



Genetic variability, character association and genetic divergence in groundnut (*Arachis hypogaea* L.) accessions

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ABSTRACT

Present investigation was conducted in 31 groundnut accessions to assess genetic divergence, characters association involving 13 quantitative characters and path coefficients in order to identify superior accessions exhibiting higher genetic diversity. Number of pods/plant, secondary branches, kernel width and pod yield displayed a higher level of coefficient of variation both at phenotypic and genotypic level. Genetic advance with higher heritability indicated preponderance of additive variance for pod length, pod yield and number of pods/plant. Number of secondary branches, kernel width, pod length and number of pods/plant revealed significant positive correlation with pod yield. Path coefficient analysis revealed exertion of high positive direct effects on pod yield through pod length, kernel width and number of pods/plant. Cluster analysis exhibited substantial diversity among 31 accessions forming 13 clusters. Two clusters [X (two accessions) and XII (one accession)] showed the largest distance, which suggests hybridization between these accessions to achieve high level of heterosis for further exploitation. Five accessions viz., TAG-24, TG-69, ICGV-02005, TG-73 and TG-80 were identified as the most divergent for future use.

Key words: Cluster analysis, Genetic advance, Heritability, Mahalanobis D², Path analysis, Squared euclidian distance.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a vital oil seed crop. It is an annual, herbaceous, and self-pollinated legume that is classified under the sub-family Papilionaceae and family Fabaceae. Groundnut covers 31.3% of the total cropped area under oilseeds and accounts for 36.1% of the overall oilseed production in the world. The maximum share of groundnut production is contributed by China, India and USA. According to latest available data (2016-17), groundnut cultivation occupies ~27.6 million ha in the world, with an annual production of 43.9 million tons (with shell). The average worldwide yield is 1590 kg/ha (with shell) (FAOSTAT, <http://www.fao.org/faostat/em/#data/QC>). It is because of its high nutritive value that groundnut is extensively used in the food and confectionery industry. Groundnut kernel, a substantial source of edible oil (48-50%) and protein (25-28%), contains considerable amounts of vitamin E, niacin, riboflavin, thiamine, minerals and flavonoids (Janila *et al.*, 2013).

Groundnut growers face multiple constraints, such as cultivating the crop on marginal and sub-marginal land along with low plant population results from using inadequate seed rate (Daudi *et al.*, 2018) and also using low-yielding and late-maturing varieties with limited genetic base (Isleib and Wynne, 1983; Gantait *et al.*, 2017). Therefore, it becomes necessary to develop varieties with broad genetic base and improved adaptability. Assessing genetic diversity among groundnut accessions can ensure development of suitable high-yielding and adapted varieties with suitable maturity period (Daudi *et al.*, 2018). Keeping the above factors in mind, the present study was carried out to: (1) identify characters that significantly contribute towards pod yield, (2) to measure the genetic diversity among available accessions and (3) to identify superior and highly divergent accessions.

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MATERIALS AND METHODS

The field experiment was carried out with 31 accessions of groundnut provided by Bhabha Atomic Research Centre (BARC), Trombay, India and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India. The experiment was conducted during the *kharif* (July to October) season for two consecutive years (2016 and 2017) at the District Seed Farm of Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India (23.5°N latitude and 89.0°E longitude; 9.75 m above mean sea level). This region is characterized by sub-tropical, humid climate, with brief and mild winter. The soil of the experimental field was alluvial and sandy loam in texture, with good water-holding capacity, medium fertility and neutral pH.

The experiment was conducted following the plan of randomized complete-block design, comprising three

replications. Accessions were sown in plots (5 m × 1.5 m plot size), with inter and intra-row spacing of 30 and 10 cm respectively. The standard cultural practices comprising of all plant protection steps and agronomical attributes were undertaken throughout the crop growth period, as required.

Ten randomly chosen plants from each individual row, belonging to a specific accession, per replication, were assessed for the morphological and yield-attributing characters, from time to time. Days-to-first flowering, days-to-50% flowering, plant height (cm), number of secondary branches, days-to-maturity, number of pods per plant, pod yield (kg/ha), 100-kernel weight (g), shelling %, length (mm) and width (mm) of pods and kernels were measured respectively.

The pooled experimental data were subjected to one-way analysis of variance using SAS[®]ver.9.3.1 (SAS Institute, Cary, NC, USA) (SAS, 2003) software package. Estimation of coefficient of variation for the given traits at phenotypic and genotypic level was done with the help of the formula devised by Burton and De Vane (1953). Probable genetic advance (GA), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV) were assessed following the methodology proposed by Johnson *et al.* (1955). The classification of different levels of GA (on the basis of mean percentage) was done as per the formula suggested by Johnson *et al.* (1955). Phenotypic and genotypic correlations among the various attributes were calculated. The path coefficient values were attained through solving of synchronized formula using SAS[®]ver.9.3.1 software package (as suggested by Kang, 2015). With the help of D² statistics, originally proposed by Mahalanobis (1936), the genetic diversity analysis was conducted.

RESULTS AND DISCUSSION

Analysis of variance exhibited highly significant dissimilarities among the accessions for the traits under study, representing substantial diversity among the accessions (Table 1). The estimates for GCV were lower

than the PCV for all the characters. The high estimates of GCV were recorded for plant height, number of pods per plant, kernel width, and pod yield; whereas high estimates of PCV were recorded for plant height, number of secondary branches per plant, number of pods per plant, kernel width and pod yield (Table 1). Abundant variation available for these traits and higher estimates indicate that selection of these traits would be effective to design a future breeding protocol for further use. The values of PCV were greater than GCV (values for each of the traits considered in our present experiment), signifying the effect of environment on these characters. The outcome of the present study is in accordance with the reports of Zaman *et al.* (2010), Vishnuvardhan *et al.* (2013) and Rao (2016). Low GCV and PCV values were documented for the traits namely, days-to-first flowering, days-to-maturity, as well as days-to-50% flowering, which indicate that there is hardly any opportunity for genetic enhancement of these characters via selection. The results comply with the previous observation of Korat *et al.* (2009) for days-to-50% flowering.

The heritability (broad sense) estimates were high in case of all the traits (Table 1). High estimates of heritability (broad sense) indicate that there is preponderance of additive gene action in the expression of these characters that is heritable and fixable in subsequent generations, which can be enhanced with the aid of individual plant selection. These results are in conformity with the findings of Upadhyaya *et al.* (2012) and Kavera and Nadaf (2017). The GA estimates were highest in case of pod yield and lowest in days-to-50% flowering (Table 1). Similar findings were reported in groundnut by Vishnuvardhan *et al.* (2013) and Rao (2016). Overall, the characters exhibiting high heritability together with maximum GA were number of pods per plant, pod length, and pod yield. Therefore, stringent screening of accessions based on these economic traits will ensure high variability and fixation of traits in subsequent generations.

Correlation analyses were conducted to study the association of traits with yield. At the genotypic level, the

Table 1: Genetic parameters for yield and yield contributing traits in groundnut accessions during *kharif* season of 2016 and 2017 (pooled).

| Characters | Range (of mean) | GCV | PCV | Heritability (%) | GA | GA as % of means |
|-------------------------|-----------------|-------|-------|------------------|---------|------------------|
| Days-to-first flowering | 23.3-27.7 | 5.14 | 5.56 | 85.40 | 2.47 | 9.78 |
| Days-to-50% flowering | 30.7-33.7 | 3.01 | 3.72 | 65.70 | 1.61 | 5.02 |
| Plant height | 32.2-85.8 | 24.29 | 24.30 | 99.90 | 25.31 | 50.01 |
| No. of sec. branches | 14.0-43.7 | 19.92 | 23.01 | 75.00 | 10.63 | 35.53 |
| Days-to-maturity | 103.3-107.7 | 1.47 | 1.55 | 89.00 | 3.00 | 2.85 |
| No. of pods per plant | 10.7-84.0 | 45.44 | 45.49 | 99.80 | 29.15 | 93.51 |
| 100-kernel weight | 28.1-57.0 | 14.70 | 14.72 | 99.70 | 13.11 | 30.24 |
| Shelling% | 51.2-79.3 | 8.75 | 8.77 | 99.70 | 12.32 | 18.00 |
| Pod length | 20.7-39.3 | 14.61 | 14.73 | 98.30 | 8.16 | 29.84 |
| Pod width | 6.7-11.7 | 11.49 | 13.28 | 74.90 | 1.76 | 20.51 |
| Kernel length | 7.7-19.0 | 18.71 | 19.07 | 96.30 | 5.45 | 37.82 |
| Kernel width | 3.3-8.7 | 20.71 | 22.76 | 82.80 | 2.13 | 38.76 |
| Pod yield | 1126.7-3466.3 | 28.32 | 28.48 | 98.90 | 1132.33 | 58.01 |

correlation values were calculated on the basis of additive variance, whereas at the phenotypic level, environmental deviations were incorporated (Lekshmanan and Vahab, 2018). In the genotypic level, significant positive correlation was recorded between number of secondary branches, pod length, number of pods available per plant as well as kernel width, individually with pod yield suggesting simultaneous improvement in both the characters. Till date, there is no report on correlation analysis for days-to-first flowering with yield or yield attributing character in groundnut, which was observed in the present investigation. Alternatively, a significant negative correlation was observed both for plant height and shelling % with pod yield. Bhargavi *et al.*, (2015) reported a significant negative correlation for plant height with pod yield that validates one of our observations. Further, pod length exhibited a significant positive correlation with pod yield at genotypic level and such outcome had not been reported in any literature till date (Table 2).

At phenotypic level, significant positive phenotypic correlations were documented for number of pods per plant and kernel width, with pod yield (Table 2). Singh *et al.* (2017) also described such results in their study with groundnut. Significant negative correlations were observed plant height and shelling %. Pod length recorded highly significant positive correlation with pod yield but exhibited negative correlation with kernel width. Pod width showed highly significant positive correlation with kernel width, which recorded a significant positive correlation with pod yield. Till date, no report is available on correlation analysis for pod- and kernel-associated dimensional characters with yield or yield attributing character in groundnut, which was observed in the present investigation for the first time.

Path coefficient analysis utilizes the correlation coefficient values and depicts whether the trait influences the yield directly or by indirect means (Lyngdoh *et al.*, 2018). At the genotypic level displayed the highest direct effects of kernel width, followed by number of pods per plant, and pod length with pod yield in a positive manner (Fig 1a). Conversely, the highest negative direct effect on pod yield was registered by shelling %. Plant height exhibited major negative indirect effects on pod yield that was expressed via pod length. Shelling % exhibited major positive indirect effect on pod yield via pod width. Kernel width displayed least indirect effects on pod yield. On the other hand, path coefficient analysis at the phenotypic level displayed highest positive direct effects of number of pods per plant on pod yield followed by kernel width and pod length (Fig 1b). Similar outcome was documented by Yang *et al.* (2018) who reported a positive direct effect of kernel weight on yield in wheat. Such (high) direct effects apparently were the prime factor behind the durable associations between the yield attributing characters and pod yield. Hereafter, effective results can be obtained if direct selection is practiced for such traits. In the present study, shelling % exhibited negative direct effect and negative association at genotypic as well as phenotypic levels. In such situations, the indirectly

Table 2: Genotypic (italics) and phenotypic correlations for yield and yield contributing traits in the groundnut accessions during Kharif season of 2016 and 2017 (pooled).

| | Days-to-first flowering | Days-to-50% flowering | No. of pods per plant | Plant height | No. of sec. branches | Days-to-maturity | 100-kernel weight | Shelling % | Pod length | Pod width | Kernel length | Kernel width | Pod yield |
|-------------------------|-------------------------|-----------------------|-----------------------|--------------|----------------------|------------------|-------------------|------------|------------|-----------|---------------|--------------|-----------|
| Days-to-first flowering | | 0.016 | 0.265* | -0.473** | 0.207 | 0.113 | 0.082 | 0.166 | 0.629** | -0.046 | 0.333** | -0.061 | 0.134 |
| Days-to-50% flowering | -0.005 | | -0.145 | 0.246* | 0.058 | 0.139 | -0.311** | -0.156 | -0.240* | -0.283* | -0.165 | -0.162 | -0.227 |
| No. of pods per plant | 0.248* | -0.114 | | -0.198 | 0.347** | 0.027 | 0.215 | -0.329** | 0.330** | 0.300** | -0.097 | 0.224 | 0.333** |
| Plant height | -0.438** | 0.198 | -0.197 | | -0.372** | -0.272* | -0.361** | 0.075 | -0.395** | -0.023 | -0.362** | -0.276* | -0.331** |
| No. of sec. branches | 0.186 | 0.049 | 0.304** | -0.323** | | 0.000 | 0.396** | -0.312** | 0.625** | 0.269* | 0.364** | 0.117 | 0.246* |
| Days-to-maturity | 0.099 | 0.067 | 0.027 | -0.257* | 0.004 | | 0.079 | -0.194 | -0.030 | 0.193 | 0.091 | 0.115 | 0.075 |
| 100-kernel weight | 0.076 | -0.249* | 0.215 | -0.360** | 0.343** | 0.077 | | -0.266* | 0.417** | 0.233 | 0.613** | 0.016 | 0.176 |
| Shelling% | 0.152 | -0.130* | -0.328** | 0.076 | -0.269* | -0.181 | -0.265* | | -0.055 | -0.473** | 0.017 | -0.261* | -0.326** |
| Pod length | 0.574** | -0.180 | 0.327** | -0.391** | 0.542** | -0.039 | 0.413** | -0.055 | | 0.281* | 0.669** | -0.094 | 0.244* |
| Pod width | -0.011 | -0.102 | 0.258* | -0.023 | 0.250* | 0.143 | 0.202 | -0.415** | 0.235 | | -0.018 | 0.648** | 0.107 |
| Kernel length | 0.298* | -0.128 | -0.094 | -0.355** | 0.291* | 0.086 | 0.599** | 0.018 | 0.644** | -0.010 | | -0.248* | 0.198 |
| Kernel width | -0.076 | -0.179 | 0.203 | -0.252* | 0.121 | 0.128 | 0.018 | -0.230 | -0.098 | 0.451** | -0.228 | | 0.314** |
| Pod yield | 0.132 | -0.173 | 0.283* | -0.329** | 0.219 | 0.053 | 0.175 | -0.325** | 0.242* | 0.100 | 0.195 | 0.273* | |

*P=0.05 level of significance**P = 0.01 level of significance.

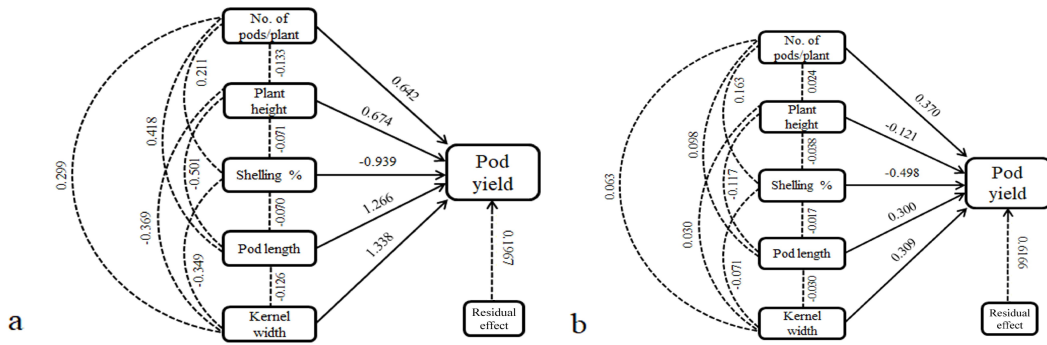


Fig 1: Path diagram (a. genotypic, b. phenotypic) showing interrelationships among major six traits of the groundnut accessions. [Solid single-head arrows represent direct effects; dotted lines represent indirect effects; dotted line with single-head arrow represents residual effects].

contributing factors have to be considered for yield improvement. Comparable results were reported earlier in groundnut (Izge *et al.*, 2004).

All the 31 accessions were grouped under 13 clusters using Mahalanobis D^2 statistics method of clustering. D^2 statistics is an effective approach for measurement of genetic diversity in any breeding program (Jyothireddy *et al.*, 2018). Among the 13 clusters designed, cluster II possessed highest number of accessions, whereas, clusters XI, XII and XIII possessed only single accession (Table 3). The clusters obtained from the D^2 statistics were compared with the dendrogram obtained from the mean values of the accessions using squared Euclidean distance (Fig 2). The maximum intra-cluster distance was recorded in cluster X (Table 4), which further suggests that the accessions available within each cluster, displayed higher degree of genetic variability and have the potential to evolve more divergent breeding material to attain maximum genetic advance (Singh *et al.*, 2010). The highest inter-cluster distance was detected between clusters X and XII tailed by clusters X and XI, clusters IX and X *etc.* (Table 4), indicating that the accessions belonging to these clusters exhibited higher divergence, thus they can be considered for designing any hybridization program. Cluster mean values displayed substantial divergence for all traits among the clusters designed. The accessions belonging to cluster XII recorded highest values for number of secondary branches, pod length and pod yield. Cluster XIII recorded higher values for pod width and kernel width, whereas, cluster I registered maximum values for days-to-maturity and kernel length. Clusters IX, X and XI had the highest values for 100-kernel weight, plant height and number of pods per plant, respectively (Table 5). Thus breeding program can be designed to utilize accessions from clusters IX, X, XI and XII in order to produce filial generations with a broad base of divergence.

The relative contribution assay of all the 13 characters towards the overall genetic divergence showed contribution of pod length to be the maximum (24.73%), which is the first kind of report and it can be a vital parameter in any future breeding programmes. The major contributing traits were number of pods per plant (10.97%), pod yield

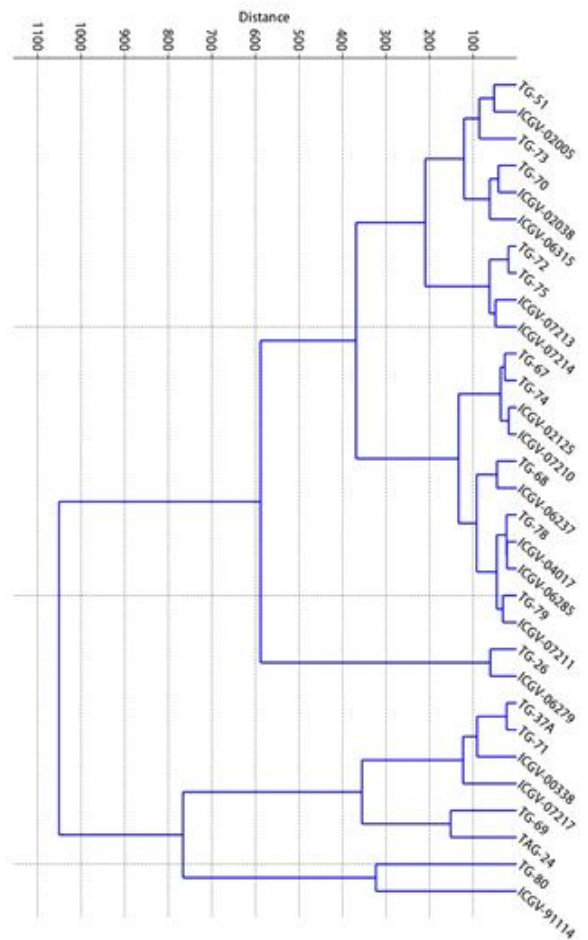


Fig 2: Dendrogram representing clustering of groundnut accessions based on Squared Euclidian distance matrix.

(16.34%), plant height (14.41%), shelling % (12.26%) and 100-kernel weight (10.97 %). The substantial contribution of 100-kernel weight towards genetic divergence supports the report of Vijayasekhar (2002) in groundnut. In addition, pod yield was reported to be the highest contributor towards genetic divergence (Gantait *et al.*, 2017). Based on the present diversity analysis, out of 31 accessions, five viz.,

Table 3: Cluster formation pattern of the groundnut accessions during *kharif* season of 2016 and 2017 (pooled).

| Cluster no | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII | XIII |
|---------------------|-------------------|--|-------------------------------|------------------------|-------------------------------|------------------------|-----------------------|------------|---------------------|----------------------|-------|-------|------------|
| No. of population | 2 | 8 | 3 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 |
| Names of accessions | TG 70, ICGV 04017 | TAG 24, TG 26, TG 37A, TG 51, TG 67, TG 68, TG 69, TG 75 | TG 71, ICGV 02038, ICGV 07210 | ICGV 02125, ICGV 06285 | TG 72, ICGV 06315, ICGV 07214 | ICGV 00338, ICGV 06237 | ICGV 07211, ICGV 9114 | ICGV 07217 | TG 79, TG 74, TG 78 | ICGV 02005, TG 06279 | TG 73 | TG 80 | ICGV 07213 |

Table 4: Intra (italics)- and Inter-cluster distances of the groundnut accessions.

| Clusters | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII | XIII |
|----------|--------|--------|--------|--------|--------|---------|--------|--------|---------|---------|---------|---------|---------|
| I | 12.227 | 55.129 | 47.845 | 53.325 | 30.535 | 75.011 | 42.967 | 63.505 | 49.625 | 139.078 | 103.416 | 85.771 | 108.880 |
| II | | 52.066 | 82.895 | 70.035 | 54.087 | 108.016 | 64.166 | 64.558 | 70.974 | 168.354 | 90.512 | 71.223 | 122.047 |
| III | | | 39.439 | 50.837 | 54.575 | 60.297 | 70.918 | 68.221 | 85.553 | 107.898 | 128.029 | 122.123 | 106.365 |
| IV | | | | 26.008 | 58.301 | 60.622 | 67.802 | 39.655 | 93.823 | 110.636 | 110.894 | 115.460 | 81.861 |
| V | | | | | 40.777 | 87.119 | 52.733 | 61.900 | 58.699 | 146.707 | 106.337 | 86.783 | 119.585 |
| VI | | | | | | 36.464 | 80.059 | 83.026 | 111.278 | 81.427 | 146.668 | 142.616 | 76.848 |
| VII | | | | | | | 46.897 | 69.292 | 63.523 | 150.222 | 117.531 | 81.416 | 110.072 |
| VIII | | | | | | | | 48.637 | 97.880 | 133.208 | 110.808 | 106.337 | 97.750 |
| IX | | | | | | | | | 50.737 | 176.042 | 104.098 | 77.921 | 136.093 |
| X | | | | | | | | | | 57.305 | 197.305 | 210.978 | 110.973 |
| XI | | | | | | | | | | | 0.000 | 87.918 | 121.713 |
| XII | | | | | | | | | | | | 0.000 | 147.407 |
| XIII | | | | | | | | | | | | | 0.000 |

Table 5: Cluster mean of the groundnut accessions.

| Clus-ter | Days-to-first flowering | Days-to-50% flowering | Plant height | No. of secondary branch | Days-to-maturity | No. of pods per plant | 100-kernel weight | Shelling % | Pod length | Pod width | Kernel length | Kernel width | Pod yield |
|----------|-------------------------|-----------------------|--------------|-------------------------|------------------|-----------------------|-------------------|------------|------------|-----------|---------------|--------------|-----------|
| I | 25.667 | 33.167 | 49.917 | 27.000 | 107.167 | 27.333 | 47.433 | 69.735 | 27.500 | 8.167 | 17.667 | 5.167 | 1669.833 |
| II | 26.375 | 31.958 | 41.708 | 33.458 | 105.083 | 35.333 | 41.911 | 69.065 | 30.000 | 8.500 | 14.500 | 5.292 | 2017.042 |
| III | 24.778 | 31.444 | 59.111 | 28.333 | 104.889 | 23.444 | 43.856 | 75.517 | 27.000 | 8.556 | 14.556 | 6.222 | 1902.667 |
| IV | 25.667 | 33.500 | 55.000 | 30.333 | 105.667 | 33.833 | 36.090 | 69.427 | 25.333 | 8.500 | 12.667 | 5.667 | 1515.167 |
| V | 26.111 | 32.667 | 47.500 | 28.333 | 105.000 | 25.889 | 44.971 | 73.062 | 28.000 | 7.667 | 14.667 | 4.667 | 1953.000 |
| VI | 23.667 | 32.167 | 64.917 | 31.167 | 104.167 | 20.000 | 42.107 | 63.307 | 25.500 | 8.000 | 14.500 | 4.333 | 2086.500 |
| VII | 23.667 | 31.667 | 44.500 | 26.167 | 105.833 | 16.000 | 46.020 | 62.973 | 24.167 | 8.333 | 16.167 | 5.500 | 2375.167 |
| VIII | 24.500 | 31.000 | 47.917 | 21.167 | 106.000 | 30.333 | 33.607 | 70.353 | 22.667 | 8.667 | 10.667 | 6.667 | 1966.000 |
| IX | 24.833 | 30.833 | 42.167 | 30.500 | 105.000 | 26.833 | 56.150 | 67.247 | 27.000 | 9.667 | 16.500 | 6.167 | 1526.667 |
| X | 23.667 | 32.333 | 83.000 | 23.500 | 105.167 | 24.667 | 35.523 | 70.823 | 23.167 | 8.333 | 11.667 | 4.000 | 1528.500 |
| XI | 26.333 | 30.667 | 44.500 | 30.667 | 105.667 | 84.000 | 52.200 | 62.650 | 32.667 | 8.667 | 16.667 | 5.000 | 1930.667 |
| XII | 25.667 | 31.667 | 33.500 | 43.667 | 107.000 | 40.333 | 52.593 | 61.610 | 35.667 | 9.667 | 19.000 | 6.667 | 3466.333 |
| XIII | 23.667 | 33.667 | 62.500 | 35.667 | 104.333 | 53.333 | 43.613 | 51.240 | 23.667 | 11.667 | 7.667 | 8.667 | 2065.000 |

TAG-24 (with high pod yield), TG-69 (with high pod yield), ICGV-02005 (with maximum plant height and high shelling %), TG-73 (with highest number of pods per plant) and TG-80 (with high 100-kernel weight) were identified as the most divergent and high yielding ones for further exploitation.

CONCLUSION

The extent of coefficient of variation signified the existence of substantial level of genetic divergence and variability among the accessions. Further, high heritability coupled with high GA recorded for number of pods per plant, pod length, and pod yield suggest that these characters can be enhanced

with the aid of simple selection procedures. Correlation data revealed that number of secondary branches, number of pods per plant, pod length and kernel width exhibited a significant positive correlation with pod yield, suggesting simultaneous improvement in these traits along with yield. Consequently, path coefficient analysis also revealed high positive direct effects of pod length, kernel width and number of pods per plant on pod yield. Thus, the traits that positively enhance yield and show prominent variation can be designated in a properly designed breeding program for harnessing divergence in our available groundnut accession. On the basis of the results obtained from cluster distance and overall cluster mean performance, the accessions that showed maximum divergence can be selected for hybridization and for future breeding programs. In this experiment, TAG-24, TG-69, ICGV-02005, TG-7 and TG-80 are the accessions that possess greater magnitude of genetic diversity due to higher inter cluster distances among them. Henceforth, the above accessions if utilized as parents in breeding program the chances of attaining heterosis in the segregating progenies will be high and pave way for more superior lines.

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REFERENCES

- Bhargavi, G., Satyanarayana Rao, V., Ratna Babu, D. and Narasimha Rao, K.L. (2015). Character association and path coefficient analysis of pod yield and yield components in Spanish bunch groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.* 6: 764-770.
- Burton, G.W. and Devane, E.W. (1953). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron. J.* 45: 478-481.
- Daudi, H., Shimelis, H., Laing, M., Okori, P. and Mponda, O. (2018). Groundnut production constraints, farming systems and farmer-preferred traits in Tanzania. *J. Crop Improvement.* 32: 812-828.
- Gantait, S., Gunri, S.K., Kundu, R. and Chatterjee, S. (2017). Evaluation of genetic divergence in Spanish bunch groundnut (*Arachis hypogaea* Linn.) genotypes. *Plant Breed. Biotechnol.* 5: 163-171.
- Isleib, T.G. and Wynne, J.C. (1983). Heterosis in testcrosses of 27 exotic peanut cultivars. *Crop Sci.* 23: 832-841.
- Izge, A.U., Alabi, S.O. and Maino, Y.T. (2004). Correlation and path analysis of pod yield and yield components of groundnut (*Arachis hypogaea* L.). *J. Sustainable Agric. Environ.* 6: 15-21.
- Janila, P., Nigam, S.N., Pandey, M.K., Nagesh, P. and Varshney, R.K. (2013). Groundnut improvement: use of genetic and genomic tools. *Front. Plant Sci.* 4: 23.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic correlations in soybean and their implications in selection. *Agron. J.* 47: 477-483.
- Jyothireddy, K., Prabhakar, B.N., Saidaiah, P. and Pandravada, S.R. (2018). Genetic divergence, variability, heritability and genetic advance for growth, pod quality and yield characters in dolichos bean (*Dolichos lablab* L. var. *typicus* Prain) germplasm. *Legume Res.* 41: 804-809.
- Kang, M.S. (2015). Efficient SAS programs for computing path coefficients and index weights for selection indices. *J. Crop Improvement.* 29: 6-22.
- Kavera and Nadaf, H.L. (2017). Genetic improvement for yield through induced mutagenesis in groundnut (*Arachis hypogaea* L.). *Legume Res.* 40: 32-35.
- Korat, V.P., Pithia, M.S., Savaliya, J.J., Pansuriya, A.G. and Sodavadiya, P. R. (2009). Studies on genetic variability in different genotypes of groundnut (*Arachis hypogaea* L.). *Legume Res.* 32: 224-226.
- Lekshmanan, D.K. and Vahab, M.A. (2018). Correlation and path coefficient analysis of yield and its component characters among different accessions of cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]. *Legume Res.* 41: 53-56.
- Lyngdoh, Y.A., Thapa, U., Shadap, A., Singh, J. and Tomar, B.S. (2018). Studies on genetic variability and character association for yield and yield related traits in french bean (*Phaseolus vulgaris* L.). *Legume Res.* 41: 810-815.
- Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proc. Natl. Acad. Sci. (India).* 2: 49-55.
- Rao, V. T. (2016). Genetic variability, correlation and path coefficient analysis under drought in groundnut (*Arachis hypogaea* L.). *Legume Res.* 39: 319-332.
- SAS. (2003). Version 9.3.1, SAS Institute Inc., Cary, NC, USA.
- Singh, P.B., Bharti, B., Kumar, A., Singh, R., Kumar, N. and Rathnakumar, A.L. (2017). Genetic characterization, character association for yield and yield component traits in groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.*, 8: 1229-1235.
- Singh, S., Singh, A. L., Kalpana, S. and Misra, S. (2010). Genetic diversity for growth, yield and quality traits in groundnut (*Arachis hypogaea* L.). *Indian J. Plant Physiol.* 15: 267-271.
- Upadhyaya, H.D., Nadaf, G.M. and Sube Singh, H.L. (2012). Variability and stability analysis for nutritional traits in the mini core collection of peanut. *Crop Sci.* 52: 168-178.
- Vijayasekhar, C. (2002). Genetic divergence studies through D² statistic and isozyme analysis in Spanish bunch groundnut (*Arachis hypogaea* L.) M.Sc., (Ag.) Thesis submitted to Acharya N.G. Ranga Agricultural University, Hyderabad, India.
- Vishnuvardhan, K.M., Vasanthi, R.P. and Reddy, K.H. (2013). Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). *Legume Res.* 36: 111-115.
- Yang, X., McMaster, G.S. and Yu, Q. (2018). Spatial patterns of relationship between wheat yield and yield components in China. *Int. J. Plant Prod.* 12: 61.
- Zaman, M.A., Tuhina-Khatun, M., Bhuiyan, M. H., Moniruzzamn, M. and Yousuf, M.N. (2010). Genetic divergence in groundnut (*Arachis hypogaea* L.). *Bangladesh J. Plant Breed. Genet.* 23: 45-49.