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## Genetic divergence studies for yield and its component traits in groundnut (*Arachis hypogaea* L.)

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**Abstract**

The genetic diversity analysis revealed the formation of eleven clusters suggested the presence of wide genetic diversity among the forty genotypes studied. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that 100 pod weight followed by shelling percent, kernel yield per plant, 100 kernel weight, plant height and days to 50% flowering contributed maximum contribution towards total divergence in the present study. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster X with IX, IX with II and cluster VIII with II which may lead to broad spectrum of favorable genetic variability for yield improvement in groundnut.

**Keywords:** Clusters, genetic divergence,  $D^2$  technique, *Arachis hypogaea*

**Introduction**

Groundnut is an allotetraploid ( $2n=4x=40$ ) with a basic chromosome number of  $x=10$  and it is highly self-pollinated crop having cleistogamous flowers. Success of plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. Choosing genetically diverse parents will enable the expansion of genetic base and development of superior types. In this regard, Mahalanobis (1936) [6] generalized distance ( $D^2$ ) technique has been extensively used to measure the genetic divergence in breeding programmes. Inter crossing between more divergent parents is expected to generate broad spectrum of variability and selection can be adopted in the segregating generations. Therefore, the present study was carried out to ascertain the nature and magnitude of genetic divergence among the forty spanish bunch groundnut genotypes, which will help to plan hybridization programmes to develop groundnut varieties with high pod yield and also oil content.

**Materials and Methods**

The experimental material consisted forty genotypes of groundnut were sown in a Randomized Block Design with three replications during Summer 2015-16. The present investigation was carried out at Research Farm of Niger Research Station, Navsari Agricultural University, Vanarasi, Tal- Vandsa, Dist- Navsari. Each entry was accommodated in a single row of 3.0 m length with a spacing of 45 x 15 cm. The experiment was surrounded by two guard rows to avoid damage and border effects. The recommended agronomical practices and plant protection measures were followed for the successful raising of the crop with eight irrigations throughout crop period. The observations were recorded on five randomly selected plants in each entry and replication for ten characters viz., day to 50% flowering, day to maturity, plant height, number of mature pods per plant, pod yield per plant, kernel yield per plant, 100- pod weight, 100- kernel weight, shelling percentage and oil content (oil content was determined by automatic soxhlet extractor as suggested by Franz von Soxhlet) and their mean values were used for the statistical analysis. The genetic divergence was assessed and the genotypes were grouped on the basis of generalized distance using the Tocher's method as suggested by Rao (1952) [8].

**Result and Discussion**

In the present study,  $D^2$ -statistic estimated on forty genotypes of groundnut for ten characters showed that the generalized distance ( $\sqrt{D^2}$ ) between two populations varied from 2.81 to 16.65 which was an indicator of considerable diversity available in the material evaluated. On the basis of  $D^2$  values, eleven clusters were formed from forty

genotypes. The clustering pattern of genotypes showed that the genotypes of different origins were clubbed into one cluster whereas the genotypes belonging to same country or origin were grouped into different clusters indicating that the geographic distribution was not the sole criterion of genetic diversity.

### Clustering pattern

The cluster VIII contained three genotypes from different origins followed by cluster III, IV, V, VI and VII contained only one genotypes. On the other hand, the clusters IX, X and XI also possessed only one genotype in each cluster. Thus, the present results indicated that geographical distribution and genetic divergence did not follow the same pattern. Similar findings have been reported by Golakiya and Makne (1992)<sup>[2]</sup>; Kutule *et al.* (1992); Dasora and Nagda (2004); Nadaf *et al.* (1986); Reddy and Reddy (1993)<sup>[9]</sup>. Therefore, it can be concluded that selection of parents for hybridization should not be based on geographical diversity only, but it should have a base of both geographical origin as well as genetic divergence.

### Intra and Inter cluster distances (D<sup>2</sup>)

In general, intra-cluster distance values were lower than the inter-cluster distances which indicated substantial diversity present among the genotypes studied. Thus, the genotypes included within a cluster tended to diverse less from each other. The lowest intra-cluster distance was in cluster I (D=5.06) indicating that genotypes within this cluster were similar whereas the highest intra-cluster distance was in cluster VIII (D=6.73). Cluster III, IV, V, VI, VII, IX, X and XI had no intra cluster distances as they were represented by only single genotype in each cluster. The maximum inter-cluster distance (D) was observed between clusters X and IX (D=16.65) followed by clusters IX and II (D=15.22) and VIII and II (D=13.81).

### Contribution towards genetic divergence

The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that 100 pod weight (38 %) followed by shelling percent (19.23 %), kernel yield per plant (14.62%), 100 kernel weight (12.18%), plant height (6.15%) and days to 50% flowering

(4.23%) contributed maximum towards divergence in the present study Those accounted near 95% per cent of total divergence among them Highest genetic divergence contributed trait was 100 pod weights (38%) in the material. The greater contribution of 100 pod weight showed by Gupta *et al.* (2015)<sup>[3]</sup>, for shelling percent reported by Golakia and Makne (1992)<sup>[2]</sup>; Reddy and Reddy (1993)<sup>[9]</sup>; Venkateswarlu *et al.* (2011)<sup>[11]</sup>, for 100 kernel weight by Vivekanand *et al.* (2015) and for kernel yield per plant reported by Kumar *et al.* (2010)<sup>[5]</sup>.

### Cluster means

Cluster mean for ten characters in groundnut clearly indicate appreciable difference among cluster means for most of the characters. Greater range of mean values among the clusters was recorded for different traits. The cluster V revealed maximum values for number of mature pod per plant (13.67 pods) and oil content (50.53). The cluster VII had high mean values for days to 50% flowering (45.00 days) and days to maturity (113.33 days). The cluster XI had high mean values for plant height (68.00cm) and 100 kernel weight (49.00g). The cluster II revealed maximum values for kernel yield per plant (14.17g) and pod yield per plant (18.19g). The cluster X revealed maximum values for 100 pod weight (90.80g) and shelling percent (75.53%). The cluster IX had lower mean values for days to 50% flowering (34.67 days). The cluster III and cluster IX both had lower mean values for days to maturity (106.33days).

**Table 1:** Average inter and intra-cluster distance ( $D = \sqrt{D^2}$ ) values for groundnut genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	5.06	9.32	6.42	7.18	7.74	7.04	6.58	8.62	8.37	11.63	8.18
II		5.89	8.61	10.13	9.07	10.06	8.71	13.81	15.22	10.52	8.62
III			0.00	2.81	3.35	3.50	9.23	7.38	10.65	6.51	6.68
IV				0.00	3.67	3.59	9.49	6.73	10.98	6.07	6.67
V					0.00	5.66	10.26	8.35	11.65	6.23	5.11
VI						0.00	9.49	6.18	11.06	7.03	9.17
VII							0.00	11.64	11.79	12.95	9.04
VIII								6.73	8.96	11.26	11.28
IX									0.00	16.65	12.29
X										0.00	9.10
XI											0.00

**Table 2:** Cluster mean for ten different characters in groundnut genotypes

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of matur pods per plant	Pod yield per Plant (g)	Kernel yield per Plant (g)	100 pod weight (g)	100 kernel weight (g)	Shelling (%)	Oil content (%)
	1	2	3	4	5	6	7	8	9	10
I	39.21	108.35	53.57	9.26	12.40	7.18	58.67	32.57	57.36	47.00
II	40.81	106.67	49.68	13.11	18.91	14.17	58.41	29.33	74.83	48.06
III	39.33	106.33	49.93	10.33	13.53	8.83	73.83	38.00	64.10	48.70
IV	39.67	107.00	59.20	9.67	12.17	7.47	78.03	37.67	62.17	49.10
V	36.67	112.33	56.53	13.67	16.77	10.40	76.23	40.33	62.10	50.53
VI	40.00	107.00	48.00	9.67	12.67	7.73	79.10	27.67	61.37	46.30
VII	45.00	113.33	64.40	9.33	11.67	7.50	49.30	27.00	64.30	41.67
VIII	39.78	109.61	53.02	9.78	9.47	4.57	77.83	30.89	48.24	47.96
IX	34.67	106.33	52.67	7.00	8.33	3.13	55.83	40.67	37.57	50.07
X	39.33	109.00	56.17	11.00	16.20	12.20	90.80	35.33	75.53	49.23
XI	41.00	109.00	68.00	12.33	18.73	11.73	63.77	49.00	62.60	50.17
MEAN	39.51	108.24	53.51	10.19	13.59	8.50	62.50	32.76	60.51	47.50
S.Em±	0.97	2.37	1.43	0.60	0.75	0.45	1.25	1.29	1.17	0.94
C.V.%	4.25	3.79	4.62	10.13	9.50	9.11	3.47	6.80	3.36	3.43
C.D. 5%	2.73	6.66	4.02	1.68	2.10	1.26	3.53	3.62	3.30	2.65

**Table 3:** Percentage contribution of various characters towards total divergence

S. No.	Characters	Number of times appearing first	% contribution toward divergence
1	Days to 50% flowering	33	4.23%
2	Days to maturity	0	0.00%
3	Plant height (cm)	48	6.15%
4	Number of mature pods per plant	21	2.69%
5	Pod yield per plant (g)	1	0.13%
6	Kernel yield per plant (g)	114	14.62%
7	100 pod weight (g)	297	38.08%
8	100 kernel weight (g)	95	12.18%
9	Shelling percentage (%)	150	19.23%
10	Oil content (%)	21	2.69

### Conclusion

It could be concluded that high yielding genotypes coupled with desirable traits like days to 50% flowering, days to maturity, plant height, number of mature pods per plant, pod yield per plant, kernel yield per plant, shelling percentage and oil content could be selected as parents for hybridization programme from cluster I, II, VIII, IX and X. Inter crossing genotypes from these clusters might result in wide array of variability for exercising effective selection. In the present investigation, based on high yielding genotypes and large inter-cluster distances or genetic distance, it is advisable to attempt crossing of the genotypes from cluster X with the genotypes of cluster IX and VIII as well as VIII with IX which may lead to broad spectrum of favourable genetic variability for yield improvement in groundnut.

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