PLANT SCIENCE TODAY
Vol x(x): xx–xx
https://doi.org/10.14719/pst.7803

eISSN 2348-1900

RESEARCH ARTICLE

Assessing the genetic diversity in large seeded confectionery groundnut (*Arachis hypogaea* L.) and association among grain quality characters

P Yogameenakshi[1], A Sheeba[2]*, V A Vijayashanthi[3], C Tamilselvi[4], S Banumathy[5], R Manimekalai[6], K Sivagamy[7] & V Vijayageetha[8]

[1]Plant Breeding and Genetics, Rice Research Station, Tamil Nadu Agricultural University, Tirur 602 025, Tiruvallur, Tamil Nadu, India
[2]Plant Breeding and Genetics, Krishi Vigyan Kendra, Tamil Nadu Agricultural University, Virudhunagar 626 107, Tamil Nadu, India
[3]Agricultural Entomology, Krishi Vigyan Kendra, Tamil Nadu Agricultural University, Tirur 602 025, Tiruvallur, Tamil Nadu, India
[4]Crop Physiology, Krishi Vigyan Kendra, Tamil Nadu Agricultural University, Tirur 602 025, Tiruvallur, Tamil Nadu, India
[5]Rice Research Station, Tamil Nadu Agricultural University, Tirur 602 025, Tiruvallur, Tamil Nadu, India
[6]Agricultural Extension, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India
[7]Agronomy, Krishi Vigyan Kendra, Tamil Nadu Agricultural University, Tirur 602 025, Tiruvallur, Tamil Nadu, India
[8]Seed Science and Technology, Krishi Vigyan Kendra, Tamil Nadu Agricultural University, Tindivanam 604 001, Tamil Nadu, India

*Correspondence email - sheeba.a@tnau.ac.in

Received: 18 February 2025; Accepted: 9 June 2025; Available online: Version 1.0: 25 July 2025

Cite this article: Yogameenakshi P, Sheeba A, Vijayashanthi VA, Tamilselvi C, Banumathy S, Manimekalai R, Sivagamy K, Vijayageetha V. Assessing the genetic diversity in large seeded confectionery groundnut (*Arachis hypogaea* L.) and association among grain quality characters. Plant Science Today (Early Access). https://doi.org/10.14719/pst.7803

Abstract

Groundnut is a principal oilseed crop cultivated in about 24 million ha worldwide mainly for oil purpose. With the arrival of other vegetable oil sources, groundnut cultivation has to be made more profitable by development and promotion of confectionary varieties which fetches better price in the local as well as international markets. The present investigation was conducted at Oilseeds Research Station, Tindivanam during 2022 using 30 bold seeded groundnut germplasm to assess the diversity existing among the germplasm for confectionary characters, association of grain quality characters with pod yield and suitability of the genotypes for improvement of confectionery characters in groundnut varieties. Significant mean performance was noticed in T 64, M522, ICGV05174, ICGV06188 for pod yield/plant, kernel weight, sound mature kernel weight/plant and sound mature kernel percentage, while T 64, TPG 41, ICGV06227, ICGV06229, ICGV06214 had significant mean performance for 100 kernel weight. The diversity analysis grouped the germplasm into eight clusters with cluster II, IV and I showing more inter cluster distance with clusters VIII and VII indicating the diverse nature of the genotypes among these clusters. Cluster Mean analysis indicated the high mean performance of genotypes in cluster IV for pod yield/plant, no. of kernels/plant and sound mature kernel/plant as compared to cluster VII with sole genotype TG 4 having high mean performance for 100 kernel weight, kernel weight per plant, sound mature kernel weight/ plant and pod yield/plant. Among the characters, 100 kernel weight (58.2 %) followed by sound mature kernel weight/plant (21.1 %) contributed maximum for diversity. Character association studies revealed that kernel weight/ plant is the most significantly correlated character followed by sound mature kernel weight/plant and no. of kernels/plant in the positive direction. High direct effect of sound mature kernel weight and indirect effect of it via kernel weight/plant on pod yield was noticed indicating the emphasis to be given on sound mature kernel weight in selection of genotypes for confectionery purposes. Principal Component Analysis (PCA) indicated the importance of first three Principal components in explaining total variation.

Keywords: confectionery; correlation; diversity; groundnut; path coefficient; PCA; sound mature kernel

Introduction

Groundnut (*Arachis hypogaea* L.) is a leguminous oilseed crop cultivated in 32.7 million ha worldwide for oil extraction and food purposes (1). Globally India ranks second after China (18.36 million tonnes) in production with 10.24 million tonnes annually (2). Among the multi various purposes of ground nut produce globally, 50 % is utilized for oil extraction, 38 % for confectionary and 12 % for seed purpose. In India, about 80 % is used for oil extraction, 11 % as seeds, 8 % as direct food and 1 % for export to other countries (3). Groundnut continues to be an important oilseed crop having maximum area among the oilseed crops in India. Even after the arrival of other oilseed crops like soybean, sunflower, oilpalm, the attraction and potential usage of groundnut for a variety of culinary purposes ranging from oil, butter, edible confectionery to protein concentrates has expanded.

In recent years, the confectionery types have assumed great significance as snack food in domestic and international markets. Edible large/bold seeded groundnut is often termed as Confectionery groundnut / Hand Picked Selection (HPS) groundnut and is put to variety of uses as peanut butter, roasted and salted kernels, preparation of candies and flakes for cake and biscuit decoration. Protein concentrates and protein isolates from HPS groundnut has also found its market in recent times. The overall quality requirements of HPS groundnut depend largely on the usage of the produce and must satisfy traits like light pink/brown testa colour, uniform shape, full development of kernels without shrivelling (sound mature kernel), 100 seed weight above 55 g, high protein and relatively low oil content (4-6). It is essential to give importance to one or more of the quality standards set for the purpose in order to release a variety for commercial purpose (7). Giving more emphasis to develop varieties specific to food purposes will improve the value chain and bring in more economic returns to the farmers and other stake holders.

Development of groundnut varieties with grain quality and high yield requires suitable selection strategies including choice of parental lines and desirable interlinked characters. The potentiality of parents under selection may be assessed based on the existing genetic diversity for the quality and yield attributes vis a vis the contribution of individual characters to diversity. Multivariate statistics like D^2 and PCA provide a more dependable measure of the genetic distance between the genotypes and thus can be used for assessment of genetic diversity (8). These techniques can thus be employed to find the genetic divergence of the gene pool, selection of parents based on their diversified nature which will ultimately assist in development of transgressive segregants (9). Any breeding strategy ultimately aims for yield enhancement. Ascertaining the component traits and their contribution to grain yield directly and indirectly is well accomplished through correlation and path coefficient analyses. Correlation coefficients reveal the nature, type and magnitude of association between characters. Path coefficient analysis allows an effective means of partitioning correlation coefficients into unidirectional pathway and alternate pathways. This analysis permits a critical examination of specific factors that produce a given correlation and can be successfully employed in formulating an effective selection strategy (10).

Substantial genetic variability exists for physical, chemical and sensory traits in groundnut (11). Breeding groundnut varieties suitable for edible purposes should aim to incorporate one or more of the quality parameters in addition to yield. Only a limited number of reports are available on genetic studies on large seeded or confectionery type groundnut (12-15). Hence the present investigation aims to study the diversity of groundnut germplasm for quality characters and correlation of quality characters with yield along with their direct and indirect effects and further down streaming the selection emphasis to few quality parameters through PCA.

Material and Methods

The present study was undertaken with thirty confectionery type germplasm obtained from DGR, Junagadh, ICRISAT, Hyderabad and TNAU, Coimbatore (Table 1) during *Kharif* and *Rabi*, 2022 at Oilseeds Research Station, Tindivanam located at 12°213886′ N latitude and 79°672351′ E longitude. The genotypes were raised in a Randomized Block Design in two replications in plot size of 4 x 2 m^2 with a spacing of 30 cm between rows and 15 cm between plants. Observations on no. of branches/plant (NB/P), no. of pods/plant (NP/P), no. of kernels/plant (NK/P), 100 kernel weight (100 KW) kernel weight/plant (KW/P), sound mature kernel weight/plant (SMK.KW/P), sound mature kernel percentage (SMK.K %) and pod yield/plant (PY/P) were recorded on five plants selected at random in each replication.

Sound Mature Kernel (SMK) refers to the kernels that are fully developed in size that fills the pod completely without any shrivelling or constriction. The weight of SMK kernels in a plant is recorded in grams and represented as SMK.KW/P and the percentage of sound mature kernel weight to total kernel weight of a plant is expressed as SMK.K percentage.

Statistical analysis

D^2 statistics was calculated involving Ward's minimum variance agglomeration method to estimate the Euclidean distance (16) and clustering using Toucher's method (17) which minimizes the within cluster variances by hierarchical clustering algorithm. Genotypic correlation coefficient analysis to find out the association of quality characters with pod yield/plant (18), path analysis (19) to assess the direct and indirect effects of quality characters on pod yield/plant and PCA (20) to identify the spatial distance among genotypes were performed using R software (21) subjecting

Table 1. Genotypes used in the study

Sl. No.	Genotypes	Source
1.	TG 1	DGR, Junagadh - X irradiated mutant variety of 'Spanish improved' from BARC, Trombay
2.	Chitra	DGR, Junagadh
3.	BAU 13	DGR, Junagadh
4.	AK 303	DGR, Junagadh
5.	T 64	DGR, Junagadh
6.	TPG 41	DGR, Junagadh
7.	Somnath	DGR, Junagadh
8.	BG 1	DGR, Junagadh
9.	BG 2	DGR, Junagadh
10.	M 522	DGR, Junagadh
11.	B 95	DGR, Junagadh
12.	T 28	DGR, Junagadh
13.	ICGV 05170	ICRISAT, Hyderabad
14.	ICGV 05174	ICRISAT, Hyderabad
15.	ICGV 05182	ICRISAT, Hyderabad
16.	ICGV 05184	ICRISAT, Hyderabad
17.	ICGV 05193	ICRISAT, Hyderabad
18.	ICGV 05198	ICRISAT, Hyderabad
19.	ICGV 05200	ICRISAT, Hyderabad
20.	ICGV 06188	ICRISAT, Hyderabad
21.	ICGV 06189	ICRISAT, Hyderabad
22.	ICGV 06211	ICRISAT, Hyderabad
23.	ICGV 06214	ICRISAT, Hyderabad
24.	ICGV 06216	ICRISAT, Hyderabad
25.	ICGV 06227	ICRISAT, Hyderabad
26.	ICGV 06229	ICRISAT, Hyderabad
27.	ICGV 06233	ICRISAT, Hyderabad
28.	TMV 13	TNAU, Coimbatore
29.	CO 6	TNAU, Coimbatore
30.	Asha	TNAU, Coimbatore

the pooled mean values of the 30 genotypes in the two seasons for each character to statistical analysis.

Results and Discussion

The Analysis of variance for the grain yield and grain quality parameters indicated significant differences among the genotypes (Table 2). Breeders must consider choosing best performers for the trait of interest for contribution of favourable alleles and genetic diversity so as to boost the overall frequency of favourable alleles (22). Hence the mean performance of genotypes was studied for selection of best performers (Table 3). The character mean values ranged from 27.4 g (B 95) to 51.5 g (TG 1) for Pod yield/plant, from 47.2-72.9 g for 100 kernel weight, from 40.0-74.0 for no. of kernels/plant, from 19.4-49.4 g for kernel weight/plant, from 13.4- 41.1 g for sound mature kernel weight/plant and from 50.1-84.6 % for sound mature kernel percentage. Among the 30 genotypes, TG1, T 64, M522, ICGV05174, ICGV06188 and Asha exhibited significant mean performance for pod yield/plant. T 64 and ICGV 06188 expressed significance for other yields attributing and grain quality characters like 100 KW, kernel weight/plant, sound mature kernel weight/plant and sound mature kernel percentage. Likewise, M 522 for no. of branches /plant, kernel weight/plant, sound mature kernel weight/plant and sound mature kernel percentage, TG05174 for no. of pods/plant, no. of kernels/plant, SMK kernel weight/plant and sound mature kernel percentage. TG 1 also expressed significant mean performance for no. of branches/plant, no. of pods/plant and no. of kernels/plant. Hence involving these genotypes in crossing programmes shall be considered for improving these quality traits in the progenies for breeding confectionery type groundnut. Per se performance of parents as one of the tools for selection of parents to obtain superior progenies in ground nuts was utilised by several workers (23, 24). Superior parents were identified for improving confectionery qualities based on high mean performance for 100 kernel weight, kernel length, kernel width, uniform pod size and shape, high pod yield per plant, high protein, moderate oil and high shelling percentage (6). Breeding lines with high pod yield and large seed size were selected by analyzing the mean performance across years in various locations (25). Significant per se performance of genotypes for days to maturity, test weight, sound mature kernels, harvest index, protein content and pod yield per plant was reported earlier (26).

Diversity studies

Genetic variability/diversity present in the initial population is imperative to obtain superior progenies (27). D^2 analysis is performed to study the genetic diversity among the

Table 2. Analysis of variance for yield and grain quality traits in groundnut genotypes

Character	Mean sum of squares		
	Replication (df: 1)	Genotypes (df: 29)	Error (df: 29)
NB/P	2.21	5.57*	1.31
NP/P	1.20	45.07*	7.57
NK/P	0.27	204.01*	31.30
100KW	0.10	77.02*	0.89
KW/P	0.28	84.61*	13.86
SMK.KW/P	0.37	87.64*	5.64
SMK.K %	1.82	208.72*	19.59
PY/P	17.42	98.29*	9.31

* denotes significant at 5 % level

Table 3. Mean performance of genotypes

Sl. No.	Genotypes	NB/P	NP/P	NK/P	100KW (g)	KW/P (g)	SMK. KW/P (g)	SMK. K%	PY/P (g)
1.	TG 1	8.10	39.25*	71.5*	57.80	37.90	24.80	65.75	51.50*
2.	Chitra	11.00*	28.50	48.0	53.55	29.15	15.85	58.25	36.55
3.	AK 303	6.50	30.50	53.5	54.00	33.95	20.50	59.35	37.00
4.	T 64	8.65	28.75	50.5	66.80*	49.35*	41.10*	82.65*	59.20*
5.	TPG 41	8.20	29.50	55.0	65.70*	31.00	20.70	67.75	35.80
6.	Somnath	6.00	35.25	62.5	55.95	36.90	18.70	50.90	48.35
7.	BAU 13	8.30	29.00	49.0	62.00*	25.95	13.40	50.90	34.10
8.	BG 1	11.50*	32.50	58.0	52.10	32.30	19.00	57.80	41.90
9.	BG 2	6.00	29.00	51.0	52.55	29.20	20.10	68.40	38.65
10.	M 522	11.60*	29.00	51.0	56.00	42.75*	31.50*	73.75*	50.80*
11.	B 95	7.80	24.75	41.0	48.95	19.35	14.05	71.10	27.35
12.	T 28	7.70	36.25*	64.0	47.15	21.25	10.70	48.80	34.70
13.	TMV 13	9.10	35.50	66.5*	47.20	31.65	17.20	53.95	41.45
14.	ICGV05170	8.50	35.75	64.5	57.90	34.65	21.15	60.60	45.90
15.	ICGV05174	6.30	43.75*	80.5*	55.95	36.95	29.15*	79.45*	54.00*
16.	ICGV05182	7.00	31.00	55.0	56.95	34.85	19.55	55.20	45.30
17.	ICGV05184	5.30	23.25	40.0	59.85	26.00	18.45	70.50	41.55
18.	ICGV05193	8.10	23.25	40.5	60.05*	33.75	20.80	58.35	44.90
19.	ICGV05198	6.00	24.25	41.5	61.05*	23.70	17.10	78.65*	30.10
20.	ICGV05200	6.10	31.75	55.0	55.85	28.90	18.90	64.95	40.40
21.	ICGV06188	5.00	30.75	55.5	63.90*	42.70*	32.80*	77.50*	51.35*
22.	ICGV06189	5.80	24.75	45.0	62.60*	35.35	30.00*	84.55*	43.00
23.	ICGV06211	8.50	34.00	61.0	60.60*	28.45	15.70	53.35	42.50
24.	ICGV06214	6.70	31.75	56.5	72.90*	33.50	24.25	72.70	46.80
25.	ICGV06216	6.90	25.00	43.0	56.40	23.20	14.85	64.55	37.55
26.	ICGV06227	8.00	30.00	52.0	64.05*	34.40	25.65	73.65*	40.40
27.	ICGV06229	9.00	28.50	51.0	67.70*	32.60	20.20	63.05	44.20
28.	ICGV06233	7.50	34.25	61.5	54.10	30.75	18.00	57.40	39.95
29.	Asha	8.00	30.75	74.0*	59.35	35.95	23.90	66.25	48.55*
30.	Co 6	9.00	31.75	57.0	49.20	27.50	14.10	50.10	36.85
	Grand mean	7.74	30.74	55.17	57.94	32.13	21.07	64.67	42.36
	Range	5.0- 11.6	23.3-43.8	40.0-74.0	47.2-72.9	19.4-49.4	13.4- 41.1	50.1-84.6	27.4-51.5
	SEd	1.143	2.75	5.60	0.94	3.70	2.37	4.43	3.05
	CD	2.35	5.65	11.50	1.94	7.6	4.88	9.10	6.27

* denotes significant at 5 % level

genotypes taken for study so as to select suitable genotypes for crossing purpose. D^2 analysis grouped the genotypes into eight clusters with cluster 1 having the maximum of 11 genotypes followed by cluster 3 with five genotypes, clusters II and IV having four genotypes each, clusters V and VI having 2 genotypes each whereas cluster VII and VIII had single genotype each (Table 4). The dendrogram (Fig. 1) shows the variable nature of the genotypes grouped into eight clusters. Presence of high inter cluster distances is indicative of more genetic diversity among the selected genotypes (28). Moreover, crossing between the genotypes in clusters having more inter cluster distance will provide more useful genotypes/transgressive segregants than crossing with clusters having less inter cluster distance (29). Accordingly, the inter cluster between clusters II and VIII (1022.45) was the highest followed by cluster II and VII (862.78), cluster I and VIII (535.18), cluster II and III (519.72), cluster I and VII (440.69), cluster IV and VIII (389.09), cluster VI and VIII (329.61) and cluster VI and VII (326.62). Hence crossing among these clusters will bring about more variability in the segregating progenies and transgressive segregants which will be utilized for further selection. Though clusters VII and VIII have single genotype each, they recorded the maximum inter cluster distance with clusters II, I, IV and VI, hence are considered ideal for utilization in crossing programmes. Among other clusters, Cluster II and IV with four genotypes each show more inter cluster distance with all other clusters and are more diverse in nature. The cluster IV with four genotypes shows more intra cluster distance followed by cluster I with 11 genotypes and cluster III with 5 genotypes (Table 5). In general, genotypes in Cluster II can be utilized for trait introgression of bold seededness with clusters VIII, VII, III and V. Similarly, the genotypes *viz*., TG 4 (cluster VII) and ICGV 06214 (cluster VIII) are considered more useful for creation of more variation.

Contribution of characters to diversity

The percentage contribution of individual characters (Fig. 2) indicated the maximum contribution of 100 kernel weight (58.2 %) followed by sound mature kernel weight/plant (21.1 %) for diversity. All other characters show relatively less contribution to the genotypic diversity. Hence due weightage should be given to 100 kernel weight and sound mature kernel weight/plant in selection of genotypes with higher yield. The characters showing maximum contribution to diversity emphasize the real variability among the genotypes for the trait in discussion and hence will provide more opportunity for improvement and to put forth transgressive segregants. Contribution of linoleic acid, free amino acid and 100 seed weight to diversity among all qualitative and

Table 4. Inter and intra cluster distances of genotypes

Cluster distance	cluster 1	cluster 2	cluster 3	cluster 4	cluster 5	cluster 6	cluster 7	cluster 8
cluster 1	**38.31**	114.75	205.61	95.84	86.72	84.68	440.69	535.18
cluster 2		**33.03**	519.72	258.91	280.48	266.31	862.78	1022.45
cluster 3			**36.80**	141.98	87.19	104.60	111.86	115.05
cluster 4				**45.045**	118.68	130.85	252.72	389.09
cluster 5					**22.025**	67.30	289.38	274.46
cluster 6						**27.82**	326.62	329.61
cluster 7							**0.000**	114.18
cluster 8								**0.000**

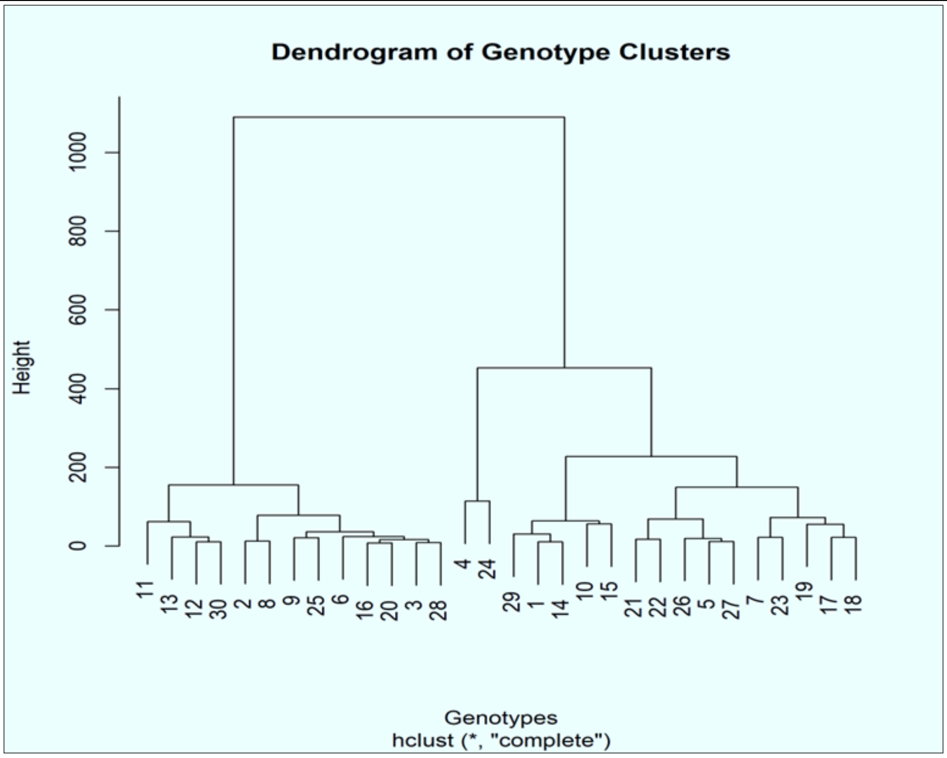

Fig 1. Dendrogram of genotypic clusters.

Table 5. Genotypes in different clusters

Clusters	Genotypes
cluster 1	ICGV05182, ICGV05200, Somnath, ICGV06233, AK 303, ICGV06216, BG 2, Chitra, ICGV05170, BG 1, ICGV05193
cluster 2	T 28, CO 6, TMV 13, B 95
cluster 3	TPG 41, ICGV06229, ICGV06227, ICGV06189, ICGV06188
cluster 4	TG 1, ICGV05174, M 522, Asha
cluster 5	BAU 13, ICGV06211
cluster 6	ICGV05184, ICGV05198
cluster 7	T 64
cluster 8	ICGV06214

quantitative traits was reported by (12) among the confectionery genotypes.

Cluster Mean analysis

Cluster mean analysis indicates that cluster VII with the sole genotype TG 4 is unique and performed well for majority of the characters related to yield and bold seededness *viz*., 100 kernel weight, kernel weight per plant, sound mature kernel weight/ plant and pod yield/plant whereas the cluster II had poor performers for yield and grain characteristics. The genotypes in cluster IV had high mean value for pod yield, no. of kernels/plant and sound mature kernel weight/plant but had average value for 100 kernel weight. Hence the genotypes in cluster IV may be combined with genotypes in cluster VII and VIII for getting good grain as well as pod yield characteristics. Considering the maximum no. of genotypes in cluster I and the genetic distance of cluster I with cluster VII and VIII and cluster mean values, crossing between the genotypes in these clusters can also be considered for improvement of pod yield and grain characteristics (Table 6). Crossing within genotypes in cluster II should be avoided owing to their poor performance. Genotypes within cluster are more similar in nature and crossing between them will not result in useful segregants (28).

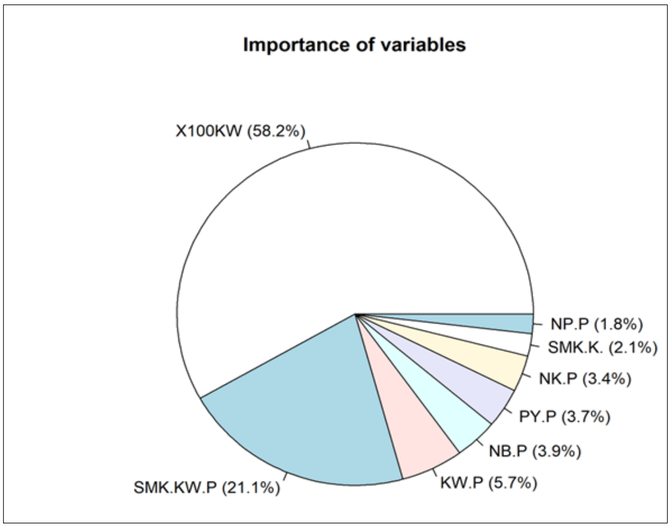

Fig 2. Contribution of characters to diversity.

Genotypic correlation coefficients

Genotypic correlation coefficients are calculated keeping Pod yield /plant as the dependent variable and all other as independent and yield contributing variables (Table 7). Among the various characters studied, kernel weight/ plant is the most significantly correlated character followed by SMK kernel weight/plant and no. of kernels/plant in the positive direction. All other characters also exhibited positive relationship with pod yield but are non-significant. Several workers have reported significant and positive correlation of 100 kernel weight with pod yield/plant (30, 31) and positive significant association of kernel yield /plant, no. of pods/plant and no. of mature pods/plant with pod yield (32). Significant and positive intercorrelation was also noticed between the traits no. of pods/plant and no. of kernels/plant; 100 kernel weight with sound mature kernel weight and sound mature kernel percentage; kernel weight / plant and sound mature kernel weight /plant; sound mature kernel weight and sound mature kernel percentage. Significant intercorrelation between characters *viz*., 100 kernel weight, kernel yield/plant

Table 6. Cluster mean analysis

Cluster	NB/P	NP/P	NK/P	100KW (g)	KW/P (g)	SMK. KW/P (g)	SMK.K %	PY/P(g)
Cluster I	7.74	30.61	53.86	55.40	31.60	18.85	59.61	41.50
Cluster II	8.40	32.06	57.13	48.13	24.94	14.01	55.99	35.09
Cluster III	7.20	28.70	51.70	64.79	35.21	25.87	73.30	42.95
Cluster IV	8.50	35.69	69.25	57.28	38.39	27.34	71.30	51.21
Cluster V	8.40	31.50	55.00	61.30	27.20	14.55	52.13	38.30
Cluster VI	5.65	23.75	40.75	60.45	24.85	17.78	74.58	35.83
Cluster VII	8.65	28.75	50.50	66.80	49.35	41.10	82.65	59.20
Cluster VIII	6.70	31.75	56.50	72.90	33.50	24.25	72.70	46.80

Table 7. Genotypic correlation coefficients for component characters with pod yield

	NB/P	NP/P	NK/P	100KW	KW/P	SMK.KW/P	SMK.K%	PY/P
NB/P	1.000	0.012	0.001	-0.183	0.079	-0.073	-0.294	**0.024**
NP/P		1.000	0.903*	-0.238	0.218	0.048	-0.246	**0.352**
NK/P			1.000	-0.182	0.275	0.108	-0.197	**0.413***
100KW				1.000	0.376	0.487*	0.464*	**0.362**
KW/P					1.000	0.874*	0.322	**0.834***
SMK.KW/P						1.000	0.713*	**0.751***
SMK.K %							1.000	**0.261**

* denotes significant at 5 % level

and no. of matured kernels/plant was reported earlier (33). The results clearly denote that the pod yield per plant can be maximized by selecting the yield contributing traits *viz*., no. of kernels/plant, kernel weight and sound mature kernel /plant. However, no. of kernels/plant exhibited negative correlation with 100 kernel weight and sound mature kernel percentage. Though not significant, care should be taken in exercising selection for high yielding genotypes with more no. of kernels and with more sound mature kernels (Fig. 3).

Path analysis

Path coefficient analysis is done to ascertain the direct and indirect effects of the genotypic correlation coefficients upon the pod yield/plant. From the results (Table 8) it could be concluded that, kernel weight per plant being the main yield contributing character, the indirect effect of it through sound mature kernel weight is the highest and also the direct effect of sound mature kernel weight on grain yield is the maximum. This clearly indicates that sound mature kernel weight should be concentrated more for selection of confectionery genotypes since it shows the high direct and indirect effect on pod yield. 100 kernel weight also has high indirect effect through sound mature kernel weight emphasizing the importance of sound mature kernel weight. High direct effect of mature pods/plant and kernel yield/plant on pod yield/plant was reported in earlier works (34, 35). Among the other characters, no. of kernels /plant show high direct effect on pod yield /plant. This is comparable to the findings of (36, 37). Hence concentrating on both of these characters keeping a balance is essential in order to select a better and ideal genotype for confectionery purpose.

Principal Component Analysis

The multivariate analysis (PCA) is conducted to restructure data sets containing many correlated variables into smaller sets of components of the original variables (38). PCA provides graphical representation of observed variation and the usefulness of the genotypes for breeding programmes based on their genotypic value (39). The results emphasized the significance of first three Principal components to be discriminative of the confectionery type groundnut. They together explained 86.12 % of the total variation and have Eigen values more than 1 (Table 9). The first principal component had an Eigen value of 3.47 and explained 43.4 % of variation while the second and the third PCs explained 29.64 % and 13.06 % of variation respectively. The cumulative percentage of variation explained by Eigen vectors is presented in Table 9 and the percentage of variation explained by various principal components as represented by the Eigen values is given as scree plot graph (Fig. 4).

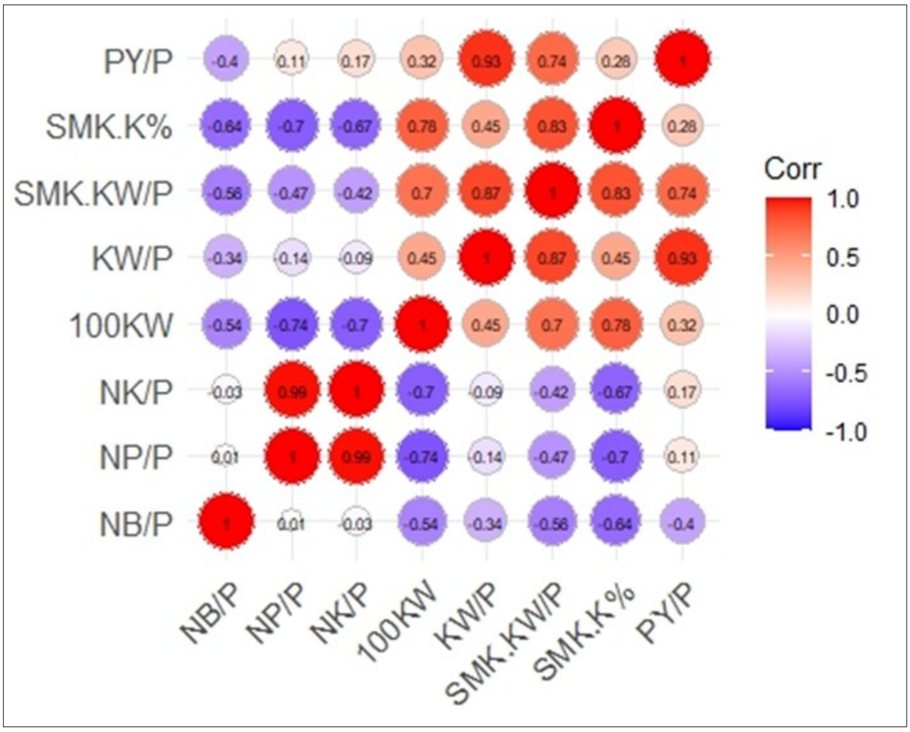

Fig 3. Corellelogram showing association of characters with pod yield.

Table 8. Direct and indirect effect of kernel and yield characters on pod yield

	NB/P	NP/P	NK/P	100 KW	KW/P	SMK. KW/P	SMK.K %	Genotypic correlation coefficient with PY/P
NB/P	**-0.014**	0.001	0.001	-0.032	0.007	-0.061	0.120	**0.024**
NP/P	-0.001	**0.039**	0.189	-0.043	0.019	0.043	0.103	**0.352**
NK/P	0.001	0.035	**0.210**	-0.036	0.023	0.095	0.082	**0.413***
100 KW	0.003	-0.009	-0.042	**0.180**	0.028	0.372	-0.182	**0.351**
KW/P	-0.001	0.009	0.057	0.060	**0.085**	0.754	-0.133	**0.834***
SMK.KW/P	0.001	0.002	0.023	0.078	0.074	**0.866**	-0.294	**0.751***
SMK.K%	0.004	-0.010	-0.042	0.079	0.027	0.615	**-0.414**	**0.261**

Residual effect - 0.225 * denotes significant at 5 % level

Table 9. Eigen values showing percentage of variance in different principal components

Principal components	Eigen values	Percentage of variance	Cumulative percentage of variance
PC1	3.475	43.44	43.44
PC2	2.373	29.64	73.07
PC3	1.044	13.06	86.12
PC4	0.554	6.92	93.04
PC5	0.382	4.78	97.82
PC6	0.096	1.20	99.03
PC7	0.068	0.85	99.87
PC8	0.010	0.13	100

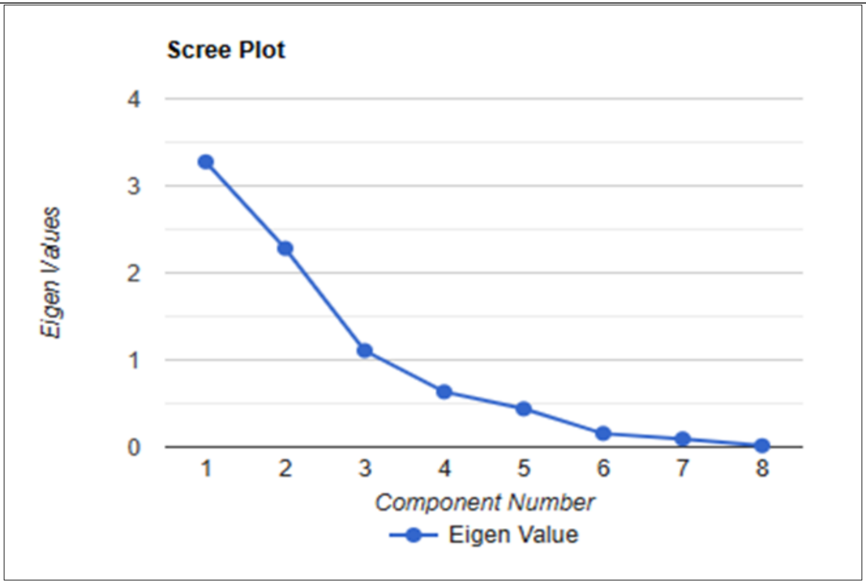

Fig 4. Scree plot graph.

High positive weight on characters *viz*., sound mature kernel weight/plant (0.952), kernel weight/plant (0.926), pod yield (0.908), sound mature kernel percentage (0.617) and 100 kernel weight (0.566) was projected by PC1, no. of pods/plant (0.897) and no. of kernels/plant (0.873) by PC2 and no. of branches /plant (0.908) by PC3. The first Principal Component is strongly associated with sound mature kernel weight/plant, kernel weight/plant, sound mature kernel percentage and pod yield/plant. (40) reported first PC to be associated with number of pods per plant, kernel yield per plant, biological yield per plant and seed yield per plant Likewise PC2 is strongly correlated with no. of pods/plant and no. of kernels/ plant while PC3 with no. of branches/plant and PC4 with 100 kernel weight (Table 10 and Fig. 5). The distribution of genotypes among the Principal Components is depicted by Fig. 6. All most equal dispersion of genotypes was noticed among the four quadrants indicating their diverse nature with minimum of 5 genotypes in first quadrant and nine genotypes in third quadrant. The trait vectors in biplot with smaller angle indicate their close relationship and the genotypes plotted closer to the trait vectors are representative of their performance for those characters (41, 42). Accordingly, the traits pod yield /plant is tightly linked with kernel weight/ plant and SMK kernel weight/plant. Likewise, 100 kernel weight is closely related with sound mature kernel percentage while no. of pods/plant and no. of kernels/plant are more closely related each other confirming the results of genotypic correlation and path analysis done in the study. The genotypes clustered around the yield contributing characters *viz*., TG1, T64, M 522, ICGV05174, ICGV06188, ICGV06214, Asha expressed high mean values for those traits. Similar results were previously reported (40, 41).

Table 10. Eigen vectors for first five principal components

Characters	Eigen vectors				
	PC 1	PC 2	PC 3	PC 4	PC 5
NB/P	-0.086	0.330	0.908	-0.009	0.243
NP/P	0.261	0.897	-0.254	0.025	0.164
NK/P	0.330	0.873	-0.248	0.038	0.180
100KW	0.566	-0.508	-0.038	0.614	0.209
KW/P	0.926	0.111	0.224	-0.012	-0.221
SMK.KW/P	0.952	-0.187	0.090	-0.195	-0.006
SMK.K %	0.617	-0.575	-0.174	-0.365	0.348
PY/P	0.908	0.246	0.068	0.060	-0.224

Conclusion

The present study conducted to analyze the genetic diversity and character association existing among the large seeded groundnut germplasm exposed the variable nature of the genotypes that were grouped in 8 clusters with 100 kernel weight and sound mature kernel weight/plant contributing to maximum variation. Clusters II and IV had maximum inter cluster distance with Clusters VII and VIII showing the usefulness of the genotypes in crossing programme. Pod yield per plant is in close association with kernel weight/plant and sound mature kernel weight/plant emphasizing the importance of these traits. The PCA analysis further simplified the importance of first 3 PCs in deciding the maximum variability of which kernel weight/plant, sound mature kernel weight/plant and 100 kernel weight are the major players. The genotypes consecrated in first and fourth quadrant expressed high mean values for the yield as well as large seededness indicating their usefulness in evolving large seeded groundnut varieties with high yield.

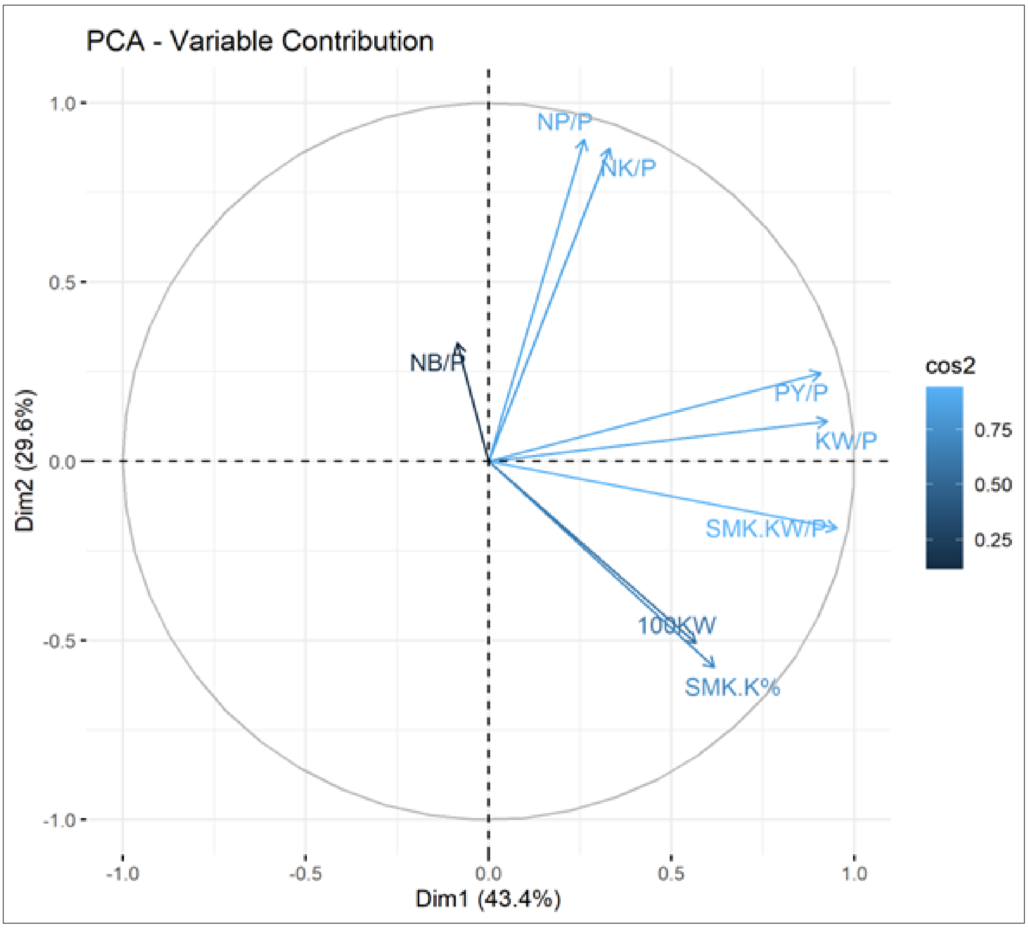

Fig 5. Contribution of variables to principal components.

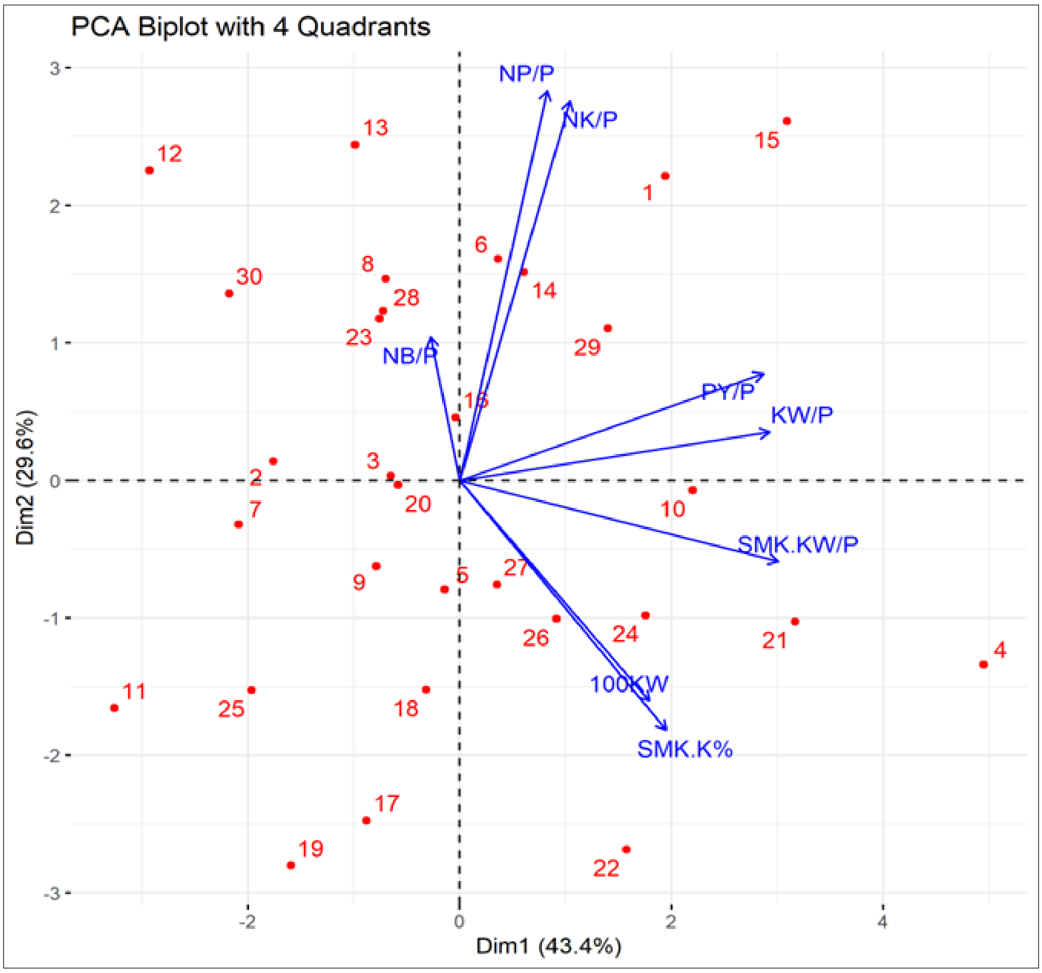

Fig 6. Biplot grouping genotypes are based on the first two principal components.

Acknowledgements

The authors profoundly thank Tamil Nadu Agricultural University for successfully conducting the research experiment.

Authors' contributions

PY conducted the experiments, analyzed the data and wrote the first draft of the research paper. AS performed statistical analysis and assisted in writing the research paper. VAV, CT, KS, RM arranged for the literary search and corrected the final draft and recorded the observations. SB participated in the design of the study data analysis and editing the manuscript. VV coordinated in the field experiments, collection and compilation of data. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

References

1. FAOSTAT. Statistical databases of the Food and Agricultural Organisation (FAO), Rome. 2021. https://www.fao.org/faostat
2. Agricultural Market Intelligence Centre, PJTSAU. Groundnut Outlook. 2024. https://pjtsau.edu.in/files/AgriMkt/2024/January/groundnut-January-2024.pdf
3. Sharma D, Joshi A, Jain D, Singh P, Choudhary R. Biochemical characterization of oil from groundnut (*Arachis hypogaea* L.) genotypes. Int J Plant Soil Sci. 2017;15(5):1-5.
4. Dwivedi SL, Thendapani K, Nigam SN. Stability of seed mass in confectionery groundnut. Int Arachis Newslett. 1988;3:14-6.
5. Patil AS, Salunke MD. Breeding for quality traits in groundnut. Popular Kheti. 2014;2(2):173-8.
6. Kona P, Mahatma MK, Gangadhara K, Ajay BC, Narendra Kumar, Kiran Kumar Reddy et al. Evaluation and identification of promising advanced breeding lines for quality and yield traits in groundnut (*Arachis hypogaea* L.). Int J Agric Sci. 2021;17(2):280-6. https://doi.org/10.15740/HAS/IJAS/17.2/280-286
7. Chunilal, Hariprasanna. Breeding for confectionery groundnut. In: Basu MS, Singh NB, editors. Groundnut research in India. Junagadh: National Research Centre for Groundnut. 2004:48-56.
8. Singh S, Pawar IS. Theory and application of biometrical genetics. India: CBS Publishers; 2005.
9. Bhandari HR, Bhanu N, Srivastava A, Singh K, Shreya, Hemantaranjan A. Assessment of genetic diversity in crop plants - an overview. Advances Plants Agric Res. 2017;7(3):279-86.
10. John K. Correlation and path coefficient analysis for yield and its related traits in groundnut - a review. East African Scholars J Agri Life Sci. 2019;2(1):4-9. https://doi.org/10.36349/easjals.2019.v02i01.002
11. Dwivedi SL, Nigam SN. Confectionery groundnut: issues and opportunities to promote export and food uses in India. J Oilseeds Res. 2005;22(1):1-4.
12. Gali Suresh DL, Reddy A, Rajesh P, John K, Sudhakar P, Rao VS. Genetic divergence analysis in confectionery peanut (*Arachis hypogaea* L.). Biological Forum. 2023;15(11):218-22.
13. Ali S, Ahmad R, Hassan MF, Ibrar D, Iqbal MS, Naveed MS et al. Groundnut genotypes' diversity assessment for yield and oil quality traits through multivariate analysis. SABRAO J Breed Genet. 2022;54(3):565-73. https://doi.org/10.54910/sabrao2022.54.3.9
14. Deepa G, Laxmi M, Patil C, Nandini B, Motagi BN. Confectionery groundnut genotypes (*Arachis hypogaea* L.): a study on genetic variability parameters with special reference to confectionery traits improvement. Int J Environ Climate Change. 2023;13(11):332-44. https://doi.org/10.9734/IJECC/2023/v13i113176
15. Abady S, Shemelis H, Pasupuleti J, Mashilo J, Chaudhari S, Manohar SS. Assessment of the genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes for kernel yield, oil and fodder quantity and quality under drought conditions. Crop Sci. 2021;1-18. https://doi.org/10.1002/csc2.20483
16. Ward JH. Hierarchical grouping to optimize an objective function. J American Stat Assoc. 1963;58:236-44.
17. Rao RC. Advanced statistical methods in biometric research. New York: John Wiley & Sons; 1952.
18. Al-Jibouri HA, Miller PA, Robinson HV. Genotypic and environmental variances and co-variances in an upland cotton cross of interspecific origin. Agron J. 1958;50:633-36.
19. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed products. Agron J. 1959;1:515-20.
20. Pearson K. On lines and planes of closest fit to systems of point in space. Philos Mag. 1901;2(11). https://doi.org/10.1080/14786440109462720
21. R Studio Team. R Studio Desktop IDE (Version 2023.06.0-421). 2023. https://posit.co/products/open-source/rstudio
22. Mumm RH. The process of cultivar development: pure line variety. In: Suza WP, Lamkey KR, editors. Cultivar Development. Iowa State University Digital Press; 2023.
23. Venkateswara Rao, Pandiyan M, Manivannan M, Chandrasekhar CN, Harisudhan C. Understanding combining ability, heterosis and relationships of pod yield and yield contributing traits in groundnut (*Arachis hypogaea* L.). 2023;15(2):1-10. https://doi.org/10.37992/2024.1502.037
24. Gangadhara K, Ajay BC, Kona P, Rani K, Kumar N, Bera SK. Performance of some early-maturing groundnut (*Arachis hypogaea* L.) genotypes and selection of high-yielding genotypes in the potato-fallow system. PLoS One. 2023;18(4):e0282438. https://doi.org/10.1371/journal.pone.0282438
25. Reddy P, Sabara P, Padhiyar SM, Kulkarni GU, Sapara GK, Tomar RS. Correlation and path analysis among agromorphological traits in groundnut (*Arachis hypogaea* L.). Annals Arid Zone. 2023;62(3):227-34. https://doi.org/10.59512/aaz.2023.62.3.5
26. Suvarna C, Vasanthi RP, Viswanath K, Kiran Kumar Reddy C, Amaravathi Y. Combining ability analysis for yield, yield attributes and quality traits in groundnut (*Arachis hypogaea* L.). Electron J Pl Breed. 2024;15(2):496-503. https://doi.org/10.37992/2024.1502.051
27. Bertan I, Fernando IF, de Carvalho A, Oliveira AC. Parental selection strategies in plant breeding programs. J Crop Sci Biotech. 2014;10(4):211-22.
28. Habite DN. Principal component analysis and genetic divergence studies for yield and yield-related trait of groundnut (*Arachis hypogaea* L.) genotypes at Pawe North Western Ethiopia. EAS J Biotechnol Genet. 2023;5(3):59-63. https://doi.org/10.36349/easjbg.2023.v05i03.005
29. Allard R. Principles of plant breeding. New York: John Wiley & Sons; 1960:485.
30. Shoba D, Manivannan N, Vindhiyavarman P. Correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.). Madras Agric J. 2012;99(1-3):18-20.
31. Sukrutha B, Reddy CK, Madhuri KV, Reddy BR, Kumar AR,

Vemireddy LN et al. Principal component analysis and path coefficient analysis for groundnut yield and seed quality attributes (*Arachis hypogaea* L.). Legume Res. LR-5075. https://doi.org/10.18805/LR-5075

32. Shankar M, Harish Babu BN, Gobu R, Sheshaiah. A study of correlation and path analysis in peanut (*Arachis hypogaea* L.). Bull Env Pharmacol Life Sci. 2018;7(12):111-4.
33. Sandhya Kiranmai M, Venkataravana P, Pushpa HD. Correlation and path analysis studies in groundnut under different environment. Legume Res. 2016;39(6):1048-50. https://doi.org/10.18805/lr.v0iOF.4484
34. Ravi Kumar D, Sekhar MR. Character association and path analysis in groundnut (*Arachis hypogaea* L.). Int J Appl Biol Pharma Technol. 2012;3(1):385-9.
35. Rajesh Kumar S, Sekhar MR. Correlation and path analysis studies on F2 generation of groundnut (*Arachis hypogaea* L.) for yield and its attributes. Bioscan. 2016;11(3):1895-8.
36. Sumathi P, Muralidharan V. Genetic analysis for quality traits in large seeded groundnut (*Arachis hypogaea* L.) genotypes. J Res ANGRAU. 2007;37(1/2):26-33.
37. Dhaliwal GPS, Nagada AK, Mittal VP. Inter trait associations and path analysis studies in groundnut (*Arachis hypogaea* L.). J Crop Improv. 2010;37(1):57-60.
38. Iezzoni AF, Pritts MP. Applications of principal component analysis to horticultural research. Hort Sci. 1991;26(4):334-8. https://doi.org/10.21273/HORT.SCI.26.4.334
39. Anderson TW. An introduction to multivariate analysis. New Delhi: Wiley Eastern Private Limited; 1972.
40. 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;SP-7(5):194-7. https://doi.org/10.33545/2618060X.2024.v7.i5Sc.781
41. Vishnuprabha RS, Viswanathan PL, Manonmani S, Rajendran L, Selvakumar T. Evaluation of variability and principal component analysis in segregating populations of groundnut (*Arachis hypogaea* L.). Plant Sci Today. 2025;12(1):1-10. https://doi.org/10.14719/pst.4025
42. Pushpa R, Shanmugam A, Arulmozhi R, Sassikumar D, Suresh R, Subrahmaniyan K. Exploring genetic variability, diversity and trait associations in sunnhemp (*Crotalaria juncea* L.) accessions for yield improvement. Plant Sci Today. https://doi.org/10.14719/pst.3929

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.