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## Research Note

### Assessment of genetic diversity for yield, yield attributes and water use efficiency related traits in groundnut [*Arachis hypogaea* L.]

S. Divya Sree<sup>1\*</sup>, B. Rupesh Kumar Reddy<sup>1</sup>, M. Shanthi Priya<sup>2</sup> and A. R. Nirmal Kumar<sup>3</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, S. V. Agricultural College, Tirupati-517 502, A.P.

<sup>2</sup>Department of Genetics and Plant Breeding, Agricultural Research Station, Perumallapalle-517 505, A.P.

<sup>3</sup>Department of Crop Physiology, S. V. Agricultural College, Tirupati-517 502, A.P.

\*E-Mail: somisettydivyasree8@gmail.com

#### Abstract

To establish the degree of genetic diversity for 14 quantitative parameters, 36 groundnut genotypes were investigated using the Mahalanobis D<sup>2</sup> Statistics. Tocher's method separated the entire genetic resource set into nine distinct, non-overlapping clusters demonstrating the presence of significant amount of genetic diversity. Cluster I had the maximum number of accessions (15), followed by cluster IV with 7 accessions, cluster VI with 5 genotypes, cluster V with 3 genotypes and cluster VII with 2 genotypes. The clusters II, III, VIII and IX were monogenotypic. The inter-cluster distance was maximum between the clusters VI and IX. Shelling percent contributed maximum to the genetic divergence followed by pod yield plant<sup>-1</sup>. Hence due emphasis should be given to these traits as improvement of these characters would result in increase in pod yield plant<sup>-1</sup>.

**Keywords:** Groundnut, D<sup>2</sup> Statistic, Tocher's technique.

The cultivated groundnut (*Arachishypogaea* L.) is an allotetraploid crop with  $2n=4x=40$ . It belongs to the sub-family Papilionaceae of the family Leguminosae. It holds the top spot in the country's edible oil business and is known as the "King of Oilseeds" and "Poor Man's Cashewnut" (Kumari and Sasidharan, 2020). It originated in South America and was domesticated in the Paraguayan valleys. It is cultivated as a main crop, an intercrop or a combination of crops (Nageswara *et al.*, 1990; Ghosh, 2004). Because of its many uses, groundnut is now a valuable cash crop for domestic and international trade in a number of developing countries.

Globally, it is grown in an area of 29.92 Mha with annual production of 55.30 Mt and productivity of 1851 kg ha<sup>-1</sup> (FAOSTAT, 2020-21). In India, groundnut covers an

area of 6.09 Mha with a production of 10.21 Mt and productivity of 1676 kg ha<sup>-1</sup>. In Andhra Pradesh, it covers an area of 0.87 Mha with a production of 0.78 Mt and productivity of 894 kg ha<sup>-1</sup> (Directorate of Economics and Statistics, 2021).

It is mostly grown as a rainfed crop under irrigated cultivation in *rabi* season. Due to depletion of ground water resources, water shortage is commonly observed during the crop period in the *rabi* season. Therefore, it is necessary to identify the genotypes of groundnut with high water use efficiency (WUE). WUE is a crucial characteristic that boosts productivity when water supplies are scarce. The crop's productivity can be increased by locating genotypes that make better utilization of the limited water resources (Arunkumar *et al.*, 2017).

Specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) are associated with WUE in groundnut as surrogate traits to select the genotypes with high WUE (Sab *et al.*, 2018) which could ultimately lead to the evolution of better genotypes adapted to drought conditions. Success of plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants (Chavadhari *et al.*, 2017). Assessment of genetic diversity among the genotypes is very essential for the evolution of transgressive segregants or superior recombinants which is aided by the selection of diverse parents based on intra cluster, inter cluster and cluster mean distances (Hampannavar *et al.*, 2018). Hence an experiment was undertaken to assess genetic diversity among 36 groundnut germplasm accessions based on Mahalanobis D<sup>2</sup> Statistics.

Thirty six genotypes of groundnut were evaluated at dry land farm of S. V. Agricultural College, Tirupati, during *rabi*, 2021-22 in a Randomised Block Design (RBD) with three replications. In each replication, every genotype was sown in three rows of 3m length with a spacing of 22.5 cm between the rows and 10 cm between the plants within the row. Data was recorded on 14 morphological traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, kernel yield plant<sup>-1</sup> (g), hundred kernel weight (g), shelling per cent, sound mature kernel per cent, harvest index (%), SPAD Chlorophyll Meter Reading at 60 DAS, Specific Leaf Area at 60 DAS (cm<sup>2</sup>

gm<sup>-1</sup>), Relative Water Content (%) and pod yield plant<sup>-1</sup> (g) were recorded in five plants per replication and the mean data were subjected to statistical analysis. The genetic divergence analysis was carried out using Mahalanobis D<sup>2</sup> (1936) statistics and clustering was done by Tocher's method as described by Rao (1952). The data analyzed was performed using INDOSTAT software.

Analysis of variance (ANOVA) was performed using INDOSTAT software. ANOVA showed significant differences for all the studied characters across all genotypes, showing the presence of high variability (Table 1). Based on the D<sup>2</sup> values, the 36 genotypes were sorted into nine distinct, non-overlapping groups (Table 2). The clustering of the genotypes revealed that Cluster I had the most accessions (15), followed by Cluster IV with 7, Cluster VI with 5, Cluster V with 3, Cluster VII with 2 genotypes and the clusters II, III, VIII and IX were monogenotypic *i.e.*, comprised of only a single genotype.

The intra and inter-cluster distances are furnished in Table 3. Cluster VI (304.88) recorded the greatest intra-cluster distance, followed by the cluster IV (235.43), cluster I (199.27), cluster V (196.14) and cluster VII (136.87). Hence genotypes from these clusters could be selected for hybridization programme for obtaining the desired segregants. Only single accession was found in each of the clusters II, III, VIII and IX indicating considerable genetic difference still exists amongst the genotypes. The greatest mean value for desirable qualities may be used as the basis for selection within these clusters. Hence the yield can be increased

**Table 1. Analysis of variance for yield, yield attributes and Water Use Efficiency (WUE) related traits in 36 genotypes of groundnut**

| S.No. | Characters                                                       | Mean sum of squares |                    |               |
|-------|------------------------------------------------------------------|---------------------|--------------------|---------------|
|       |                                                                  | Replications (df:2) | Treatments (df:35) | Error (df:70) |
| 1     | Days to 50% flowering                                            | 2.815               | 14.701**           | 2.710         |
| 2     | Days to maturity                                                 | 1.861               | 18.198**           | 1.680         |
| 3     | Plant height (cm)                                                | 1.685               | 56.210**           | 4.728         |
| 4     | Number of primary branches plant <sup>-1</sup>                   | 0.328               | 3.831**            | 0.109         |
| 5     | Number of secondary branches plant <sup>-1</sup>                 | 0.180               | 1.659**            | 0.069         |
| 6     | Kernel yield plant <sup>-1</sup> (g)                             | 0.108               | 9.454**            | 0.476         |
| 7     | Hundred Kernel Weight (g)                                        | 39.433              | 73.824**           | 24.466        |
| 8     | Shelling per cent (%)                                            | 1.757               | 157.744**          | 17.271        |
| 9     | Sound Mature Kernel (%)                                          | 112.236             | 270.267**          | 84.253        |
| 10    | Harvest Index (%)                                                | 64.824              | 367.870**          | 67.886        |
| 11    | SPAD Chlorophyll Meter Reading at 60 DAS                         | 1.629               | 11.539**           | 4.670         |
| 12    | Specific leaf area at 60 DAS (cm <sup>2</sup> gm <sup>-1</sup> ) | 259.032             | 3595.106**         | 407.379       |
| 13    | Relative Water Content (%)                                       | 32.903              | 54.532**           | 23.053        |
| 14    | Pod Yield Plant <sup>-1</sup> (g)                                | 0.285               | 19.792**           | 0.923         |

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

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

| S. No. | Cluster Number | Number of Genotypes | Genotypes                                                                                                                                     |
|--------|----------------|---------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| 1      | I              | 15                  | TCGS-2057, Rohini, TCGS-2227, TCGS-2038, TCGS-2219, TCGS-2068, TCGS-1798, TCGS-2044, Narayani, Dheeraj, TCGS-2004, TAG-24, Dharani, TCGS-2060 |
| 2      | II             | 1                   | TCGS-2039                                                                                                                                     |
| 3      | III            | 1                   | TCGS-2055                                                                                                                                     |
| 4      | IV             | 7                   | TCGS-2052, K9, TCGS-2233, TCGS-2317, TCGS-2278, TCGS-2041 and TCGS-2217                                                                       |
| 5      | V              | 3                   | TCGS-1694, TCGS-2049 and Greeshma                                                                                                             |
| 6      | VI             | 5                   | TCGS-2235, Tirupati-1, Tirupati-4, K6 and TCGS-2229                                                                                           |
| 7      | VII            | 2                   | TCGS-2040 and TCGS-2223                                                                                                                       |
| 8      | VIII           | 1                   | TCGS-2230                                                                                                                                     |
| 9      | IX             | 1                   | TCGS-2053                                                                                                                                     |

**Table 3. Average Inter (above diagonal) and Intra cluster (diagonal) D<sup>2</sup> and D values (in parenthesis) for 9 clusters in 36 genotypes of groundnut**

| Clusters | I                 | II                | III               | IV                | V                 | VI                 | VII                | VIII               | IX                 |
|----------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| I        | 199.27<br>(14.12) | 286.18<br>(16.92) | 366.21<br>(19.14) | 507.07<br>(22.52) | 680.75<br>(26.09) | 421.19<br>(20.52)  | 738.93<br>(27.18)  | 1390.32<br>(37.29) | 2080.02<br>(45.61) |
| II       |                   | 0.00<br>(0.00)    | 24.99<br>(5.00)   | 201.24<br>(14.19) | 652.22<br>(25.54) | 587.38<br>(24.24)  | 273.79<br>(16.55)  | 879.19<br>(29.65)  | 1004.15<br>(31.69) |
| III      |                   |                   | 0.00<br>(0.00)    | 199.08<br>(14.11) | 710.73<br>(26.66) | 740.62<br>(27.21)  | 274.24<br>(16.56)  | 770.98<br>(27.77)  | 874.55<br>(29.57)  |
| IV       |                   |                   |                   | 235.43<br>(15.34) | 439.56<br>(20.97) | 953.21<br>(30.87)  | 712.88<br>(26.70)  | 626.30<br>(25.03)  | 981.72<br>(31.33)  |
| V        |                   |                   |                   |                   | 196.14<br>(14.00) | 1146.57<br>(33.86) | 1634.98<br>(40.43) | 816.51<br>(28.57)  | 1846.08<br>(42.97) |
| VI       |                   |                   |                   |                   |                   | 304.88<br>(17.46)  | 882.38<br>(29.70)  | 2438.09<br>(49.38) | 2611.50<br>(51.10) |
| VII      |                   |                   |                   |                   |                   |                    | 136.87<br>(11.70)  | 1684.13<br>(41.04) | 1064.39<br>(32.62) |
| VIII     |                   |                   |                   |                   |                   |                    |                    | 0.00<br>(0.00)     | 1071.40<br>(32.73) |
| IX       |                   |                   |                   |                   |                   |                    |                    |                    | 0.00<br>(0.00)     |

through the use of recombination breeding by selecting the genotypes from these clusters. Similar results were earlier reported by John and Mylaswamy (1998).

Clusters VI and IX had the greatest intercluster distance (2611.50), followed by clusters VI and VIII (2438.09), I and IX (2080.02), V and IX (1846.08) and clusters VII and VIII (1684.13) which were all found to be divergent in decreasing order of their magnitude and could be utilized as parents for crossing programmes to produce high heterotic effects and transgressive segregants with high variability. A cluster diagram was made to depict the interrelationships between the various genotypes. Clusters VI and IX, which were the farthest apart (2611.50) displayed the greatest degree of divergence. On the other hand, of the nine clusters established, the inter cluster distance between cluster II and cluster III was the shortest (24.99) and thereby least genetic divergence.

Character-wise score across all nine clusters, as well as the cluster mean for traits are shown in **Table 4**. The cluster means were derived for all characters after the 36 genotypes were divided into nine groups. The clusters were ranked based on the aggregate score obtained from 14 attributes. Cluster-VII which received a total score of 39 for all the 14 characters ranked first followed by clusters-IX, II, III, VIII, IV, VI, I and V. These clusters demonstrated the presence of the promising genotypes and could be extensively used in upcoming breeding programmes for development of high yielding varieties with high water use efficiency.

The data suggested that for all the characters studied, genotypes with higher performance for one trait has the average performance for the other traits. Hence the idea of selecting a single genotype for immediate use was eliminated because no cluster in the current analysis

Table 4. Cluster means for yield, yield attributes and Water Use Efficiency (WUE) related traits in 36 genotypes of groundnut

| Clusters | Characters |           |          |         |         |          |          |          |          |          |          |           | Productivity Traits |          |             |            |
|----------|------------|-----------|----------|---------|---------|----------|----------|----------|----------|----------|----------|-----------|---------------------|----------|-------------|------------|
|          | DFF        | DM        | PH       | NPB     | NSB     | KYP      | HKW      | SHF      | SMK      | HI       | SCMR     | SLA       | RWC                 | PYP      | Total Score | Final Rank |
| I        | 27.20(9)   | 106.73(7) | 33.69(3) | 4.88(7) | 1.36(6) | 10.48(7) | 50.88(3) | 74.84(3) | 51.33(5) | 45.33(9) | 47.27(7) | 211.89(5) | 82.79(9)            | 14.00(7) | 87          | 8          |
| II       | 26.33(5)   | 107.00(8) | 34.60(5) | 5.80(3) | 2.40(2) | 11.99(4) | 53.93(1) | 71.05(4) | 60.03(2) | 45.63(7) | 48.47(6) | 218.43(7) | 85.56(4)            | 16.88(6) | 61          | 3          |
| III      | 27.00(7)   | 107.33(9) | 33.33(2) | 4.52(8) | 1.47(5) | 12.31(3) | 48.53(8) | 70.17(5) | 57.33(4) | 51.73(6) | 48.63(4) | 165.61(1) | 88.60(1)            | 17.54(3) | 66          | 4          |
| IV       | 26.29(4)   | 106.05(5) | 37.15(7) | 5.59(4) | 1.33(7) | 11.06(6) | 50.34(5) | 65.79(6) | 49.38(6) | 55.5(5)  | 48.77(3) | 202.32(3) | 85.70(3)            | 16.82(5) | 69          | 6          |
| V        | 25.78(3)   | 106.67(6) | 39.50(9) | 5.29(5) | 1.0(8)  | 8.04(9)  | 48.22(9) | 60.10(8) | 43.70(9) | 59.58(4) | 46.07(8) | 219.78(8) | 85.82(2)            | 13.41(9) | 97          | 9          |
| VI       | 26.53(6)   | 105.60(4) | 38.65(8) | 4.91(6) | 1.91(4) | 11.25(5) | 49.73(7) | 81.06(1) | 48.25(8) | 45.41(8) | 45.71(9) | 209.33(4) | 83.57(8)            | 13.87(8) | 86          | 7          |
| VII      | 25.33(2)   | 105.50(3) | 34.65(6) | 6.74(2) | 2.23(3) | 14.43(2) | 51.03(2) | 75.84(2) | 58.93(3) | 64.46(3) | 49.70(1) | 171.71(2) | 85.03(6)            | 19.03(2) | 39          | 1          |
| VIII     | 24.33(1)   | 103.67(1) | 26.13(1) | 3.87(9) | 2.47(1) | 10.00(8) | 50.80(4) | 57.26(9) | 49.20(7) | 69.79(2) | 48.53(5) | 226.22(9) | 85.23(5)            | 17.46(4) | 66          | 4          |
| IX       | 27.33(8)   | 104.67(2) | 34.11(4) | 8.82(1) | 0.80(9) | 15.36(1) | 50.13(6) | 63.60(7) | 63.80(1) | 71.45(1) | 49.50(2) | 217.65(6) | 84.25(7)            | 24.14(1) | 56          | 2          |
| Mean     | 26.24      | 105.91    | 34.65    | 5.60    | 1.67    | 11.66    | 50.40    | 68.86    | 53.55    | 56.55    | 48.07    | 204.77    | 85.17               | 17.02    |             |            |

**Note:** Numbers in the parenthesis indicates the ranks based on cluster mean. Total score is the summation of rank numbers for all characters, based on which final rank indicated. Bold numbers indicated highest mean values for each character.

DFF : Days to 50% flowering      DM : Days to maturity      PH : Plant height (cm)  
 NPB : No. of primary branches plant<sup>-1</sup>      NSB : No. of secondary branches plant<sup>-1</sup>      KYP : Kernel yield plant<sup>-1</sup> (g)  
 HKW : Hundred Kernel Weight (g)      SP : Shelling per cent (%)      SMK : Sound Mature Kernel (%)  
 HI : Harvest Index (%)      SCMR : SPAD Chlorophyll Meter Reading at 60 DAS      SLA : Specific Leaf Area at 60 DAS (cm<sup>2</sup> gm<sup>-1</sup>)  
 RWC : Relative Water Content (%)      PYP : Pod Yield Plant<sup>-1</sup> (g)

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

| S.No. | Characters                                                       | Number of times ranked first | Contribution (%) |
|-------|------------------------------------------------------------------|------------------------------|------------------|
| 1     | Days to 50% flowering                                            | 0                            | 0.00%            |
| 2     | Days to maturity                                                 | 0                            | 0.00%            |
| 3     | Plant height (cm)                                                | 0                            | 0.00%            |
| 4     | No. of primary branches plant <sup>-1</sup>                      | 0                            | 0.00%            |
| 5     | No. of secondary branches plant <sup>-1</sup>                    | 5                            | 0.79%            |
| 6     | Kernel yield plant <sup>-1</sup> (g)                             | 24                           | 3.81%            |
| 7     | Hundred Kernel Weight (g)                                        | 0                            | 0.00%            |
| 8     | Shelling Per cent                                                | 234                          | 37.14%           |
| 9     | Sound Mature Kernel (%)                                          | 0                            | 0.00%            |
| 10    | Harvest Index (%)                                                | 0                            | 0.00%            |
| 11    | SPAD Chlorophyll Meter Reading at 60 DAS                         | 136                          | 21.59%           |
| 12    | Specific Leaf area at 60 DAS (cm <sup>2</sup> gm <sup>-1</sup> ) | 2                            | 0.32%            |
| 13    | Relative Water Content (%)                                       | 0                            | 0.00%            |
| 14    | Pod Yield Plant <sup>-1</sup> (g)                                | 229                          | 36.35%           |

was discovered to have at least one genotype with all the desirable characters. As a result, hybridization between the chosen genotypes from different clusters is necessary to properly combine all the desirable traits. (Gupta *et al.*, 2015).

Additionally, it was found that the relative contributions of several plant traits to divergence (**Table 5**) can assist breeders in selecting the ideal parents for hybridization and in developing efficient selections in succeeding generations. The trait, shelling percent was ranked first for 234 times and contributed the most to genetic divergence (37.14%). It was followed by pod yield plant<sup>-1</sup> (36.35%), SPAD chlorophyll meter reading at 60 DAS (21.59%), kernel yield plant<sup>-1</sup> (3.81%), number of secondary branches plant<sup>-1</sup> (0.79%) and specific leaf area at 60 DAS (0.32%).

There was no genetic divergence associated with the attributes plant height, number of primary branches plant<sup>-1</sup>, sound mature kernel percentage, hundred kernel weight, days to 50% flowering, days to maturity, harvest index and relative water content.

It could be concluded that it would be advantageous to hybridise genotypes across divergent clusters with highest mean values for the specific characters to produce superior hybrids. By comparing the genetic divergence between the clusters and *per se* performance of genotypes, the cross combinations K-6 × TCGS-2053 and TCGS-2235 × TCGS-2053 could be recommended to increase water use efficiency related traits in groundnut, whereas the cross combinations Greeshma × TCGS-2053 and TCGS-2223 × TCGS-2230 could be recommended

to obtain transgressive segregants for yield and yield attributes.

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