Biological Forum – An International Journal **15(11): 218-222(2023)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Divergence analysis in Confectionery Peanut (*Arachis hypogaea* L.)

Suresh Gali[1*], D.L. Reddy[2], A. Prasanna Rajesh[3], K. John[4], P. Sudhakar[5] and V. Srinivasa Rao[6]

[1]Research Scholar, Department of Genetics and Plant Breeding, Agricultural College, ANGRAU, Bapatla (Andhra Pradesh), India.
[2]Professor & Uni. Head (Retd.), Department of Genetics and Plant Breeding, S.V. Agricultural College ANGRAU, Tirupati (Andhra Pradesh), India.
[3]Principal Scientist (Oilseeds), Department of Genetics and Plant Breeding, Agricultural Research Station, ANGRAU, Kadiri (Andhra Pradesh), India.
[4]Principal Scientist (Plant Breeding), Department of Genetics and Plant Breeding, RARS, ANGRAU, Tirupati (Andhra Pradesh), India.
[5]Professor, Department of Crop Physiology, ANGRAU, Lam, Guntur (Andhra Pradesh), India.
[6]Professor & Head, Department of Statistics and Computer Applications, Agricultural College, ANGRAU, Bapatla (Andhra Pradesh), India.

(Corresponding author: Suresh Gali[*])
(Received: 09 September 2023; Revised: 07 October 2023; Accepted: 19 October 2023; Published: 15 November 2023)
(Published by Research Trend)

ABSTRACT: Genetic diversity in the experimental material is generally measured as a very important criterion for choosing hereditarily dissimilar parents necessary for well-organized and successful hybridization programme, which in turn results in the production of high yielding lines. There is a greater likelihood of promising and desired cultivars emerging in crop species with higher genetic variability. Quantifying the degree of genetic diversity among genotypes can be most effectively accomplished with the D^2 methodology, which Mahalanobis (1936) developed based on multivariate analysis. The 65 genotypes were divided into 10 clusters, with cluster IV having the highest number of genotypes (28) and clusters VI, VII and X had only single genotype. Maximum inter cluster D^2 value was observed between cluster IX and cluster X. Diversity analysis concluding that geographic diversity was not associated to genetic diversity, as genotypes from the same eco-geographic origin were divided into separate clusters without creating a single cluster. Cluster VI, VII, VIII, IX and X recorded high cluster mean values for most of the yield contributing and quality characters. The trait linoleic acid content contributed maximum variation to total variation.

Keywords: D^2 analysis, Genetic divergence, Peanut.

INTRODUCTION

The peanut (*Arachis hypogaea* L.) is an annual legume crop planted for its superior edible oil and easily absorbed protein found in its seeds. It is a self-pollinated crop with a chromosome number of 2n = 4x = 40 (Deepthi *et al*., 2022). In India, Gujarat and Andhra Pradesh are the major groundnut growing states. India ranks second in peanut production (67.27 lakh tonnes) after China (175 lakh tonnes) with an export of 6,41,125 tonnes of confectionery types (FAO, 2019). India is the largest exporter to Asean countries with the worth of 1836.12 crores in 2009-10, 4398.01 crores in 2014-15 and it has decreased to 2535.06 crores in 2018-19 (Palanisingh *et al*., 2020). The fluctuating trend of peanut exports in India is mainly due to instability of yields due to environmental effect, cultivation practices and lack of large seeded genotypes. Large seeded varieties catch the attention of high price for edible nuts on the global market. One of the earliest varieties of confectionery to be grown in India was Birsa Bold 1 (Rahman *et al*., 1995). Genetic diversity in the experimental material is generally considered as a vital criterion for choosing genetically diverse parents required for efficient and successful hybridization programme, which in turn results in the production of high yielding lines. Greater the genetic diversity in crop species better is the chance of evolving promising and desired types. The D^2 technique based on multivariate analysis developed by Mahalanobis (1936) is the most valuable method for quantifying the extent of genetic diversity among genotypes. It is generally accepted that genetically diverse parents when crossed will show maximum heterosis and offer the utmost chance of isolating transgressive segregants.

MATERIALS AND METHODS

The present investigation comprised of 65 peanut genotypes, obtained from ICRISAT (Hyderabad), ARS (Kadiri) and RARS (Tirupati). Two rows of each

genotype, each measuring 4 m in length, were sowed in the experiment in two replications using a randomized block design, with a spacing of 45 cm between the rows and 15 cm between the plants for the period of *kharif* - 2019 at Agricultural College Farm, Bapatla, Guntur, Andhra Pradesh. The experimental plot at growing season was done with recommended agronomic practices to raise healthy crop. The data were recorded from five randomly selected plants in each of the genotype per replication for yield traits. Days to 50% flowering and days to maturity were recorded on plot basis. Quality traits like oil content, protein content and fatty acids were estimated by using NIRS (model XDS RCA-FOSS Analytical AB, ICRISAT). Total soluble sugars content and free amino acids were estimated by adopting the method suggested by Sadasivam and Manickam (1961). The recorded data was statistically analyzed in INDOSTAT 9.2 Ver. The data collected on different yield contributing characters was analyzed using Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1936). The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The 65 peanut genotypes were grouped into 10 clusters using Tocher's method (Table 1 and Fig. 1). The maximum number of genotypes (28) were comprised into cluster IV followed by cluster V (12), cluster II (7), cluster III (6), cluster VIII (4) and cluster I (3) and cluster IX (2). The least number of genotypes (1) were comprised into clusters VI, VII and X. Due to a unidirectional selection effect, the genotypes analysed in this study with varied family backgrounds may fall into the same cluster, resulting in genotypes that were genetically closer than their parents. Based on the growth habit, the peanut was classified into two major groups namely, Spanish and Virginia. Present study examined 65 peanut genotypes (32 Spanish bunch types and 33 Virginia bunch types) for divergence. Tocher's clustering indicated that clusters I (3), II (7), IX (2) and X (1) had only Spanish type of peanut genotypes and clusters III (6), VI (1) and VII (1) had contained only Virginia type of peanut genotypes. These findings are clearly differentiating the two groups of peanut. Moreover, the clusters IV (14 SB and 14 VB), V (10 VB and 2 SB) and VIII (3 VB and 1 SB) were comprised with both Spanish and Virginia peanut types indicating that the genotypes included in these clusters might have exchanged their genetic material to each other in past and share genes from common gene pool. The genotypes obtained from ICRISAT were distributed over all the 10 clusters while Kadiri genotypes scattered under 2 clusters (III and V) and genotypes from diverse geographical regions were distributed in the same cluster (V) indicating that clustering of genotypes did not follow their geographic or location distribution and thus indicating that there is no relationship between geographical origin and genetic diversity. Similar findings of non correspondence of geographic origin with genetic diversity were also reported by Ravikumar (2005); Suneetha (2007); Ravikumar *et al*. (2012).

Based on D^2 values in which the genotypes belonging to same cluster had an average minimum D^2 value, than that of genotypes present in different clusters. The average intra and inter - cluster distances D^2 value was estimated and are presented in Table 2 and Fig. 2**.** In the present investigation, the maximum inter cluster D^2 value was observed between cluster IX and cluster X (10781.20) followed by cluster V and cluster IX (9751.07) and cluster II and cluster IX (8396.00). Intra cluster distance was observed to be minimum for cluster I (40.88) and maximum for cluster IX (642.23), while it was zero for the mono genotypic clusters VI, VII and X.

Among all the quantitative and qualitative characters studied, the character linoleic acid content (41.11 %) showed maximum contribution towards total divergence followed by free amino acids (22.07 %) and 100 seed weight (13.85). Maximum diversity of linoleic acid content may be due to wide range of linoleic acid per cent among all genotypes and also the genotypes namely, ICGV 171002 and ICGV 171004 were recorded very high oleic acid content among all genotypes studied. Results revealed that most of the qualitative characters contributed highest variation towards total divergence as they are significantly varies among the genotypes (Table 3).Venkatesh *et al*. (2016); Saini *et al*. (2020) were also reported that 100 seed weight contributed maximum towards diversity in their study.

Occasionally breeder needs to refine a specific trait of a variety for improvement which is diversely suitable. Cluster means for 21 traits of all the 10 clusters were presented in the Table 4. Clusters VI, VII, VIII, IX and X had recorded desirable cluster mean values for yield and quality contributing characters like days to maturity, number of primary branches per plant, number of secondary branches per plant, number of mature pods per plant, number of immature pods per plant, pod yield per plant, kernel yield per plant, sound mature kernel per cent, shelling percentage, 100 seed weight, protein content, free amino acids, total soluble sugars, palmitic acid content, stearic acid content, oleic acid content, linoleic acid content and oleic linoleic acid ratio. Therefore, intercrossing of genotypes included in these clusters could be effective for creating variability in the respective traits and improving their justification for enhancing peanut production.

Table 1: Clustering pattern of 65 peanut genotypes by Tocher's method.

Cluster number	Number of genotypes	Name of genotypes
I	3	ICGV 12266, ICGV 171304, ICGV 171334
II	7	ICGV 11321, ICGV 11353, ICGV 171341, ICGV 05182, ICGV 171436, ICGV 171376, ICGV 171363
III	6	K 1578, K 1643, K 1799, K 2075, K 1735, ICGV 171277
IV	28	ICGV 171285, ICGV 171309, ICGV 16326, ICGV 171401, ICGV 171307, ICGV 171305, ICGV 01369, ICGV 10237, ICGV 98432, ICGV 03133, ICGV 171274, ICGV 171346, ICGV 171377, ICGV 16330, ICGV 06211, ICGV 15366, ICGV 171276, ICGV 15364, ICGV 06229, ICGV 171278, ICGV 171371, ICGV 98412, ICGV 10209, ICGV 99105, ICGV 93058, ICGV 92160, ICGV 00440, ICGV 171385
V	12	K 1501, K 1574, K 1736, Nithya haritha, ICGV 00441, ICGV 10213, Kadiri 8 bold, Kadiri 7 bold, K 1924, ICGV 06214, ICGV 95165, ICGV 11310
VI	1	ICGV 12218
VII	1	ICGV 86564
VIII	4	ICGV 02249, ICGV 05200, ICGV 94215, ICGV 06188
IX	2	ICGV 171002, ICGV 171004
X	1	ICGV 03137

Table 2: Average intra and inter D^2 values among 10 clusters with 65 peanut genotypes.

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	40.88									
II	105.57	80.72								
III	285.67	294.38	120.34							
IV	178.96	201.95	379.64	239.73						
V	544.67	397.77	520.61	509.64	358.64					
VI	183.14	375.40	470.72	338.69	913.17	0.00				
VII	127.42	232.88	351.37	314.91	654.73	269.81	0.00			
VIII	360.82	533.12	621.08	448.94	1035.27	320.11	517.91	508.58		
IX	7868.91	8396.00	8186.27	8339.81	9751.07	6883.74	7977.68	7675.51	642.23	
X	2836.41	2838.41	3103.18	2409.16	2646.98	2522.90	3409.40	2380.83	10781.20	0.00

Table 3: Contribution of different characters towards divergence in 65 peanut genotypes.

Sr. No.	Character	Contribution (%)	Times Ranked 1st
1.	Days to 50 % flowering	0.14	3
2.	Days to maturity	0.48	10
3.	Plant height (cm)	0.0	0
4.	Number of primary branches per plant	0.0	0
5.	Number of secondary branches per plant	0.05	1
6.	Number of mature pods per plant	0.0	0
7.	Number of immature pods per plant	0.0	0
8.	Pod yield per plant (g)	1.01	21
9.	Kernel yield per plant (g)	0.63	13
10.	Sound mature kernel per cent	2.60	54
11.	Shelling percentage	0.14	3
12.	100 seed weight (g)	13.85	288
13.	Oil content (%)	0.0	0
14.	Protein content (%)	0.38	8
15.	Free amino acids (μg g^{-1})	22.07	459
16.	Total soluble sugars (%)	11.68	243
17.	Palmitic acid content (%)	0.05	1
18.	Stearic acid content (%)	1.30	27
19.	Oleic acid content (%)	1.10	24
20.	Linoleic acid content (%)	41.11	885
21.	Oleic linoleic acid ratio	3.37	70

Table 4: Mean values of 10 clusters for different kernel yield traits estimated by Tocher's method among 65 peanut genotypes.

Sr. No.	Character	Cluster number									
		I	II	III	IV	V	VI	VII	VIII	IX	X
1.	Days to 50 % flowering	28.00	28.00	35.92	31.77	34.04	37.00	32.50	33.50	33.75	36.00
2.	Days to maturity	123.00	122.29	124.00	120.39	121.13	120.00	123.50	121.00	125.00	118.50
3.	Plant height (cm)	23.19	25.19	16.10	25.09	20.38	25.09	29.25	21.98	20.67	23.66
4.	Number of primary branches per plant	5.40	5.03	5.72	5.17	5.54	5.65	5.07	5.43	6.17	5.83
5.	Number of secondary branches per plant	3.91	3.79	4.82	4.32	4.69	5.35	4.93	4.51	4.57	4.78
6.	Number of mature pods per plant	14.74	13.60	12.90	14.93	13.62	16.11	16.04	15.80	25.10	11.23
7.	Number of immature pods per plant	5.97	4.68	4.62	5.95	5.99	6.25	7.76	4.59	11.25	2.67
8.	Pod yield per plant (g)	19.95	21.18	14.83	21.61	18.28	20.93	19.48	22.82	22.41	15.90
9.	Kernel yield per plant (g)	13.44	11.91	8.82	13.34	11.30	15.74	16.15	15.69	15.84	9.49
10.	Sound mature kernel per cent	83.60	78.01	79.48	83.18	82.79	81.46	89.09	87.40	77.92	88.90
11.	Shelling percentage	68.16	59.84	66.98	64.94	66.49	74.81	73.87	66.98	66.21	66.71
12.	100 seed weight (g)	94.40	91.31	47.58	97.21	64.81	86.29	107.97	63.65	63.50	101.24
13.	Oil content (%)	46.22	46.38	45.93	46.32	46.13	46.73	50.37	44.37	45.56	46.13
14.	Protein content (%)	28.71	27.99	27.15	28.41	28.28	26.64	26.40	29.66	28.43	29.01
15.	Free amino acids (µg g^{-1})	0.58	0.50	0.55	0.80	0.73	0.93	0.40	1.07	0.57	3.49
16.	Total soluble sugars (%)	7.18	6.64	13.36	7.43	6.30	5.90	4.66	9.89	7.36	3.21
17.	Palmitic acid content (%)	9.35	8.92	8.77	8.83	9.31	9.56	7.55	8.91	5.91	8.49
18.	Stearic acid content (%)	2.80	2.91	3.04	3.05	3.03	3.64	2.83	2.86	2.67	3.05
19.	Oleic acid content (%)	57.58	54.79	54.52	54.89	50.16	59.39	48.80	57.05	78.85	53.49
20.	Linoleic acid content (%)	26.11	28.46	27.56	27.92	32.92	22.52	24.64	24.45	3.28	32.45
21.	Oleic linoleic acid ratio	2.21	1.93	1.98	1.99	1.54	2.64	1.98	1.65	24.50	1.65

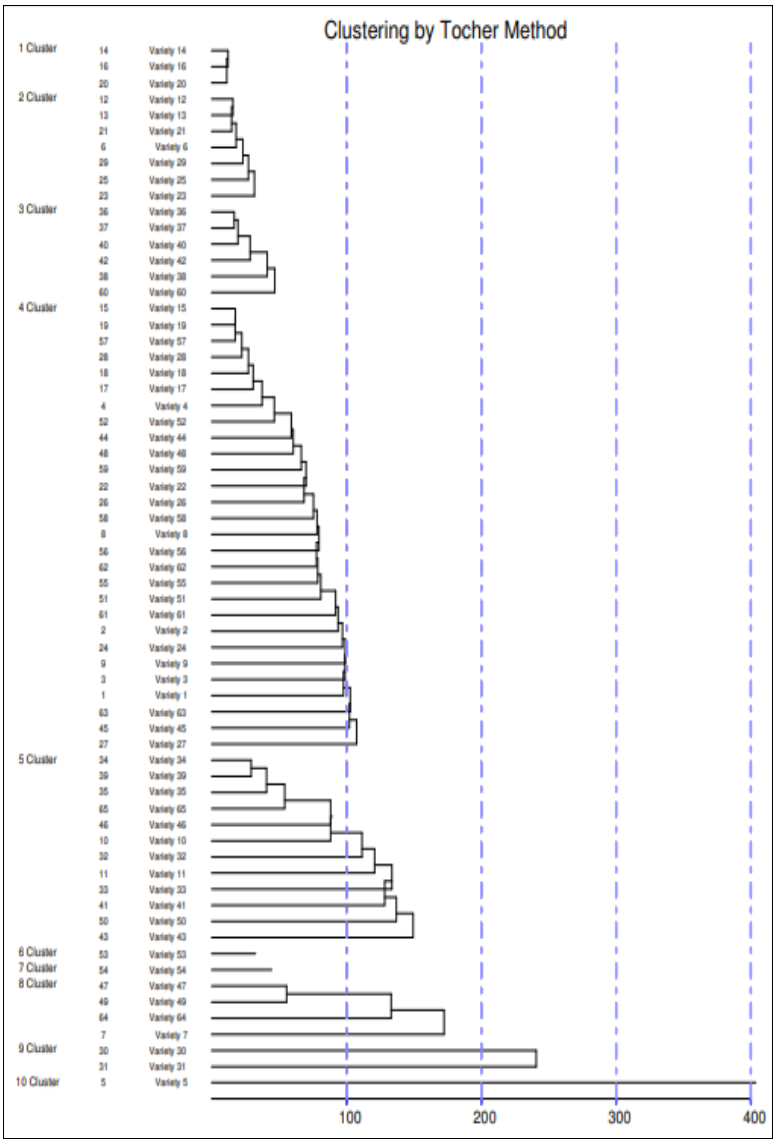

Fig. 1. Dendrogram showing relationship among 65 peanut genotypes in 10 clusters based on D^2 values.

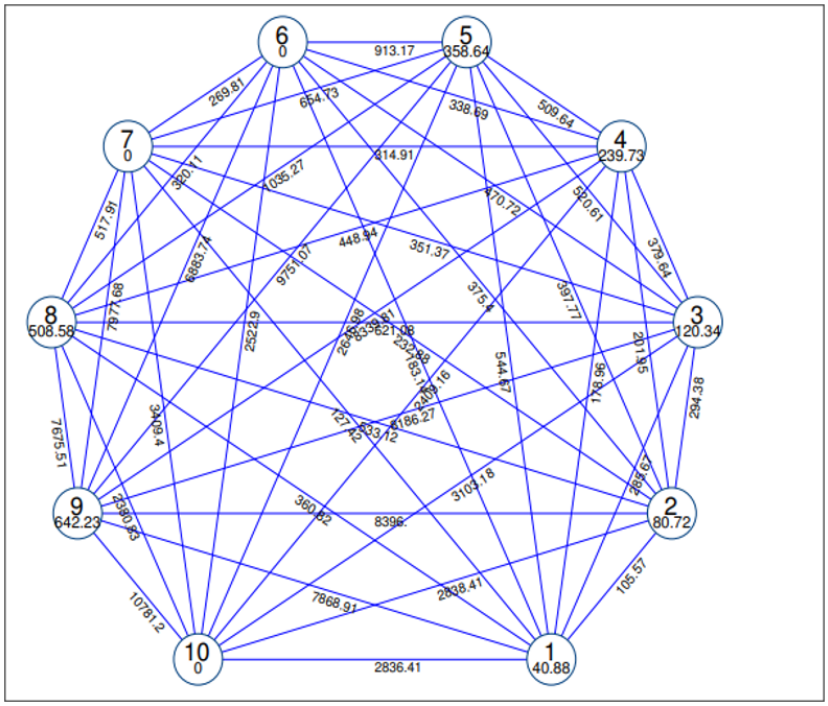

Fig. 2. Intra and inter cluster distances of 65 peanut genotypes in 10 clusters based on dendrogram.

CONCLUSIONS

It is recommended that the character with highest contribution towards divergence should be given significance in selection of parents for hybridization programme. In view of the cluster distances and cluster means in the current examination, importance should be given to crosses between genotypes belonging to cluster IX and cluster X in order to get transgressive segregants. Genotypes namely, ICGV 171004 and ICGV 171002 recorded significantly very high oleic content and so, these genotypes may be used as sources for increasing of oleic acid in peanut lines in future breeding programmes.

Acknowledgement. Authors are thankful to Acharya N.G. Ranga Agricultural University (ANGRAU) and ICRISAT for providing required facilities. Also, special thanks to Department of Genetics and Plant Breeding, Agricultural College, Bapatla.

Conflict of interest. None.

REFERENCES

Deepthi, K., John, K., Bharathi, D. and Sudhakar, P. (2022). Genetic variability studies in large seeded genotypes of peanut (*Arachis hypogaea* L.). *Biological Forum–An International Journal*, *14*(2), 1146-1151.

FAO (2019). Food and agricultural organization statistical database available at www.faostat.org.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of National Institute of Science*. India, *12*, 49-55.

Palanisingh, V., Vijayalakshmi, R., Sathishkumar, R. and Palanichamy, V. (2020). Groundnut exports of India direction and trends. *International Journal of Scientific and Technology Research*, *9(6)*, 397-400.

Rahman, M. H., Sinha, P. K. and Basu, M. S. (1995). Birsa Bold 1, a promising new confectionery variety of groundnut. *International Arachis Newsletter*, *15*, 12.

Rao, C. R. (1952). Advanced Statistical Methods in Biometerical Research. *John Wiley and Sons Inc*., New York.

Ravikumar, D. (2005). Genetic divergence studies in groundnut (*Arachis hypogaea* L.). *M.Sc. (Ag.) Thesis*, Acharya N.G. Ranga Agricultural University, Hyderabad.

Ravikumar, D., Reddisekhar, M., Rajareddy, K. and Ismail, S. (2012). Comparison of cluster formation by Mahalanobis' D^2 and metroglyph analyses in groundnut (*Arachis hypogaea* L.). *International Journal Applied Biology and Pharmaceutical Technology*, *30*(1), 395-399.

Sadasivam, S. and Manickam, A. (1961). Biochemical methods for Agricultural Sciences, *Wiley Eastern Limited*, New Delhi, 187-188.

Saini, H., Sharma, M. M. Saini, L. K., Solanki, K. L. and Singh, A. G. (2020). Genetic divergence analysis in groundnut (*Arachis hypogaea* L.). *International Journal of Chemical Studies*, *8*(1), 1781-1784.

Suneetha, N. (2007). Morphological and RAPD based genetic diversity studies among released cultivars and pre-release cultures of groundnut (*Arachis hypogaea* L.). *M.Sc. (Ag.) Thesis*, Acharya N.G. Ranga Agricultural University, Hyderabad.

Venkatesh, K., Rajesh, A.P., Srinivas, T. and Umamaheswari, P. (2016). Assessment of genetic diversity for kernel yield and quantitative traits in drought tolerant groundnut genotypes. *Electronic Journal of Plant Breeding*, *7*(1), 29-36.

How to cite this article: Suresh Gali, D.L. Reddy, A. Prasanna Rajesh, K. John, P. Sudhakar and V. Srinivasa Rao (2023). Genetic Divergence analysis in Confectionery Peanut (*Arachis hypogaea* L.). *Biological Forum – An International Journal, 15*(11): 218-222.