Research Article

Genetic divergence analysis in Groundnut (*Arachis hypogaea* L.) genotypes

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Abstract

The Mahalanobis D2 statistic was utilized to quantify genetic dissimilarity among groundnut genotypes for thirteen features. Tocher's approach was used to divide genotypes into groups. In all, ten clusters were established from 40 genotypes. Cluster I has sixteen genotypes subsequently cluster II has eight, clusters IV and VI contain three, cluster III contains five, and clusters V, VII, VIII, IX, and X had a single genotype. This classification revealed a greater amount of variation among genotypes. Cluster II had a desirable rating for the number of pods per plant. The cluster IX had a desirable rating for the highest plant height, number of branches per plant, and kernel yield per plant. Cluster X had a desirable rating for the highest germination percentage, earliness flowering, the highest number of kernels per plant, and shelling percentage. Cluster III reported the greatest intra-cluster distance. Cluster IV and Cluster VII were established to possess the greatest inter-cluster distance.

Keywords cluster diagram, diversity, groundnut

Introduction

Groundnut (*Arachis hypogaea* L.) is taken from two Greek words: "Arachis" means a legume, and "hypogaea" means the production of pods in the soil. In India groundnut (*Arachis hypogaea* L.) is a dominant oilseed crop. Cultivated groundnut is an autotetraploid legume crop with 2n=4x=40 chromosomes that belongs to the Fabaceae family and is self-pollinated (1). Groundnuts are high in edible oil (47-54%), high-quality protein (22-30%), carbohydrate (6-24%), cellulose (1-2%), minerals (2-3%), and calories (5-6 percent). Groundnut is prized for its edible oil as well as confectionary. The genetic divergence analysis determines the variation pattern in the collection of genotypes, identifies the characters, and differentiates the genotypes into different groups that could be used in the crop improvement program. Genetic variety is significant because hybrids between lines with different genetic backgrounds tend to have more heterosis than hybrids between closely related parents, which might result in broad-spectrum genetic variety in separate generations.

Methodology

The present study on Groundnut was undertaken to study variability analysis using 40 genotypes. The experiment was performed at the

Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, S. K. Nagar during the summer of 2020 with three replications. Each entry was grown in a single row with a 30 cm row to row distance and a 10 cm plant to plant distance. For a satisfactory crop, all recommended agronomic practices were followed. The present study consisted of 40 diverse genotypes collected from germplasm materials maintained at the Main oilseed Research Station, Junagadh Agricultural University, Junagadh.
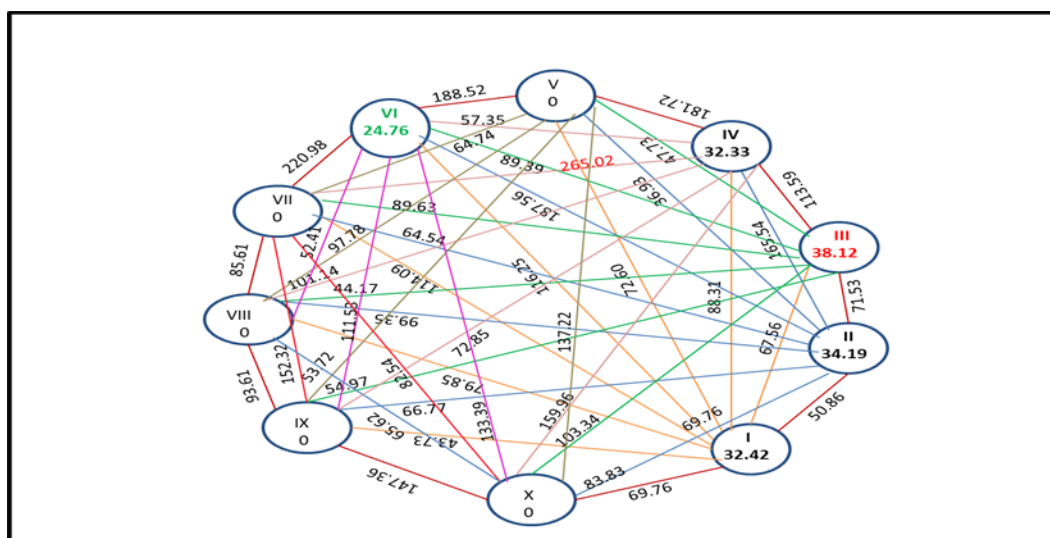

Figure 1. Cluster diagram

Table 1. The genotypes of groundnuts studied are listed below.

Sr.No.	Genotype	Sr.No.	Genotype	Sr.No.	Genotype	Sr.No.	Genotype
1	JB-1494	11	JB-1491	21	JB-1450	31	JB-1481
2	JB-1488	12	TG-88	22	GG-6	32	JB-1422
3	JB-1497	13	JB-1464	23	JB-1418	33	JB-1474
4	JB-1496	14	JB-1503	24	JB-1406	34	JB-1432
5	JB-1493	15	JB-1463	25	JB-1511	35	JB-1517
6	JB-1500	16	JB-1516	26	JB-1501	36	GG-34
7	JB-1492	17	JB-1506	27	JB-1509	37	TG-37A
8	JB-1487	18	JB-1515	28	GJG-31	38	TAG-24
9	JB-1505	19	JB-1519	29	JB-1442	39	GJG-33
10	JB-1498	20	JB-1480	30	JB-1504	40	TPG-41
Source: Main Oil seed Research Station, Junagadh							

The genotypes were selected based on diverse performance for various traits. For the quantitative analysis of 13 traits including the percentage of germination, flowering days, maturity days, height of plant (cm), branches present in every plant, pods present in each plant, kernels present in each plant, per plant, 100 seed weight (g), shelling percentage, harvest index (percent), oil content (percent), protein content (percent), and kernel yield per plant (g) the average value was utilized.

<p style="text-align:center">**Table 2. Distribution of genotypes evaluated for seed yield into different clusters of groundnuts**</p>

Cluster	No. of Genotype	Name of Genotype
I	16	JB-1505, JB-1450, JB-1491, TG-88, JB-1418, JB-1487, JB-1498, GJG-33, JB-1497, JB-1488, JB-1406, JB-1432, JB-1463, JB-1481, JB-1442, GG-6
II	8	TG-37A, GG-34, JB-1474, JB-1494, JB-1509, JB-1511, JB-1501, JB-1422
III	5	JB-1496, TPG-41, JB-1493, JB-1480, JB-1504
IV	3	JB-1516, JB-1506, JB-1503
V	1	GJG-31
VI	3	JB-1515, JB-1519, JB-1492
VII	1	JB-1517
VIII	1	TAG-24
IX	1	JB-1464
X	1	JB-1500

Results and Discussion

The genotypes were categorized using Tocher's approach [2], with a theory regarding the genotype of clusters i.e. genotypes within a cluster have lower D2 values than genotypes from separate clusters. A total of 40 genotypes were used to generate ten clusters. Table 2 shows the genotype distributions divided into ten groupings. The largest cluster, Cluster I, has sixteen genotypes. Cluster II has eight genotypes, clusters IV and VI have three genotypes each, cluster III has five genotypes, and clusters V, VII, VIII, IX, and X only have one genotype each.

Similar findings of [3-21] corroborated that the clustering of genotypes from various eco-geographical areas was done randomly, illustrating that geographic distribution does not always indicate genetic divergence.

The average D2 values within each cluster ranged from 24.76 to 38.12. Cluster III had the greatest intra-cluster distance among the clusters (38.12), Cluster II comes afterward (34.19), while the minimum intra-cluster distance was studied for cluster VI (24.76). Clusters V, VII, VIII, IX, and X

<p style="text-align:center">**Table 3. The average intra- and inter-cluster D2 score of 40 Groundnut genotypes**</p>

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	32.42	50.86	67.56	88.31	72.60	116.25	114.09	79.85	43.73	69.76
II		34.19	71.53	165.54	36.93	187.56	64.54	99.35	66.77	83.83
III			38.12	113.59	47.73	89.39	89.63	44.17	54.97	103.34
IV				32.33	181.72	57.35	265.02	101.14	72.85	159.96
V					0	188.52	64.74	97.78	53.72	137.22
VI						24.76	220.98	52.41	111.53	133.39
VII							0	85.61	152.32	82.54
VIII								0	93.61	65.62
IX									0	147.36
X										0

were found to have zero intra-cluster distance. The four clusters V, VI, VIII, I, and X were all solitary clusters (Table 3). Inter-cluster distances were considerably large than intra-cluster distances, indicating that the genotypes differed significantly. The selection of parents for crossing from different clusters may result in heterotic expression for yield and quality traits.

Table 4. Cluster means for seed yield and its components in Groundnut

Cluster	Germin-ation %	Days to flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Number of kernels per plant	100-seed weight	Kernel yield Per plant	Harvest index	Shelling %	Oil content	Protein content
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)
I	87.20	34.19	104.34	45.43	17.24	12.82	18.13	37.77	14.97	26.45	57.23	37.27	31.88
II	86.22	32.97	106.09	38.83	15.56	13.24	17.84	37.47	15.38	28.97	60.93	39.94	32.48
III	86.10	35.50	106.25	45.31	17.20	11.10	16.27	39.55	11.46	26.28	56.52	38.03	33.34
IV	85.83	33.50	104.92	48.09	17.92	10.91	14.80	36.54	13.03	24.13	58.63	31.31	32.31
V	88.00	34.50	107.00	40.70	15.12	13.00	18.00	36.87	14.37	28.66	59.43	39.60	34.19
VI	90.17	37.42	104.58	46.86	18.05	9.74	14.65	39.46	8.87	24.23	52.58	33.96	31.98
VII	83.25	35.00	108.75	34.10	13.45	12.05	16.80	32.75	11.52	35.92	59.71	43.99	32.08
VIII	88.00	37.25	105.00	42.07	17.00	9.25	12.65	34.75	9.47	23.03	64.90	38.32	32.14
IX	84.25	35.75	106.75	52.82	19.92	10.90	15.65	35.62	15.57	24.34	44.79	35.67	33.62
X	91.25	32.25	104.75	37.00	14.60	11.90	20.10	39.50	11.72	24.87	67.22	40.74	29.86

For some traits, there were wider ranges of average values among the clusters. The cluster I had the maximum mean values and a decent maturity rating (104.34 days). Cluster II had a desirable rating for the number of pods per plant (13.24). For 100-seed weight, cluster III had the maximum mean values and favorable rating (39.55 g). Cluster V had the maximum average values and the most desirable protein content rating (34.19 percent). Cluster VII had the highest average values for harvest index (35.92), and oil content (43.99 %). The cluster IX had a desirable rating for the highest plant height (52.82 cm), number of branches per plant (19.92), and kernel yield per plant (15.57 g). Cluster X had a desirable rating for the highest germination percentage (91.25%), earliness flowering (32.25 days), the highest number of kernels per plant (20.10), and shelling percentage (67.22) (Table 4).

Table 5. Groundnut genotypes were examined for kernel yield and the relative contribution of different traits to genetic diversity

No.	Character	Time ranked 1st	Contribution to divergence%
1	Germination percentage	1	0.13
2	Days to flowering	3	0.38
3	Days to maturity	3	0.38
4	Plant height (cm)	0	0
5	Number of branches per plant	0	0
6	Number of pods per plant	2	0.25
7	Number of kernels per plant	14	1.79
8	100-seed weight (g)	5	0.64
9	kernel yield per plant (g)	249	31.92
10	Harvest index (%)	50	6.41
11	Shelling percentage	10	1.28
12	**Oil content (%)**	**275**	**35.25**
13	Protein content (%)	168	21.54

Oil content (35.25 percent) contributed the most to the diversity of all the characters, taking first place 275 times out of 780 combinations, subsequently kernel yield per plant (31.92%) with 249 times, protein content (21.54%) with168 times, harvest index (6.41%) with 50 times. While, the number of kernels per plant (1.79%) with 14 times, shelling percentage (1.28%) with 10 times, 100-seed weight (0.64%) with 5 times, days to flowering (0.38%) with 3 times, days to maturity (0.38%) with 3 times, number of pods per pod (0.25%) with 2 times and germination percentage (0.13 %) with 1 time contributed minimum towards total genetic divergence. Characters like plant height and number of branches per plant, on the other hand, had no effect on the overall genetic divergence, as shown in Table 5.

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