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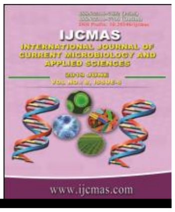

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Genetic Diversity Studies in Yield and its Contributing Traits in Groundnut (*Arachis hypogaea* L.) Genotypes using D2 Statistics

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ABSTRACT

Keywords

D2 statistics, Groundnut, Cluster, Yield, Cluster distance and Percent of contribution

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An experimental trial consisting of 40 groundnut genotypes, study was conducted during *kharif,* 2017 at Agricultural College Farm, Bapatla, to study the genetic divergence in different characters with yield and yield related traits. The genetic diversity among 40 genotypes for 15 characters was estimated by employing D^2 statistic. The 40 groundnut genotypes were grouped under seven clusters. Among seven clusters, cluster I was the largest which comprising of 26 genotypes fallowed by clusters II with nine genotypes. The rest of clusters like III, IV, V, VI and VII had shown solitary in nature. The average D2 values of inter cluster distances, showed maximum distance between Cluster-IV and VI (819.41) followed by inter cluster distance (732.17) between IV and VII. It indicates that crossing between these clusters helps in production of transgressive segregates or better recombinants. Each character had their own contribution to total divergence where, the Oil content and protein content had maximum contribution of 38.59% and 30.39% respectively to the divergence of genotypes.

Introduction

Oil and fats are essential things in human diet since they supply energy; improve taste and palatability of food. Oilseed crops next to cereals in respect to production of agricultural commodities in India, Oilseeds occupy a place of prime importance in Indian economy. Groundnut (*Arachis hypogaea* L.) is a leading oilseed crop in India. In tropical and subtropical regions of the world it is an important oilseed crop. In India most of the farmers considered Groundnut as the most remunerative crop with relatively less chance of crop losses despite an unpredictable monsoon. In North coastal zone farming community of Andhra Pradesh, Groundnut is gaining popularity and farmers are growing groundnut by practicing high input management and is being cultivated throughout the year *viz., Kharif, Rabi and Summer* season.

Genetic diversity is the first and foremost thing for any crop improvement programme. For finding the gene source for the particular trait within the available germplasm, the evaluation of genetic diversity present in the trait is very important. So, it is pre-requisite to know the genetic diversity of the existing genotypes before conducting any crop improvement programme. To assess the genetic diversity present among the genotypes Mahalanobis (1936) D2 technique is widely used in crop improvement programmes. Therefore, the present study was carried out to evaluate 40 groundnut genotypes for the nature and magnitude of genetic diversity present in it.

Materials and Methods

An experimental study was carried out at the Agricultural college farm, Bapatla using 40 diverse genotypes obtained from various research stations which were located across Andhrapradesh *viz.*, Agricultural Research Station, Kadiri, RARS Tirupati and RARS jagityal. The list of genotypes together with their pedigree and origin is presented in table 1. The experimental field is laid out in randomized block design with three replications during the year *kharif* 2017. The experiment had plot size of 4 x 1.2 m2 of each genotype having 3 rows. Row to row 30cm and plant to plant 10 cm distance were maintained. At regular intervals weeding was carried out, and Earthing up operation was taken up after gypsum application. All the recommended practices were followed to raise a healthy crop. The following observations were recorded on five randomly selected plants per replication for each genotype for all the 15 characters *viz.*, Days to 50 % flowering, Plant height(cm), SPAD chlorophyll meter reading (SCMR) at 60 DAS and 80 DAS, days to maturity, number of mature pods per plant, pod yield per plant (g), harvest index, shelling percentage, kernel yield per plant(g), hundred kernel weight(g), oil content (%), protein content(%), oil yield/plant(g) and hundred pod weight(g). Except days to 50% flowering and days to maturity data were recorded on the plot basis. The genotypes were grouped into different cluster by using the Tocher's method. Average intra (diagonal) and inter-cluster distance and Cluster mean values for various yield and yield attributing characters. The relative contributions of different characters towards genetic divergence were also worked out.

Results and Discussion

The genetic diversity among 40 genotypes for 15 characters was measured by using D^2 statistic. Based on D^2 values, the genotypes were clustered using Tocher's method as given by Rao (1952).

Group constellation

Based on the D^2 statistics 40 groundnut genotypes were grouped into seven clusters (Table 2 and Fig. 1) by using Tocher's method. The distribution of genotypes into seven clusters is presented in table 2. Among seven clusters, cluster I was the largest comprising of 26 genotypes fallowed by clusters II with 9 genotypes. The cluster III, IV, V, VI and VII are solitary in nature.

Intra and inter relation of clusters

The average D2 values of intra and inter cluster distances are given in table 3 and figure 2. Maximum difference among the genotypes within the same cluster was shown by cluster-I (80.78) and fallowed by cluster II (66.65). Some clusters like III, IV, V, VI and VII intra cluster value was zero due to solitary nature.

Table.1 List of Genotypes together with their pedigree and origin

Sl. No	Genotypes	Pedigree	Origin
1	kadiri 6	JL24 X AH316 S	ARS Kadiri
2	kadiri 7 Bold	ICGV86522 X ICGVFDRS X ICGV 91172	ARS Kadiri
3	Kadiri 8 Bold	ICGV86522 X ICG 10 X ICGV 91172	ARS Kadiri
4	kadiri 9	K-4 X Vemana	ARS Kadiri
5	kadiri Harithandra	91-57-2 X P1-47-6177	ARS Kadiri
6	K 1454 red	Vemana X Tirupai	ARS Kadiri
7	K 1501	K-4 X ICGX 930179 P2	ARS Kadiri
8	K1574	Vemana x JSSP-6-VB	ARS Kadiri
9	K1609	K-8 X JL-24	ARS Kadiri
10	K1621	ICGV99099 X K-4	ARS Kadiri
11	K1715	Germplasm collections	ARS Kadiri
12	K1719	K-7 X TAG 24	ARS Kadiri
13	K1725	K-7 X TAG 24	ARS Kadiri
14	K1735	K-7 X JL 24	ARS Kadiri
15	K1787	ICGX020063-F2-B1-SSD-P23-B2	ARS Kadiri
16	K1789	ICGX020066-F2-B1-SSD-P2-B1	ARS Kadiri
17	K1800	ICGV96176(Floriant X 2597447 XICGV88312)	ARS Kadiri
18	K1805	ICGV020047-F2-SSD-SSD-P18-B1	ARS Kadiri
19	K1811	ICGV020055-F2-SSD-SSD-P18-B1	ARS Kadiri
20	K1812	ICGV020055-F2-SSD-SSD-P20-B1	ARS Kadiri
21	K1813	ICGV020055-F2-SSD-SSD-P25-B1	ARS Kadiri
22	K1847	K-8 X K-4	ARS Kadiri
23	K1924(VGLS)	VG9521 X R 8808	ARS Kadiri
24	K1924(SB)	VG9521 X R 8808	ARS Kadiri
25	K2014	K-9 X 3 X 155-005	ARS Kadiri
26	K2064	K-7 X K-4	ARS Kadiri
27	K2066	K 1468 X K-4	ARS Kadiri
28	K2075	K-7 X TKG 19-A	ARS Kadiri
29	K2077	K-7 X ICGV99073	ARS Kadiri
30	K2104	K-8 X ICGV99073	ARS Kadiri
31	TCGS1416	Germplasm collections	RARS, Tirupati
32	TCGS1426	Germplasm collections	RARS, Tirupati
33	TCGS1073	Germplasm collections	RARS, Tirupati
34	TCGS894	Germplasm collections	RARS, Tirupati
35	TCGS1157	Germplasm collections	RARS, Tirupati
36	Dharani	VRI 2-XTCGP-6	RARS, Tirupati
37	Narayani	JL-24 x Ah316/s	RARS, Tirupati
38	Abhaya	K-134XTAG-24	RARS, Tirupati
39	TAG 24	TGS-2 X TGE-1	BARC Trombay, Mumbai
40	JCG-88-2	J 11 x TG (E) 1	RARS,Jagityal
41	Girnar-3	Girnar 1 x ICGS 11	DGR, Junagadh
42	Girnar-2	M 13 x R 33-1	DGR, Junagadh

Table.2 Distribution of 40 Groundnut genotypes in different clusters based on D^2 statistics

Clusters	No of genotypes	Genotypes
Cluster. I	26	K1574, K1621, K 1501,Kadiri 8 Bold, K1735, kadiri 7 Bold, JCG-88-2, K2077, K1847, K2104, K2014, K2075, K1609, K2064, K1715, K1725, TCGS1157, Dharani, kadiri 9, K1811, K1800, K1924(VGLS), Narayani, K1813, TCGS1416, K1789.
Cluster. II	9	TCGS1426, Abhaya, TAG 24, K1812, K1805, K1787, kadiri 6, kadiri Harithandra, K 1454 red
Cluster. III	1	TCGS1073
Cluster. IV	1	TCGS894
Cluster. V	1	K1924(SB)
Cluster. VI	1	K2066
Cluster. VII	1	K1719

Table.3 Average intra (diagonal) and inter-cluster distance of 40 Groundnut genotypes

Clusters	Cluster. I	Cluster. II	Cluster. III	Cluster. IV	Cluster. V	Cluster. VI	Cluster. VII
Cluster. I	**80.78**	**150.87**	**168.18**	**412.16**	**198.60**	**269.49**	**317.47**
Cluster. II		66.65	166.65	196.02	165.76	332.43	280.37
Cluster. III			0.00	190.90	106.99	589.98	618.81
Cluster. IV				0.00	185.46	819.41	732.17
Cluster. V					0.00	668.87	619.74
Cluster. VI						0.00	107.70
Cluster. VII							0.00

Table.4 Cluster mean values for various yield and yield attributing characters

Character	Cluster. I	Cluster. II	Cluster. III	Cluster. IV	Cluster. V	Cluster.VI	Cluster. VII
DFF	27.12	25.96	25.33	26.33	24.67	29	26
PH	45.67	48.21	44.33	35.53	55.60	48.07	48.40
NPP	28.71	28.42	15.53	22.67	48.80	38.47	21.27
Pod Yield/Plant(g)	30.64	26.18	19.23	24.07	31.50	40.37	25.33
HI	0.53	0.50	0.65	0.70	0.38	0.53	0.62
100 Pod Weight(g)	111.12	91.20	101	101.83	88.17	126.33	118.83
Protein content (%)	25.95	24.89	25.90	23.70	25.20	25.90	25.20
Oil content (%)	46.29	46.30	48.10	48.30	48.40	43.40	43.50
SHP	67.85	66.68	70.88	73.85	64.51	68.72	71.74
DM	112.81	107.93	107.67	107.67	109.33	114	107.33
SPAD@60 DAS	50.69	50.66	53.40	54.73	54.87	50.03	49.30
SPAD @80 DAS	49.39	47.29	49.80	53.60	54.67	52.17	52
KY/Plant	9.63	8.39	3.06	5.50	16.42	15.67	5.37
Oil Yield/Plant	445.73	386.19	147	266	794.67	680	233.33
100 KW	50.34	40.73	56.77	42.50	43	64.50	62

DFF=Days o 50% flowering, PH=plant height (cm), NPP= No. of mature pods per plant, HI=Harvest index, SHP=shelling percentage, DM=Days to maturity, KYP=Kernal yield per plant (g), 100KW=100 Kernal weight

Table.5 Relative contribution of 15 traits towards divergence in groundnut genotypes

Source	Contribution %	Times ranked 1st
Days o 50% flowering	0 %	0
Plant Height (cm),	0.13%	1
No. of mature pods per plant	2.05%	16
Kernel Yield /Plant	0.13%	1
Pod Yield/Plant	0.13%	1
Harvest Index	0%	0
100 Pod Weight(g)	0%	0
Oil content (%)	38.59%	301
Protein content (%)	30.38%	237
100 Kernel Weight(g)	1.15%	9
Oil Yield/Plant(g)	0.77%	6
SPAD @60 DAS	0%	0
SPAD@80 DAS	0.77%	6
Shelling Percenage(%)	0%	0
Days to maturity	25.9%	202
Total	100	

Fig.1 Clustering of 40 groundnut genotypes by Tocher's method

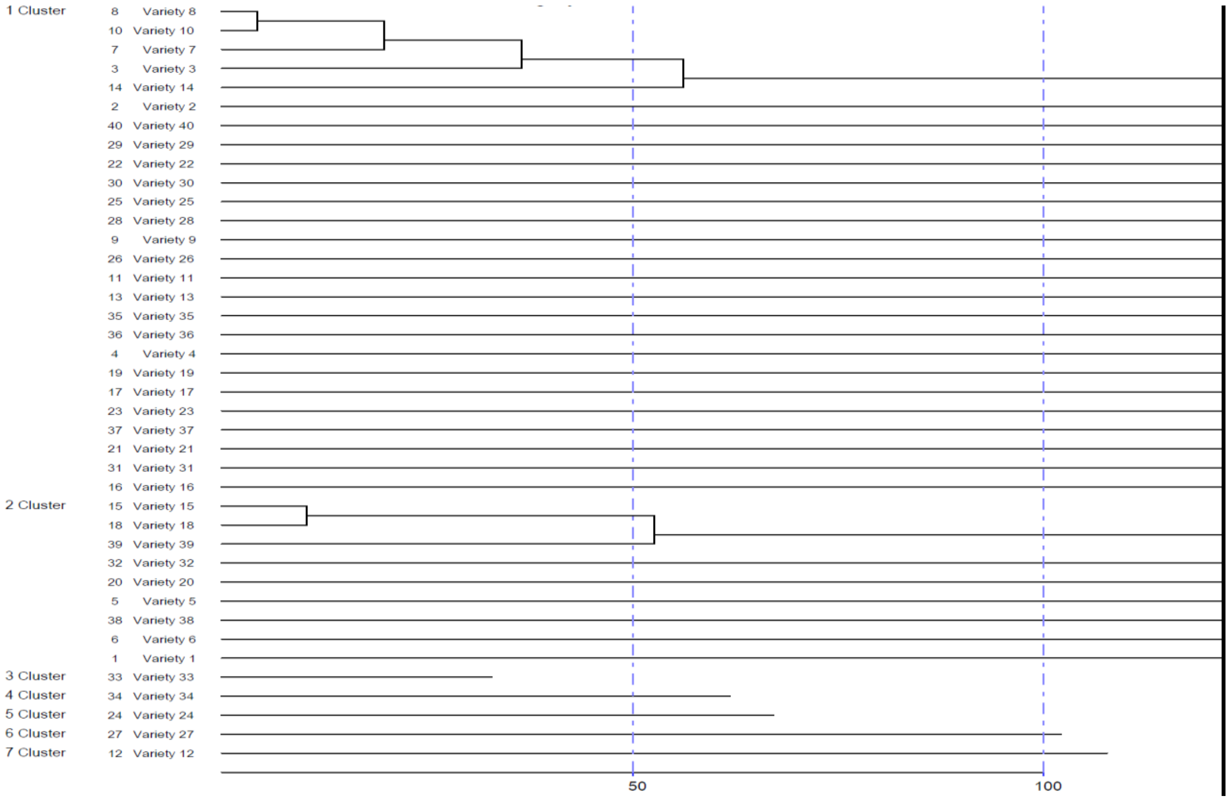
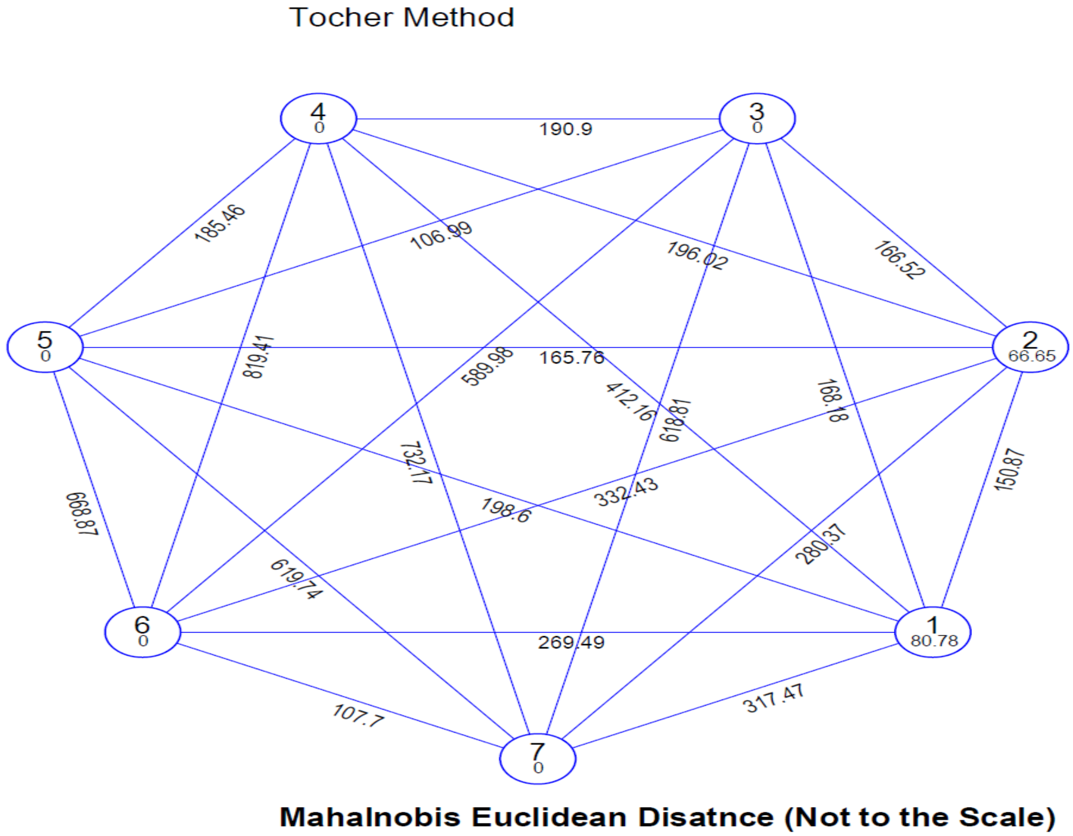


Fig.2 Average D2 values of intra and inter cluster distances



Cluster-IV and VI showed maximum inter cluster distance (819.41) followed by inter cluster distance (732.17) between IV and VII (Table 3). These clusters are quite divergent from each other and the genotypes belonging to these clusters can be used as parents for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give better recombinants. The lowest inter cluster distance (106.99) was noticed between cluster-III and V. Similarly Dhakar *et al.*, (2017) and Namrata *et al.*, (2018) also reported relatively low genetic diversity with respect to morphological characters in peanut.

Cluster means

The cluster means for 15 characters and over all character wise across the seven clusters are presented in (Table 4). All the 40 genotypes were spread over seven clusters and means of each character in each cluster were scored for all the seven clusters for all the 15 characters.

Cluster means were found highest for different characters *viz.*, Cluster V showed highest mean performance for oil yield per plant (794.67), No. of mature pods/plant (48.80), plant height (55.60), days to maturity (109.33), SPAD @ DAS (54.87), SPAD @80 DAS (54.67), Kernel yield per plant (16.42) and cluster VI showed highest mean performance for Days to 50% flowering (29) pod yield per plant (40.37), 100 pod weight (126.33), 100 kernel weight (64.50) for harvest index (0.70) and shelling percentage (73.85) cluster IV showed highest. Cluster I showed highest for protein content (25.95).

Contribution of different characters towards divergence

Difference in proportion of contribution of each character to total D2 statistics was observed and presented in table 5. The Oil content contributed 38.59 per cent to the total divergence of genotypes followed by protein percentage (30.38%), days to maturity (25.9%), number of mature pods per plant (2.05%), 100 Kernel Weight (1.15%), both Oil Yield/Plant (g) and SPAD@80 DAS (0.77) respectively, similarly the traits like Kernel Yield /Plant, Plant Height and Pod Yield/Plant (0.13). contributed to the divergence. Some of the characters like days to 50% flowering, SPAD @60 DAS, 100 Pod Weight(g), Harvest Index, shelling percentage not shown their contribution to total divergence. These observations were in accordance with observations of Foundra *et al.*, (2000) and Hampannavar and Khan. (2018).

In conclusion, the diversity is prerequisite for hybridization programme. Genotypes belonging to clusters separated by high genetic distance may be used in hybridization program to obtain a wide spectrum of variation. The most of times selecting parents only based on phenotype won't give the expected result. The selections of parents based on intra and inter cluster distance and cluster mean helps in development of transgressive segregants or better recombinants.

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