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Studies on Genetic Divergence for Yield, Yield Components and Quality Traits in Peanut (*Arachis hypogaea* L.)

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ABSTRACT

Forty groundnut genotypes were evaluated for their genetic diversity with regards to pod yield, yield attributing characters and oil content. The genotypes were classified into eight clusters, based on Mahalanobis D^2 statistic. Geographical origin, habit group and genetic diversity were observed to be unrelated, as genotypes from the same center and habit group were grouped into different clusters. Results on inter-cluster distances revealed maximum diversity between genotypes of cluster II and VIII. Intra-cluster distance was maximum for cluster II, indicating the existence of high variability within the cluster. A perusal of the results on cluster means revealed early flowering, early maturity and highest sound mature kernel per cent for cluster VII; low mean for number of immature pods, highest mean performance for primary branches per plant, dry pod yield, fresh pod yield and high oil content for cluster V; Low plant height for the cluster, VI; high mean for mature pods and shelling per cent for cluster III; and more number of secondary branches and high 100 kernel weight for cluster II; indicating the importance of selection of genotypes from the corresponding clusters in hybridization programs for effecting improvement of the respective traits. Further, secondary branches per plant was observed to contribute maximum, followed by 100 kernel weight towards the total divergence of the genotypes studied in the present investigation.

Keywords D^2 analysis, Genetic divergence, Groundnut, Dry pod yield, Yield components.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the most important oil seed crops of India and contributes to about 30 % of the total domestic vegetable oil supply. In Andhra Pradesh, it occupies an area of 0.74 M ha with a production of 1.05 M t and a productivity of 1426 kg ha^{-1} (Ministry of Agriculture 2019-20). Major constraints in production are abiotic stresses, namely, drought and low light in addition to biotic stresses, namely, late leaf spot, rust, sucking insects and leaf webber. Keeping these constraints in view, high yield-

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ing groundnut varieties with improved performance have been bred and released in Andhra Pradesh from time to time. For bringing about further improvement in yield of groundnut, it is essential to know the extent of diversity among the genotypes for yield, yield components and oil content. In this direction, studies on genetic divergence among the identified groundnut genotypes are essential for planning an efficient and successful hybridization program, since the cross involving genetically diverse parents is likely to produce high heterotic effects and also more variability in the segregating generations for effective selections (Reddy *et al*. 2017). Further, biometric techniques such as multivariate analysis based on Mahalanobis D^2 statistic (Mahalanobis 1936) quantifies the degree of genetic divergence amongst biological populations and assesses the relative contribution of various attributes to total divergence. Genetic diversity studies also help to determine the inherent potential of a cross for heterosis and frequency of the desirable recombinants in advanced generations. In this context, the present study was undertaken to classify and understand the nature and magnitude of genetic diversity among the groundnut genotypes of Agricultural Research Station, Kadiri of Andhra Pradesh state using Mahalanobis D^2 statistic.

MATERIALS AND METHODS

Experimental material for the present investigation comprised of 40 groundnut genotypes obtained from Agricultural Research Station, Kadiri of Acharya N.G. Ranga Agricultural University (Table 1). These genotypes were sown during *rabi*, 2020-21. Each genotype was sown in continuous three row plots of 5 m row length at a spacing of 30 cm between rows and 10 cm between plants within the row in a Random-

Table 1. Details of the groundnut genotypes studied in the present investigation.

Variety	Genotypes	Pedigree	Origin	Habit group
1	K1501	Kadiri4 X ICGV930179/P2	ARS Kadiri	Virginia bunch
2	K1577	K1341 X TAG24	ARS Kadiri	Virginia bunch
3	K1578	K1341 X TAG24	ARS Kadiri	Virginia bunch
4	K1628	ICGV99099 X Kadiri4	ARS Kadiri	Virginia bunch
5	K1643	K1340 X TAG24	ARS Kadiri	Virginia bunch
6	K1687	K1341 X JL24	ARS Kadiri	Virginia bunch
7	K1706	K1341 X JL24	ARS Kadiri	Virginia bunch
8	K1707	K1341 X JL24	ARS Kadiri	Virginia bunch
9	K1715	K1340-092ANP	ARS Kadiri	Virginia bunch
10	K2317	K1510 X ICGV00350	ARS Kadiri	Virginia bunch
11	K1736	K1340 X JL24	ARS Kadiri	Virginia bunch
12	K2238	K1470 X K1341	ARS Kadiri	Virginia bunch
13	K1800	ICGV96176{(Florigiant X NCAc17090) (Dh-3-20 X PI259747)} X ICGV88312	ARS Kadiri	Virginia bunch
14	K2270	DRT43-008	ARS Kadiri	Virginia bunch
15	K8	ICGV86522 X ICG 10 X ICGV 91172	ARS Kadiri	Virginia bunch
16	K2316	K1482 X ICGV00348	ARS Kadiri	Virginia bunch
17	K2330	K1535 X AIS2009-1	ARS Kadiri	Virginia bunch
18	K2331	K1570 X AIS2009-1	ARS Kadiri	Virginia bunch
19	K7	ICGV86522 X ICGVFDRS X ICGV 91172	ARS Kadiri	Virginia bunch
20	K2314	K1482 X ICGV00348	ARS Kadiri	Virginia bunch
21	K1621	ICGV99099 X Kadiri4	ARS Kadiri	Spanish bunch
22	K1622	ICGV99099 X Kadiri4	ARS Kadiri	Spanish bunch
23	K1660	K1341 X Kadiri4	ARS Kadiri	Spanish bunch
24	Amaravathi	K6 X NCAc2242	ARS Kadiri	Spanish bunch
25	K1702	K1341 X JL24	ARS Kadiri	Spanish bunch
26	K1721	K1340 X TAG24	ARS Kadiri	Spanish bunch
27	Chithravathi	K7(Bold) X TAG 24	ARS Kadiri	Spanish bunch
28	Harithandra	91-57-2 X P1-47-6177	ARS Kadiri	Spanish bunch
29	K1801	ICGV96177{(Florigiant X NCAc17090) (Dh-3-20 X PI259747)} X ICGV88312	ARS Kadiri	Spanish bunch

Table 1. Continued.

Variety	Genotypes	Pedigree	Origin	Habit group
30	K2246	K1577 X ICGV86564	ARS Kadiri	Spanish bunch
31	K1809	ICGX020054-F2-SSD-P18-B1	ARS Kadiri	Spanish bunch
32	Kadiri Lepakshi	(ICGV92069 X ICGV93184) X (SIL4ICGV98300)	ARS Kadiri	Spanish bunch
33	K2313	K1482 X ICGV00348	ARS Kadiri	Virginia bunch
34	K1677	K1340 X JL24	ARS Kadiri	Spanish bunch
35	Anantha	Vemana X Girnar	ARS Kadiri	Spanish bunch
36	K4	DH3-30 X NCAc-2230	ARS Kadiri	Spanish bunch
37	K6	JL24 X AH316 S	ARS Kadiri	Spanish bunch
38	K9	K-4 X Vemana	ARS Kadiri	Spanish bunch
39	TAG 24	TGS-2 X TGE-1	BARCTrombay, Mumbai	Spanish bunch
40	K2017	K1375x3x155-005	ARS Kadiri	Virginia bunch

ized Complete Block Design with three replications. The crop was raised under irrigated conditions and all recommended practices were followed to raise a healthy crop. Observations were recorded on yield and quality traits namely, days to 50 % flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, number of mature pods per plant, number of immature pods per plant, sound mature kernel per cent, dry pod yield per plant (g), fresh pod yield per plant (g), 100 kernel weight (g), shelling percent and oil content. All observations were recorded from five randomly selected plants for each genotype in each replication, except for days to 50% flowering and days to maturity which were recorded on plot basis; and 100 kernel weight (g), shelling percent and oil content (%) which were recorded from a random sample obtained from each plot. The data collected was subjected to standard statistical procedures. Genetic diversity in the material was analyzed using Mahalanobis D^2 statistic (Rao 1952) and the varieties were grouped into different clusters according to Tocher' method.

RESULTS AND DISCUSSION

Analysis of variance (Table 2) revealed highly significant differences for all characters studied indicating the existence of sufficient variability for effective selection. The 40 genotypes studied in the present

Table 2. Analysis of variance for yield and yield components in groundnut. ** Significant at 1 % level.

Source of variation	Degrees of freedom	Mean sum of squares						
		Days to 50 % flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Mature pods per plant	Immature pods per plant
Replications	2	0.36	0.97	13.82	0.01	0.11	5.47	0.98
Genotypes	39	49.43**	194.68**	42.61**	0.73**	10.46**	26.35**	6.18**
Error	78	4.72	12.29	7.2	0.29	0.22	1.9	0.42

Table 2. Continued.

Source of variation	Degrees of freedom	Mean sum of squares					
		Sound mature kernel per cent	Fresh pod yield per plant	Dry pod yield per plant	Shelling per cent	100 kernel weight	Oil content (%)
Replications	2	9.39	22.16	19.43	7.8	26.34	4.23
Genotypes	39	50.32**	65.25**	49.49**	16.997**	273.9**	30.53**
Error	78	26.07	9.58	6.97	7.22	13.27	4.48

Table 3. Clustering pattern of 40 genotypes for yield and yield components in groundnut.

Cluster number	Number of genotypes	Genotypes	Source	Habit group
I	13	K1621, K1721, Chitravathi, K1702, K1622, K2246, K1677, K1801, K1660, Harithandra, Anantha, K1809, K9	Kadiri	Spanish bunch
II	21	K1577, K2316, K1628, K1736, K2017, K1578, K8, K1707, K2313, K1715, K1643, K2317, K1706, K1501, K2330, K7, K2331, K2270, K1800, K2238, K1687	Kadiri	Virginia bunch
III	1	K 2314	Kadiri	Virginia bunch
IV	1	K1628	Kadiri	Spanish bunch
V	1	K 1812	Kadiri	Spanish bunch
VI	1	TAG 24	BARC, Trombay, Mumbai	Spanish bunch
VII	1	K6	Kadiri	Spanish bunch
VIII	1	K4	Kadiri	Spanish bunch

investigation were grouped into eight clusters based on the relative magnitude of D^2 values such that genotypes belonging to same cluster had an average smaller D^2 value than those belonging to different

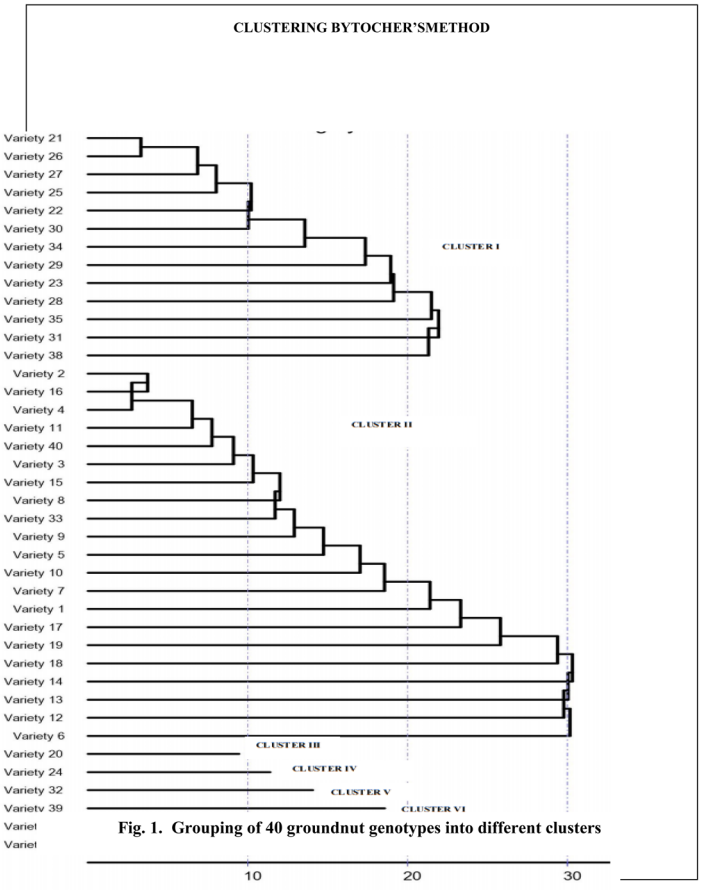

Fig. 1. Grouping of 40 groundnut genotypes into different clusters

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clusters. The distribution of genotypes into various clusters is presented in Table 3 and Fig. 1. Among the eight clusters, cluster II consisted of maximum genotypes (21), while cluster I had thirteen collections the clusters III, IV, V, VI, VII and VIII were however, monogenotypic and consisted of single genotype.

Genotypes chosen from the same eco-geographic region were observed to be present in different clusters as well as in the same cluster. The findings are in conformity with the reports of Venkatesh *et al*. (2016). The production of greater diversity by genetic drift and selection, compared to that produced by geography was also observed in the present study, as the genotypes developed at agricultural research station, Kadiri were noticed to be distributed across different clusters. A further, classification of the genotypes in each cluster based on habit group also revealed the distribution of genotypes to be at random indicating that habit group and genetic diversity were also not related. Genotypes from the same habit group were also observed to be present in different clusters (clusters II and III for the Virginia habit group and clusters I, IV, V, VI and VII for the Spanish bunch habit group) The results are in broad agreement with the reports of Venkatesh *et al*. (2015).

An analysis of inter and intra-cluster distances (Table 4 and Fig. 2) revealed maximum inter-cluster distance between clusters II and VIII (125.05) followed by II and VII (103.75) indicating that genotypes from these clusters were highly divergent meriting their consideration in selection of parents for hybridization. Similar greater diversity between genotypes from different clusters based on their inter cluster distance has also been reported earlier in the crop (Kumar *et al*. 2012). Minimum inter-cluster distance was observed between the clusters, V and VII (19.2)

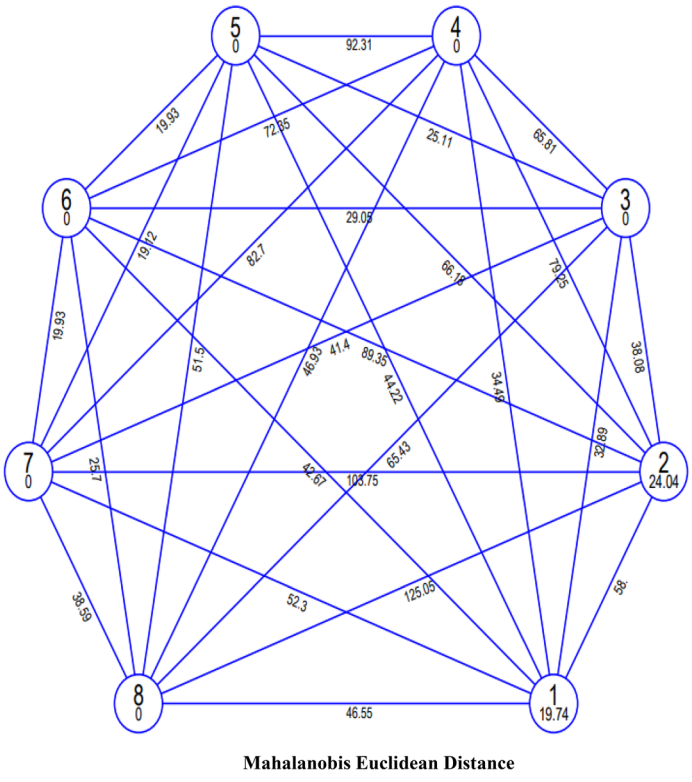

Fig. 2. Inter and intra-cluster distance of 40 groundnut genotypes in eight clusters.

Table 4. Average intra-and inter–cluster D^2 values among eight clusters of groundnut genotypes for yield and yield components.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	19.74	58.00	32.89	34.49	44.22	42.67	52.30	46.55
II		24.04	38.08	79.25	66.18	89.35	103.75	125.05
III			0.00	65.81	25.11	29.05	41.40	65.43
IV				0.00	92.31	72.35	82.70	46.93
V					0.00	19.93	19.12	51.50
VI						0.00	19.93	25.70
VII							0.00	38.59
VIII								0.00

indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be maximum for cluster II (24.02), while it was zero for the monogenotypic clusters, namely, clusters III, IV, V, VI, VII and VIII as they included only single genotype. The genotypes included in cluster II, exhibiting maximum intra-cluster distance, are inferred to be more divergent than those in other clusters. The study indicates the need for hybridization between the genotypes of clusters II with cluster VIII (K4) and the cluster VII (K6) for realization of greater variability and transgressive segregates towards effective selection and improvement of yield components and quality characters.

A perusal of the results on cluster means for yield and yield components revealed considerable differences between the clusters for all characters under study. The cluster mean values for the characters studied are presented in Table 5 and Fig. 3. The data indicated a wide range of mean values between the clusters. Days to 50 % flowering had a range of 26.33 days in cluster VIII to 38.83 days in cluster II; days to maturity ranged from 94 days in cluster VIII to 123.87 days in cluster II; plant height from18.20 cm in cluster VI to 31.37 cm in cluster VIII; primary branches per plant from 4.73 in cluster VIII to 6.47 in cluster V; secondary branches per plant from 5.64 in cluster II to 1.33 in cluster VIII; mature pods per plant from 5.87 for cluster II to 17.27 for cluster III; immature pods per plant from 3.67 for cluster V to 9.4 for cluster IV; sound mature kernel per cent from 71.33 for cluster IV to 85.87 for cluster VIII; fresh pod yield per plant from 20.24 g for cluster VIII to 35.27 g for cluster V; dry pod yield per plant from10.23 g for cluster IV to 25.00 g for cluster V, 100 kernel weight from 36.23 g for cluster VI to 62.59 g for cluster II and oil content (%) from 42.21 for cluster II to 51 in cluster V. None of the clusters, were however, superior for all the traits studied in the present investigation.

Number of times each of the thirteen characters appeared first and their respective per cent contribution towards diversity is presented in Table 6. Information on the relative contribution of various plant characters towards the divergence was also reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations (Suneetha *et al*. 2012). Among all the characters

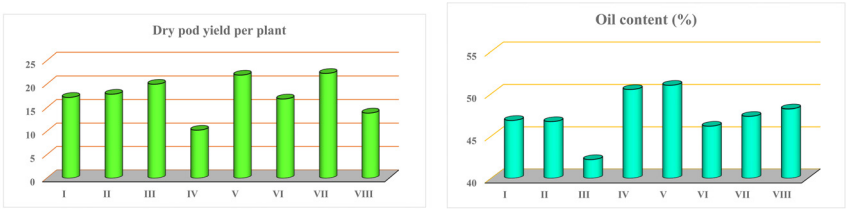

Fig. 3. Dry pod yield per plant and oil content of different clusters obtained in the present study.

Table 5. Cluster means of 40 groundnut genotypes for yield and yield components.

Clusters	Days to 50 % flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Mature pods per plant	Immature pods per plant
I	35.23	111.90	23.94	5.71	2.04	12.19	6.53
II	38.83	123.87	21.33	5.92	5.64	11.34	6.98
III	32.67	112.67	23.83	6.33	4.40	17.27	7.33
IV	30.67	108.00	26.67	5.40	1.80	5.87	9.40
V	33.67	114.33	26.47	6.47	3.00	14.13	3.67
VI	30.33	110.00	18.20	4.93	2.27	16.47	5.80
VII	28.33	108.00	31.37	5.53	2.20	14.89	4.60
VIII	26.33	94.00	19.57	4.73	1.33	8.20	6.60

Table 5. Continued.

Clusters	Sound mature kernel per cent	Fresh pod yield per plant	Dry pod yield per plant	Shelling per cent	100 kernel weight	Oil content
I	77.19	25.45	17.18	71.92	59.68	46.86
II	74.86	25.70	17.86	70.63	62.59	46.72
III	75.33	26.62	19.97	72.62	53.90	42.21
IV	71.33	21.26	10.23	67.45	58.86	50.50
V	84.17	35.27	25.00	72.45	41.79	51.00
VI	75.50	24.32	16.84	72.00	36.23	46.18
VII	78.17	34.43	22.27	67.73	37.22	47.34
VIII	85.87	20.24	13.87	71.00	45.44	48.21

studied, secondary branches contributed maximum (47.69%) towards diversity, followed by 100 kernel weight (16.41%), immature pods per plant (11.79%), mature pods per plant (7.18%), oil content (5.51%), fresh pod yield per plant (3.21%), days to maturity (1.79 %), the traits namely, plant height, shelling percentage, days to 50 % flowering, primary branches per plant, sound mature kernel per cent and dry pod yield per plant contributed 1.67, 1.67, 1.54, 1.28, 0.13 and 0.13, respectively to the total divergence. Cluster means together with information on the traits that contribute maximum towards divergence would help in selection of parents. It has been suggested that divergence should be given importance for undergoing hybridization program (Venkatesh *et al*. 2015).

Table 6. Relative contribution of characters studied towards genetic divergence in groundnut.

Source	Contribution %	Times ranked 1st
Days to 50 % flowering	1.54 %	12
Days to maturity	1.79 %	14
Plant height	1.67 %	13
Primary branches per plant	1.28 %	10
Secondary branches per plant	47.69 %	372
Mature pods per plant	7.18 %	56
Immature pods per plant	11.79 %	92
Sound mature kernel per cent	0 .13 %	1
Fresh pod yield per plant	3.21 %	25
Dry pod yield per plant	0.13 %	1
Shelling per cent	1.67 %	13
100 kernel weight	16.41 %	128
Oil content	5.51 %	43

Among the clusters, cluster V had recorded highest number of primary branches per plant coupled with minimum immature pods per plant resulting in maximum fresh and dry pod yield per plant. The genotype K1812 in the cluster is a high yielding Spanish bunch variety released in 2021 as Kadiri Lepakshi from the state of Andhra Pradesh may be utilized in further groundnut breeding programs. The genotypes of cluster II had recorded maximum kernel weight (62.59 g) and included several bold varieties,

such as K7 and K8. Hence, these genotypes may be utilized for development of bold seeded confectionary type groundnut varieties for table purpose. Cluster VIII showed early flowering (26.33), early maturity (94) and high sound mature kernel per cent (85.87); while low plant height (18.20) were noticed for cluster VI and cluster III for high number of mature pods (17.27) and shelling per cent (72.62) indicating the importance of selection of genotypes from the corresponding clusters in hybridization programs for effecting improvement of the respective traits.

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