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Research Article

Assessment of the genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes for kernel yield

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Abstract
The current study was conducted to determine the genetic diversity present among the popular varieties and advanced cultures of groundnut. Genotypic correlation between single plant yield with number of pegs/plant and number of pods/plant was significant and positive. High heritability along with high genetic advance as a percentage of mean was found for plant height, no. of branches/plant, no. of pegs/plant, no. of pods/plant, hundred kernel weight and pod yield/plant. The 46 genotypes were grouped into five clusters based on D^2 analysis. The highest intra-cluster distance was recorded for cluster VI followed by clusters II, I, III and V. Maximum inter-cluster distance was observed between clusters IV and V followed by clusters II and V. Minimum inter-cluster distance was observed between clusters I and II. PCA was used to estimate the relative contribution of various traits to the total variability. Three components (PC1, PC2 and PC3) were found to have more than one eigenvalue and they accounted for 67.23 *per cent* of the variability of the genotypes used.

Keywords: Groundnut, Variability, Heritability, Correlation, D^2 analysis, PCA.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a member of the *Fabaceae* family, a legume crop, cultivated for food and oil around the world. It is cultivated widely throughout the world and the top five groundnut-producing countries are Nigeria (13.09%), China (15.20%), Sudan (10.57%), and Senegal (3.75%) (https://www.fao.org/faostat/ 2021). India is one of the world's leading cultivators of groundnut, with an annual area coverage of 54.2 lakh hectares and the second-largest producer with an annual production of 101 lakh tonnes and a productivity of 1863 kg per hectare during 2021–22 (https://agricoop.gov.in/ en/StatHortEst). The oil (48–50%) and protein (25-28%) in groundnut kernels are considered an important source of energy. The haulms supply animals with nutrient-rich fodder which are rich in carbohydrate (38–45%) than typical cereal fodder, containing 8-15% of protein, 1-3% of lipids, 9-17% of minerals, and 8-15% of fat. Groundnut is a rich source of oil, protein, carbohydrates, minerals (*e.g.*, P, Ca, Mg, and K), and vitamins (E, K, and B). When designing breeding programs for crops with high yield potential, knowledge of genetic diversity is very important. Understanding the existing variability, the strength of the correlation between the yield-contributing features, and the respective contributions of each to the yield are necessary for creating high-yielding varieties of groundnut. Breeders can utilize heritability and genetic advancement to determine the direction and strength of selection (Jain. 2000). Studies of correlation offer the chance to examine the strength and direction of the relationship between yield and also among various components.

Calculating genetic divergence between genotypes and relating geographic origin to clustering patterns are both possible using the Mahalanobis D^2 (Rao, l952) statistics. Cluster analysis and Principal Component Analysis (PCA) are the most recommended methods for estimating

genetic variability and is used to investigate the patterns of variation among the genotypes. Through the use of principal component analysis (PCA), potential breeding sources could be identified, and evaluation of variations based on a variety of agronomic parameters could be made as potential selection methods (Sudhir *et al*., 2010). Hence, for refining selection and yield levels in groundnut study of genetic variability, heritable variation, character association, and diversity was carried out.

MATERIALS AND METHODS

Forty-six groundnut genotypes including released varieties were raised during *rabi* 2022 at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore in Randomised block design (RBD) with three replications (**Table 1**). The genotypes were raised with the spacing of 30x10 cm and all agronomic practices were carried out at precise stages of crop growth. Observations were recorded on five randomly selected plants in each genotype in each replication for the characters *viz*., plant height (PH), number of primary branches/plant (NB), number of matured pods/plant (NP), number of peg/plant (NPeg), 100-kernel weight (100Kwt) and pod yield/plant (SPY) and for days to 50% flowering (DFF) on plot basis. Genetic variability parameters like genotypic, phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, and genetic advance were calculated using R Studio software. The phenotypic and genotypic components of variances based on analysis of variance were estimated as per Johnson *et al*. (1955). Genetic diversity among genotypes was analysed by Mahalanobis's generalized distance D^2 (1936) method using TNAUSTAT software and the grouping of genotypes was done based on Tocher cut-off value, as described by Rao (1952).

PCA was computed from correlation matrices using SAS Procedure PRINCOMP in order to assess the patterns of phenotypic trait variation considering all variables simultaneously.

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed significant differences among 46 genotypes for all the characters suggesting the presence of extensive amount of variability among the genotypes studied (**Table 2**). The genotypic and phenotypic variances were calculated using respective mean square values from the variance table. It was observed that there was a closer correspondence between GCV and PCV (**Table 3**) for all the traits. The components

Table 1. List of groundnut genotypes used for the study

S. No	Genotype	Botanical group	Habit	S. No	Genotype	Botanical group	Habit
1	ALR 1	Virginia	Semi-spreading	24	K9	Spanish	Bunch
2	ALR 2	Spanish	Bunch	25	DHARANI	Spanish	Bunch
3	ALR 3	Spanish	Bunch	26	TAG 24	Virginia	Semi-spreading
4	BSR 1	Spanish	Bunch	27	TG 37-A	Spanish	Bunch
5	BSR 2	Spanish	Bunch	28	GPBD 4	Spanish	Bunch
6	CO 1	Spanish	Bunch	29	JL 24	Spanish	Bunch
7	CO 2	Spanish	Bunch	30	WESTERN 44	Virginia	Semi-spreading
8	CO 3	Spanish	Bunch	31	ASHA	Virginia	Semi-spreading
9	CO 4	Spanish	Bunch	32	AK 303	Virginia	Bunch
10	CO 5	Virginia	Semi-spreading	33	GANGAPURI	Valencia	Bunch
11	CO 6	Virginia	Semi-spreading	34	R 2001/2	Spanish	Bunch
12	CO 7	Spanish	Bunch	35	COG 0537	Spanish	Bunch
13	TMV 1	Virginia	Spreading	36	COG 0539	Spanish	Bunch
14	TMV 10	Virginia	Semi-spreading	37	CHICO	Spanish	Bunch
15	VRI 4	Spanish	Bunch	38	COG 17007	Spanish	Bunch
16	VRI 5	Spanish	Bunch	39	GIRNAR 4	Virginia	Bunch
17	VRI 6	Spanish	Bunch	40	GIRNAR 5	Virginia	Bunch
18	VRI 7	Virginia	Semi-spreading	41	TMV 2	Spanish	Bunch
19	VRI 8	Spanish	Bunch	42	TMV 7	Spanish	Bunch
20	GG 20	Virginia	Semi-spreading	43	TMV 13	Spanish	Bunch
21	GG 33	Virginia	Semi-spreading	44	TMV 14	Spanish	Bunch
22	GG 7	Spanish	Bunch	45	VRI 3	Spanish	Bunch
23	K 6	Spanish	Bunch	46	VRI 2	Spanish	Bunch

Table 2. Analysis of variance for eight quantitative characters in groundnut genotypes

Source of variation	df	DFF	PH (cm)	NB	Npeg	NP	100 Kwt (g)	SPY (g)
Replications	2	3.41	39.12	8.46	13.19	3.51	19.25	42.083
Genotypes	45	36.48**	68.57**	27.85**	280.11**	238.97**	103.45**	61.57**
Error	90	0.836	1.487	1.4712	5.28	7.7	2.5	1.856

* and **= Significant at 5% probability level and highly significant at 1% probability level respectively
DFF= Days to 50% flowering, PH=Plant height (cm), NB=Number of branches per plant, Npeg=Number of pegs per plant, NP=Number of pods per plant, 100Kwt=100 kernel weight(g), SPY=Pod yield/plant (g).

Table 3. Estimates of variability parameters for groundnut genotypes

Characters	δ^2 g	δ^2 p	GCV %	PCV %	h^2_b%	GA	GAM
DFF (days)	11.88	12.71	7.44	7.69	93.00	6.86	14.81
PH (cm)	22.36	23.85	13.68	14.13	94.00	9.43	27.30
NB	8.79	10.26	30.81	33.29	86.00	5.65	58.75
Npeg	91.61	96.89	23.71	24.38	95.00	19.17	47.49
NP	77.09	84.78	37.48	39.32	91.00	17.25	73.64
100Kwt (g)	33.65	36.15	17.74	18.39	93.00	11.53	35.26
SPY (g)	19.90	21.76	25.52	26.69	91.00	8.79	50.28

σ^2g = Genotypic variance, σ^2p= Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2_b= Heritability in broad sense, GA= Genetic advance, GAM = Genetic advance as percentage of mean.

of variance showed that the phenotypic coefficients of variance (PCV) were higher than the genotypic coefficients of variance (GCV). Similar results were also reported by Bhargavi *et al*. (2016) and Chaudhari *et al*. (2017). Higher GCV and PCV values observed for the number of pods per plant (37.48), number of branches per plant (30.81), single plant yield (25.52), and moderate values for the number of pegs per plant (23.71), yield (22.97), hundred kernel weight (17.71) and plant height (13.68). Higher the genetic component of variation in these characters, the greater the scope for its improvement through selection. These results are confirmative with the findings of John *et al*. (2007) for kernel yield per plant and pod yield per plant. Low differences between phenotypic and genotypic coefficients of variation suggest less influence of environment on the expression of the traits.

Heritability estimates provide information about the variation attributes due to additive genetic effect and the phenotype strongly reflects the genotype. In the present study, all the characters recorded high heritability indicating that these characters were less influenced by the environment. High heritability coupled with high genetic advance as percent of mean was observed for plant height (27.3), number of primary branches/plant (58.75), number of pegs/plant (47.49), number of pods/plant (73.64), 100 kernel weight (35.26) and pod yield/plant (50.28) showed the presence of lesser environmental impact and occurrence of additive gene action in their expression and suggesting the possibility of improving these characters through selection. These results are in accordance with earlier reports of Sawargaonkar *et al*. (2010) for kernel yield per plant and pod yield per plant.

The genotypic correlation coefficients obtained from 46 genotypes for seven yield components are presented in **Table 4.** The study of the interactions and relative contributions of many traits to crop development is greatly facilitated by genetic association. Correlation coefficients were categorized as weak (0.0–0.4), moderate (0.4–0.6) and strong (0.6–1.0) (Belsley *et al*., 2005).

The estimation of the genotypic correlation coefficient revealed that the single plant yield exhibited positive and highly significant association with number of pegs per plant (r=0.415) and number of pods per plant (r=0.487) (**Table 4**). Similar kind of results were observed between the no. of pods/plant and single plant yield by Reddy *et al*. (2017). Hence, these characters could be given due emphasis in formulating selection criterion for improvement of yield in groundnut. Considering intercorrelation between yield component traits, 100 kernel weight had a positive and significant correlation (p<0.001) with days to 50% flowering (r=0.366) and number of pegs per plant showed a positive and significant association with number of primary branches/plant and the number of pegs per

Table 4. Estimates of Genotypic correlation coefficient among yield and yield Contributing characters in groundnut

	DFF	PH	NB	Npeg	NP	100 Kwt (g)	SPY(g)
DFF (Days)	1.000	0.031	0.151	0.017	-0.223	0.366**	-0.16
PH (cm)		1.000	0.196	0.11	0.170	0.168	0.040
NB			1.000	0.404**	0.213	0.229	0.117
Npeg				1.000	0.099	0.103	0.415**
NP					1.000	-0.185	0.487**
100 KWt (g)						1.000	0.066
SPY (g)							1.000

plant had a positive and significant correlation with the number of branches per plant (r=0.40) and single plant yield (r=0.42) and non-significantly correlated with other characters.

Based on Mahalanobis D² statistic, total 46 genotypes were grouped into five clusters. The highest numbers of groundnut genotypes were grouped in cluster I (35 entries) followed by cluster II which contained seven entries, Cluster IV which contained two genotypes. The cluster III and V were represented by a single genotype each (**Table 5**).

Among the clusters, maximum intra-cluster distance was recorded by Cluster IV (378.74) followed by cluster II (259.55). Maximum inter-cluster distance was recorded between the clusters IV and V (D^2=2398.73) followed by cluster I and V (D^2=1296.37) (**Table 6**).

Hybridization between genotypes of such wide clusters could result in hybrids with high heterosis and they are also likely to result in better segregants. The minimum inter-cluster distance was observed between the clusters I and II (D^2=309.61). Similar results were observed by Mahesh (2017) and Yadav *et al*. (2023), who revealed grouping of 40 genotypes into six clusters and 96 genotypes were grouped into eight clusters in groundnut respectively. Cluster mean values of all the characters are depicted in **Table 7**. Among the mean values of different characters, cluster II had a low mean value for days to 50% flowering (early maturing genotypes).

The mean value of the number of branches per plant was high in cluster III, hence it showed superior vegetative growth. The cluster mean value for single plant yield was high in cluster II followed by cluster IV. Genotypes in the above clusters could be used as parents for the improvement of yield (Upadhya *et al*., 2005 and Leonard and Peter, 2009).

Principle component analysis: The purpose of PCA is to obtain a small number of factors that account for

Table 5. Clustering pattern of 46 genotypes and name of the genotypes

Cluster No.	Number of genotypes	Name of genotypes
Cluster I	35	ALR 1, ALR 2, CO 2, C0 3, C0 4, CO 5, CO 6, CO 7, TMV1, TMV 7, TMV10, TMV13, VRI2, VRI3, VRI5, VRI6, VRI7, VRI 8, GG 20, GG33, GG 7, K 6, K9, DHARANI, TAG 24, GPBD 4, JL 24, WESTERN 44, AK 303, GANGAPURI, R2001/1, CO0539, COG 17007, GIRNAR 4, GIRNAR 5
Cluster II	7	ALR 3, BSR 1, BSR 2, CO 1, TG 37 A, TMV 2, TMV 14
Cluster III	1	CHICO
Cluster IV	2	VRI 4, ASHA
Cluster V	1	COG 0537

Table 6. Inter and Intra (diagonal) cluster distance in groundnut

Cluster	I	II	III	IV	V
I	**200.60**	309.61	463.82	428.10	1296.37
II		**259.55**	621.72	581.99	1696.69
III			**0.00**	1194.74	408.82
IV				**378.74**	2398.73
V					**0.00**

Table 7. Mean performance of clusters for seven traits in groundnut

	DFF (Days)	PH (cm)	NB	NPeg	NP	100Kwt (g)	SPY (g)
I	46.70	33.65	9.82	39.82	22.46	32.93	17.20
II	43.19	39.71	8.57	44.86	31.57	29.90	**20.21**
III	49.67	38.60	**13.33**	49.67	23.33	32.10	16.77
IV	48.67	35.37	8.50	28.33	13.17	38.77	12.45
V	48.67	24.50	8.67	43.00	20.67	32.33	18.87

Table 8. Proportion of variance and Eigen values of PCs

Principal Components	Eigen Values	Proportion of Variance (%)	Cumulative Proportion (%)
PC1	**2.012**	28.74	28.74
PC2	**1.703**	24.32	53.07
PC3	**1.002**	15.16	67.23
PC4	0.803	11.39	78.62
PC5	0.722	10.23	88.85
PC6	0.561	8.01	96.86
PC7	0.219	4.14	100

maximum variability out of the total variability. The results of the principal component analysis for seven characters of 46 groundnut genotypes are depicted in table 8. The PCA of 46 accessions based on the correlation matrix yielded seven eigenvectors. The disparity among 46 groundnut genotypes was assessed through principal component analysis based on the morphological traits. Principal components (PCs) with eigenvalues greater than unity, and component lodgings greater than ± 0.3 were considered to be meaningful and valuable (Hair et al., 1998).

In the present study, among the seven principal components PC1, PC2 and PC3 had greater than one eigen value (2.012, 1.703 and 1.002 respectively). The first three principal components for (PCs) accounted 67.23% of the total variation. The first principal component had an eigen value of 2.012 and explained 28.74% of the total variation.

The variation in principal component (1) was mainly due to the positive loading effect of pod yield/plant (SPY) (0.521), number of pegs/plant (0.493), number of pod per plant (0.458) and number of branches/plant (0.438) mostly traits which have ± 0.3 are important contributors for the total variation. Similar results, were reported by Patil et al. (2020), Ali et al. (2022) and Habite and Sendekie (2023).

The biplot diagram depicts how the characters interact as well as which genotypes are more advantageous for the attributes. High levels of variation were observed both in the biplot diagram and between the genotypes and parameters. Each trait's vector length showed its greater contribution to the total divergence (**Fig. 1)**. Biplot between PC1 and PC2 explained the variation between seven quantitative characters along one and two principal component vectors PC1 and PC2, whose variation accounted for 28.74% and 24.32% respectively. Similarly, the principal components 1 and 2 whose variation accounted for 25.89% and 16.21% respectively taken into consideration by Kumar *et al*. (2010).

Single plant yield showed maximum vector length indicating its contribution to the total divergence followed

Table 9. Character differentiation for Principal components

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DFF	-0.059	0.583	0.1074	0.2558	-0.4061	0.6438	0.0147
PH	0.255	0.1713	-0.8291	-0.0251	0.3720	0.2483	0.1330
NB	0.438	0.3160	-0.0405	-0.4899	-0.466	-0.3465	0.3600
Npeg	0.493	0.1282	0.3882	-0.4061	0.4005	0.2885	-0.4253
NP	0.458	-0.3602	-0.2475	0.2760	-0.4927	0.0015	-0.5294
100Kwt	0.123	0.5786	0.0328	0.4665	0.2219	-0.5573	-0.2677
SPY	**0.521**	-0.2236	0.2938	0.485	0.1649	0.1000	0.5654

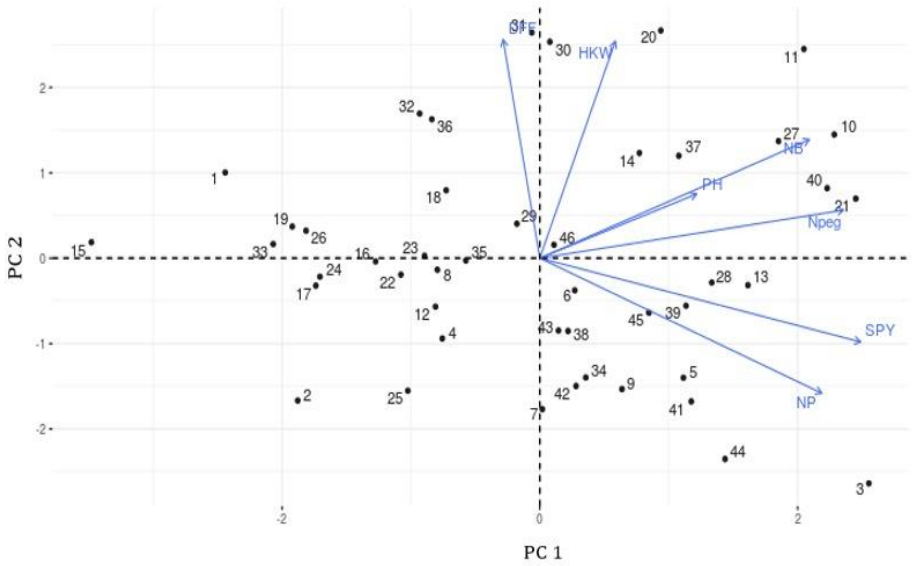

Fig 1. Biplot between PC1 and PC2

by number of pods per plant, number of pegs per plant and number of branches per plant. The direction of association between the traits indicated by the angle between the trait vectors. An acute angle (<90^0) between vectors indicates a positive correlation and a right angle (90^0) indicates no correlation and an obtuse angle (>90^0) indicates that there is a negative correlation between characters. Out of seven traits studied except hundred kernel weight and days to 50% flowering, all other traits showed positive correlation towards single plant yield. The genotypes that are present near the trait vector were found to be best performing for that particular trait. The genotypes *viz.*, TMV 1, GIRNAR 4, VRI 2, VRI 3, BSR 2, CO 1 and GPBD 4 along with other genotypes in the particular quadrant perform better for the trait yield single plant yield. Similar findings were reported by Ali *et al*. (2022) that genotypes in the particular quadrant along with PC4 was positively correlated with the characters like days to flower initiation, pods per plant, dry pod yield, and stearic acid, while negatively correlated for 20 pod length.

Pod yield/plant was the highest contributor for the variation in the first component The genotypes. TMV 1, BSR 2, TG 37 A, CHICO, GIRNAR 4, CO 1 and GPBD4 were identified as putative parents based on principal component analysis and the traits *viz.,* number of pods per plant, single plant yield, number of pegs per plant, plant height, number of branches per plant as important and they were also present in different clusters indicates that the selection would be effective for these genotypes.

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