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D^2 Analysis to Evaluate the Genetic Diversity of Peanut (*Arachis hypogaea* L.)

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ABSTRACT

Background: A complex quantitative characteristic, yield is heavily impacted by the environment. The productivity of groundnuts can be increased less effectively through direct selection for grain yield. The study aimed to determine the genetic diversity.

Methods: The Mahalanobis D^2 statistic was used to quantify the genetic diversity among 24 genotypes of groundnut for seven quantitative and six qualitative criteria.

Result: There is sufficient diversity among genotypes, as evidenced by the fact that all of the features in the ANOVA showed significance. High GCV and PCV values were seen for the traits primary-branches/plant (PB), secondary-branches/plant (SB), pod yield/plant (PY), sucrose content (SC), total free aminoacids (TFA), total soluble solids (TSS) and iron content (IC), demonstrating that these traits were well chosen. High heritability and genetic progress as a percentage of mean were observed for plant height, PB, SB, PY, Hundred-pod weight (100-PW), SC, TFA, TSS and IC, demonstrating additive gene-action is in charge of these traits. Twenty-four genotypes were divided into nine clusters using Tocher's method of clustering, with cluster I being the biggest with sixteen genotypes. Cluster VII and Cluster IX had the greatest inter-cluster distance, which showed that their individuals were more diverse (26.91). In order to obtain transgressive segregants for yield and yield parameters, taking into consideration the cluster distances and cluster means in the current experiment, an emphasis should be focused on establishing crossings between genotypes from clusters VII and VIII that are promising.

Key words: D^2, Genetic divergence, Groundnut.

INTRODUCTION

Groundnut is not only a major crop for oilseeds, but it is also a major crop for food and feed. It is a member of the 'Leguminosae' family and is endemic to South America. With a 2n = 40 diploid chromosome number, it is an allotetraploid crop that is self-pollinated. It is used for a wide range of things, including making particleboard from the shell and using the kernel for food or crushing it for oil. Its leaves can also be used as animal feed. Polyunsaturated fatty acids (PUFA) make up 32% and 46%, respectively, of the fats in groundnut oil. With its annual yield of 37.1 million tonnes and a productivity of 1405 kg ha^{-1}, it covers an area of 26.4 million ha worldwide India ranks second among different countries in groundnut production with an area of 6.01 million ha, 10.24 million tons of production and 1703 kg/ha of productivity (Ministry of Agriculture and Farmers Welfare, Govt of India 2020-21). In Andhra Pradesh, it is cultivated in an area of 0.87 Mha with production of 0.77 Mt and average productivity of 891 kg/ha (AICRP-Annual Report 2020-2021).

Increased production while concurrently enhancing one or more characteristics is the main objective of plant breeding projects (Mandal *et al*., 2017; Yusuf *et al*., 2017). It has been established that grain yield is a complex quantitative feature due to the interaction of various related components (Acquaah, 2009; Kiranmai *et al*., 2016). It has a low hereditary component and is greatly influenced by the environment in which one is raised (Luz *et al*., 2011; Mukherjee *et al*., 2016). Therefore, directly selecting for yield to increase groundnut output is less successful. However, the effectiveness of yield improvement can be improved by utilising the relationship between yield and the accompanying qualities it is correlated with. The most essential traits that contribute to progress could be clarified by employing correlation and path-coefficient analysis (Zaman *et al*., 2011). Compared to other crops, groundnut pods are more pertinent to trait association study because they may make correct selection prior to harvest impossible. But it has been proposed that the environment and/or the genotypes used could affect their estimates (Kiranmai *et al*., 2016)

A successful breeding programme requires the selection of genetically varied parents because it allows for the creation of new, enhanced cultivars with desirable

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features (Govindaraj, 2015; Niveditha *et al*., 2016). For the purpose of crop development, cluster and principal component analysis (PCA) are helpful tools for determining the genetic relationships among genotypes. This is because they combine genotypes that are genetically related and provide a scatter plot of genotypes with geometrical distances between them that accurately reflect their genetic distances with the least amount of distortion, respectively.

Because hybrids between genetically varied parents exhibit stronger heterosis than those between more closely related parents, genetic diversity assessment is a crucial stage in every crop development programme. We need good, various, favourable parental lines in order to have an improved line. In order to evaluate the type and extent of genetic diversity found in 24 groundnut genotypes, the current experiment was conducted.

MATERIALS AND METHODS

On a dry-land farm at the Regional Agricultural Research Station (RARS), Tirupati, ANGRAU which is located at an altitude of 182.9 metres above mean sea level, a field experiment was carried out in *Kharif* 2019 using a randomized block design (RBD) with three replications and a total of 24 groundnut genotypes (Table 1) released from RARS, Tirupati and Agricultural Research Station (ARS), Kadiri, ANGRAU and a few other popular varieties grown throughout India.

For each genotype of groundnut, observations on five competitive plants at random from each genotype were made on seven quantitative and six qualitative parameters, including plant height, number of primary and secondary branches per plant, pod yield per plant, hundred pod weight, hundred kernel weight, shelling percentage, oil content, protein content, total sucrose content, total free amino acids, total soluble sugars and seed iron and zinc content.

According to Lush (1940), Burton (1952), Allard (1960) and Johnson *et al*., (1955) genetic parameters, genotypic co-efficient of variation, heritability (h^2) and genetic progress as a percentage of mean were computed. Mahalanobis's D^2 statistics were used to analyse genetic divergence (1936). The Tocher's approach was used to cluster genotypes into groups as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA) was employed to analyze the genetic divergence and the outcomes revealed substantial differences for all examined variables, demonstrating that the

Table 1: Details of 24 groundnut genotypes used in the study.

Genotype	Pedigree	Released institute
JL-24	Selection from EC94943	ORS, Jalgaon
TPT-1	E.C-106983 × 3	RARS, Tirupati
TPT-2	GAUG- 1 × Nc.Ac.FLA.14	RARS, Tirupati
TPT-3	Selection from TMV-10, a Virginia bunch variety with variegated testa	RARS, Tirupati
TAG 24*	TGS-2 × TGE-1	BARC, Mumbai
TPT-4	JL-24 × Ah316/S	RARS, Tirupati
Narayani	JL 24 × Ah316/S	RARS, Tirupati
Kalahasti	TCG1709 × TCG1518	RARS, Tirupati
Kadiri-6 (K-6)	JL-24 × Ah 316/s	ARS, Kadiri
Prasuna	TCG1717 × TCG1518	RARS, Tirupati
Abhaya	K-134 × TAG 24	RARS, Tirupati
Greeshma	TIR46 × JUG37	RARS, Tirupati
Kadiri-7 (K-7)	{(ICGV 86522 × ICGV (FDRS) 10} × ICGV 91172	ARS, Kadiri
Kadiri-8 (K-8)	{(ICGV 86522 × ICGV (FDRS) 10} × ICGV 91172	ARS, Kadiri
Kadiri-9 (K-9)	Kadiri 4 × Vemana	ARS, Kadiri
KadiriHarithandra	91/57-2 × P I – 476177 (ICG × 930181P3)	ARS, Kadiri
Rohini	Tirupati 4 × TIR 45	RARS, Tirupati
Bheema	TAG 24 × TG 19	RARS, Tirupati
ICGV-00350	ICGV-87290 × ICGV-87846	RARS, Tirupati
Dharani	VRI-2 × TCGP-6	RARS, Tirupati
Kadiri Amaravati	Kadiri 6 × Nc.Ac. 2242	ARS, Kadiri
TCGS-1073	Narayani × JAL30	RARS, Tirupati
TCGS-1157	TAG 24 × Jyothi	RARS, Tirupati
TCGS-894	TIR 46 × Kadiri 134	RARS, Tirupati

*Hybridization with mutant TGS-2 obtained by irradiation with gamma rays (200 Gy) and mutant TGE-1 obtained by irradiation with X-rays (750 Gy).

ORS: Oil Seed Research Station; RARS: Regional Agricultural Research Station, Tirupati; BARC: Baba Atomic Research Station; ARS: Agricultural Research Station.

genotypes had sufficient variation (Table 2). The analysis of variance results agreed with those of Chandrasekhara *et al*. (2020), Jahanzaib *et al*. (2020), Shrotri *et al*. (2021), Preeti and Sikarwar (2022), John *et al*. (2013), Maurya *et al*. (2014), Vasanti *et al*. (2015) and Narasimhulu *et al* (2012). High phenotypic variety among genotypes makes it typically recommended to use them as donors in breeding programmes or to release them as commercial varieties.

High GCV and PCV values for the characters demonstrated successful character selection. These traits included the number of major branches (GCV-22.44%; PCV-27.07%), secondary branches (GCV-97.34%; PCV-119.9%), pod yield (GCV-22.41%; PCV-28.66%), sucrose content (GCV-38.61%; PCV-39.25%) and total free amino acids (GCV-29.0%; PCV-39.25%) (Table 3).

GCV and PCV were moderate for plant height (19.73% and 22.55%), hundred pod weight (18.49% and 23.3%), shelling percentage (14.78% and 21.81%), zinc content (14.16%) and shelling percentage (27.19%). Low values for the 100-kernel weight, oil content and protein content were discovered (GCV: 6.49%; PCV: 8.54%, respectively). Studies by Zaman *et al*. (2011), Mahesh *et al*. (2018), Bhargavi *et al*. (2016) and Shrotri *et al*. (2021) reported high GCV and PCV for the number of primary branches per plant, which was consistent with the findings of the current article. Similar high GCV estimates were found by Rathod and Toprope (2018) for the total soluble sugars and sucrose content.

In a broad sense, heritability ranged from 27.12% for zinc content to 99.13% for TFA. Pod yield/plant (H-61.15%; GAM-36.10), hundred pod weight (H- 62.97%; GAM-30.22),

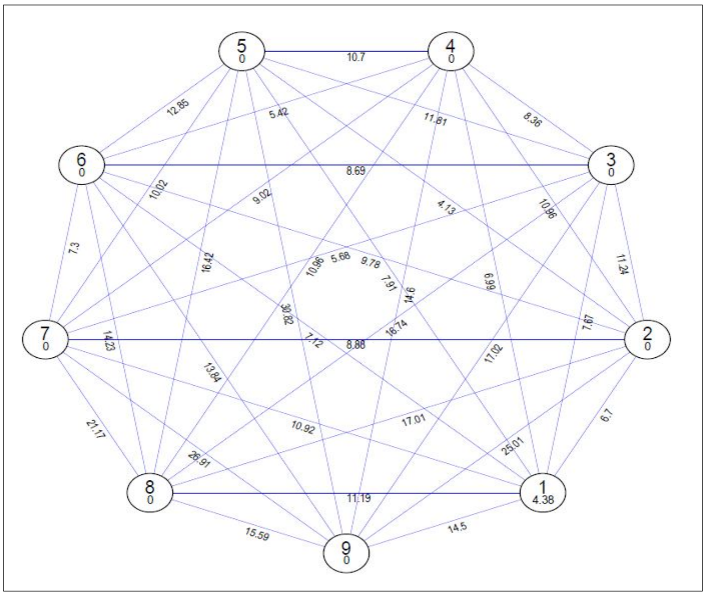

Fig 1: Mahalanobis euclidean distance by tochers method.

Table 2: Analysis of variance for yield and seed quality traits in groundnut.

Character	Mean sum of squares		
	Replications (df: 2)	Treatments (df : 23)	Error (df : 46)
Plant height	133.08	298.827**	27.71
Primary branches per plant	2.94	4.243**	0.56
Secondary branches per plant	0.13	2.660**	0.08
Pod yield per plant	4.97	30.948**	5.04
Hundred pod weight	285.89	1329.038**	217.79
Hundred kernel weight	36.15	144.416**	15.12
Shelling percentage	12.26	83.413**	16.33
Oil content	0.49	1.708**	0.06
Protein content	0.06	0.282**	0.07
Total free aminoacids (TFA)	6.31	22218.767**	64.76
Total soluble sugars (TSS)	0.02	0.062**	0.00
Total sucrose content	1.38	264.623**	2.91
Fe content	134.11	4359.679**	357.81
Zn content	48.76	194.429*	91.88

Table 3: Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as percent of mean for yield and seed quality traits in groundnut.

Character	General mean	Range		Variance		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance	Genetic advance as per cent of mean
		Max	Min	Genotypic	Phenotypic	Genotypic	Phenotypic			
Plant height (cm)	49.05	64.49	39.29	93.70	122.32	19.73	22.55	76.53	17.13	35.55
No. of primary branches	5.09	7.93	3.07	1.30	1.90	22.44	27.07	68.67	1.89	38.30
No. of secondary branches	0.69	2.13	0.00	0.45	0.69	97.34	119.92	65.89	1.46	162.78
Pod yield per plant (g)	13.20	18.80	10.40	8.76	14.29	22.41	28.66	61.15	4.75	36.10
Hundred pod weight (g)	106.61	149.33	76.00	388.48	617.03	18.49	23.30	62.97	31.46	30.22
Hundred kernel weight (g)	47.55	66.00	38.67	9.55	16.48	6.49	8.54	57.77	7.40	10.16
Shelling percentage (%)	73.29	80.82	63.05	117.29	255.68	14.78	21.81	45.94	15.56	20.64
Oil content (%)	47.92	48.87	45.87	0.55	0.61	1.55	1.63	90.60	1.46	3.04
Protein content (%)	26.17	26.80	25.57	0.07	0.14	1.01	1.44	49.64	0.39	1.47
Sucrose content (µg g^{-1})	24.19	38.22	8.86	87.24	90.06	38.61	39.25	96.78	18.93	78.25
Total free aminoacids (µg g^{-1})	296.33	586.60	196.80	7383.96	7449.42	29.00	29.13	99.13	176.25	59.48
Total soluble sugars (g/g)	0.37	0.60	0.14	0.02	0.02	38.54	39.48	95.30	0.29	77.51
Fe content (ppm)	83.09	206.67	37.83	1333.71	1691.68	43.96	49.50	78.85	66.81	80.41
Zn content (ppm)	41.30	57.33	28.23	34.22	126.11	14.16	27.19	27.12	6.27	15.19

Table 4: Distribution of the 24 groundnut genotypes in various clusters using Tocher's method.

Cluster	Number of genotypes	Genotypes
I	16	JL-24, TPT-1, TPT-2, TPT-4, Kadiri-6, Prasuna, Abhaya, Greeshma, Kadiri-9, K-Harithandra, Rohini, Dharani, Bheema, ICGV-00350, K-Amaravati, Dheeraj
II	1	TPT-3
III	1	Kadiri-8
IV	1	Nitya Haritha
V	1	TAG-24
VI	1	Narayani
VII	1	Kadiri-7
VIII	1	Pragathi
IX	1	Kalahasti

plant height (H-76.53%; GAM-35.55), number of primary branches/plant (H-68.67%; GAM-38.30), number of secondary branches/plant (H-65.89%; GAM-162.78), sucrose content (H-96.78%; GAM-78.25), total free aminoacids (H The percentage of kernels in a hundred (H-57.77%; GAM-10.16) and the shelling percentage (H-45.94%; GAM-20.64) both showed moderate heritability and GAM. Oil content showed high heritability and low GAM (H-90.6%; GAM-3.04).

Strong heritability and substantial genetic progress as a percentage of mean were found for pod yield/plant, as reported by Narasimhulu *et al*. (2012), Singh *et al*. (2017), Kumar *et al*. (2019) and Shrotri *et al*. (2021). Similar to the findings of Patil *et al*. (2014), there was a moderate heritability and a slight genetic advance as a percentage of the mean for 100 kernel weight. In the current investigation, the amounts of protein and oil showed small GCV and PCV levels. These results matched those from Mahesh *et al*. (2018), Omprakash and Nadaf (2017) and Vasanthi *et al* (2015).

Using D^2 values, 9 clusters were created from 24 genotypes (Table 4). The largest number of genotypes (16 genotypes) were found in cluster I, while all the other clusters only had one genotype. The categorization of genotypes in the current study did not match to breeding location or pedigree. There was more variation among the genotypes of different clusters, as evidenced by the fact that the inter-cluster distance (Table 5, Fig 1) was greater than the intra-cluster distance (Zaman *et al*., 2010). Cluster I recorded the most intra-cluster distance (4.38), while the other clusters with only one genotype each did not record any distance. The inter-cluster distance ranged from 4.13 to 26.91 on average. Clusters VII and IX had the greatest inter-cluster distance (26.91), indicating that their members were more diverse from one another. Elite genotypes from these various clusters can be used as parents in hybridization in order to produce transgressive segregants for yield and traits related to yield in later generations. Crossing between these genotypes will be advantageous for both generating

Table 5: Average intra- and inter cluster D^2 values among 24 groundnut genotypes.

	cluster I	cluster II	cluster III	cluster IV	cluster V	cluster VI	cluster VII	cluster VIII	cluster IX
Cluster I	**4.38**	6.7	7.67	6.99	7.91	7.12	10.92	11.19	14.5
Cluster II		**0**	11.24	10.96	4.13	9.78	8.88	17.01	25.01
Cluster III			**0**	8.36	11.81	8.69	5.68	16.74	17.02
Cluster IV				**0**	10.7	5.42	9.02	10.96	14.6
Cluster V					**0**	12.85	10.02	16.42	30.82
Cluster VI						**0**	7.3	14.23	13.84
Cluster VII							**0**	21.17	26.91
Cluster VIII								**0**	15.59
Cluster IX									**0**

Figures in bold indicate Intra cluster D^2 values.

Table 6: Cluster means for yield and seed quality traits in 24 groundnut genotypes (Mahalanobis's D^2 method).

Cluster no	Plant height	Primary branches/ plant	Secondary branches/ plant	Pod yield/ plant	100 Pod weight	100 Kernel weight	Shelling per cent
I	48.48	4.77	0.58	12.71	100.84	74.08	74.31
II	56.56	5.27	1.33	11.33	87.33	70.12	61.67
III	47.6	6.4	1.93	19.6	114	74.62	84
IV	40.04	5.2	1.13	13.35	110.33	69.94	77.47
V	33.01	4.4	1.6	9.87	67.33	74.62	50.33
VI	56.69	5	1.13	14.67	119.33	71.22	84.67
VII	43.99	7.87	3.13	18.53	140.67	70.58	99.33
VIII	19.27	1.73	0.8	5.73	64	42.01	40.33
IX	48.78	4.53	1.2	14.27	143.33	65.97	94
Cluster no	Oil content	Protein content	Total sucrose content	Total free aminoacids	Total soluble sugars	Iron content	Zinc content
I	48.12	26.14	25.58	285.93	0.35	81.28	39.13
II	47.9	25.77	16.05	279.45	0.33	161.97	47.55
III	46.9	26.6	15.92	253.67	0.24	55.92	49.12
IV	47.63	26.77	25.79	303.79	0.56	54.3	54.26
V	48	25.8	27.02	284.4	0.29	104.43	36.26
VI	47.73	26.37	27.77	501.6	0.53	92.23	49.19
VII	45.9	26.33	24.67	358.15	0.3	70.36	51.62
VIII	32.17	17.07	8.11	194.85	0.35	24.97	17.12
IX	47.83	26.3	22.2	278.53	0.6	109.17	49.19

diversity for desired characteristics and choosing superior recombinants for trait enhancement. John and Mylaswamy (1998) and Choudhary *et al*., (1998) published similar findings. The inter-cluster distance was found to be lowest (4.13) between clusters II and V, indicating a close link between the genotypes in these clusters.

The largest pod yield per cluster was in cluster VII (18.53) and the lowest pod yield per cluster was in cluster VIII (5.73) (Table 6). The shelling percentage varied from 99.33% (cluster VII) to 40.33%. (cluster VIII). Cluster VIII had the lowest cluster mean for 100-seed weight whereas Cluster III and V had the highest mean (74.62 g) for 100-Kernel weight (42.01 g). It has been suggested that elite genotypes from these clusters be crossed to produce a wide range of variability.

CONCLUSION

In order to obtain transgressive segregants for yield and yield characteristics, taking into account the cluster distances and cluster means in the current experiment, an emphasis should be focused on establishing crossings between genotypes from clusters VII and VIII that are promising. Similar to this, crosses between genotypes in clusters VI and VIII may result in transgressive segregants for seed quality measures. The information on cluster distance and cluster means for different objective traits will be useful to breeders in selecting genotypes for hybridization programmes.

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