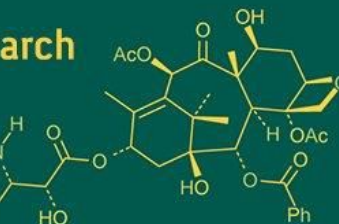
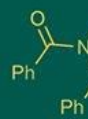


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(3): 18-25
www.biochemjournal.com
Received: 24-12-2025
Accepted: 30-01-2026

Darshini TK

Ph.D. Scholar, Genetics & Plant Breeding Department, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Sai Harini

Associate Professor, Genetics & Plant Breeding Department, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Konreddy Sathish

Assistant Professor, Genetics & Plant Breeding Department, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Gudla Mahesh

Assistant Professor, Department of Crop Physiology, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Mamata

Assistant Professor, Department of statistics, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Mahesh S Pujar

Research Associate, Genetics & Plant Breeding Department, ICRIAT, Patancheru, Hyderabad, Telangana, India

Dachani Sruthi

Assistant Professor, Genetics & Plant Breeding Department, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Corresponding Author:**Darshini TK**

Ph.D. Scholar, Genetics & Plant Breeding Department, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India

Genetic diversity and yield trait analysis in groundnut Germplasm based on DUS and multivariate approaches

Darshini TK, Sai Harini, Konreddy Sathish, Gudla Mahesh, Mamata, Mahesh S Pujar and Dachani Sruthi

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i3Sa.7794>

Abstract

Improving pod yield and kernel quality in groundnut requires systematic exploration of genetically diverse germplasm for key yield and developmental traits. Accordingly, this study evaluated Distinctness, Uniformity, and Stability (DUS), genetic variability, trait associations, and phenotypic diversity among 54 groundnut (*Arachis hypogaea* L.) germplasm accessions and two check varieties during the Summer and Kharif seasons of 2025 at Malla Reddy University, Hyderabad, Telangana, India. Seven DUS traits and eleven yield-related traits were assessed using an alpha-lattice design. Analysis of variance revealed highly significant differences ($p < 0.001$) among genotypes. Wide variation was observed for pod yield per plant (21.48-57.40 g), 100-kernel weight (19.93-60.91 g), and plant height (9.86-43.81 cm). Most traits exhibited high heritability (64.69-95.09%) and moderate to high genetic advance (13.46-60.50%). Pod yield showed strong association with kernel weight ($r = 0.89$; $p < 0.01$). The first four principal components explained 66.91% of total variation, and cluster analysis grouped genotypes into four clusters. The observed genetic diversity offers significant potential for groundnut improvement.

Keywords: DUS, germplasm accessions, heritability, genetic diversity, correlation analysis

Introduction

Groundnut (*Arachis hypogaea* L.) is a major oilseed and cash crop cultivated extensively in tropical and subtropical regions for its high nutritional and economic value. It is predominantly autogamous and an allotetraploid species with a chromosome constitution of $2n = 4x = 40$. Globally, groundnut occupies 32.7 million hectares with an annual production of 31.43 million tonnes and an average productivity of $1,648 \text{ kg ha}^{-1}$ (ANGRAU, 2023) [3]. India, the second-largest producer, cultivates groundnut on 5.97 million hectares, producing 10.2 million tonnes annually with an average productivity of $1,716 \text{ kg ha}^{-1}$ (Ambast *et al.*, 2023) [1]. The kernel, the edible portion of the crop, contains 35-56% oil and 25-30% protein and serves as a rich source of carbohydrates, essential minerals such as phosphorus, calcium, magnesium, and potassium, and vitamins E, K, and B (Gulluoglu *et al.*, 2016) [7].

In view of its economic and nutritional importance, efficient utilization of genetic resources through systematic characterization and evaluation of germplasm is essential, as mandated under the Plant Varieties and Farmers' Rights (PPV&FR) Act, 2001, for varietal registration. Groundnut exhibits substantial genetic variability and is classified into two major subspecies, hypogaea and fastigiata (Krapovickas and Gregory, 1994) [14], comprising distinct botanical groups that differ in plant architecture, pod morphology, and seed traits. Key morphological and yield-related traits, including pod reticulation, number of kernels per pod, number of primary branches, and pod and seed dimensions, contribute directly or indirectly to kernel yield and serve as reliable selection criteria. Accordingly, systematic evaluation of diverse germplasm is necessary for identifying superior genotypes with desirable attributes such as increased kernels per pod, higher kernel yield per plant, larger kernel size, and early flowering. In India, early-flowering varieties are particularly important for efficient crop rotation systems and enhanced adaptability.

Genetic variability for these traits is assessed through estimates of variance components, heritability, and genetic diversity, which form the foundation of effective breeding strategies.

Since kernel yield is a complex trait governed by multiple genes and strongly influenced by environmental factors, a clear understanding of heritable variation and trait associations is essential for achieving sustainable genetic improvement. Therefore, the present study was undertaken to assess genetic variability, diversity, and interrelationships among groundnut germplasm accessions, with particular emphasis on early flowering and kernel yield-related traits.

Materials and Methods

Genetic Material and Field Evaluation

The experimental material comprised 56 groundnut genotypes, including 54 germplasm accessions obtained from the ICRISAT Genebank, Patancheru, Hyderabad, India, and two locally adapted check varieties, Kadiri 6 and JL 24 (Table 1). Field evaluation was conducted during the summer and rainy seasons of 2025 at the School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana (17.3850° N, 78.4867° E). The summer season was hot and dry, with temperatures of 38-42 °C (maximum) and 25-28 °C (minimum), relative humidity of 35-45%, and negligible rainfall, whereas the rainy season had moderate temperatures (28-32 °C and 20-24 °C), higher humidity (60-75%), and annual rainfall of 700-800 mm.

The experiment was laid out in an alpha-lattice design with two replications. Sowing was done manually with two seeds per hill in two continuous rows of 1.3 m length at 40 cm spacing, accommodating about 26 plants per plot. Crops were harvested at physiological maturity (110-120 days) and sun-dried for 10-15 days. Seven DUS traits were recorded following National Test Guidelines and UPOV descriptors. Observations on five representative plants per plot were recorded for flowering, growth, and yield traits. Morphological traits were measured in millimeters, yield traits in grams, and shelling percentage as percent.

Statistical analysis

Analysis of variance (ANOVA) was performed using an alpha-lattice design, treating genotypes and replications as fixed effects and incomplete blocks as random effects. Trait relationships were assessed using Pearson's correlation, and correlation matrices and scatter plots were generated in R (version 4.5.0), with significance tested at $p < 0.05$ and $p < 0.01$ (R Core Team.). Principal component analysis was conducted using standardized data following Hatcher (1994)^[11]. Genetic distances were estimated using Euclidean distance, and hierarchical clustering was performed using Ward's method (Murtagh and Legendre, 2011)^[15]. Cluster analysis was carried out using the dendextend (Galili, 2015)^[6] and circlize (Gu *et al.*, 2014)^[8] packages.

Results and Discussion

Distinctness, Uniformity, and Stability

Following the DUS test guidelines for groundnut (Anonymous, 2009)^[2], 54 genotypes were evaluated using qualitative and quantitative descriptors (Table 2). The number of primary branches varied widely, with 22 genotypes classified as few, 24 as medium, and 8 as profuse. Pod reticulation ranged from absent to strong, with 3 genotypes lacking reticulation, 30 showing weak, 20 medium, and one (ICG 12921) showing strong expression. Kernel number per pod showed limited variation, as 46 genotypes had two kernels, while 8 had two or more. Pod and seed size traits also showed considerable diversity, with

21, 25, and 8 genotypes classified as short, medium, and long for pod length; 10, 20, and 24 as narrow, medium, and broad for pod width; 11, 38, and 5 as short, medium, and long for seed length; and 17, 32, and 5 as narrow, medium, and broad for seed width, respectively. Overall, the observed variability reflects substantial genetic diversity and provides valuable scope for selection, consistent with earlier reports (Yasmine *et al.*, 2025; Karthikeyan *et al.*, 2023; Rajesh *et al.*, 2025; Darshini *et al.*, 2025)^[21, 12, 17, 5].

Genetic Variance Components

Analysis of variance revealed highly significant differences ($p < 0.001$) for yield and its associated traits (Table 3), indicating substantial variability among the evaluated germplasm. Genotypic effects were the major source of variation, ranging from 66.84% for number of primary branches to 91.67% for plant height, demonstrating strong genetic control of the studied traits. Block effects remained below 20% and replication effects were negligible, reflecting uniform field conditions and high experimental precision. The low error variance further confirmed data reliability and suggested that phenotypic selection would be effective for improving yield and related traits.

Estimation of Genetic Parameters for Yield and Associated Traits

The evaluated groundnut genotypes exhibited wide genetic variability for yield and its associated traits during the rainy season of 2025, as reflected by broad trait ranges and moderate to high genetic parameters (Table 4 and Figure 1). Days to 50% flowering ranged from 17.10 to 31.00 days and showed moderate GCV (13.90%) and PCV (14.97%) along with high heritability (86.17%) and GAM (26.57%). Plant height varied from 9.86 to 43.81 cm and recorded high GCV (30.12%), PCV (30.89%), heritability (95.09%), and GAM (60.50%), indicating strong genetic control. The number and length of primary branches also exhibited moderate to high variability, with GCV values of 15.12% and 13.26%, PCV values of 18.01% and 14.30%, and heritability estimates of 70.50% and 86.02%, respectively.

Pod and seed traits showed moderate variability and heritability, with GAM ranging from 13.93% to 27.25%. Pod yield per plant exhibited wide variation (21.48-57.40 g) and recorded high GCV (21.69%), PCV (23.59%), heritability (84.53%), and GAM (41.07%), while 100-kernel weight also showed high heritability (89.02%) and GAM (39.28%). Shelling percentage exhibited comparatively lower variability but moderate heritability (72.91%) and GAM (13.46%). The predominance of moderate to high heritability coupled with substantial genetic advance as percentage for most traits indicates the major role of additive gene action, suggesting that direct phenotypic selection would be effective for yield improvement, in agreement with earlier reports (Patel *et al.*, 2024; Gurjar *et al.*, 2025; Behera *et al.*, 2025)^[16, 9, 4].

Traits association among yield and yield related traits

Correlation analysis revealed predominantly positive and significant associations among pod yield and its component traits (Figure 2). Pod length showed strong positive correlations with seed length, seed width, pod yield, and 100-kernel weight, while pod width and seed size traits were also significantly associated with yield. Kernel weight exhibited an exceptionally strong correlation with pod yield

($r = 0.89$; $p < 0.01$), highlighting its major contribution to productivity. In contrast, plant architectural traits showed relatively weaker associations. A negative association between pod width and days to 50% flowering was observed, consistent with earlier reports (Thakur *et al.*, 2013; Korale *et al.*, 2022) [20, 13]. Overall, the predominance of positive correlations among pod size, seed size, kernel weight, and yield supports simultaneous selection for these traits as an effective strategy for groundnut improvement, in agreement with previous studies (Gurjar *et al.*, 2025) [9].

Principal component analysis

Principal component analysis revealed substantial multivariate variation among the evaluated groundnut genotypes, with 11 principal components extracted (Figure 3a and 3b). The first four components, with eigenvalues of 3.010, 1.787, 1.375, and 1.188 for PC1, PC2, PC3, and PC4, respectively, jointly explained 66.91% of the total variation, indicating that a limited number of components captured most of the phenotypic diversity (Table 5). Pod yield per plant (0.501) and 100-kernel weight (0.501) showed the highest positive loadings on PC1, while number of primary branches (-0.463) and pod width (-0.463) contributed most negatively to PC2. Shelling percentage (0.689) and plant height (0.639) were the major contributors to PC3 and PC4, respectively (Supplementary Table 1).

The PCA biplot showed that pod yield, kernel weight, pod length, seed length, and seed width formed closely aligned vectors with acute angles ($<45^\circ$), indicating strong positive associations and coordinated expression. In contrast, branching traits and shelling percentage were oriented in the opposite direction, reflecting their contrasting contribution to variability. The wide dispersion of genotypes across all quadrants confirmed substantial phenotypic diversity. Genotypes located on the positive side of PC1, including ICG 3240, ICG 14985, ICG 9418, and ICG 118, were associated with superior pod and seed traits, whereas those separated along PC2 (ICG 8083, ICG 11249, ICG 6407, and ICG 4911) reflected variation mainly governed by plant height, flowering time, and branching. Overall, the predominance of yield and seed-pod related traits in the major principal components highlights the effectiveness of PCA in identifying genetically diverse groundnut genotypes with desirable trait combinations, as also reported by Rajput *et al.* (2024) [18] and Hariharan *et al.* (2025) [10].

Diversity analysis and cluster mean

Phenotypic diversity analysis based on 11 yield and yield-related traits grouped 54 groundnut genotypes (excluding two check varieties) into four distinct clusters, indicating substantial genetic divergence (Table 6 and Figure 4)). Cluster II was the largest, comprising 27 genotypes, and recorded higher mean values for pod length, seed length, pod yield per plant, and 100-kernel weight, reflecting the predominance of pod and kernel size-associated yield traits. Cluster I, with 13 genotypes, exhibited the highest means for days to 50% flowering and shelling percentage, indicating variation in flowering behaviour and shelling efficiency. Cluster III consisted of 8 genotypes and was characterized by the highest mean for length of primary branch, while Cluster IV, the smallest with 6 genotypes, showed higher means for plant height, number of primary branches, pod width, and seed width, suggesting distinct plant stature and pod-seed dimensional traits.

The differentiation of genotypes into trait-specific clusters demonstrates that yield-related, architectural, and developmental traits contributed independently to phenotypic variation. The predominance of pod and seed size traits in the largest cluster highlights their major role in genetic divergence and yield performance, while smaller clusters indicate the presence of unique genotypes with contrasting attributes. These genetically diverse and complementary genotypes can be effectively utilized as parents in hybridization programmes to combine high yield potential with desirable plant architecture and adaptive traits, thereby enhancing groundnut improvement.

Table 1: Details of groundnut germplasm accessions evaluated in the present study

S. No.	Genotype
1	ICG 36
2	ICG 81
3	ICG 118
4	ICG 434
5	ICG 442
6	ICG 1137
7	ICG 1415
8	ICG 1519
9	ICG 1711
10	ICG 1973
11	ICG 2019
12	ICG 2106
13	ICG 3102
14	ICG 3240
15	ICG 3343
16	ICG 3421
17	ICG 3584
18	ICG 3746
19	ICG 3775
20	ICG 4543
21	ICG 4684
22	ICG 4729
23	ICG 4750
24	ICG 4911
25	ICG 4955
26	ICG 5195
27	ICG 5236
28	ICG 5494
29	ICG 5779
30	ICG 6263
31	ICG 6375
32	ICG 6407
33	ICG 6654
34	ICG 7190
35	ICG 7906
36	ICG 7969
37	ICG 8083
38	ICG 9157
39	ICG 9249
40	ICG 9418
41	ICG 9507
42	ICG 10384
43	ICG 11249
44	ICG 11515
45	ICG 11651
46	ICG 11687
47	ICG 12189
48	ICG 12697
49	ICG 12879
50	ICG 12921
51	ICG 12988
52	ICG 13491
53	ICG 14118
54	ICG 14985

Selected Pod, Plant, and Seed Traits for DUS Characterization in Groundnut

Trait	Code	States	No. of genotypes	Frequency distribution %
No. of primary branches	3	Few	22	41
	5	Medium	24	44
	7	Many	8	15
Pod reticulation	1	Absent or very weak	3	6
	3	Weak	30	56
	5	Medium	20	37
	7	Strong	1	2
	9	Very strong	0	0
Kernal per pod	1	Mostly one kernel	0	0
	2	Mostly two kernels	46	85
	3	Three or more kernels	8	15
Pod length	3	Short	21	39
	5	Medium	25	46
	7	Long	8	15
Pod width	3	Narrow	10	19
	5	Medium	20	37
	7	Broad	24	44
Seed length	3	Short	11	20
	5	Medium	38	70
	7	Long	5	9
Seed width	3	Narrow	17	31
	5	Medium	32	59
	7	Broad	5	9

Table 3: ANOVA for Yield and Related Traits in 56 Groundnut Genotypes (Rainy Season, 2025)

Source	Df	MSS													
		DDF	PH	NPB	LPB	PL	PW	SL	SW	PY	SP	KW			
Replication	1	2.703	33.474	0.009	3.782	7.917	1.406	1.721	0.877	11.668	0.018	0.922			
Block	14	21.369***	38.370***	1.160***	15.593	12.491*	0.491	2.527**	1.161*	63.105**	35.620**	105.647***			
Genotypes	55	24.086***	144.513***	0.805***	66.186***	20.328***	2.394***	4.852***	2.738***	158.463***	64.983***	130.632***			
Residuals	41	1.789	3.640	0.139	4.975	3.908	0.513	0.410	0.377	13.282	10.181	7.587			

Note: Df = Degrees of freedom, MSS = Mean Sum of Squares, DFF = Days to 50% Flowering, PH = Plant height (cm), NPB = Number of primary branches, LPB = Length of primary branch, PL = Pod length (mm), PW = Pod width (mm), SL = Seed length (mm), SW = Seed width (mm), PY = Pod yield per plant (g), SP = Shelling percentage (%), KW = 100 Kernel weight: *, **, ***, significant at probability 0.05, 0.01 and 0.001

Table 4: Genetic Parameter Estimates in Groundnut

Trait	Range		Mean	GCV	PCV	Heritability	GAM	CV
	Minimum	Maximum						
DDF (days)	17.10	31.00	23.68	13.90	14.97	86.17	26.57	5.57
PH (cm)	9.86	43.81	27.74	30.12	30.89	95.09	60.50	6.85
NPB	2.59	5.82	3.80	15.12	18.01	70.50	26.15	9.78
LPB (mm)	31.03	55.14	41.83	13.26	14.30	86.02	25.33	5.35
PL (mm)	18.03	32.46	25.18	11.32	13.75	67.75	19.19	7.81
PW (mm)	8.88	14.11	11.58	8.41	10.45	64.69	13.93	6.21
SL (mm)	8.37	16.34	11.72	12.65	13.77	84.41	23.94	5.44
SW (mm)	5.19	10.28	7.14	15.19	17.45	75.81	27.25	8.58
PY (g)	21.48	57.40	39.26	21.69	23.59	84.53	41.07	9.28
SP (%)	53.05	83.75	68.26	7.65	8.96	72.91	13.46	4.67
KW (g)	19.93	60.91	38.87	20.21	21.42	89.02	39.28	7.10

Note: GCV-Genotypic Coefficient of Variation, PCV-Phenotypic Coefficient of Variation =, GAM-Genetic Advance as Percentage of Mean, CV-Coefficient of Variation

Table 5: Principal Component Analysis: Eigenvalues and Variance Explained

PCA	Eigen value	Variance (%)	Cumulative variance (%)
PC1	3.010	27.362	27.362
PC2	1.787	16.244	43.606
PC3	1.375	12.500	56.106
PC4	1.188	10.799	66.905
PC5	0.874	7.949	74.854
PC6	0.785	7.141	81.995
PC7	0.684	6.219	88.214
PC8	0.540	4.913	93.126
PC9	0.398	3.622	96.748
PC10	0.279	2.540	99.289
PC11	0.078	0.711	100.000

Note: PC = Principal Component Analysis, PC = Principal Component

Table 6: Cluster means of traits for groundnut germplasms

Clusters	No of Genotypes	Traits										
		DFF (days)	PH (cm)	NPB	LPB (mm)	PL (mm)	PW (mm)	SL (mm)	SW (mm)	PY (g)	SP (%)	KW (g)
Cluster 1	13	27.10	21.32	3.37	39.51	25.40	11.03	11.42	6.86	38.65	72.64	39.32
Cluster 2	27	22.58	30.06	3.70	42.21	26.60	11.73	12.39	7.37	44.98	65.56	43.66
Cluster 3	8	22.38	27.72	4.15	44.23	21.98	11.05	9.79	5.96	24.87	67.08	25.21
Cluster 4	6	22.97	31.24	4.74	41.96	22.63	12.80	11.87	8.29	34.02	72.47	34.52

Supplementary Table 1: Principal component loadings for traits

Traits	PCA Loadings for each trait			
	PC1	PC2	PC3	PC4
DFF	0.043	0.384	0.560	0.118
PH	0.120	-0.266	0.182	0.639
NPB	-0.067	-0.461	0.193	0.432
LPB	-0.039	-0.398	0.093	-0.236
PL	0.397	0.085	-0.163	-0.025
PW	0.201	-0.462	0.067	-0.463
SL	0.363	-0.038	-0.114	-0.093
SW	0.381	-0.330	0.286	-0.077
PY	0.501	0.175	-0.079	0.080
SP	-0.031	0.148	0.689	-0.294
KW	0.501	0.168	0.031	0.110

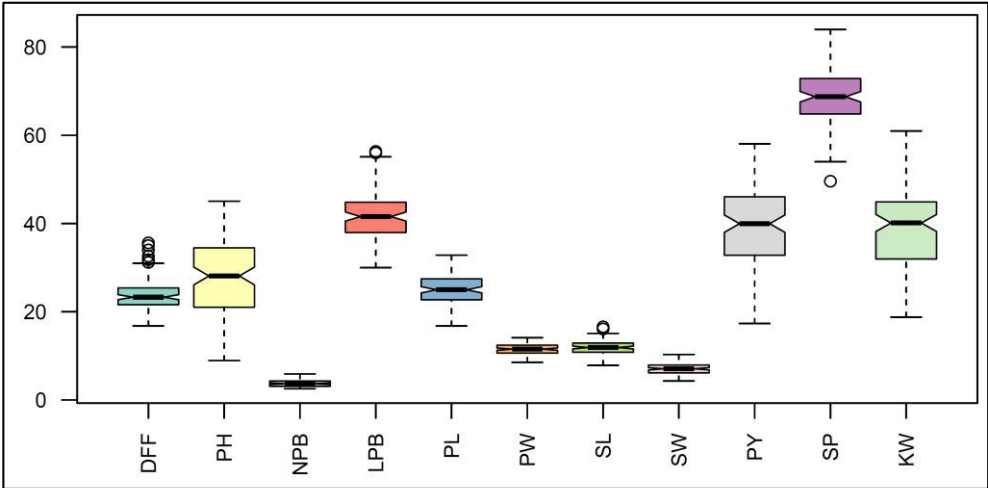


Fig 1: Box plot representation of variation in evaluated traits among 56 genotypes.

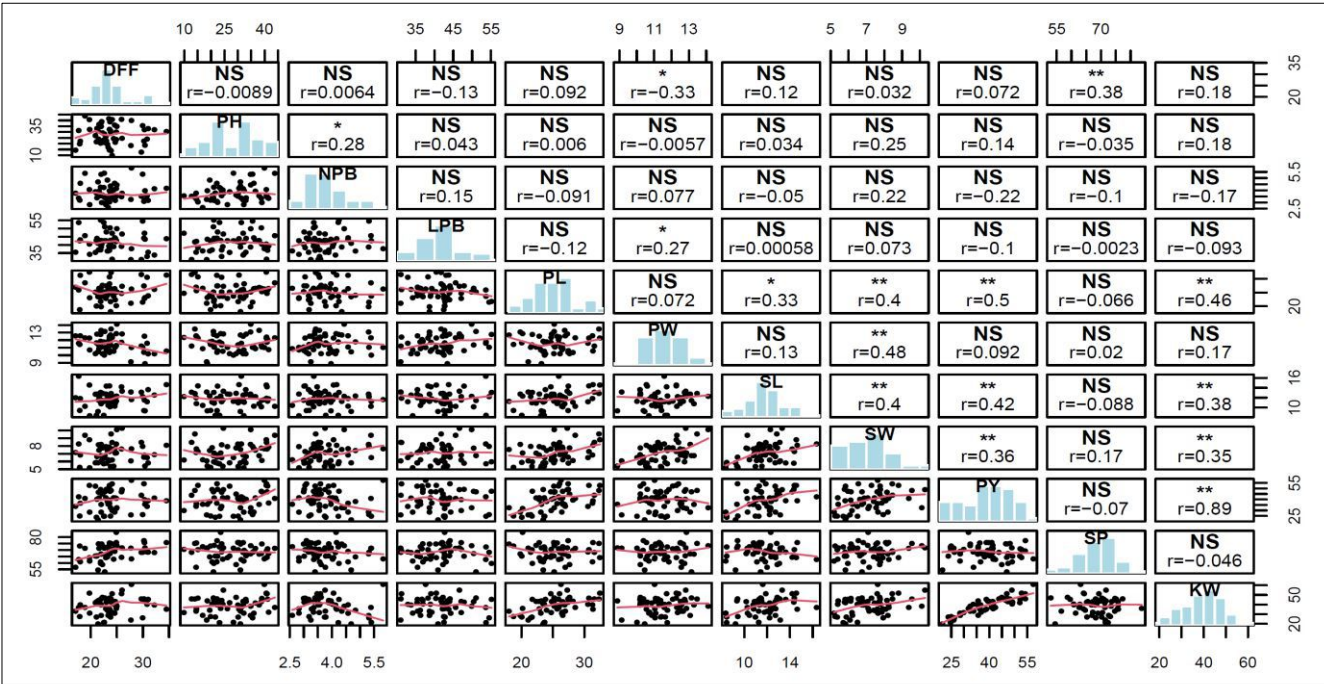
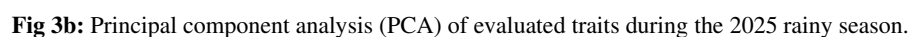


Fig 2: Scatter plot depicting correlations among traits in 56 genotypes.



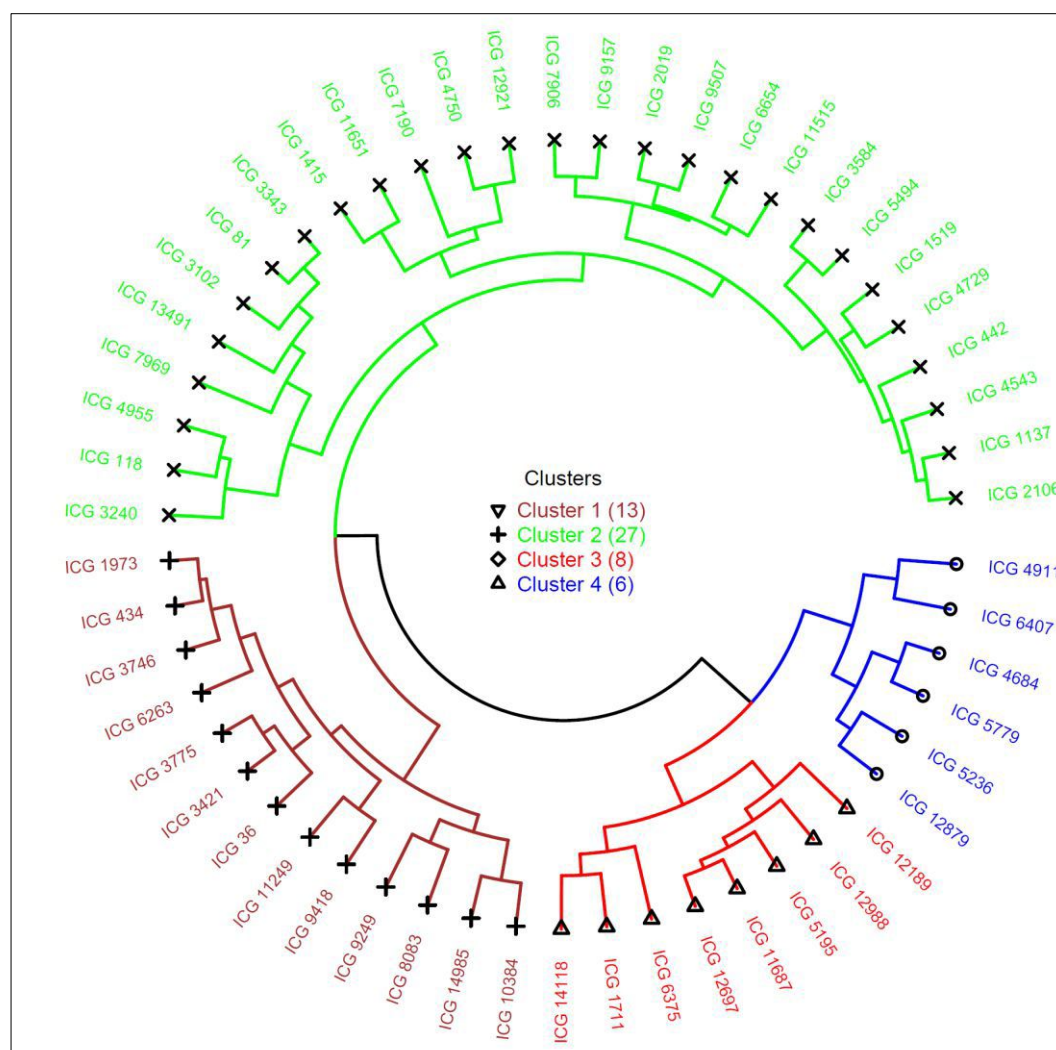


Fig 4: Circular cluster dendrogram showing genetic divergence among 54 evaluated genotypes based on measured phenotypic traits during the 2025 rainy season.

Conclusion and Future Prospects

The study revealed substantial genetic variability and phenotypic diversity among groundnut genotypes for yield and related traits. High heritability and genetic advance for most characters indicated the effectiveness of direct phenotypic selection. Pod length, seed size traits, and kernel weight were identified as key contributors to pod yield. Multivariate and cluster analyses confirmed wide genetic divergence and distinct genotype groupings. Integration of DUS characterization with genetic analyses facilitated reliable identification of superior genotypes. Future studies should focus on utilizing promising genotypes in hybridization programmes and validating their performance across environments.

Acknowledgments

The authors acknowledge the School of Agricultural Sciences, Malla Reddy University, Hyderabad, India, and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India, for providing field facilities and technical support.

References

1. Ambast SK, Varatharajan G, Upadhyaya HD, Vadez V. High-value crops' embedded groundnut-based production systems. *Front Plant Sci.* 2023;14:1298946.
2. Anonymous. Guidelines for the conduct of test for distinctiveness, uniformity and stability (DUS) on soybean (*Glycine max* (L.) Merrill). Plant Var J India. 2009;3:289-298.
3. ANGRAU. Groundnut outlook report: June to May 2023-24. Agril Market Intelligence Centre, Acharya N.G. Ranga Agricultural University; 2023. p. 91.
4. Behera PP, Deshmukh D, Vemula AK, Bangaru K, Bagudam R, Mathew A, *et al.* Realized genetic gain for yield and yield attributes in groundnut breeding at International Crops Research Institute for the Semi-Arid Tropics from an era trial. *Front Plant Sci.* 2025;16:1640041.
5. Darshini TK, Harini S, Satish K, Patel M. Morphological characterization of groundnut (*Arachis hypogaea* L.) accessions using DUS descriptors. *J Adv Biol Biotechnol.* 2025;28:401-411.
6. Galili T. Dendextend: An R package for visualizing, adjusting, and comparing trees of hierarchical clustering. *Bioinformatics.* 2015;31:3718-3720.
7. Gulluoglu L, Basal H, Onat B, Kurt C, Arioglu H. The effect of harvesting on some agronomic and quality characteristics of peanut grown in the Mediterranean region of Turkey. *Field Crops Res.* 2016;21:224-232.
8. Gu Z, Gu L, Eils R, Schlesner M, Brors B. Circlize implements and enhances circular visualization in R. *Bioinformatics.* 2014;30:2811-2812.

9. Gurjar JK, Meena AK, Yadav MR, Rathore JS. Genetic variability and heritability in groundnut (*Arachis hypogaea* L.) for yield and quality traits. *Plant Arch.* 2025;25:929-933.
10. Hariharan K, Satheeskumar K, Mahendran R. Multivariate analysis in groundnut (*Arachis hypogaea* L.) germplasm accessions for yield traits by principal component analysis. *Indian J Agric Res.* 2025;1:1-5.
11. Hatcher LA. Step-by-step approach to using the SAS system for factor analysis and structural equation modelling. Cary: SAS Institute Inc.; 1994. p. 296-297.
12. Karthikeyan AR, Ezhilkumar S, Karthikeyan P. Characterization of groundnut (*Arachis hypogaea* L.) varieties as per DUS guidelines. *Journal Name.* 2023;29:758-762.
13. Korale OD, Dhuppe MV, Patil SS, Gite NG, Mirkad SB. Correlation and path analysis for yield and yield contributing characters in groundnut (*Arachis hypogaea* L.). *Int J Theor Appl Sci.* 2022;14:22-25.
14. Krapovickas A, Gregory WC. Taxonomia del genero *Arachis* (Leguminosae). *Bonplandia.* 1994;8:1-186.
15. Murtagh F, Legendre P. Ward's hierarchical clustering method: Clustering criterion and agglomerative algorithm. *Sci Found Ireland.* 2011;31:274-295.
16. Patel JK, Sapara GK, Parmar RS, Riya. Genetic variability, heritability and genetic advance for pod yield and its related traits in F_3 populations of Spanish bunch groundnut (*Arachis hypogaea* L.). *Asian Res J Agric.* 2024;17:1072-1082.
17. Rajesh J, Kumar A, Saha S, Chauhan JS, Nautiyal PC. Evaluation of groundnut for growth, yield and seed quality for cultivation in Uttarakhand hill agro-ecosystem. *Plant Arch.* 2025;25:433-439.
18. Rajput LS, Sikarwar RS, Ingle SV, Tripathi MK, Prajapati PK, Yadav RK. Principal component analysis for groundnut yield and seed attributes (*Arachis hypogaea* L.). *Int J Res Agron.* 2024;194-197.
19. R Core Team. R: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing; 2025.
20. Thakur SB, Ghimire SK, Chaudhary NK, Shrestha SM, Mishra B. Determination of relationship and path coefficient between pod yield and yield component traits of groundnut cultivars. *Nepal J Sci Technol.* 2013;14:1-8.
21. Yasmine F, Begum M, Sikder MR, Kamruzzaman M, Sultana MR, Rahman MA. Assessment of groundnut genetic diversity through DUS descriptor. *Bangladesh J Nucl Agric.* 2025;39:1-12.