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Research Note

Genetic diversity studies in groundnut genotypes (*Arachis hypogaea* L.)

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Abstract
The present study was done to study the extent of diversity among the released and popular varieties of India and advanced cultures in groundnut. D^2 analysis for 15 characters resulted in the formation of nine clusters among the 30 genotypes studied. Highest intra-cluster distance was recorded for cluster VI followed by III, V, II and VII. Maximum inter-cluster distance was recorded between clusters VIII and IX followed by between clusters III and IX and between clusters VII and VIII. Based on mean performance, intra and inter-cluster distance, the genotypes of cluster VI (ALR 1 and COG0539) could be used for increasing the shelling per cent, oil content, pod yield / plant and no. of primary branches / plant. The genotypes in cluster III (CO 1, COG0549 and BSR 2) can be used for improving number of mature pods/ plant, hundred kernel weight, leaf area index and cluster VIII (JL 24) for total biomass and kernel yield / plant for trait based improvement programme.

Keywords : Groundnut, Diversity, D^2 analysis, Intra and inter cluster distance

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop of the world. It contains 48-50 *per cent* oil, 25-28 *per cent* easily digestible protein, 10-20 *per cent* carbohydrates and provides 564 k cal. of energy for every 100 g of kernel. Also, groundnut is a rich source of many micronutrients and health improving components, like minerals, antioxidants, vitamins, some biologically active polyphenols, flavonoid and isoflavones (Janila *et al.,* 2013). Groundnut is cultivated in an area of 27.66 m. ha. in the global level. In India, groundnut covering an area of 5.80 m ha. but its productivity is low (1631 kg/ha) when compared to the USA (4254 kg/ha), China (3906 kg/ha) and Argentina (3498 kg/ha) (FAO, 2020). In increasing the crop productivity, it is essential to evolve a genotype with fairly high kernel yield potential than the cultivated varieties. One of the major steps in developing genotypes with high yield potential in groundnut is to collect and evaluate diverse germplasm. The knowledge on genetic diversity in any crop is essential in order to design breeding programmes for high yield potential. Understanding of the available genetic variability in any crop will help in the selection of superior plants with diverse genetic background which will help in the crop improvement programme.

Because of highly self pollinated nature of groundnut, this crop has very narrow genetic base stressing the need for creation of more variability. Knowledge of genetic and phenotypic diversity is essential to identify the genotypes with similar genetic background for conserving, evaluating, and utilizing the genetic resources for pre-breeding and crop improvement (Franco *et al.*, 2001). Availability of diverse plant genetic resources provides an opportunity for plant breeders to evolve new and improved cultivars with desirable characteristics. Hence the present study was undertaken to study the diversity among the

groundnut genotypes for utilizing the genetically diverse sources for groundnut improvement.

The experimental material consisted of thirty varieties of groundnut released from various states of India (**Table 1**). The crop was raised in randomized block design with two replications during *Rabi*, 2021-22 at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore. The data was observed for fifteen characters, *viz.* plant height(cm), no. of primary branches / plant, days to first flowering, no, of flowers in main stem, total no. of pods / plant, no. of mature pods / plant, total biomass / plant(g), 100 kernel weight (g), shelling percent, oil content (percent), SPAD chlorophyll index, Leaf Area Ratio (cm^2g^{-1}), Leaf Area Index, pod yield / plant(g) and kernel yield / plant(g). In each replication, five plants in each of the genotype were randomly selected and observed. The mean values were used for further analysis. The recommended package of practice was adopted to raise a good crop.

Using the statistical method suggested by Fisher (1918), the mean value of the recorded data was subjected to analysis of variance (ANOVA). Multivariate analysis of D^2 was performed for all fifteen characters studied as suggested by Mahalonobis (1936) and clusters were formed by following the Ward (1963) method.

Prior knowledge about the nature and extent of genetic diversity present in the available genetic resources will help the plant breeder in identifying the most diverse parents which in turn is expected to produce the genotypes

Table 1. Details of groundnut genotypes with parentage

S. No.	Name of the genotypes	Pedigree
1	ALR 1	POL-2 × PPG-4
2	ALR 2	Selection from ICGV-86011
3	ALR 3	(R 33-1 × ICGV-68) × (NCAc-17090 × ALR-1)
4	BSR 1	ICGV-44 × (Robut-33-1 × NCAc-2821)
5	BSR 2	VRI-2 × TVG-0004
6	CO 1	Ah-6279 ×TMV-3
7	CO 2	EMS mutant variety of Pollachi-1
8	CO 3	VRI-3 × JL-24
9	CO(Gn)4	TMV-10 × ICGS-82
10	CO(Gn)5	Multiple cross derivative
11	CO 7	ICGV-87290 × ICGV-87846
12	COG0539	CO 7 × ICGV 03042
13	COG0549	GG2 × ICGV 00203
14	GG 7	S 206 x FESR 8-1-9-B-B
15	GG 20	GAUG-10 x R-33-1
16	GJG 33	(ICGV 92069 x ICGV 93184)
17	GPBD 4	KRG-1 × ICGV-86855
18	JL 24	Selection from EC-94943
19	K9	Kadiri-4 x Vemana
20	TAG 24	Selection from TGS-2 × TGE-1
21	TMV 1	Selection from west African variety ‘Saloum’
22	TMV 2	Selection from ‘Gudiyatham’
23	TMV 13	Selection from Pollachi red
24	TMV 14	VRI-6 × R 2001-2
25	VRI 2	JL-24 × CO-2
26	VRI 3	J-11 × R 33-1
27	VRI 4	VG-5 × NCAc-17090
28	VRI(Gn)5	CG-26 × ICGS-44
29	VRI(Gn)6	ALR-2 × VG-9513
30	VRI 8	ALR 3/AK 303

with high vigour and yield (Kumari and Singh 2015; Reddy, 2017). Information on already existing genetic diversity is the basic need of any crop improvement program so as to explore for more diverse genotypes or to make use of the available resources for increasing the yield of any crop (Bhakal and Lal, 2015). The significance in treatment mean square of the present study indicated the presence of variability among the genotypes for most of the characters, except days to fifty percent flowering, number of flowers in main stem, leaf area ratio **(Table 2**) which showed the presence of considerable variation among the groundnut genotypes used for the traits studied. The intra-cluster distance was lesser than the inter cluster distance, indicating the greater diversity present among the genotypes studied as reported by Yaikhom *et al.* 2015. Hence by utilizing the elite genotypes from the diverse clusters as parents for hybridization programme, it would generate promising segregants in filial generations, which was earlier mentioned by Saritha *et al.* (2018).

Based on the observed magnitude of the D^2 value (**Table 3**), the thirty entries were grouped into nine clusters based on Tocher's cut off value. Among the nine clusters, Cluster I was the largest with 9 genotypes and thus may have similar genetic background due to unidirectional selection pressure for pod yield and other contributing traits. Cluster III and V had three genotypes each. Clusters VI and VII possessed two genotypes each. Cluster VIII and IX were the smallest and solitary ones. Though the genotypes, VRI 3 and GG 20 having the common parent R 33-1 are grouped in cluster 1 and CO

Table 2. ANOVA for fifteen characters studied in groundnut genotypes

Source of variation	Mean sum of squares		
	Replication	Entries	Error
df	1	29	29
Plant height (cm)	232.06	32.42*	198.50
Number of primary branches / plant	1.41	5.76**	23.96
Days to 50% flowering (days)	17.15	17.95	0.26
Number of flowers in main stem	23.19	2.93	15.73
Total number of pods / plant	63.65	10.64*	1.49
Number of mature pods / plant	50.05	11.74*	32.41
Total biomass per plant (g)	1.30	5.65*	1.14
Hundred kernel weight (g)	740.6	199.3**	1.52
Shelling per cent	9.23	44.30**	2325.36
Oil content (%)	4.229	177.28**	9747.31
SPAD chlorophyll Index	51.56	421.76	35.29
Leaf Area Ratio (cm^2/g)	209.92	55.13	0.03
Leaf Area Index	5.34	31.54**	36.42
Pod yield per plant (g)	14.27	23.51**	37.08
Kernel yield per plant (g)	57.62	3.25*	10.19

* Significance at 5% level ** Significance at 1% level

Table 3. Clustering of genotypes based on D^2 analysis in groundnut

Clusternumber	Number ofentries	Name of the entries
I	9	CO 7, TMV 14, VRI 3, TMV 13, VRI(Gn) 5, GG 20, GJG 33, GPBD 4, ALR 2.
II	5	CO(Gn) 4, VRI 2, BSR 1, CO 3, CO 2.
III	3	CO 1, COG0549, BSR 2.
IV	4	VRI 4, TMV 1, GG 7, TAG 24.
V	3	ALR 3, K 9, CO(Gn) 5.
VI	2	ALR 1, COG0539.
VII	2	VRI 8, TMV 2.
VIII	1	JL-24
IX	1	VRI(Gn) 6

2 one of the parent of VRI 2 in cluster II, new genotypes developed by using old and popular genotypes as one of the parent are not grouped under the same cluster. For example, CO 3 having the parentage of VRI 3 x JL 24, in which, CO 3, VRI 3 and JL 24 were grouped in cluster II, I and VIII respectively. Also, CO 7 is one of the parents of COG 0539, in which CO 7 and COG 0539 were grouped in cluster I and VI respectively. Similarly, JL 24 and CO 3, VRI 3 and CO 3 were grouped in different clusters. Hence the parentage, geographical distance between the varieties were not related to the genetic divergence as the varieties from same source grouped in different clusters as well as entries from different sources were clustered in same group. This was earlier confirmed by Islam *et al*. (2005) and Namrata *et al*. (2018).

When the mean values of different traits from different clusters are considered (**Table 4**), the genotypes in cluster III *i.e.,* CO 1, COG 0549 and BSR 2 recorded the highest mean performance for no. of pods / plant (14.26), no. of mature pods / plant (13.23) , hundred kernel weight (60.51) and Leaf Area Index (5.79). This was followed by cluster VI for shelling percent (53.84), oil content (52.75) and pod yield (15.59) and cluster VIII for days to fifty percent flowering (28.0), biomass (65.78) and kernel yield per plant (6.58). Hence trait-based selection could be done for the entries from different clusters to get desirable transgressive segregants upon hybridization for making effective selection.

From the inter and intra-cluster distance between different clusters (**Table 5**), the maximum intra-cluster distance was recorded for cluster VI followed by III and V. Hence, the genotypes falling in these clusters are more diverse among them. Maximum inter-cluster distance was recorded between clusters VIII and IX followed by between cluster III and IX and between cluster VII and VIII. Hybridization of the genotypes from the above clusters would increase heterosis and increase variability in the segregating generations. As the clusters VIII and IX were having solitary genotypes, JL 24 and VRI(Gn) 6 respectively and were found to have more inter cluster distance with many other clusters based on the fifteen traits observed, and hence these two genotypes can

Table 4. Mean performance of clusters for fifteen traits in groundnut

Cluster	PH	NB	DFF	NF	NP	NMP	BM	HKW	SP	Oil	SPAD	LAR	LAI	PY	KY
I	22.99	6.96	29.00	36.00	10.97	9.82	42.93	39.44	49.77	48.41	34.40	40.16	4.12	11.05	5.51
II	27.39	5.66	29.40	35.66	11.58	9.66	46.37	53.72	48.24	45.68	34.79	30.69	3.43	12.01	5.35
III	27.22	7.13	29.00	35.33	**14.26**	**13.23**	56.37	**60.51**	48.87	47.82	34.85	43.98	**5.79**	14.22	6.53
IV	23.86	7.95	32.50	**36.25**	9.77	8.50	40.27	40.96	52.98	47.07	33.87	36.44	3.83	9.87	5.24
V	27.22	6.23	**28.00**	32.66	9.20	8.36	27.97	40.38	52.90	50.35	33.85	35.77	2.57	9.23	4.85
VI	23.28	**10.0**	31.00	34.00	11.95	11.00	52.26	38.09	**53.84**	**52.75**	38.72	39.02	4.93	**15.59**	6.11
VII	27.29	5.55	33.00	34.45	6.70	5.55	30.33	49.97	48.84	42.37	**38.83**	44.81	3.80	6.76	3.25
VIII	27.33	6.80	**28.00**	34.00	13.00	11.70	**65.78**	44.21	51.60	50.73	32.41	28.80	4.21	12.80	**6.58**
IX	**19.15**	5.60	33.00	33.60	10.60	7.70	26.55	34.50	53.11	49.00	27.61	**48.76**	3.81	7.75	4.05

PH - Plant Height(cm), NB- No. of primary branches / plant, DFF- Days to 50% flowering, NF- No. of flowers in main stem, NP- Total no. of pods / plant, NMP- No. of mature pods / plant, BM- Total biomass / plant (g), HKW- Hundred kernel weight (g), SP- Shelling percent, Oil- Oil content (Percent), SPAD- SPAD Chlorophyll index, LAR- Leaf Area Ratio (cm^2g^{-1}), LAI- Leaf Area Index, PY - Pod yield / plant (g), KY- Kernel yield / plant (g).

Table 5. Intra (diagonal) and inter-cluster distance in groundnut

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**43.51**	99.17	149.59	58.22	96.76	115.89	134.75	126.51	151.74
II		**61.92**	92.31	110.73	152.41	191.39	121.50	144.65	232.63
III			**71.11**	175.13	280.02	166.78	237.86	87.89	407.82
IV				**55.73**	102.40	117.65	99.41	177.23	126.74
V					**66.68**	250.81	95.90	314.07	83.10
VI						**82.71**	267.37	112.41	330.81
VII							**58.73**	347.18	107.64
VIII								**0.00**	437.61
IX									**0.00**

be utilized for the crop improvement programme. The closest proximity was found between cluster I and V followed by III and VIII, indicated that the genotypes in these clusters slightly differ from one another. Therefore, hybridization among them might not provide the intended level of genetic diversity in future generations.

From this study, based on mean performance, inter and intra-cluster distance, it was found that the genotypes from cluster VI (ALR 1 and COG0539) could be used for increasing the shelling per cent, oil content, pod yield / plant and no. of primary branches / plant. The genotypes in cluster III (CO 1, COG0549 and BSR 2) could be utilized for improving total no. of pods / plant, number of mature pods / plant, hundred kernel weight, leaf area index and cluster VIII (JL 24) for enhancing total biomass and kernel yield / plant for trait based improvement programme.

REFERENCES

Bhakal, M., Lal, G.M., 2015. Studies on Genetic Diversity in Groundnut (*Arachis hypogaea* L.) Germplasm. *Journal of Plant Science Research* **2(2)**, 128.

FAOSTAT (2020). Food and Agriculture Organization of the United Nations. http://www.fao.org/faostat/en/.

Fisher, R.A., 1918. The correlations among relatives on the supposition of Mendelian inheritance. Transactions Royal Society, Edinburg, **52**, 399–433. [Cross Ref]

Islam, M.T., Alam, S., Islam, M.Z., Hossain. M.K., 2005. Genetic variability and diversity of groundnut (*Arachis hypogaea* L.) *The Agriculturist* **3(1&2)**, 96-103.

Janila, P, S Nigam, MK Pandey, P Nagesh, and RK Varshney. 2013. “Groundnut improvement: use ofgenetic and genomic tools.” *Frontiers in plant science* 4:23. [Cross Ref]

Kumari, S., Singh, S.K., 2015. Assessment of genetic diversity in promising finger millet (*Eleusine coracana* L.) genotypes. *The Bioscan* **10(2)**, 825–830.

Mahalonobis, P.C., 1936. A statistical study at chinese head measurement. *Journal of Asiatic Society of Bengal* **25**, 301–377.

Namrata, Hemlata Sharma, Prashant Bisen, Bhumica Singh and Surbhi Jain. 2018. Assessment of Genetic Diversity Among Groundnut (*Arachis Hypogaea* L.) Genotypes. *International Journal of Bio-resource and Stress Management.* **9(3)**:383-386. [Cross Ref]

Reddy, A.L., Reddy, C.M.M., Srinivas, T., 2017. Assessment of multivariate analysis for kernel yield and yield component traits in drought tolerant groundnut genotypes. *Plant Archives* **17(2)**, 985–987.

Saritha, K., Vasanthi, R.P., Shanthi Priya, M. and Latha P. 2018. Genetic divergence analysis in groundnut (*Arachis hypogaea* L.) *Electronic Journal of Plant Breeding* 9**(4)** : 1355-1361. [Cross Ref]

Ward, J.H., 1963. Hierarchical grouping to optimize an objective function. *Journal of American statistical Association* **58**, 236–244. [Cross Ref]

Yaikhom Vivekananda, Pramesh Khoyumthem and Brajendra Singh, N. 2015. Genetic divergence analysis in groundnut (*Arachis hypogaea* L.) *Electronic Journal of Plant Breeding* **6(1)** : 315 - 317