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Research Note

Assessment of genetic diversity for yield, yield attributes and water use efficiency related traits in groundnut [*Arachis hypogaea* L.]

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Abstract
To establish the degree of genetic diversity for 14 quantitative parameters, 36 groundnut genotypes were investigated using the Mahalanobis D^2 Statistics. Tocher's method separated the entire genetic resource set into nine distinct, non-overlapping clusters demonstrating the presence of significant amount of genetic diversity. Cluster I had the maximum number of accessions (15), followed by cluster IV with 7 accessions, cluster VI with 5 genotypes, cluster V with 3 genotypes and cluster VII with 2 genotypes. The clusters II, III, VIII and IX were monogenotypic. The inter-cluster distance was maximum between the clusters VI and IX. Shelling percent contributed maximum to the genetic divergence followed by pod yield plant^{-1}. Hence due emphasis should be given to these traits as improvement of these characters would result in increase in pod yield plant^{-1}.

Keywords: Groundnut, D^2 Statistic, Tocher's technique.

The cultivated groundnut (*Arachishypogaea* L.) is an allotetraploid crop with 2n=4x=40. It belongs to the sub-family Papilionaceae of the family Leguminosae. It holds the top spot in the country's edible oil business and is known as the "King of Oilseeds" and "Poor Man's Cashewnut" (Kumari and Sasidharan, 2020). It originated in South America and was domesticated in the Paraguayan valleys. It is cultivated as a main crop, an intercrop or a combination of crops (Nageswara *et al.,* 1990; Ghosh, 2004). Because of its many uses, groundnut is now a valuable cash crop for domestic and international trade in a number of developing countries.

Globally, it is grown in an area of 29.92 Mha with annual production of 55.30 Mt and productivity of 1851 kg ha^{-1} (FAOSTAT, 2020-21). In India, groundnut covers an area of 6.09 Mha with a production of 10.21 Mt and productivity of 1676 kg ha^{-1}. In Andhra Pradesh, it covers an area of 0.87 Mha with a production of 0.78 Mt and productivity of 894 kg ha^{-1} (Directorate of Economics and Statistics, 2021).

It is mostly grown as a rainfed crop under irrigated cultivation in *rabi* season. Due to depletion of ground water resources, water shortage is commonly observed during the crop period in the *rabi* season. Therefore, it is necessary to identify the genotypes of groundnut with high water use efficiency (WUE). WUE is a crucial characteristic that boosts productivity when water supplies are scarce. The crop's productivity can be increased by locating genotypes that make better utilization of the limited water resources (Arunkumar *et al.,* 2017).

Specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) are associated with WUE in groundnut as surrogate traits to select the genotypes with high WUE (Sab *et al.,* 2018) which could ultimately lead to the evolution of better genotypes adapted to drought conditions. Success of plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants (Chavadhari *et al.,* 2017). Assessment of genetic diversity among the genotypes is very essential for the evolution of transgressive segregants or superior recombinants which is aided by the selection of diverse parents based on intra cluster, inter cluster and cluster mean distances (Hampannavar *et al.,* 2018). Hence an experiment was undertaken to assess genetic diversity among 36 groundnut germplasm accessions based on Mahalanobis D^2 Statistics.

Thirty six genotypes of groundnut were evaluated at dry land farm of S. V. Agricultural College, Tirupati, during *rabi,* 2021-22 in a Randomised Block Design (RBD) with three replications. In each replication, every genotype was sown in three rows of 3m length with a spacing of 22.5 cm between the rows and 10 cm between the plants within the row. Data was recorded on 14 morphological traits *viz.,* days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, kernel yield plant^{-1} (g), hundred kernel weight (g), shelling per cent, sound mature kernel per cent, harvest index (%), SPAD Chlorophyll Meter Reading at 60 DAS, Specific Leaf Area at 60 DAS (cm^2 gm^{-1}), Relative Water Content (%) and pod yield plant^{-1} (g) were recorded in five plants per replication and the mean data were subjected to statistical anlaysis. The genetic divergence analysis was carried out using Mahalonobis D^2 (1936) statistics and clustering was done by Tocher's method as described by Rao (1952). The data analyzed was performed using INDOSTAT software.

Analysis of variance (ANOVA) was performed using INDOSTAT software. ANOVA showed significant differences for all the studied characters across all genotypes, showing the presence of high variability (**Table 1**). Based on the D^2 values, the 36 genotypes were sorted into nine distinct, non-overlapping groups (**Table 2**). The clustering of the genotypes revealed that Cluster I had the most accessions (15), followed by Cluster IV with 7, Cluster VI with 5, Cluster V with 3, Cluster VII with 2genotypes and the clusters II, III, VIII and IX were monogenotypic*i.e.,* comprised of only a single genotype.

The intra and inter-cluster distances are furnished in **Table 3**. Cluster VI (304.88) recorded the greatest intra-cluster distance, followed by the cluster IV (235.43), cluster I (199.27), cluster V (196.14) and cluster VII (136.87). Hence genotypes from these clusters could be selected for hybridization programme for obtaining the desired segregants. Only single accession was found in each of the clusters II, III, VIII and IX indicating considerable genetic difference still exists amongst the genotypes. The greatest mean value for desirable qualities may be used as the basis for selection within these clusters. Hence the yield can be increased

Table 1. Analysis of variance for yield, yield attributes and Water Use Efficiency (WUE) related traits in 36 genotypes of groundnut

S.No.	Characters	Mean sum of squares		
		Replications (df:2)	Treatments (df:35)	Error (df:70)
1	Days to 50% flowering	2.815	14.701**	2.710
2	Days to maturity	1.861	18.198**	1.680
3	Plant height (cm)	1.685	56.210**	4.728
4	Number of primary branches plant^{-1}	0.328	3.831**	0.109
5	Number of secondary branches plant^{-1}	0.180	1.659**	0.069
6	Kernel yield plant^{-1}(g)	0.108	9.454**	0.476
7	Hundred Kernel Weight (g)	39.433	73.824**	24.466
8	Shelling per cent (%)	1.757	157.744**	17.271
9	Sound Mature Kernel (%)	112.236	270.267**	84.253
10	Harvest Index (%)	64.824	367.870**	67.886
11	SPAD Chlorophyll Meter Reading at 60 DAS	1.629	11.539**	4.670
12	Specific leaf area at 60 DAS (cm^2 gm^{-1})	259.032	3595.106**	407.379
13	Relative Water Content (%)	32.903	54.532**	23.053
14	Pod Yield Plant^{-1} (g)	0.285	19.792**	0.923

*Significant at 5% level; ** Significant at 1% level

Table 2. Clustering of genotypes of groundnut based on Tocher's method

S. No.	Cluster Number	Number of Genotypes	Genotypes
1	I	15	TCGS-2057, Rohini, TCGS-2227, TCGS-2038, TCGS-2219, TCGS-2068, TCGS-1798, TCGS-2044, Narayani, Dheeraj, TCGS-2004, TAG-24, Dharani, TCGS-2060
2	II	1	TCGS-2039
3	III	1	TCGS-2055
4	IV	7	TCGS-2052, K9, TCGS-2233, TCGS-2317, TCGS-2278, TCGS-2041 and TCGS-2217
5	V	3	TCGS-1694, TCGS-2049 and Greeshma
6	VI	5	TCGS-2235, Tirupati-1, Tirupati-4, K6 and TCGS-2229
7	VII	2	TCGS-2040 and TCGS-2223
8	VIII	1	TCGS-2230
9	IX	1	TCGS-2053

Table 3. Average Inter (above diagonal) and Intra cluster (diagonal) D^2 and D values (in parenthesis) for 9 clusters in 36 genotypes of groundnut

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	199.27 (14.12)	286.18 (16.92)	366.21 (19.14)	507.07 (22.52)	680.75 (26.09)	421.19 (20.52)	738.93 (27.18)	1390.32 (37.29)	2080.02 (45.61)
II		0.00 (0.00)	24.99 (5.00)	201.24 (14.19)	652.22 (25.54)	587.38 (24.24)	273.79 (16.55)	879.19 (29.65)	1004.15 (31.69)
III			0.00 (0.00)	199.08 (14.11)	710.73 (26.66)	740.62 (27.21)	274.24 (16.56)	770.98 (27.77)	874.55 (29.57)
IV				235.43 (15.34)	439.56 (20.97)	953.21 (30.87)	712.88 (26.70)	626.30 (25.03)	981.72 (31.33)
V					196.14 (14.00)	1146.57 (33.86)	1634.98 (40.43)	816.51 (28.57)	1846.08 (42.97)
VI						304.88 (17.46)	882.38 (29.70)	2438.09 (49.38)	2611.50 (51.10)
VII							136.87 (11.70)	1684.13 (41.04)	1064.39 (32.62)
VIII								0.00 (0.00)	1071.40 (32.73)
IX									0.00 (0.00)

through the use of recombination breeding by selecting the genotypes from these clusters. Similar results were earlier reported by John and Mylaswamy (1998).

Clusters VI and IX had the greatest intercluster distance (2611.50), followed by clusters VI and VIII (2438.09), I and IX (2080.02), V and IX (1846.08) and clusters VII and VIII (1684.13) which were all found to be divergent in decreasing order of their magnitude and could be utilized as parents for crossing programmes to produce high heterotic effects and trangressive segregants with high variability. A cluster diagram was made to depict the interrelationships between the various genotypes. Clusters VI and IX, which were the farthest apart (2611.50) displayed the greatest degree of divergence. On the other hand, of the nine clusters established, the inter cluster distance between cluster II and cluster III was the shortest (24.99) and thereby least genetic divergence.

Character-wise score across all nine clusters, as well as the cluster mean for traits are shown in **Table 4**. The cluster means were derived for all characters after the 36 genotypes were divided into nine groups. The clusters were ranked based on the aggregate score obtained from 14 attributes. Cluster-VII which received a total score of 39 for all the 14 characters ranked first followed by clusters-IX, II, III, VIII, IV, VI, I and V. These clusters demonstrated the presence of the promising genotypes and could be extensively used in upcoming breeding programmes for development of high yielding varieties with high water use efficiency.

The data suggested that for all the characters studied, genotypes with higher performance for one trait has the average performance for the other traits. Hence the idea of selecting a single genotype for immediate use was eliminated because no cluster in the current analysis

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Table 4. Cluster means for yield, yield attributes and Water Use Efficiency (WUE) related traits in 36 genotypes of groundnut

Clusters	Characters														Productivity Traits	
	DFF	DM	PH	NPB	NSB	KYP	HKW	SHP	SMK	HI	SCMR	SLA	RWC	PYP	Total Score	Final Rank
I	27.20(9)	106.73(7)	33.69(3)	4.88(7)	1.36(6)	10.48(7)	50.88(3)	74.84(3)	51.33(5)	45.33(9)	47.27(7)	211.89(5)	82.79(9)	14.00(7)	87	8
II	26.33(5)	107.00(8)	34.60(5)	5.80(3)	2.40(2)	11.99(4)	**53.93(1)**	71.05(4)	60.03(2)	45.63(7)	48.47(6)	218.43(7)	85.56(4)	16.88(6)	61	3
III	27.00(7)	107.33(9)	33.33(2)	4.52(8)	1.47(5)	12.31(3)	48.53(8)	70.17(5)	57.33(4)	51.73(6)	48.63(4)	**165.61(1)**	**88.60(1)**	17.54(3)	66	4
IV	26.29(4)	106.05(5)	37.15(7)	5.59(4)	1.33(7)	11.06(6)	50.34(5)	65.79(6)	49.38(6)	55.5(5)	48.77(3)	202.32(3)	85.70(3)	16.82(5)	69	6
V	25.78(3)	106.67(6)	39.50(9)	5.29(5)	1.0(8)	8.04(9)	48.22(9)	60.10(8)	43.70(9)	59.58(4)	46.07(8)	219.78(8)	85.82(2)	13.41(9)	97	9
VI	26.53(6)	105.60(4)	38.65(8)	4.91(6)	1.91(4)	11.25(5)	49.73(7)	**81.06(1)**	48.25(8)	45.41(8)	45.71(9)	209.33(4)	83.57(8)	13.87(8)	86	7
VII	25.33(2)	105.50(3)	34.65(6)	6.74(2)	2.23(3)	14.43(2)	51.03(2)	75.84(2)	58.93(3)	64.46(3)	**49.70(1)**	171.71(2)	85.03(6)	19.03(2)	39	1
VIII	**24.33(1)**	**103.67(1)**	**26.13(1)**	3.87(9)	**2.47(1)**	10.00(8)	50.80(4)	57.26(9)	49.20(7)	69.79(2)	48.53(5)	226.22(9)	85.23(5)	17.46(4)	66	4
IX	27.33(8)	104.67(2)	34.11(4)	**8.82(1)**	0.80(9)	**15.36(1)**	50.13(6)	63.60(7)	**63.80(1)**	**71.45(1)**	49.50(2)	217.65(6)	84.25(7)	**24.14(1)**	56	2
Mean	**26.24**	**105.91**	**34.65**	**5.60**	**1.67**	**11.66**	**50.40**	**68.86**	**53.55**	**56.55**	**48.07**	**204.77**	**85.17**	**17.02**		

Note: Numbers in the parenthesis indicates the ranks based on cluster mean. Total score is the summation of rank numbers for all characters, based on which final rank indicated. Bold numbers indicated highest mean values for each character.

DFF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPB : No. of primary branches plant^{-1}
NSB : No. of secondary branches plant^{-1}
KYP : Kernel yield plant^{-1} (g)
HKW : Hundred Kernel Weight (g)
SP : Shelling per cent (%)
SMK : Sound Mature Kernel (%)
HI : Harvest Index (%)
SCMR : SPAD Chlorophyll Meter Reading at 60 DAS
SLA : Specific Leaf Area at 60 DAS (cm^2 gm^{-1})
RWC : Relative Water Content (%)
PYP : Pod Yield Plant^{-1} (g)

Table 5. Relative contribution of various characters towards genetic diversity in groundnut

S.No.	Characters	Number of times ranked first	Contribution (%)
1	Days to 50% flowering	0	0.00%
2	Days to maturity	0	0.00%
3	Plant height (cm)	0	0.00%
4	No. of primary branches plant^{-1}	0	0.00%
5	No. of secondary branches plant^{-1}	5	0.79%
6	Kernel yield plant^{-1} (g)	24	3.81%
7	Hundred Kernel Weight (g)	0	0.00%
8	Shelling Per cent	234	37.14%
9	Sound Mature Kernel (%)	0	0.00%
10	Harvest Index (%)	0	0.00%
11	SPAD Chlorophyll Meter Reading at 60 DAS	136	21.59%
12	Specific Leaf area at 60 DAS (cm2 gm^{-1})	2	0.32%
13	Relative Water Content (%)	0	0.00%
14	Pod Yield Plant^{-1} (g)	229	36.35%

was discovered to have at least one genotype with all the desirable characters. As a result, hybridization between the chosen genotypes from different clusters is necessary to properly combine all the desirable traits. (Gupta *et al.,* 2015).

Additionally, it was found that the relative contributions of several plant traits to divergence (**Table 5**) can assist breeders in selecting the ideal parents for hybridization and in developing efficient selections in succeeding generations. The trait, shelling percent was ranked first for 234 times and contributed the most to genetic divergence (37.14%). It was followed by pod yield plant^{-1}(36.35%), SPAD chlorophyll meter reading at 60 DAS (21.59%), kernel yield plant^{-1} (3.81%), number of secondary branches plant^{-1} (0.79%) and specific leaf area at 60 DAS (0.32%).

There was no genetic divergence associated with the attributes plant height, number of primary branches plant^{-1}, sound mature kernel percentage, hundred kernel weight, days to 50% flowering, days to maturity, harvest index and relative water content.

It could be concluded that it would be advantageous to hybridise genotypes across divergent clusters with highest mean values for the specific characters to produce superior hybrids. By comparing the genetic divergence between the clusters and *per se* performance of genotypes, the cross combinations K-6 × TCGS-2053 and TCGS-2235 × TCGS-2053 could be recommended to increase water use efficiency related traits in groundnut, whereas the cross combinations Greeshma× TCGS-2053 and TCGS-2223 × TCGS-2230 could be recommended to obtain transgressive segregants for yield and yield attributes.

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