GENETIC DIVERGENCE IN CONFECTIONARY TYPES OF GROUNDNUT (ARACHIS HYPOGAEA L.)

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ABSTRACT

Seventy four genotypes representing diverse geographic origin were studied for genetic divergence using Mahalanobis $D^2$ statistic. These genotypes were grouped into twelve clusters. The mode of distribution of genotypes to various clusters was at random suggesting that there is no relationship between geographical distribution and genetic diversity. Based on inter-cluster distances, the clusters VII vs X, VI vs XII and X vs XII were found as divergent. Hence, selection of genotypes from these clusters namely ICGV 99032 (cluster VI), TCGS 647, JL 220 (cluster VII), ICGV 95477, JL 24, ICGV 99054, ICGV 86699 (cluster X) and ICGV 99029 (cluster XII) for hybridization programme may result into good recombinants. The characters 100-kernel weight, shelling percentage and harvest index contributed maximum towards genetic divergence in both $D^2$ analysis and canonical root analysis. Further, canonical root analysis confirmed the clustering pattern obtained by $D^2$ analysis.

Key words: Genetic divergence, Groundnut.

INTRODUCTION

Groundnut (Arachis hypogaea L.) is one of the premier oilseed crops in our country. More than 80% of groundnut production in the country is used for extraction of oil and 1-3% is exported for confectionery purpose. The large seeded confectionery groundnut has a greater demand as snack food in domestic as well as international market and fetches a higher price. However, the groundnut export trade in India is restricted to hand picked selected seeds only. Hybridization, followed by selection has been one of the breeding strategies recommended to increase productivity in groundnut (Norden, 1973). The information on genetic diversity in a crop is essential in order to have breeding programmes for higher yield potentials. Choosing genetically diverse parents will enable the expansion of genetic base and development of superior genotypes. In this regard, $D^2$ statistics has been extensively used to measure the genetic divergence in breeding programmes. Intercrossing between more divergent parents is expected to generate a broad spectrum of variability and selection can be adopted in the segregating generations. Hence, an attempt was made to assess the magnitude of genetic divergence in groundnut genotypes and to identify genetically divergent parents, which can be utilized in a hybridization programme.

MATERIALS AND METHODS

Seventy four groundnut genotypes obtained from various research stations of India were studied
in a randomized block design with three replications at Regional Agricultural Research Station, Tirupati during kharif, 2007. The soil of the experimental site is sandy loam and the crop was raised under irrigated situation and high input management conditions. Each genotype was raised in three rows of five meter length spaced at 30 cm between rows and 10 cm within the row. Ten plants were selected randomly from each plot and observations for sixteen characters were recorded for yield, quality, physiological and yield attributes viz., plant height, number of primary branches per plant, number of mature pods per plant, harvest index, shelling percentage, sound mature kernel percent (SMK%), 100-kernel weight, protein content, total sucrose content, oil percentage, SPAD chlorophyll Meter Reading (SCMR), specific leaf weight, specific leaf area, pod yield and kernel yield per plant. The analysis of genetic divergence was carried out using Mahalanobis’s D² statistics (1936). The seventy four genotypes were grouped into 12 clusters. Out of the 12 clusters formed, the maximum numbers of genotypes (22) were included in cluster III, followed by cluster I and X with 14 genotypes each, while cluster II had 13 genotypes. Cluster VII had four genotypes and the remaining clusters had one genotype each (Table 1). The formation of largest cluster III comprising 22 genotypes might be due to a free flow (or) exchange of breeding material from one place to another or/and the unidirectional selection practiced by breeders of different locations. Seven genotypes were not included in any other cluster as they maintained separate identity from all others. They were grouped into different clusters viz., IV, V, VI, VIII, IX, XI and XII, each exhibiting high genetic diversity with most of the other clusters. The

### RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes for all the sixteen characters studied. The D² values of the possible 2701 combinations ranged from 7.83 (between cluster IV and VI) to 101.82 (between cluster VII and X). The seventy four genotypes were grouped into 12 clusters. Out of the 12 clusters formed, the maximum numbers of genotypes (22) were included in cluster III, followed by cluster I and X with 14 genotypes each, while cluster II had 13 genotypes. Cluster VII had four genotypes and the remaining clusters had one genotype each (Table 1). The formation of largest cluster III comprising 22 genotypes might be due to a free flow (or) exchange of breeding material from one place to another or/and the unidirectional selection practiced by breeders of different locations. Seven genotypes were not included in any other cluster as they maintained separate identity from all others. They were grouped into different clusters viz., IV, V, VI, VIII, IX, XI and XII, each exhibiting high genetic diversity with most of the other clusters. The

### Table 1: Clustering pattern of 74 groundnut genotypes during Kharif, 2007.

<table>
<thead>
<tr>
<th>Cluster No.</th>
<th>No. of genotypes</th>
<th>Genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>14</td>
<td>TIRUPATI-3, TCGP 10, ICGV 94358, ICR-40, VG 229, TIRUPATI-2, ICG 10, TCGP – 5, KADIRI-6, NARAYANI, PRASUNA, ICGV 9560, ICG 7416, KALAHASTHI</td>
</tr>
<tr>
<td>II</td>
<td>13</td>
<td>ICG 7791, VG 9513, ICG 7216, TIR – 43, VG 9521, TCGP 7, VG 210, K-1375, KADIRI 4, TIR-09, ICG 11987, VG 36, JUG-43</td>
</tr>
<tr>
<td>IV</td>
<td>1</td>
<td>VG 137</td>
</tr>
<tr>
<td>V</td>
<td>1</td>
<td>ICGV 95454</td>
</tr>
<tr>
<td>VI</td>
<td>1</td>
<td>ICGV 99032</td>
</tr>
<tr>
<td>VII</td>
<td>4</td>
<td>TCGC 647, JL 220, TCGP-6, TG 47</td>
</tr>
<tr>
<td>VIII</td>
<td>1</td>
<td>ICG 9930</td>
</tr>
<tr>
<td>IX</td>
<td>1</td>
<td>ICGV 86325</td>
</tr>
<tr>
<td>X</td>
<td>14</td>
<td>VG 39, CSMG 84-1, ICR 04, ICGV 95492, JL – 24, ICGV 95469, ICGV 95322, ICGV 98383, ICGV 00350, JAL 39, ICGV 99054, ICGV 98163, ICGV 86699, ICGV 95477</td>
</tr>
<tr>
<td>XI</td>
<td>1</td>
<td>GANGAPURI</td>
</tr>
<tr>
<td>XII</td>
<td>1</td>
<td>ICGV 99029</td>
</tr>
<tr>
<td>Cluster</td>
<td>I</td>
<td>II</td>
</tr>
<tr>
<td>--------</td>
<td>-----</td>
<td>-----</td>
</tr>
<tr>
<td>I</td>
<td>10.07</td>
<td>20.67</td>
</tr>
<tr>
<td></td>
<td>(3.17)</td>
<td>(4.55)</td>
</tr>
<tr>
<td>II</td>
<td>12.88</td>
<td>29.59</td>
</tr>
<tr>
<td></td>
<td>(3.59)</td>
<td>(5.44)</td>
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<tr>
<td>III</td>
<td>18.63</td>
<td>29.86</td>
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<td>(4.32)</td>
<td>(5.46)</td>
</tr>
<tr>
<td>IV</td>
<td>0.00</td>
<td>19.18</td>
</tr>
<tr>
<td></td>
<td>(0.00)</td>
<td>(4.38)</td>
</tr>
<tr>
<td>V</td>
<td>0.00</td>
<td>18.37</td>
</tr>
<tr>
<td></td>
<td>(0.00)</td>
<td>(4.29)</td>
</tr>
<tr>
<td>VI</td>
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<td>80.21</td>
</tr>
<tr>
<td></td>
<td>(0.00)</td>
<td>(8.96)</td>
</tr>
<tr>
<td>VII</td>
<td>29.76</td>
<td>65.87</td>
</tr>
<tr>
<td></td>
<td>(5.46)</td>
<td>(8.12)</td>
</tr>
<tr>
<td>VIII</td>
<td>0.00</td>
<td>25.24</td>
</tr>
<tr>
<td></td>
<td>(0.00)</td>
<td>(5.02)</td>
</tr>
<tr>
<td>IX</td>
<td>0.00</td>
<td>26.86</td>
</tr>
<tr>
<td></td>
<td>(0.00)</td>
<td>(5.18)</td>
</tr>
<tr>
<td>X</td>
<td>39.48</td>
<td>72.61</td>
</tr>
<tr>
<td></td>
<td>(6.28)</td>
<td>(8.52)</td>
</tr>
<tr>
<td>XI</td>
<td>0.00</td>
<td>22.81</td>
</tr>
<tr>
<td></td>
<td>(0.00)</td>
<td>(4.78)</td>
</tr>
<tr>
<td>XII</td>
<td>0.00</td>
<td></td>
</tr>
</tbody>
</table>

D² values in parenthesis.
| Clusters | Days to maturity (cm) | Plant height (cm) | Primary branches / plant | Matute pods / plant | Pod yield (g) | 100-kernel weight (g) | Shelling Sound maturity % | SLA at 60 DAS (cm g⁻²) | SLW at 60 DAS (g cm⁻²) | SCMR Harvest index | Sucrose content (%) | Protein content (%) | Oil content (%) | Kernel yield/plant (g) |
|----------|-----------------------|-------------------|--------------------------|-------------------|--------------|----------------------|---------------------------|--------------------------|----------------------|------------------|-------------------|------------------|-----------------|----------------|------------------|
| I        | 108                   | 38                | 5.4                      | 19                | 16.6         | 32.99               | 68                         | 74                        | 175                  | 0.006            | 37.8             | 46               | 3.41            | 19.58           | 49.51           | 11.50            |
| II       | 109                   | 41                | 5.3                      | 17                | 15.2         | 34.60               | 58                         | 72                        | 168                  | 0.006            | 39.4             | 48               | 3.22            | 19.27           | 48.74           | 8.77             |
| III      | 108                   | 37                | 5.6                      | 19                | 16.9         | 39.11               | 69                         | 75                        | 163                  | 0.006            | 38.6             | 48               | 3.48            | 19.92           | 48.15           | 11.91            |
| IV       | 110                   | 40                | 5.2                      | 20                | 16.7         | 32.52               | 69                         | 72                        | 135                  | 0.007            | 41.3             | 39               | 2.14            | 18.40           | 49.82           | 11.50            |
| V        | 108                   | 40                | 6.6                      | 15                | 14.5         | 28.64               | 73                         | 67                        | 169                  | 0.006            | 38.5             | 52               | 4.09            | 15.70           | 48.20           | 10.42            |
| VI       | 107                   | 41                | 5.7                      | 17                | 16.5         | 31.55               | 70                         | 66                        | 140                  | 0.007            | 44.4             | 37               | 3.73            | 20.62           | 47.97           | 13.44            |
| VII      | 109                   | 37                | 6.1                      | 18                | 15.8         | 44.98               | 70                         | 76                        | 164                  | 0.006            | 39.6             | 52               | 3.70            | 19.71           | 50.48           | 15.06            |
| VIII     | 109                   | 42                | 4.1                      | 22                | 19.1         | 31.40               | 73                         | 84                        | 176                  | 0.006            | 34.1             | 50               | 5.14            | 17.81           | 50.03           | 16.44            |
| IX       | 110                   | 43                | 4.7                      | 16                | 14.5         | 30.50               | 66                         | 80                        | 143                  | 0.006            | 41.1             | 50               | 4.27            | 18.64           | 51.07           | 9.53             |
| X        | 105                   | 40                | 5.6                      | 19                | 17.0         | 29.37               | 66                         | 72.25                     | 162                  | 0.006            | 39.4             | 46               | 3.25            | 20.43           | 49.46           | 11.62            |
| XI       | 107                   | 39                | 6.1                      | 18                | 16.0         | 40.51               | 53                         | 77                        | 174                  | 0.006            | 37.5             | 54               | 2.56            | 21.71           | 46.80           | 8.13             |
| XII      | 98                    | 38                | 4.6                      | 18                | 15           | 43.71               | 56                         | 68                        | 169                  | 0.006            | 36.0             | 52               | 4.44            | 17.14           | 49.19           | 8.46             |
genotypes originated from different eco-geographical regions were grouped together into different clusters. The clustering pattern in the present study revealed that there is no correlation between geographic diversity and genetic diversity. This inference is substantiated by the reports of Golakia and Makne (1991), Reddy and Reddy (1993), Nayak and Patra (1997), Venkataravana et al., (2000) and Garajappa et al., (2005) in groundnut. Random genetic drift and selection exercised for specific characters in specified environments could cause greater diversity than geographical distance (Murthy and Arunachalam, 1966).

Inter cluster distances were employed conforming the presence of diversity among clusters. The maximum inter-cluster distance was observed between cluster VII and X (101.83) followed by cluster VI and XII (91.4) indicating wide diversity among these genotypes (Table 2). Hence, genotypes from these clusters may be utilized as parents for hybridization which would result in high heterotic expression for yield components and wider segregation in filial generations. By using such genotypes as parents in a hybridization programme, superior recombinants can be obtained. Similar results were also suggested by Choudhary et al., (1998) and John Joel and Mylaswamy (1998). The minimum inter-cluster distance between clusters IV and VI (7.84) indicated that most of the characters had similar values in these clusters. Maximum intra-cluster distance was observed in cluster X (39.48) followed by cluster VII (29.76) and cluster III (18.63) wherein closely related genotypes were grouped into each cluster and indicates less divergence among them.

Major emphasis has been given on cluster means for selecting the best parents for the crossing programme. Cluster means for different characters showed considerable differences among the clusters for all the characters (Table 3). The cluster IV recorded high specific leaf weight at 60 DAS (0.007), whereas cluster V showed highest cluster means for the number of primary branches per plant (6.63) and shelling percentage (73.4). The genotype of

<table>
<thead>
<tr>
<th>Sl.No.</th>
<th>Character</th>
<th>Times ranked first</th>
<th>% contribution towards divergence</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Days to maturity</td>
<td>186</td>
<td>6.89</td>
</tr>
<tr>
<td>2.</td>
<td>Plant height (cm)</td>
<td>10</td>
<td>0.37</td>
</tr>
<tr>
<td>3.</td>
<td>No. of primary branches per plant</td>
<td>21</td>
<td>0.78</td>
</tr>
<tr>
<td>4.</td>
<td>Mature pods per plant</td>
<td>26</td>
<td>0.96</td>
</tr>
<tr>
<td>5.</td>
<td>Pod yield per plant (g)</td>
<td>1</td>
<td>0.04</td>
</tr>
<tr>
<td>6.</td>
<td>100-kernel weight (g)</td>
<td>1189</td>
<td>44.02</td>
</tr>
<tr>
<td>7.</td>
<td>Shelling percentage (%)</td>
<td>687</td>
<td>25.44</td>
</tr>
<tr>
<td>8.</td>
<td>Sound mature kernel per cent (SMK %)</td>
<td>11</td>
<td>0.41</td>
</tr>
<tr>
<td>9.</td>
<td>SLA at 60 DAS (cm² g⁻¹)</td>
<td>29</td>
<td>1.07</td>
</tr>
<tr>
<td>10.</td>
<td>SLW at 60 DAS (g cm⁻²)</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>11.</td>
<td>SCMR (SCMR) at 60 DAS</td>
<td>77</td>
<td>2.85</td>
</tr>
<tr>
<td>12.</td>
<td>Harvest index (%)</td>
<td>202</td>
<td>7.48</td>
</tr>
<tr>
<td>13.</td>
<td>Sucrose content (%)</td>
<td>66</td>
<td>2.44</td>
</tr>
<tr>
<td>14.</td>
<td>Protein content (%)</td>
<td>45</td>
<td>1.67</td>
</tr>
<tr>
<td>15.</td>
<td>Oil content (%)</td>
<td>54</td>
<td>2.00</td>
</tr>
<tr>
<td>16.</td>
<td>Kernel yield per plant (g)</td>
<td>97</td>
<td>3.59</td>
</tr>
</tbody>
</table>
cluster VI showed high values for SCMR at 60 DAS (44.4). Similarly, the genotypes of cluster VII possessed high mean values for 100-kernel weight (44.97), whereas the genotypes of cluster VIII had highest values for mature pods per plant (21.46), pod yield per plant (19.05), sound mature kernel per cent (83.7), specific leaf area at 60 DAS (175.78), sucrose content (5.143) and kernel yield per plant (16.43). In a similar fashion, the genotypes of cluster IX had highest values for plant height (43.23), oil content (51.07) and long duration (110 days) and the genotypes of cluster XI had highest mean values for harvest index (53.64) and protein content (21.71). Inter-crossing of the genotypes from these clusters could be suggested to generate a wide range of variability followed by effective selection for these characters.

The relative contribution of different characters to the total genetic divergence estimated by $D^2$ analysis indicated that 100-kernel weight contributed the maximum (44.02%) towards the divergence followed by shelling percentage (25.44%) and harvest index (7.48%) (Table 4). Cluster means together with information on the traits that contribute maximum towards divergence would help in selection of parents. The highest contribution of 100-kernel weight towards divergence was also earlier reported by Golakia and Makne (1991), Reddy and Reddy (1993) and Lakshmidevamma et al., (2006). The greater contribution of harvest index towards genetic divergence is in consonance with the reports of Anuradha (1995) in groundnut. The group constellations formulated on the basis of Mahalanobis’s $D^2$ statistic were confirmed by canonical root analysis. The five canonical roots were responsible for 81.82 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 5). The relative distribution of genotypes reflected existence of parallelism between grouping obtained by $D^2$ analysis and canonical root analysis.

From the above discussion, it is clear that the characters viz., 100-kernel weight, shelling percentage, harvest index and days to maturity contributed more towards the divergence in a set of 74 genotypes involved in the present study. Based on inter-cluster distance, per se performance of genotypes included in clusters and contribution of characters towards divergence, the following Promising genotypes of groundnut identified from different clusters for inclusion in the hybridization programme.

<table>
<thead>
<tr>
<th>Cluster No.</th>
<th>Genotypes</th>
<th>Desirable characters</th>
</tr>
</thead>
<tbody>
<tr>
<td>II</td>
<td>JUG-43</td>
<td>High sucrose content</td>
</tr>
<tr>
<td>VI</td>
<td>ICGV-99032</td>
<td>High SCMR</td>
</tr>
<tr>
<td>VII</td>
<td>TCGS-647</td>
<td>High 100-kernel weight</td>
</tr>
<tr>
<td></td>
<td>JL-220</td>
<td>High kernel yield/plant</td>
</tr>
<tr>
<td>X</td>
<td>JL-24</td>
<td>High sound mature kernel per cent</td>
</tr>
<tr>
<td></td>
<td>ICGV-99054</td>
<td>High protein content</td>
</tr>
<tr>
<td></td>
<td>ICGV-86699</td>
<td>High oil content</td>
</tr>
<tr>
<td></td>
<td>ICGV-95477</td>
<td>High no. of mature pods/plant, high pod yield/plant, high shelling percentage</td>
</tr>
<tr>
<td>XII</td>
<td>ICGV-99029</td>
<td>Early maturity</td>
</tr>
</tbody>
</table>
genotypes were identified from each divergent cluster for inclusion in a hybridization programme. The crosses between these genotypes would create desirable transgressive segregants for combining all important yield components and physiological and quality characters in groundnut varieties.

REFERENCES