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## Genetic divergence analysis in groundnut (*Arachis hypogaea* L.)

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### Abstract

Genetic diversity among RILs of groundnut were estimated using Mahalanobis  $D^2$  statistic for seventeen characters. The analysis of variance revealed significant differences among the RILs for all characters. Based on Tocher's method, 149 RILs were grouped into fifteen clusters. Cluster II was the largest, holding 40 RILs followed by cluster I (34 RILs), cluster IV (14 RILs), cluster VI (14 RILs), VIII cluster (10 RILs), cluster V (7 RILs), cluster VII (6 RILs), cluster X (6 RILs), cluster IX (4 RILs), cluster XIII (4 RILs), cluster XI (3 RILs), cluster XIV (3 RILs), III cluster (2 RILs). Whereas cluster XII and XV were unique with only one RILs in each. This grouping indicated considerable diversity among the RILs. Cluster III had RILs with desirable characters like number of kernels per pod, 100-kernel weight, kernel yield per plant and biological yield per plant. Similarly, other clusters like VIII and were also possessed different character combinations. Intra-cluster distance was highest for cluster VI while inter-cluster distance between cluster III and cluster VII was maximum, indicating the existence of high variability within and between clusters.

**Keywords:** Groundnut,  $D^2$  and genetic divergence

### Introduction

Groundnut is one of the important oilseeds crop grown among? Countries of the world. It is native to South America and it belongs to the family 'Leguminosae'. It is a self-pollinated crop, allotetraploid with diploid chromosome number  $2n = 40$ . It has wide variety of uses viz., kernel directly used for table purposes or can be crushed for oil, vine with leaves as fodder and shell can be made to particleboard. Groundnut oil contains 46 and 32 percent of monounsaturated fatty acids (MUFA) and polyunsaturated fatty acids (PUFA), respectively. This analysis provides the basis for grouping the germplasm collections into different homogenous groups and therefore, it is helpful in reducing the size of germplasm collection to be evaluated. The  $D^2$  statistic for multivariate analysis has been successfully used to select divergent genotypes in order to exploit heterosis and for bringing together higher frequency of desirable genes in the segregates. Thus, the knowledge of genetic variability and genetic divergence in combination with character association allows a breeder to select suitable and divergent genotypes for their use in breeding strategies and to formulate a suitable selection scheme.

### Materials and Methods

The experimental material included single seed descent method derived 150 Recombinant Inbred Lines (RILs) of groundnut parental lines CHICO and ICGV 12473, which were procured from International Crops Research Institute for the Semi-Arid Tropics Patancheru, Hyderabad, India, through All India Coordinated Research Project on Groundnut, ARS Bikaner.

The experiment was conducted during Kharif 2016 in alpha lattice design (15 x 10) with a spacing of 30 cm between rows and 10 cm between plant to plant within the rows. The experiment material was sown on June 30, 2016 and one line (No. 49) germinated after 30 days and could not produced pods, therefore, could not be included in the study and the remaining 149 RILs were evaluated for traits related to yield and quality. The experiment was harvested on November 4, 2016.

The observations were recorded on the basis of five randomly selected representative plants from each replication for ten characters viz., days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, pod yield per plant, number of kernels per pod, kernel yield per plant (g), 100-kernel weight (g), shelling percentage, biological yield per plant, harvest index, protein content, oil content and fatty acids.

The genetic diversity between genotypes was worked out using Mahalanobis  $D^2$  (1936) [6] extended by Rao (1952) [7]. On the basis of  $D^2$  values the genotypes were grouped into clusters according to Tocher's method (Rao, 1952) [7]. The method of Singh and Chaudhary (1985) [9] were used to calculate the intra and inter-cluster distances. All the statistical calculations were done using excel stat based computer software.

Results and Discussion: The 149 RILs of groundnut were grouped into fifteen clusters based on  $D^2$  value (Table 1). Among the clusters, cluster II contained maximum number of RILs (40) followed by cluster I with 34 RILs, cluster IV and VI with 14 RILs, VIII cluster with 10 RILs, cluster V with 7 RILs, cluster VII, X with 6 RILs, cluster IX, XIII with 4

RILs, XI, XIV cluster with 3 RILs, III cluster with 2 RILs, whereas cluster XII and XV were unique, since, each had only one RILs. This grouping indicated considerable diversity among the RILs.

The inter-cluster distance (Table 2) was larger than the intra-cluster distance which indicated that greater diversity is present among the genotypes of distant group (Zaman *et al.*, 2010) [12]. The inter-cluster distance analysis shows that the maximum divergence was observed between cluster III and cluster VII (94.866). The inter-cluster distance between cluster III and cluster VII, followed by cluster III and cluster XV, cluster I and cluster III, cluster III and cluster IV were relatively high as compared to other, so the genotypes in these clusters can be utilized for selection of parents for hybridization. Similar results were also suggested by Choudhary *et al.* (1998) [2]. Minimum inter-cluster distance was observed between cluster II and cluster VI (6.573). The highest intra-cluster distance was observed in cluster VI (28.682), followed by cluster V (25.962), cluster III (25.803) and cluster IX (23.882). The intra cluster distance was not present in cluster XII and XV as these clusters had only one RILs each.

**Table 1:** Distribution of one hundred forty-nine groundnut RILs into different clusters

Cluster	Number of RILs	Composition of clusters
I	34	RILs No. 1,2,10,11,12,14,15,17,18,19,20,21,24,27,33,34,54,56,72,73,78,79,84,92,96,100,102,105,106,110,118,123,128,137
II	40	RILs No. 3,7,13,25,29,30,31,32,36,44,47,48,50,51,58,63,68,69,71,75,85,88,98,99,104,107,111,112,115,124,129,133,135,138,139,140,145,146,147,148
III	2	RILs No. 4,28
IV	14	RILs No. 5,38,39,41,45,46,55,62,64,65,86,95,108,120
V	7	RILs No. 6,23,40,77,113,117,136
VI	14	RILs No. 8,16,22,26,35,57,76,83,90,94,114,125,127,141
VII	6	RILs No. 9, 60,61,81, 89,103
VIII	10	RILs No. 37,42,43,59,70,74,97,109,116,142
IX	4	RILs No. 52, 53, 93,101
X	6	RILs No. 66, 121,122,130,131,134
XI	3	RILs No. 67,126,144
XII	1	RILs No. 80
XIII	4	RILs No. 82, 87,143,149
XIV	3	RILs No. 91,132,150
XV	1	RILs No. 119

**Table 2:** Average intra and inter cluster distances ( $D=\sqrt{D^2}$ ) in groundnut RILs

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	23.206	24.685	80.368	27.918	31.156	21.218	22.244	30.392	50.224	44.229	42.262	58.401	25.408	50.919	24.148
II		21.300	64.912	18.144	12.092	6.573	31.959	10.248	27.855	24.893	20.930	36.841	10.371	33.606	18.297
III			25.803	77.072	55.513	64.669	94.866	61.720	44.904	49.950	56.498	56.230	69.350	42.636	80.763
IV				18.840	23.257	19.662	24.216	23.424	37.582	29.959	33.662	42.408	24.295	40.021	9.236
V					25.962	11.994	40.653	12.932	20.627	16.398	21.023	35.311	20.798	23.729	26.308
VI						28.682	31.088	10.858	29.913	26.508	23.288	41.296	13.985	34.596	19.943
VII							16.985	36.500	57.645	51.800	49.061	62.428	31.972	60.911	19.244
VIII								21.291	25.193	25.865	19.642	37.361	14.788	33.871	24.097
IX									23.882	16.171	20.162	27.142	34.340	22.404	42.163
X										18.364	25.086	26.151	33.300	13.527	35.575
XI											20.338	30.456	24.095	32.985	35.307
XII												0.000	40.125	30.817	46.197
XIII													19.710	40.516	21.068
XIV														17.763	45.029
XV															0.000

**Table 3:** Cluster means for seventeen characters in groundnut

Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
Days to 50% flowering	33.59	33.82	34.47	33.86	34.56	33.22	33.47	33.39	33.56	36.07	35.73	33.55	33.59	33.78	37.17
Days to maturity	127.23	127.28	127.24	127.16	127.28	127.35	127.29	127.04	127.15	127.17	127.29	127.32	127.08	127.09	127.91
Number of branches per plant	7.18	7.52	7.47	7.3	8.17	7.32	7.4	7.58	7.31	7.58	7.3	8.38	7.44	7.65	7.27
Number of pods per plant (g)	17.74	22.28	24	17.08	21.1	20.22	19.04	25.08	24.97	15.69	17.77	17.72	25.98	15	19.22
Pod yield per plant (g)	21.41	23.43	20.6	14.59	21.74	24.21	18.27	26.95	21.87	14.39	32.19	13.63	28.1	15.59	18.35
Shelling percentage	64.63	62.22	66.3	62.3	64.62	64.96	63.09	62.69	69.21	64	66.28	51.17	56.87	58.41	58.86
Number of kernels per pod	1.64	1.68	1.8	1.49	1.66	1.62	1.67	1.63	1.59	1.58	1.53	1.68	1.51	1.49	1.53
Kernel yield per plant(g)	12.85	13.66	24.88	9.19	13.12	14.44	10.61	15.35	13.74	8.95	18.23	8.92	15.43	8.11	10.97
100 kernel weight (g)	61.94	49.79	77.14	41.57	54.74	53.48	43.37	48.24	47.43	51.16	43.66	36.88	49.18	59.71	42.57
Bio. yield per plant(g)	62.84	83.07	140.52	75.41	91.65	81.52	53.41	87.54	109.49	103.42	98.2	111.84	79.32	110.44	69.9
Harvest index (%)	22.89	18.64	20.66	11.59	14.63	19.73	19.39	21.32	15.2	12.06	21.06	22.31	21.84	8.23	13.51
Protein content (%)	24.66	24.98	24.96	25.48	23.91	24.99	23.34	24.49	24.83	24.88	23.09	23.64	25.27	24.73	24.78
Oil content (%)	49.71	49.58	49.24	48.34	49.6	49.24	51.56	49.62	48.54	49.1	51.3	48.6	51.56	51.26	47.36
Palmitic acid (%)	11.96	12.07	11.76	11.47	11.97	11.98	11.38	11.08	12.29	12.07	12.79	13.06	12.42	11.76	11.45
Stearic acid (%)	2.75	2.85	2.98	2.7	2.71	2.7	3.06	2.71	2.7	2.55	2.82	2.62	3.46	3.13	2.46
Oleic acid (%)	34.08	32.7	34.59	36.39	35.57	35.29	38.2	38.38	32.95	34.36	29.09	25.7	30.69	34.93	35.68
Linoleic acid (%)	45.26	46.46	44.56	42.96	43.1	44.06	42.54	42.18	45.63	45.23	49.21	52.31	49.1	44.06	44.71

The Cluster mean value (Table 3) for different clusters indicated that cluster III recorded the highest cluster mean for number of kernels per pod, 100-kernel weight, kernel yield per plant (g) and biological yield per plant. Cluster XIII was the best source for number of pods per plant, pod yield per plant, oil content and stearic acid. Cluster XV was the best source for days to 50% flowering and days to maturity. Contribution of character towards divergence (Table 4) was

observed maximum in harvest index (15.15). Anuradha (1995) [1] also recorded the similar results in groundnut. However, the differences were clearer for kernel yield per plant followed by pod yield per plant, biological yield per plant, 100-kernel weight and number of pods per plant. The present findings are in conformity with those reported earlier in groundnut (Dashora and Nagda (2004) [3]; Sonone and Thaware (2009) [10].

**Table 4:** Contribution of various characters to divergence

S. No.	Characters	Contribution (%)
1	Days to 50% flowering	1.18
2	Days to maturity	0.06
3	Number of branches per plant	2.78
4	Number of pods per plant (g)	8.81
5	Pod yield per plant (g)	13.04
6	Shelling percentage	3.77
7	Number of kernels per pod	3.27
8	Kernel yield per plant(g)	13.26
9	100-kernel weight (g)	10.91
10	Biological yield per plant (g)	11.7
11	Harvest index (%)	15.15
12	Protein content (%)	1.75
13	Oil content (%)	1.17
14	Palmitic acid (%)	2.16
15	Stearic acid (%)	3.76
16	Oleic acid (%)	4.37
17	Linoleic acid (%)	2.85

The greatest contribution of 100-kernel weight towards divergence was also earlier reported by Golakia and Makne (1991) [4], Reddy and Reddy (1993) [8], Lakshmidivamma *et al.* (2006) [5] and Venkatesh *et al.* (2015) [11]. It has been suggested that the character with maximum contribution towards divergence should be given importance for undergoing hybridization programme. Considering the cluster distances and cluster means in the present investigation, emphasis should be given to genotypes belonging cluster III, VIII, XV, XIII and VII for exploitation as parents in hybridization programme.

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