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Genetic Diversity Analysis in Groundnut (*Arachis hypogaea* L.) Genotypes Employing Mahalanobis D^2 statistic

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Abstract

Genetic divergence among 35 genotypes of groundnut (*Arachis hypogaea* L.) was estimated by Mahalanobis D^2 statistics during *Kharif* - 2022 at the Instructional Farm, College of Technology and Engineering, Maharana Pratap University of Agriculture and Technology, Udaipur for thirteen characters. Mean Square for genotypes was found significant for all the characters, indicated the presence of adequate variability among the genotypes. Genotypes were grouped into XIII clusters. Cluster I had maximum number of genotypes *i.e.*, 19 genotypes, cluster III, IV and V each had 2 genotypes, whereas the remaining clusters *i.e.*, cluster VI, VII, VIII, IX, X, XI, XII, XIII, had only one genotype in each cluster. The largest intra-cluster distance was found for cluster V (6.90), followed by cluster IV (6.75). The largest inter-cluster distance was between clusters XIII and X (15.86), which were followed by clusters XI and VIII (15.25). This indicated that the genotypes in these clusters (UG-239, UG-231, UG-225, and UG-243, respectively) had a diverse genotype and could be used in a hybridization programme to increase groundnut yield. The genotype included in the diverse clusters can be used as promising parents for hybridization programme to obtain high heterotic response and thus better segregants in groundnut. The genotypes UG-220, UG-238, UG-239, UG-242, JL-501, and PM-3 were determined to be superior based on this investigation.

Key words *: Genetic divergence, cluster analysis, D^2 analysis, groundnut.*

Introduction

Groundnut is an essential oilseed legume primarily cultivated in Asia, Africa and America and it is easily cultivated in semi-arid tropics. In India, it is considered as “king of oilseeds.” Groundnut was originated from Brazil and it was popularly known as peanut in America and it is well known as Mungphali in India. Groundnut, being an oilseed crop, contains 40 to 53 per cent oil and 24 to 36 per cent protein content in kernels. Also, groundnut is a good source of calcium, phosphorus, iron, zinc and boron. Groundnuts also contain vitamin E and small amounts of the vitamin B complex.

Groundnut occupies first position in terms of area and second position in terms of production after soybean in world. Groundnut is cultivated globally in over 29.6 million hectares with a yield of 48.8 million tons. China is the top producer of groundnut in the world with 17.5 million tons, while India is the second largest producer of groundnut with yield of 6.7 million tons. In India the area of groundnut cultivation during 2021-22 was 6.09 M. ha, production was 10.21 million tonnes with productivity of 1676 kg ha^{-1} (1).

India is the world’s leading producer of groundnut but its productivity is much lower than others. The production of cultivars via selection and hybridization demands a large quantity of resources for the use of available genetic diversity to adapt to diverse environmental circumstances. In plant breeding, genetic diversity plays an important role and it arises due to geographical separation or due to genetic barriers to cross ability. The evaluation of diversity is important to know the source of genes for particular trait within the available germplasm. So, it is essential to know the genetic diversity of the existing genotypes before undertaking any crop improvement programme. Therefore, the present study was carried out to estimate the nature and magnitude of genetic diversity present in a collection of 35 genotypes of groundnut.

Materials and Methods

Thirty five groundnut genotypes (including four checks) were used for this experiment which were obtained by AICRP on Groundnut, MPUAT, Udaipur. The experiment was laid out in Randomized Block Design with three replications during *Kharif* 2022 at the Instructional Farm, College of Technology and Engineering, Maharana Pratap University of Agriculture and Technology, Udaipur. Five rows per genotype were sown in a plot of 5.0m x 1.5m with inter and intra row spacing 30 x 10 cm and 5m row length. Another recommended agronomic practice for zone IVA was followed to raise a healthy crop.

Traits observed : Observations were recorded on plant basis, 5 individual plants were randomly selected for all the genotypes in each replication for all the characters *viz.*, number of branches per plant, plant height (cm), pods per plant, shelling percentage (%), sound mature kernel (%), dry pod yield per plant (gm), biological yield per plant

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Table-1 : Clustering pattern of different genotypes in different clusters.

Clusters	Number	Members/genotypes
I	19	UG-220, UG-221, UG-222, UG-223, UG-224, UG-226, UG-228, UG-229, UG-230, UG-233, UG-235, UG-236, UG-240, UG-241, UG-242, UG-259, UG-260, UG-261, UG-262
II	2	UG-219, UG-244
III	2	UG-232, TG37A
IV	2	UG-227, UG-263
V	2	UG-234, UG-238
VI	1	GG-7
VII	1	JL-501
VIII	1	UG-239
IX	1	UG-237
X	1	UG-231
XI	1	UG-225
XII	1	PM-3
XIII	1	UG-243

Table-2 : Mean values of different characters for 35 genotypes in thirteen clusters.

Cluster	Days to 50 per cent flowering	Days to maturity	Number of branches per plant	Plant height (cm)	Pods per plant	Shelling percent-age	100-Kernels weight (g)	Dry pod yield per plant(g)	Sound mature kernel (%)	Biological yield per plant(g)	Harvest index (%)	Oil content (%)	Protein content (%)
I	33.07	106.22	7.48	24.26	13.08	71.50	39.05	10.37	86.18	27.40	43.14	42.83	21.68
II	31.18	103.13	8.25	25.93	9.62	70.12	44.00	8.99	82.29	17.89	46.23	43.78	20.50
II	32.06	101.38	11.70	23.93	10.89	73.81	43.93	11.06	88.73	22.56	34.76	45.57	23.45
IV	31.47	97.41	6.42	23.17	13.52	68.04	37.89	10.55	83.24	26.51	51.16	41.51	23.17
V	31.86	98.42	6.12	21.43	9.51	71.48	40.55	14.95	88.63	26.62	38.03	42.89	21.06
VI	34.10	102.58	11.83	26.04	15.79	68.96	34.42	15.99	89.17	34.74	54.93	45.49	23.75
VII	32.37	101.35	10.50	18.00	20.44	69.37	44.79	16.76	89.97	37.26	48.26	42.38	22.49
VIII	32.78	107.23	7.83	22.62	22.93	72.46	35.67	13.13	78.72	34.43	37.58	42.95	22.71
IX	34.17	109.30	9.43	15.21	9.34	69.15	42.42	13.27	81.78	21.92	37.81	45.83	23.25
X	36.22	106.30	8.90	17.50	15.01	68.77	32.79	10.32	84.79	26.43	40.78	42.06	20.85
XI	31.65	101.26	5.23	21.59	7.02	65.40	45.16	7.50	88.01	14.78	33.31	42.31	21.42
XII	33.23	104.17	8.83	26.68	20.44	73.24	40.67	14.02	91.18	23.31	50.21	43.87	22.03
XIII	32.23	99.08	7.53	25.10	13.05	70.08	46.52	7.93	85.17	35.68	48.04	46.94	22.72

(gm), harvest index (%), oil content (%), protein content (%) except days to 50 per cent flowering, days to maturity and 100-kernel weight, which were recorded on plot basis. Shelling percentage, biological yield plant, harvest index were calculated by using formulas. Oil content was determined by the Soxhlet's Method (A.O.A.C., 1965) and average oil content in per cent was worked out, and for calculating protein content, nitrogen content of kernels was obtained by the standard Micro Kjeldahl method (2) then value of nitrogen obtained was converted to crude protein per cent by multiplying with a factor of 6.25 and average protein per cent was worked out. The mean data for all characters were computed for the statistical analysis.

Statistical analysis : The genetic divergence among 35 genotypes was estimated by Mahalanobis D^2 statistics (generalized distance) as suggested by (3). Based on the estimated inter-se genetic distances between the genotypes, the genetic divergence between various genotypes is calculated. The steps used to calculate D^2 values was according to Singh and Choudhary, 1985.

Results and Discussion

Genotypes under the study were divided into XIII clusters following Tocher's method (Rao, 1952). Cluster I had maximum number of genotypes *i.e.*, 19 genotypes (UG-220, UG-221, UG-222, UG-223, UG-224, UG-226, UG-228, UG-229, UG-230, UG-233, UG-235, UG-236, UG-240, UG-241, UG-242, UG-259, UG-260, UG-261, UG-262) followed by cluster II (UG-219, UG-244), III (UG-232, TG37A), IV (UG-227, UG-263) and V(UG-234, UG-238), each had 2 genotypes, whereas the remaining clusters *i.e.*, cluster VI, VII, VIII, IX, X, XI, XII, XIII, had only one genotype in each cluster presented in table-1.

The mean values for different characters in different clusters are given in table 2. The results revealed that the range for the divergence was highest for harvest index (%) followed by biological yield per plant, pods per plant, 100-kernels weight, days to maturity, plant height, sound

Table-3 : Average intra and inter-cluster distance based on corresponding D^2 values.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	6.68	8.40	8.30	8.74	9.12	8.99	10.60	8.03	8.89	9.02	9.74	8.05	9.84
II		3.45	8.34	9.64	11.95	11.05	11.27	11.00	10.08	10.38	8.50	8.60	11.15
III			4.68	11.00	9.24	8.71	10.38	9.42	8.47	12.34	11.71	9.43	10.46
IV				6.75	10.04	9.94	10.44	8.64	11.27	10.86	9.11	10.86	11.19
V					6.90	10.04	10.65	12.54	10.27	12.05	10.66	11.61	12.00
VI						0.00	8.22	12.70	9.03	8.49	14.88	8.75	10.93
VII							0.00	11.47	11.70	13.40	14.90	10.82	13.10
VIII								0.00	8.62	11.39	15.25	11.43	13.25
IX									0.00	9.76	9.27	14.23	11.70
X										0.00	8.85	12.95	15.86
XI											0.00	12.70	11.30
XII												0.00	13.31
XIII													0.00

Table-4 : Per cent contribution of each character towards total divergence.

S. No.	Characters	Contribution %
1.	Days to 50 per cent flowering	1.84
2.	Days to maturity	9.26
3.	Number of branches per plant	1.76
4.	Plant height (cm)	11.22
5.	Pods per plant	14.14
6.	Shelling percentage	2.66
7.	100-Kernels weight (g)	9.92
8.	Dry pod yield per plant(g)	4.14
9.	Sound mature kernel (%)	7.25
10.	Biological yield per plant(g)	12.44
11.	Harvest index (%)	23.92
12.	Oil content (%)	0.93
13.	Protein content (%)	0.53

mature kernel (%), dry pod yield per plant, shelling percentage, number of branches per plant, oil content, days to 50 per cent flowering and protein content.

The maximum intra-cluster distance was observed within cluster V (6.90) followed by cluster IV (6.75). The maximum inter-cluster distance was found between cluster XIII and cluster X (15.86) followed by inter cluster distance between cluster XI and cluster VIII (15.25). Table 3 shows the average intra and inter-cluster distance and these were calculated from the D^2 values, within and between the clusters, of the respective genotypes. Contribution of individual character towards divergence is given in table 4. The highest contribution was estimated for harvest index (%) (23.92), followed by pods per plant (14.14) and biological yield per plant (12.44), whereas protein content (0.53) contributed least towards total divergence. Dry pod yield per plant contributed only 4.14% towards total divergence. These finding are in close agreement to earlier reported (4, 5, 6, 7, 8, 9).

Conclusions

Geographical distance between the genotypes had no relation with the divergence genetically present among them. Genotypes from distantly situated clusters like cluster III and VIII could be used to produce the desirable transgressive segregants and selecting better genotypes for those characters which are having high mean values in these clusters for future groundnut improvement

programme. Cluster XIII and cluster X having highest inter-cluster distance; therefore, selection of parents should be done from these two clusters to get more variability and heterotic effect. Cluster XIII and cluster X having highest divergence between them so that they can be used in recombinant as well as heterotic breeding, whereas between cluster I and VIII lowest inter-cluster distance was found, indicates lesser divergent genotypes from each other.

References

1. Anonymous. 2022. Directorate of Economics and Statistics, Department of Agriculture and Cooperation, Govt. of India.
2. AOAC 1965. Official methods for oil analysis for association of Official Agricultural Chemists. 10th (Edn.). Washington, D.C.
3. Rao, C. R. 1952. Advanced Statistical Methods in Biotmetric Research. Edn. 1., John Willey & Sons, New York.
4. Dhakar, T.R., Hemlata, S. and Prashant, B. 2017. Genetic diversity analysis in groundnut (*Arachis hypogaea* L.) genotypes using D^2 statistics. *Indian Journal of Ecology*, **44**(4): 175-181.
5. Dudhatra, R.S., Viradiya, Y. A., Joshi, K.B., Desai, T.A. and Vaghela, G.K. 2022. Genetic divergence analysis in groundnut (*Arachis hypogaea* L.) genotypes. *Emergent Life Sciences Research*, **8**: 114-118.
5. Gantait, S., Gunri, S.K., Kundu, R. and Chatterjee, S. 2017. Evaluation of genetic divergence in Spanish bunch groundnut (*Arachis hypogaea* L.) genotypes. *Plant breeding and biotechnology*, ***5***(3): 163-171.
6. Mitra, M., Gantait, S. and Kundu, R. 2021. Genetic variability, character association and genetic divergence in groundnut (*Arachis hypogaea* L.) accessions. *Legume Research*, ***44***: 164-169.
7. Motasara, N., Sharma, H., Bisen, P., Singh, B., and Jain, S. 2018. Assessment of Genetic Diversity Among Groundnut (*Arachis hypogaea* L.). *International Journal of Bio-resource and Stress Management*, **9**(3): 383-386.
8. Joshi, D., Singh, P.B., Yadav, V., Pareek, V., Regar, H. and Mariyam, A. 2022. Diversity Analysis in Spanish Bunch Type Groundnut (*Arachis hypogaea* L.). *Frontiers in Crop Improvement,* **10**(11): 918-923.
9. Janila, P., Nigam, S.N., Pandey, M.K., Nagesh, P. and Varshney, R.K. 2013. Groundnut improvement: use of genetic and genomic tools. *Frontiers in plant science*, **4**: 23.
9. Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of National Institute of Sciences of India*, **2**: 49-55.
2. Lindner RC 1944. Rapid analytical method for some of the more common inorganic constituents of plant tissues. *Plant Physiology* **19**: 76–89.
13. Reddy, A.L., Reddy, C.M.M. and 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.
14. Singh, R.K. and Chaudhary, B.D. 1985. Biometrical Methods in Quantitative Genetics Analysis. Kalyani Publishers, New Delhi.