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STUDIES ON DIVERGENCE IN GROUNDNUT (*Arachis hypogaea* L.)

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Abstract–The present experiment was conducted to the diversity present in 33 genotypes of groundnut collected from different parts of the country and world for yield and yield components and their contribution towards divergence. The analysis of variance indicated sufficient variability among the genotypes for all the characters. The D^2 analysis revealed presence of considerable diversity among the 33 genotypes and were grouped into six clusters using Tocher's method. The maximum number of genotypes (11) were present in the cluster II followed by cluster I with 10 genotypes and cluster III with nine genotypes. Clusters IV, V and VI formed solitary clusters with single genotype each. The maximum contribution towards genetic divergence was recorded from the traits, 100 kernel weight followed by days to 50 % flowering and harvest index. The inter cluster distance ranged from 52.40 to 298.70 and was observed between the clusters V and VI followed by clusters IV and V, clusters III and V, clusters I and V, clusters III and IV, clusters II and V, clusters II and III, clusters II and IV, clusters I and VI, clusters II and VI. Thus, genotypes from these clusters having maximum inter cluster distance can be included in hybridization programme in order to obtain superior and desirable recombinants based on the cluster mean values.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the important oilseed crop of the world grown in tropical and subtropical regions. It is a segmental allopolyploid with self pollination mechanism and belongs to the Fabaceae sub-family Papilionoideae. It is an annual herbaceous legume. It is fifth most important vegetable oil crop among the nine major oilseed crops of world (Tillman *et al.*, 2009). Groundnut is mainly cultivated for its oil (36-54%) and protein (22-36%). The oil is rich in essential polyunsaturated fatty acids *i.e.,* linolenic acid and linoleic acids (Desai *et al*., 1999). The groundnut productivity is low, one ton per hectare indicating the importance of germplasm for the improvement of yield and other yield contributing traits (Mace *et al*., 2006). The available generic diversity for various yield traits in groundnut is low and there is an urgent need to evaluate the world genetic resources for the exploitation in breeding programmes to generate variability. Sound knowledge on genetic diversity is important for selecting parents in hybridization programme as diverse parents in a cross allows creation of more variation and high heterotic effect in the segregating population. This is confirmed and exploited many crops for heterosis (Asha *et al*. (2013), Haritha and Lal Ahamed (2013), Jadhav *et al*. (2014), Radhika Ramya *et al*. (2017), Mounika *et al*. (2018), Roy *et al*. (2018), Sateesh Babu *et al*. (2019) and Shalini *et al*. (2020)).. Mahalanobis D^2 statistic, a powerful tool for quantifying the degree of divergence and Tocher's method was utilized for grouping the genotypes into different clusters. Keeping this in view, the present investigation was planned to study the genetic divergence in the material collected from Directorate of Groundnut Research, Junagarh, Gujarat and Regional Agricultural Research Station, Tirupati, Andhra Pradesh.

MATERIALS AND METHODS

The experimental material comprised of thirty three Indian as well as exotic groundnut genotypes obtained from Directorate of Groundnut Research, Junagarh, Gujarat and Regional Agricultural Research Station, Tirupati, Andhra Pradesh. The genotypes were sown during *kharif* 2016 in randomized block design with two replications at Regional Agricultural Research Station farm, ANGRAU, Tirupati. Observations were recorded from five randomly selected plants for eleven characters *viz*., days to 50 % flowering, SCMR 40 DAS, SCMR 50 DAS, SCMR 60 DAS, SCMR 70 DAS, days to maturity, harvest index, shelling percentage, 100 kernel weight, kernel yield per plant and oil content. The number of days taken to flowering from the day of sowing to opening of flowers in 50 per cent of plants was taken as days to 50 per cent flowering. SCMR was measured on the leaflets of third leaf from the apex on the main axis at 40, 50, 60 and 70 DAS under normal sunlight using SPAD chlorophyll meter of Minolta Company, New Jersey, USA (SPAD-502). Number of days taken for maturity was counted when more than 75 % of the pods attained physiological maturity in the random samples tested in a genotype. Oil content in the seed was estimated with the help of Universal Grain analyzer in which dried seed samples (8-12 % moisture content) of 100g was taken and fed into the grain analyzer and the oil content was recorded directly as percentage of oil. The genetic diversity was assessed by Mahalonobis' D^2 Statistic (Mahalanobis, 1936) and the genotypes were clustered using Tocher's method as described by Rao (1952). The average intra and inter-cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Analysis of variance for yield and yield attributes revealed significant differences for all the characters studied which indicated the presence of considerable amount of variation among the genotypes.Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the Wilk's criterion 'Ù'. The Wilk's criterion thus obtained was used in calculations of 'V' statistic. The statistic was highly significant indicating that genotypes differ significantly when all the characters were considered simultaneously. The value of 'V' statistic was 784.57 in the present investigation.

Number of times each of the eleven characters appeared first and their respective per cent contribution towards diversity is presented in Table 1. Among all the characters studied, 100 kernel weight contributed maximum (39.58 %) towards diversity by taking first rank 209 times followed by days to 50 % flowering (20.45 %) ranking 108 times first, harvest index (16.48 %) ranking 87 times first, SCMR 70 DAS (8.33 %) ranking 44 times first, shelling percentage (4.73 %) ranking 25 times first, SCMR 60 DAS (3.98 %) ranking 21 times first and kernel yield per plant (2.46 %) ranking 13 times first. The traits *viz.* SCMR 40 DAS, SCMR 50 DAS, oil content and days to maturity contributed 1.52, 1.33, 0.95, 0.19, respectively to the total divergence by ranking 8, 7, 5, 1 times first, respectively.

Grouping of Genotypes into Clusters

The 33 genotypes were grouped into six clusters using Tocher's method with a criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values (Table 2). The random grouping of genotypes revealed maximum number of genotypes (11) present in cluster II followed by cluster I with 10 genotypes and cluster III with 9 genotypes. Clusters IV, V and VI formed solitary clusters with single genotype. The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster D^2 values. The tree like structure called dendrogram (Fig. 1) was constructed based on clustering by Tocher's method.

The average intra and inter-cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977) and are presented in the Table 3. The maximum intra cluster distance was observed in the cluster II (55.96) followed by clusters III (51.56), I (31.12) while it was zero in the clusters, IV, V and VI. The intra and inter cluster distances revealed that inter cluster distance values were greater than intra-cluster distance values. The high intra-cluster distance in cluster II indicates the presence of wide genetic diversity among the genotypes present within this cluster. Genotypes grouped in the same cluster presumably differ little from one another as the aggregate of characters measured.

In the present study, inter-cluster distances

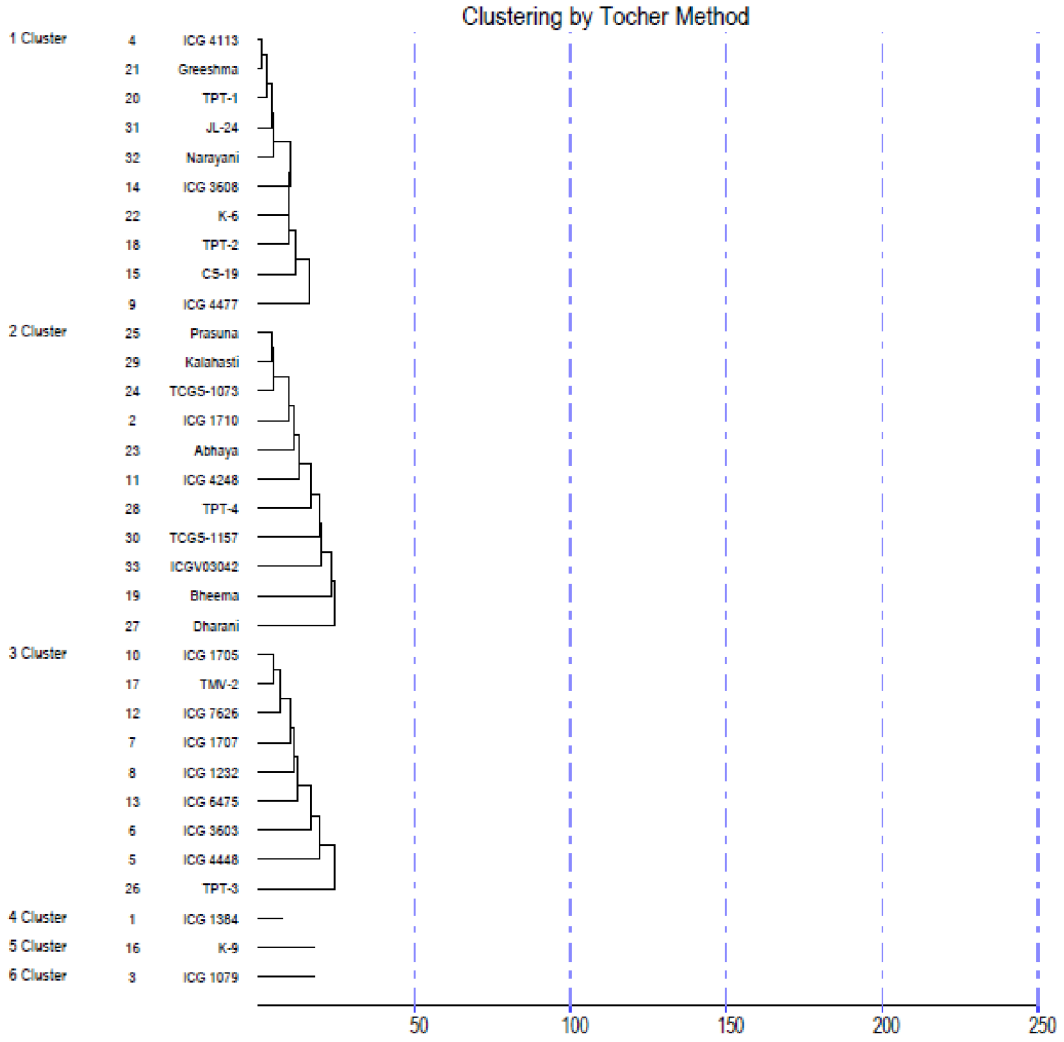

Fig. 1. Clustering of 33 genotypes of groundnut using Tocher's method.

Table 1. Contribution of different characters towards genetic divergence in 33groundnut (*Arachishypogaea* L.) genotypes.

S.No.	Source	Times Ranked first	Contribution %
1	Days to 50% Flowering	108	20.45
2	SCMR 40 DAS	8	1.52
3	SCMR 50 DAS	7	1.33
4	SCMR 60 DAS	21	3.98
5	SCMR 70 DAS	44	8.33
6	Days to Maturity	1	0.19
7	Harvest Index	87	16.48
8	Shelling %	25	4.73
9	Kernel Yield Per Plant	13	2.46
10	100 Kernel Weight	209	39.58
11	Oil Content	5	0.95

ranged from 52.40 (between clusters IV and I) to 298.70 (between clusters V and VI). The maximum inter cluster distance was 298.70 (between clusters V and VI) followed by 227.22 (between clusters IV and V), 172.76 (between clusters III and V), 152.21 (between clusters I and V), 143.65 (between clusters III and IV), 140.25 (between clusters II and V), 131.62 (between clusters II and III), 124.04 (between clusters II and IV), 119.73 (between clusters I and VI), 114.28 (between clusters II and VI). Thus, it indicated that sufficient diversity was present between these clusters and crosses involving genotypes from these clusters having higher inter-cluster distance will be rewarding.

The cluster mean values for the characters are presented in Table 4. The data indicated a wide range of mean values between the clusters. Days to 50 % flowering had a range of 24.00 days in cluster IV to 38.00 days in cluster VI; SCMR 40 DAS had a range of 34.40 in cluster IV to 49.30 in cluster V; SCMR 50 DAS had a range of 35.55 in cluster VI to 47.30 in cluster V; SCMR 70 DAS had a range of 33.30 in cluster VI to 51.20 in cluster V; days to maturity had a range of 107.50 days for cluster IV to 122.00 days for cluster VI; harvest index had a range of 35.77 for cluster III to 47.85 for cluster IV; shelling percentage had a range of 60.10 for cluster VI to 70.00 for cluster V; kernel yield per plant had a range of 5.79 g for cluster III to 8.75 g for cluster VI; 100 seed weight had a range of 30.35 g for cluster IV to 48.74 g for cluster II and oil content had a range of 45.80 for cluster VI to 48.15 for cluster II.

Higher mean values for 100 kernel weight were observed in clusters II and V; for days to 50 %

Table 2. Clustering pattern of 33 groundnut (*Arachis hypogaea* L.) genotypes by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype (s)
I	10	ICG 4113, Greeshma, TPT-1, JL-24, Narayani, ICG 3608, K-6, TPT-2, CS-19, ICG 4477
II	11	Prasuna, Kalahasti, TCGS-1073, ICG 1710, Abhaya, ICG 4248, TPT-4, TCGS-1157, ICGV03042, Bheema, Dharani
III	9	ICG 1705, TMV-2, ICG 7626, ICG 1707, ICG 1232, ICG 6475, ICG 3603, ICG 4448, TPT-3
IV	1	ICG1384
V	1	K-9
VI	1	ICG 1079

Table 3. Average intra-and inter –cluster D^2 values among six clusters in 33 genotypes of groundnut (*Arachishypogaea* L.).

Cluster no.	I	II	III	IV	V	VI
I	**31.12**	109.87	72.44	52.40	152.21	119.73
II		**55.96**	131.62	124.04	140.25	114.28
III			**51.56**	143.65	172.76	106.21
IV				**0.00**	227.22	109.38
V					**0.00**	298.70
VI						**0.00**

Note: Bold and diagonal values indicate intra-cluster D^2 distance.

Table 4. Mean values of six clusters estimated by Tocher 'smethod from 33 genotypes of groundnut (*Arachishypogaea* L.).

	Days to 50% flowering	SCMR 40DAS	SCMR 50DAS	SCMR 60 DAS	SCMR 70 DAS	Days to maturity	Harvest index	Shelling %	Kernel yield per plant (g)	100 kernel weight (g)	Oil content (%)
1 Cluster	27.10	39.51	36.44	39.16	35.77	108.40	39.56	66.94	7.11	35.64	47.42
2 Cluster	32.82	43.01	40.83	42.22	38.58	111.91	45.78	66.02	8.61	**48.74**	**48.15**
3 Cluster	35.00	40.48	38.08	39.67	37.85	113.67	**35.77**	62.89	**5.79**	38.94	47.24
4 Cluster	**24.00**	**34.40**	36.40	39.60	34.45	**107.50**	**47.85**	69.65	8.40	**30.35**	46.85
5 Cluster	26.00	**49.30**	**47.30**	**50.40**	**51.20**	118.50	46.90	**70.00**	8.30	46.00	47.65
6 Cluster	**38.00**	39.10	**35.55**	**35.90**	**33.30**	**122.00**	45.75	**60.10**	**8.75**	35.45	**45.80**

Note: Bold figures are minimum and maximum values

flowering were seen in clusters VI and III and for harvest index were seen in clusters IV and V which are the main contributors for improving kernel yield per plant. Based on mean values, series of crosses in diallel fashion may prove highly successful for increasing the yield and its components.

The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence has been studied by Venkataravana *et al.* (2000); Muralidharan and Manivannan (2004); Mahalakshmi *et al.* (2005); Lakshmidevamma *et al.* (2006); Mane *et al.* (2008); Dolma *et al* (2010); Kumar *et al.* (2012); Suneetha *et al.* (2013); Bhakal and Lal (2015); Vasanthi *et al.* (2015); Ashutosh *et al.* (2016); Niveditha *et al.* (2017) and Waghmode *et al.* (2017).

Thus, from the present study it was recorded that the traits 100 kernel weight (39.58 %), days to 50 % flowering (20.45 %) and harvest index (16.48 %) contributed maximum towards genetic divergence. The genotypes were grouped into six clusters using Tocher's method. The traits *viz.* days to 50 % flowering, days to maturity and kernel yield per plant recorded highest mean value in cluster VI; for SCMR 40 DAS, SCMR 50 DAS, SCMR 60 DAS, SCMR 70 DAS and shelling percentage in cluster V; for harvest index cluster IV; for 100 kernel weight and oil content cluster II. Therefore, the genotypes placed in clusters V and VI can be used as parents in breeding programmes for obtaining more heterotic hybrids or transgressiveseggregants.

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Authors' declaration

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