

Genetic divergence and cluster analysis for yield, yield attributing & quality traits in groundnut (*Arachis hypogaea* L.)

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Abstract

An experimental trail consisting of twenty seven advanced breeding lines of groundnut, including two check varieties (Visishta and K6), was evaluated in a randomized block design with three replications to assess genetic divergence for sixteen physiological, yield attributing and quality traits. Genetic diversity among the genotypes was estimated using Mahalanobis D² statistic, and the genotypes were grouped into seven clusters by Tocher's method. Cluster I was the largest, comprising fourteen genotypes, followed by cluster III with five and cluster II with four genotypes; clusters IV, V, VI and VII were solitary in nature. The maximum inter-cluster distance was recorded between cluster II and cluster IV (720.07), followed by cluster IV and cluster V (718.78) and cluster I and cluster IV (562.17), indicating wide genetic divergence among the genotypes of these clusters, whereas the minimum inter-cluster distance (150.80) was observed between cluster I and cluster VI. Among the sixteen characters studied, kernel yield per plant contributed maximum (23.60%) towards total genetic divergence, followed by hundred pod weight (14.60%) and plant height (8.00%). Based on genetic divergence and per se performance, crosses involving genotypes from clusters II and IV are suggested for obtaining desirable transgressive segregants in future groundnut improvement programmes.

Keywords: Groundnut, D² statistics, genetic divergence, Tocher's Method, cluster distance, percent contribution

Introduction

Groundnut (*Arachis hypogaea* L.) is a self-pollinating legume valued for its oil-rich kernels and nitrogen-fixing roots. It is a rich source of edible oil, protein, and essential nutrients, contributing to nutritional security and farmers livelihoods. However, groundnut productivity remains low due to various biotic and abiotic constraints. Since yield is a complex trait governed by multiple genes and influenced by environmental factors, direct selection for yield is often less effective (Gangurde *et al.*, 2022) [13].

Groundnut is grown extensively in Gujarat, Rajasthan, Andhra Pradesh, Karnataka, and Tamil Nadu, with Gujarat leading India's kharif 2025-26 production of about 110.93 lakh tonnes. Globally, groundnut covers 30.19 million hectares, yielding 51.2 million tonnes at 1,700 kg/ha (USDA, 2026). India ranks first in area (5.87 million ha) and second in production (13.07 million tonnes) at 2,228 kg/ha productivity, after China. Andhra Pradesh contributes 0.29 million ha and 0.430 million tonnes, with a comparatively low productivity of 1,476 kg/ha, largely due to moisture stress under rainfed conditions (Ministry of Agriculture, 2025-26) [5].

Pod yield in groundnut is a complex, environment-sensitive trait governed by several interacting characters, so selection must consider component traits rather than yield alone this also requires exploiting genetic variability, as a narrow genetic base increases stress vulnerability. Since hybridization success depends on parental divergence, Mahalanobis' D² statistic (1936, elaborated by Rao, 1952) [4, 7] is widely used to quantify diversity, identify suitable parents, and assess trait contributions. Accordingly, this

study examined genetic diversity among advanced groundnut breeding lines for physiological, yield, and quality traits to identify divergent parents for hybridization.

Materials and Methods

The present investigation comprised twenty seven groundnut genotypes, developed at the Regional Agricultural Research Station, Tirupati, along with two check varieties Visishta and K-6. The genotypes were evaluated in a Randomized Block Design with three replications during the kharif season at the research farm. Recommended agronomic and plant protection practices were followed uniformly across replications to raise a healthy crop.

Observations were recorded on five randomly selected plants per replication for each genotype (plot basis for days to 50% flowering and days to maturity) for sixteen physiological, yield attributing and quality characters, viz., days to 50% flowering, days to maturity, SPAD chlorophyll meter reading (SCMR) at 60 DAS, specific leaf area (SLA) at 60 DAS, plant height, number of primary branches per plant, number of mature pods per plant, hundred pod weight, hundred kernel weight, shelling percentage, dry haulms yield per plant, harvest index, kernel yield per plant, oil content, protein content and pod yield per plant.

The data recorded were subjected to analysis of variance to test for significant differences among genotypes. Genetic divergence among the twenty seven genotypes was estimated by employing Mahalanobis (1936) [4] D² statistic, and the genotypes were grouped into clusters following Tocher's method as described by Rao (1952) [7]. Average

intra and inter-cluster distances were computed, cluster means were worked out for all sixteen characters, and the relative contribution of each character towards total genetic

divergence was estimated based on the number of times it ranked first in the pair-wise D² comparisons.

Table 1: List of groundnut genotypes

S. No	Entry	Pedigree
1	TCGS-2578	K-6 × TCGS-1862
2	TCGS-2580	K-6 × TCGS-1862
3	TCGS-2581	K-6 × TCGS-1862
4	TCGS-2583	K-6 × TCGS-1862
5	TCGS-2584	K-6 × TCGS-1862
6	TCGS-2585	K-6 × TCGS-1862
7	TCGS-2586	K-6 × TCGS-1862
8	TCGS-2631	K-6 × TCGS-1837
9	TCGS-2635	TAG-24 × TCGS-1837
10	TCGS-2636	K-6 × TCGS-1837
11	TCGS-2642	K-6 × TCGS-1837
12	TCGS-2643	TAG-24 × TCGS-1837
13	TCGS-2644	K-6 × TCGS-1915
14	TCGS-2645	K-6 × TCGS-1915
15	TCGS-2647	K-6 × TCGS-1915
16	TCGS-2648	K-6 × TCGS-1915
17	TCGS-2649	K-6 × TCGS-1915
18	TCGS-2650	TAG-24 × TCGS-1915
19	TCGS-2651	K-6 × TCGS-1915
20	TCGS-2652	TAG-24 × TCGS-1915
21	TCGS-2654	TAG-24 × TCGS-1915
22	TCGS-2656	TAG-24 × TCGS-1915
23	TCGS-2657	TAG-24 × TCGS-1915
24	TCGS-2658	TAG-24 × TCGS-1915
25	TCGS-2660	K-6 × TCGS-1915
26	VISISTHA (C)	K-6 × ICD(FDRS)79
27	K-6 (C)	JL-24 × Ah-316/s

Results and Discussion

Analysis of Variance

The analysis of variance (Table 2) revealed highly significant differences among genotypes for all sixteen

characters studied, indicating the existence of substantial genetic variability in the material and providing ample scope for effective selection in the groundnut breeding programme.

Table 2: Analysis of variance for physiological, yield attributing and quality traits in groundnut

S.no	Characters	Mean sum of squares		
		Replication (df:2)	Genotypes (df:26)	Error (df:52)
1	Days to 50% flowering	2.259	3.641**	0.90
2	Days to maturity	5.086	9.596**	2.176
3	SCMR at 60 DAS	17.900	33.826**	6.362
4	Specific leaf area at 60 DAS (cm ² g ⁻¹)	33.407	2360.99**	235.634
5	Plant height(cm)	5.463	141.905**	5.415
6	Number of primary branches plant ⁻¹	0.319	5.241**	0.256
7	Number of mature pods plant ⁻¹	2.100	17.261**	1.515
8	Hundred pod weight (g)	2.285	328.595**	8.044
9	Hundred kernel weight (g)	11.353	35.971**	3.755
10	Shelling per cent	3.890	56.471**	1.752
11	Dry haulms yield plant ⁻¹ (g)	1.851	38.665**	2.479
12	Harvest index (%)	10.663	77.351**	3.918
13	Kernel yield plant ⁻¹ (g)	1.945	25.710**	1.125
14	Oil content %	0.854	6.155**	0.961
15	Protein content%	1.099	35.716**	1.986
16	Pod yield plant ⁻¹ (g)	4.167	46.760**	1.493

** Significant at 1% level of probability.

Genetic Divergence (D² Analysis)

Genetic divergence plays a crucial role in groundnut improvement, as knowledge of diversity guides the choice of parents in hybridization programmes; the wider the

genetic distance among parents, the greater the likelihood of recovering desirable transgressive segregants. In the present study, the twenty seven genotypes were quantitatively assessed using Mahalanobis D² statistic.

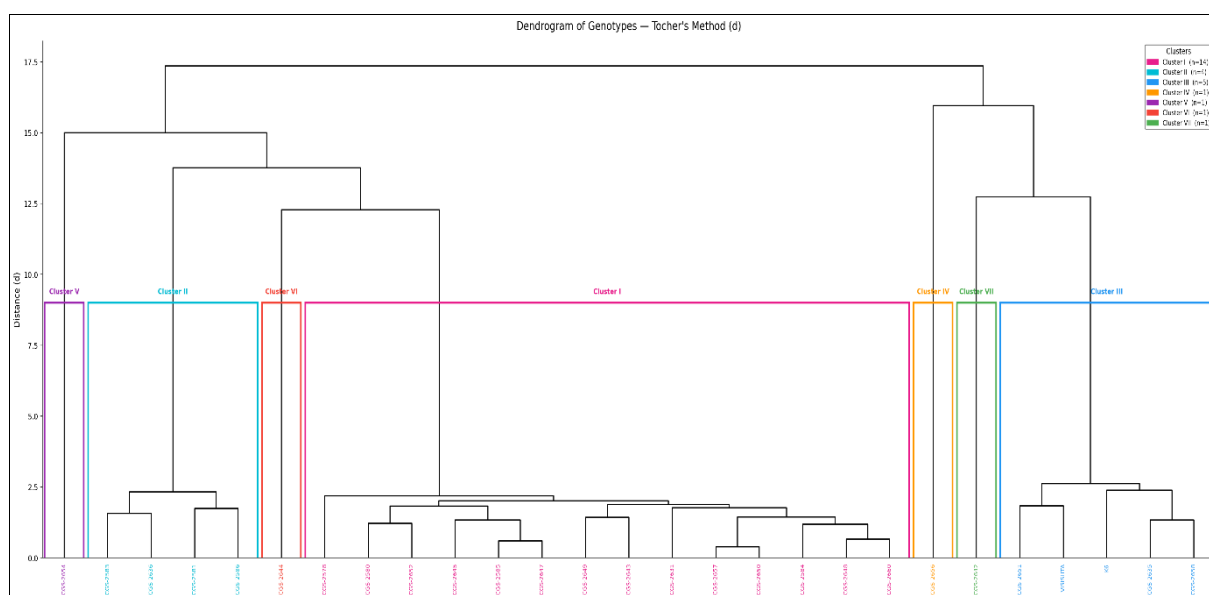
Table 3: Distribution of 27 groundnut genotypes into clusters based on D² statistics (Tocher's method)

Cluster No.	Number of genotypes	Genotypes
1.	14	TCGS-2648, TCGS-2657, TCGS-2645, TCGS-2585, TCGS-2660, TCGS-2584, TCGS-2631, TCGS-2650, TCGS-2580, TCGS-2578, TCGS-2652, TCGS-2649, TCGS-2643, TCGS-2647
2.	4	TCGS-2583, TCGS-2581, TCGS-2636, TCGS-2586
3.	5	TCGS-2635, TCGS-2651, TCGS-2658, K6, VISISHTA
4.	1	TCGS-2656
5.	1	TCGS-2654
6.	1	TCGS-2644
7.	1	TCGS-2642

Grouping of Genotypes

Based on D² values, the twenty seven genotypes were grouped into seven clusters (Table 3 and Fig. 1) by Tocher's method (Rao, 1952)^[7]. Cluster I was the largest, comprising fourteen genotypes, followed by cluster III with five genotypes and cluster II with four genotypes. Clusters IV, V, VI and VII were solitary, each represented by a single genotype (TCGS-2656, TCGS-2654, TCGS-2644 and TCGS-2642, respectively). The presence of several Mon

genotypic clusters indicates a high degree of genetic divergence among these particular lines, suggesting their usefulness as distinct parents in hybridization, and is in agreement with the findings of Vivekananda *et al.* (2015)^[12], Shinde *et al.* (2019)^[9] and Koraddi *et al.* (2019)^[2], who similarly reported groundnut germplasm resolving into a few large clusters together with several solitary ones under Tocher's grouping.

**Fig 1:** Clustering pattern of 27 groundnut genotypes into clusters using Torcher's method**Table 4:** Average intra (diagonal) and inter-cluster D² distances among seven clusters of groundnut genotypes

Clusters	I	II	III	IV	V	VI	VII
I	104.14 (10.21)	185.86 (13.63)	257.63 (16.05)	562.17 (23.71)	177.48 (13.32)	150.80 (12.28)	182.55 (13.51)
II		93.57 (9.67)	320.26 (17.90)	720.07 (26.83)	384.72 (19.61)	241.07 (15.53)	213.30 (14.60)
III			122.02 (11.05)	220.77 (14.86)	394.18 (19.85)	261.28 (16.16)	162.09 (12.73)
IV				0.00 (0.00)	718.78 (26.81)	490.37 (22.14)	458.66 (21.42)
V					0.00 (0.00)	400.66 (20.02)	287.40 (16.95)
VI						0.00 (0.00)	261.20 (16.16)
VII							0.00 (0.00)

Figures in parenthesis indicates D values

Intra and Inter Cluster Distances

Average intra- and inter-cluster D² values are presented in Table 4 and Fig. 2. The maximum inter-cluster distance was recorded between cluster II and cluster IV (720.07), followed by cluster IV and cluster V (718.78), cluster I and cluster IV (562.17), cluster IV and cluster VI (490.37), and cluster V and cluster VI (400.66), indicating that genotypes belonging to these cluster pairs are highly divergent and their crossing is likely to produce a broad spectrum of variability and superior transgressive segregants. In contrast, the minimum inter-cluster distance (150.80) was observed

between cluster I and cluster VI, followed by cluster I and cluster V (177.48), cluster I and cluster VII (182.55) and cluster I and cluster II (185.86), suggesting that genotypes of these clusters are genetically similar and share a larger number of common gene complexes. The maximum intra-cluster distance was recorded for cluster I (104.14), followed by cluster III (122.02) and cluster II (93.57), reflecting considerable genetic variability even within these multi-genotype clusters. These results corroborate the earlier reports of Bhakal and Lal (2015)^[1], Saritha *et al.* (2019)^[8] and Sudhishna *et al.* (2022)^[10].

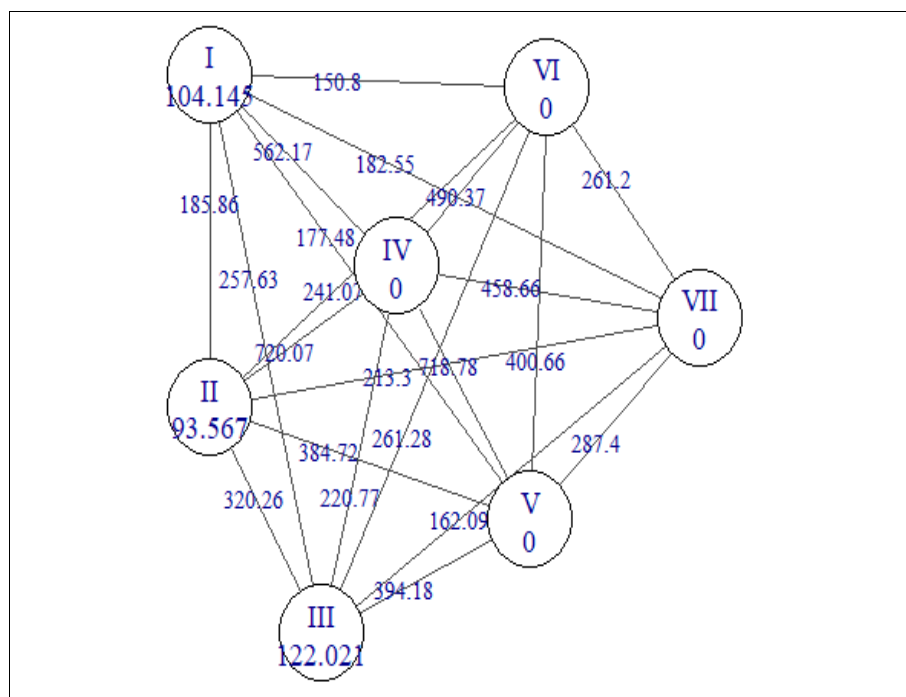


Fig 2: Tocher's diagram depicting inter and intra cluster (D^2) distances among seven clusters of groundnut

Table 5: Cluster Means of groundnut genotypes for physiological, yield attributing and quality traits in groundnut

Cluster	DFF	DM	SCMR	SLA	PH	NPP	NMP	HPW	HKW	SP	DHY	HI	KYP	OC	PC	PYP
Cluster-1	28.8	102.4	38.93	149.11	39.96	6.32	14.62	95.85	43.15	65.82	24.99	37.44	10.03	48.7	22.5	15.2
Cluster-2	29.2	102.33	42.61	172.38	41.38	6.6	13.82	105.74	46.97	65.62	25.15	40.7	11.74	45.8	28.7	17.7
Cluster-3	29.8	102.13	37.79	149.31	41.74	5.61	13.47	95.82	43.89	63.86	26.71	35.6	9.16	47.59	25.3	14.4
Cluster-4	26	98	36.07	154.21	51.23	5.6	16	95.49	48.09	62.77	32.71	39.19	13.13	47.47	26.2	21.1
Cluster-5	29	101.67	42.63	158.56	44.62	5.22	9.8	100.54	45.53	68.5	26.81	36.18	10.4	48.39	24.7	15.2
Cluster-6	28.7	103.33	34.7	168.46	47.27	6.93	19.6	104.01	45	75.3	28.09	41.78	15.18	46.68	25.9	20.2
Cluster-7	29.7	102.67	43.47	105.89	37.14	4.73	14.2	116.25	47.79	73.79	24.11	47.78	15.92	47.89	25.8	22.1
Mean	28.7	101.79	39.46	151.13	43.33	5.86	14.5	101.96	45.78	67.95	26.94	39.81	12.22	47.5	25.6	18

DFF = Days to 50% flowering; DM = Days to maturity; SCMR = SPAD chlorophyll meter reading at 60 DAS; SLA = Specific leaf area at 60 DAS ($\text{cm}^2 \text{g}^{-1}$); PH = Plant height (cm); NPB = Number of primary branches plant⁻¹; NMP = Number of mature pods plant⁻¹; HPW = Hundred pod weight (g); HKW = Hundred kernel weight (g); SP = Shelling percent (%); DHY = Dry haulm yield plant⁻¹ (g); HI = Harvest index (%); KYP = Kernel yield plant⁻¹ (g); OC = Oil content (%); PC = Protein content (%); PYP = Pod yield plant⁻¹ (g)

Cluster means for the sixteen characters (Table 5) revealed wide variation among clusters. Cluster IV recorded the earliest flowering (26.00 days) and earliest maturity (98.00 days), while cluster VI was the latest for both traits, against a general mean of 28.73 and 101.79 days respectively indicating that cluster IV harbours genotypes suited for developing short-duration cultivars. Cluster VI recorded the tallest plants (47.27 cm) and the highest number of mature pods per plant (19.60), while cluster VII recorded the highest hundred pod weight (116.25 g) and highest harvest index (47.78%). Cluster IV showed the highest hundred kernel weight (48.09 g), and cluster VI the highest shelling

percentage (75.30%). Notably, cluster VII recorded the highest pod yield per plant (22.06 g) and kernel yield per plant (15.92 g), both well above their respective general means of 17.97 g and 12.22 g, marking it as an agronomically promising cluster despite being solitary in nature. Cluster I recorded the highest oil content (48.70%), whereas cluster II recorded the highest protein content (28.67%). Such contrasting cluster means for yield and quality traits reinforce the scope for combining complementary clusters in hybridization to recover recombinants superior for multiple traits simultaneously.

Table 6: Relative contribution of physiological, yield attributes and quality traits towards genetic diversity of groundnut genotypes.

S.no	Characters	Number of times ranked first	% Contribution
1.	Days to 50% flowering	6	1.80
2	Days to maturity	9	2.60
3	SPAD chlorophyll meter reading at 60 DAS	7	2.00
4	Specific leaf area at 60 DAS ($\text{cm}^2 \text{g}^{-1}$)	18	5.10
5	Plant height(cm)	28	8.00
6	Number of primary branches plant ⁻¹	27	7.60
7	Number of mature pods plant ⁻¹	15	4.40

8	Hundred pod weight (g)	51	14.60
9	Hundred kernel weight (g)	17	4.90
10	Shelling per cent	6	1.70
11	Dry haulms yield plant ⁻¹ (g)	7	2.00
12	Harvest index (%)	24	6.90
13	Kernel yield plant ⁻¹ (g)	83	23.60
14	Oil content %	10	2.70
15	Protein content%	24	6.90
16	Pod yield plant ⁻¹ (g)	18	5.20

Contribution of Individual Characters towards Divergence

The relative contribution of each character to total genetic divergence is presented in Table 6. Kernel yield per plant ranked first most frequently (83 times) and contributed maximum (23.60%) to overall divergence, followed by hundred pod weight (14.60%), plant height (8.00%), number of primary branches per plant (7.60%), protein content and harvest index (6.90% each), pod yield per plant (5.20%), specific leaf area at 60 DAS (5.10%), hundred kernel weight (4.90%), number of mature pods per plant (4.40%), oil content (2.70%), days to maturity (2.60%), SCMR at 60 DAS and dry haulms yield per plant (2.00% each), shelling percentage (1.70%) and days to 50% flowering (1.80%). These findings are in close agreement with the reports of Mitra *et al.* (2021) ^[6] and Kumar *et al.* (2024) ^[3], who also identified yield and its immediate component traits as the principal contributors to genetic divergence in groundnut.

Conclusion

The study revealed the presence of considerable genetic divergence among the twenty seven groundnut genotypes evaluated, which grouped into seven clusters by Tocher's method, with several solitary clusters pointing to distinct genetic backgrounds among specific breeding lines. The hybridization success depends on both divergence and per se performance, crosses between cluster II and IV (maximum distance, 720.07), cluster IV and V (718.78), and cluster I and IV (562.17) are expected to yield the widest variability and best scope for transgressive segregants. Genotypes TCGS-2636, TCGS-2656, TCGS-2648, TCGS-2654, and TCGS-2644, being from divergent clusters with superior yield performance, may be prioritized as parents, while cluster I × VI crosses (minimum distance, 150.80) are less desirable due to expected lower genetic variance. Kernel yield per plant, hundred pod weight and plant height emerged as the principal contributors to total genetic divergence. Genotypes drawn from the widely separated clusters II and IV, and IV and V, offer the best prospects for hybridization aimed at generating superior transgressive segregants, while selection based on cluster mean performance alongside D² based divergence should be adopted for a more targeted and efficient groundnut improvement programme,

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