAS ($cm^2$ $g^{-1}$) | 167 | 33.67 |
| 3. | RWC at 80 DAS (%) | 160 | 32.26 |
| 4. | Shelling percentage (%) | 1 | 0.20 |
| 5. | 100-seed weight (g) | 164 | 33.06 |
| 6. | Pod yield per plant (g) | 3 | 0.60 |

SCMR - SPAD chlorophyll meter reading; SLA - Specific leaf area; RWC – Relative Water Content

**Table 8. Canonical root values, per cent of variation expected and cumulative variation expected for 32 genotypes of groundnut**

| Sl. No. | Values of canonical root | Per cent of variation expected | Cumulative total Variation expected |
|---|---|---|---|
| $Z_1$ | 3.24152 | 54.02530 | 54.02530 |
| $Z_2$ | 1.41600 | 23.59991 | 77.62521 |
| $Z_3$ | 0.86534 | 14.42236 | 92.04757 |