

Assessment of Genetic Diversity in Groundnut Genotypes: Identifying Promising Clusters Via Mahalanobis D² Analysis

Shrishti Srivastava¹, Soni Singh^{2*}, Ganesh Phatate¹ and Shiva Chaturvedi³

^{1,2}Department of Genetics and Plant Breeding, ITM University, Gwalior 474 001, M.P., India

³Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur 208 002, U.P., India

(Received 26 July, 2025; Accepted 23 September, 2025)

ABSTRACT

Groundnut (*Arachis hypogaea* L.) is a leguminous, annual crop also known as, king of oilseed crop as it contains 46% oil. Research was conducted on groundnut genotypes in Kharif season 2024 using randomized block design. Genetic diversity among 32 genotypes was estimated using Mahalanobis D² statistics. Genotypes were grouped into five clusters by Tocher's method. The maximum intra-cluster distance was observed for clusters IV (22.41) followed by cluster II (19.98) and cluster I (16.69). The maximum inter-cluster distance value was observed in between cluster IV and II. Therefore Nithya Haritha, Bheema, Tirupati, RG 559-3, Kadiri Leepakshi, GJG-32 will be efficient for hybridization program. The minimum inter-cluster distance recorded was recorded for cluster II and I which indicates lesser divergence in these genotypes. On the basis of cluster mean value of traits, selection of genotype which falls under cluster V will be better for yield enhancement.

Key words: Genetic diversity, Inter and intra-cluster distance, Hybridization, Divergence.

Introduction

Groundnut is an annual, self-pollinated crop that belongs to family Fabaceae. Botanically, groundnut is termed as *Arachis hypogaea* L. *Arachis* is divided into two sub-species i.e. *hypogaea* and *fastigiata* (Holbrook and Stalker, 2003). The cultivated groundnut is allotetraploid (AABB, 2n = 4x = 40) (Chen *et al.*, 2019) and have narrow genetic diversity (Gantait *et al.*, 2017). Groundnut is a legume crop mainly grown for its edible seeds and also referred as monkey-nut, peanut, goober it is native to South America. Peanut (*Arachis hypogaea* L.) is a Kharif crop

ranked fourth in the world among oilseed and it is grown for its high oil content i.e., 48% (Akram *et al.*, 2018). Pod yield in addition to being polygenically controlled, is also influenced by its component characters (Sravanti *et al.*, 2024). According to DA&FW (GOI), during the year 2023-24, India's total area under groundnut cultivation, 47.07 lakh ha and total production is 101.80 lakh tons. As per DA&FW (GOI), major groundnut producing states are Gujarat (46%), Rajasthan (20%), Madhya Pradesh (10%), Tamil Nadu (9%), Andhra Pradesh (3%).

The production of cultivars through selection and hybridization demands a large quantity of resources

(*Research Scholar, ²Faculty)

for the use of available genetic divergence for adaptation to unfavourable environmental conditions. A successful breeding program requires genetically diverse parents for creating novel and elite cultivars (Govindraj, 2015). Productivity and quality attributes have historically been the main criteria used to assess groundnut genetic diversity (Yadav *et al.*, 2014). Multivariate analysis based on Mahalanobis D² statistics (Mahalanobis, 2018) is a biometrical technique that measures the level of genetic divergence among genotypes (Suthar *et al.* 2023) and evaluates the contribution of various traits to the total divergence.

Materials and Method

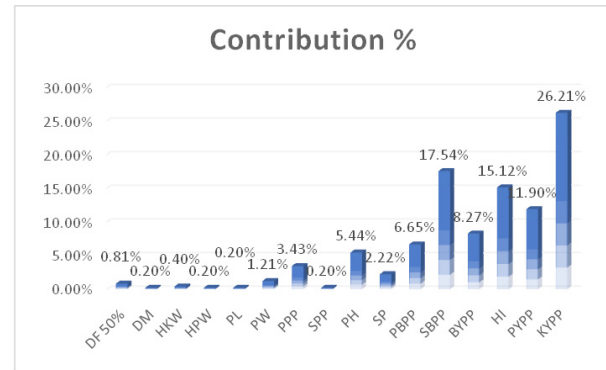
An experiment comprising 32 groundnut genotypes including two checks *i.e.*, GJG-32 and TAG-24 was conducted in a RBD with three replications at Crop Research Centre-1, Department of Genetics and Plant Breeding, School of Agriculture, ITM University, Sithouli, Gwalior during the *Kharif*-2024. Spacing maintained was 30 × 20cm. The soil of experimental site is sandy loam, red and light shallow soil with pH 5.5 and with an annual rainfall of 800 - 1000mm. In order to grow a healthy crop stand, the suggested set of procedures and plant protection measures were implemented on time and consistently. The study for genetic divergence was done using Mahalanobis D² statistics (Mahalanobis, 2018 and Rao, 1952). Genotypes were divided into several clusters via Tocher's method and D² statistics. Multivariate Statistical analysis based on Mahalanobis D² was performed by INDOSTAT.

Results and Discussion

Characters' contribution towards genetic divergence

The observations on character wise contribution towards genetic divergence (Fig. 1) depicts that kernel yield had highest contribution (26.21%) by ranking first 130 times followed by secondary branches per plant (17.54%) by 87, harvest index (15.12%) by 75 times, pod yield per plant (11.9%) by 59 times, biological yield per plant (8.27%) by ranking 41 times. The lowest contribution was observed for days to maturity (0.20%) by 1 time, hundred pod weights (0.20%) by 1, pod length (0.20%) by 1, seeds per pod (0.20%) by 1 time (Table 1). Similarly, higher contri-

bution by kernel yield and harvest index was reported by Dudhatra *et al.* (2022). Higher contribution for biological yield and harvest index was also observed in research done by Sharma *et al.* (2024). It has been recommended that the traits with the greatest contribution to divergence should be used in future hybridization programs.



DF- days to 50% flowering, DM- days to maturity, HKW- hundred kernel weight, HPW- hundred pod weight, PL- pod length, PW- pod width, PPP- number of pods per plant, SPP- seeds per pod, PH- plant height, SP- shelling percentage, PBPP- number of primary branches per plant, SBPP- number of secondary branches per plant, BYPP- biological yield per plant, HI- harvest index, KYPP- kernel yield per plant, PYPP- pod yield per plant.

Fig. 1. Contribution of traits towards genetic divergence

Table 1. Contribution of yield attributing traits towards genetic divergence in 32 genotypes of groundnut

Source	Times Ranked 1st	Contribution %
DF 50%	4	0.81%
DM	1	0.20%
HKW	2	0.40%
HPW	1	0.20%
PL	1	0.20%
PW	6	1.21%
PPP	17	3.43%
SPP	1	0.20%
PH	27	5.44%
SP	11	2.22%
PBPP	33	6.65%
SBPP	87	17.54%
BYPP	41	8.27%
HI	75	15.12%
PYPP	59	11.90%
KYPP	130	26.21%

Clustering by tocher's method

Assessment of genetic divergence is one of the primary objectives of a breeding program. The hybrid-

ization programme is believed to be effective as it brings together genetically distinct parents, which allows the heterotic expression and segregation potential of crosses. To study genetic diversity in 32 released genotypes of groundnut Mahalanobis (2018) D^2 statistics and clustering of genotypes were done based on D^2 values using Tocher's method (Rao, 1952) (Table 2). Based on D^2 analysis, 32 genotypes were grouped into five clusters (Fig. 2). Cluster I was largest consisting of 24 genotypes. Similar

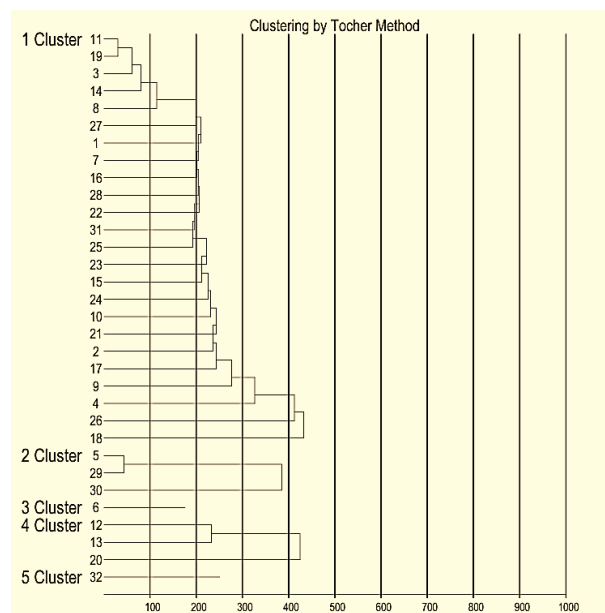


Fig. 2. Dendrogram based on tocher's method showing diversity among 32 genotypes of groundnut.

results were reported by Sukrutha *et al.* (2022) for consisting the largest number of genotypes (16) in cluster I. Cluster II and IV consists of three genotypes each respectively, cluster III and V consists of one genotype each.

Intra and Inter-cluster Distance

Intra-cluster distance ranged from 0 to 22.41. As mentioned in Table 3 the maximum intra-cluster distance was seen for clusters IV (22.41) followed by cluster II (19.98) and cluster I (16.69). While, minimum intra-cluster distance (zero) was observed for cluster III. The maximum inter-cluster distance value was observed between cluster IV and II (47.37) which shows that genotypes in these clusters are diverse and can be used in hybridization program and results in transgressive segregation (Bhakal *et al.* 2015). Cluster II and cluster I had the smallest inter-cluster distance (23.89), which depicts that genotypes which falls in these cluster are closely related. Similar results were reported in study by Zaman *et al.* (2011), Saritha *et al.* (2018) for inter-cluster distance being greater than the intra-cluster distance.

Cluster means for yield attributing traits

As shown in the Table 4, cluster I revealed high mean values for 100 kernel weight (32.36), 100 pod weight (13.54), pod length (15.84). Cluster II revealed high mean values for traits which included days to 50% flowering (29.33), days to maturity (30.67), pod width (4.33), plant height (30.33), shell-

Table 2. Cluster classification of 32 groundnut genotypes using tocher's method

Cluster no.	Genotypes	No. of genotypes
I	TAG-24, Kadiri-6, ITMU-Purulia, Kadiri-9, Kadiri-8, KDG-123, Dharini, TG-39A, Dheeraj, Kadiri Amravati, TG-26, TG-22, Kadiri Anantha, RG-456, Kurnool, Kadiri-7 Bold, RG-382, Tyagulu, Kadiri-3, TPT-3, RG-582, TPG-41, 26, RG-510	24
II	RG 559-3, Kadiri Leepakshi, GJG-32	3
III	Kadiri Haritandhra	1
IV	Nithya Haritha, Bheema, Tirupati-1	3
V	JL-24	1

Table 3. Average inter and Intra (diagonal) cluster distances between 5 clusters

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	16.69	23.89	24.32	37.59	28.36
Cluster II		19.98	35.12	47.37	29.09
Cluster III			0	43.36	37.66
Cluster IV				22.41	28.74
Cluster V					0

Table 4. Cluster means for quantitative traits in 32 groundnut genotypes

Cluster	DF 50%	DM	HKW	HPW	PL	PW	PPP	SPP
Cluster I	28.74	29.42	32.36	13.54	15.84	4.21	18.36	4.28
Cluster II	29.33	30.67	31.67	12.67	15.33	4.33	17.33	4.33
Cluster III	27.67	28.17	31.33	12.33	14.67	4.11	16.67	4.22
Cluster IV	28.44	29.33	31.78	12.56	15.44	4.22	18.44	4.33
Cluster V	28.67	28.89	32	12.89	15.56	4.19	18.78	4.33
Cluster	PH	SP	PBPP	SBPP	BYPP	HI	PYPP	KYPP
Cluster I	29.45	45.63	5.29	3.86	7.21	13.28	7.46	15.36
Cluster II	30.33	46.67	5.33	3.67	7.33	13.33	7.33	16.89
Cluster III	28.67	45	5.11	3.44	7.11	12.67	7.11	14.67
Cluster IV	29.33	45.89	5.22	3.78	7.22	13.11	7.33	22.22
Cluster V	29.56	46.33	5.44	3.89	7.44	13.44	7.56	24

ing percentage (46.67), In contrast seeds per pod shows high mean value of 4.33 in cluster II, IV, V. In cluster V high mean values for pods per plant (18.78), harvest index (13.44), biological yield plant⁻¹ (7.44), pod yield per plant (7.56), primary branches per plant (5.44), secondary branches plant⁻¹ (3.89) which resulted in highest kernel yield per plant. Selection of genotype JL-24 can be useful for enhancement in yield (Vaggar *et al.*, 2022).

Conclusion

Groundnut is self-pollinated crop with high oil content. Traits such as kernel yield per plant, followed by secondary branches per plant are highly contributing for genetic divergence. Genotypes in cluster I, II and V have high values of mean for more than a single trait. Genotypes with high inter cluster distances have divergence and can be used in hybridization programs. Therefore, Nithya Haritha, Bheema, Tirupati, RG 559-3, Kadiri Leepakshi, GJG-32 will be efficient for hybridization programs.

Acknowledgement

The author would like to thank all the committee members of this research for providing experiment materials and for guiding throughout the experiment.

Conflict of Interest- There is no conflict of Interest.

Source of Funding -No external sources of funding

References

Akram, N.A., Shafiq, F. and Ashraf, M. 2018. Peanut (*Arachis hypogaea* L.): A prospective legume crop to offer multiple health benefits under changing climate.

Comprehensive Reviews in Food Science and Food Safety. 17(5): 1325-1338. <https://doi.org/10.1111/1541-4337.12383>

Bhakal, M. and Lal, G.M. 2015. Studies on genetic diversity in groundnut (*Arachis hypogaea* L.) germplasm. *Journal of Plant Science & Research*. 2(2): 1-4.

Chen, X., Lu, Q., Liu, H., Zhang, J., Hong, Y., Lan, H. and Liang, X. 2019. Sequencing of cultivated peanut, *Arachis hypogaea*, yields insights into genome evolution and oil improvement. *Molecular Plant*. 12(7): 920-934. <https://doi.org/10.1016/j.molp.2019.03.005>

Department of Agriculture & Farmers Welfare Ministry of Agriculture & Farmers Welfare Government of India Krishi Bhawan, New Delhi-110 001 www.agriwelfare.gov.in

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. <https://doi.org/10.31783/elsr.2022.81114118>.

Gantait, S., Gunri, S.K., Kundu, R. and Chatterjee, S. 2017. Evaluation of genetic divergence in Spanish bunch groundnut (*Arachis hypogaea* Linn.) genotypes. *Plant Breeding and Biotechnology*. 5(3): 163-171.

Govindaraj, M., Vetriventhan, M. and Srinivasan, M., 2015. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics research international*. 2015(1), p.431487.

Holbrook, C.C. and Stalker, H.T., 2003. Peanut breeding and genetic resources. *Plant breeding reviews*, 22, pp.297-356.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Sankhyâ: The Indian Journal of Statistics, Series A*. 1936 (80): S1-S7.

Rao, C.R. 1952. Advanced statistical methods in biometric research. *John Wiley & Sons, Inc., New York, N. Y.* 390 pp.

Saritha, K., Vasanthi, R.P., Priya, M.S. and Latha, P. 2018. Genetic divergence analysis in groundnut (*Arachis*

- hypogaea* L.). *Electronic Journal of Plant Breeding*. 9(4): 1355-1361. <https://doi.org/10.5958/0975-928X.2018.00169.2>
- Sharma, R., Singh, P., Dashora, A., Mahla, P., Joshi, D. and Gupta, S. 2024. Genetic diversity analysis in groundnut (*Arachis hypogaea* L.) genotypes employing Mahalanobis D² statistic. *Frontiers in Crop Improvement*. 11: 775-778 <https://doi.org/10.13140/RG.2.2.28650.70080>
- Sravanti, K., Reddy, V.R., Mamatha, K., Shankar, M., Rani, V.D., Sujatha, M. and Goverdhan, M. 2024. Variability studies for yield and related traits in groundnut (*Arachis hypogaea* L.) genotypes. *International Journal of Advanced Biochemistry Research*. SP-8(12): 1377-1381 <https://doi.org/10.33545/26174693.2024.v8.i12Sq.3509>
- Sukrutha, B., Kumar, A.N. and Akkareddy, S. 2022. D² Analysis to Evaluate the Genetic Diversity of Peanut (*Arachis hypogaea* L.). *Agricultural Science Digest*. 1-6.
- Suthar, D.M., Patel, D.G., Patel, P. R. and Soni, N.V. 2023. Studies on variability for Yield and Yield Attributing Traits in Groundnut [*Arachis hypogaea* (L.)]. *Biological Forum – An International Journal* 15(11): 520-525.
- Vaggar, S., Kumar, U., Prasad, K., Yadav, L.M. and Sinha, B.M. 2022. Study of genetic divergence for yield and quality traits in cowpea [*Vigna unguiculata* (L.) walp.]. *Legume Research-An International Journal*. 45(4): 410-414.
- Yadav, S.R., Rathod, A.H., Shinde, A.S., Patade, S.S., Patil, C.N. and Vaghela, P.O. 2014. Genetic variability and divergence studies in groundnut (*Arachis hypogaea* Linn.). *International Journal of Agricultural Sciences* 10(2): 691-694
- Zaman, M.A., Tuhina-Khatun, M., Ullah, M.Z., Moniruzzamn, M. and Alam, K.H. 2011. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). *The Agriculturists*. 9(1-2): 29-36.
-