Genetic Divergence for Yield and its Component Traits in Groundnut Germplasm

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Eighty-one genotypes of groundnut (*Arachis hypogaea* L.) representing different groundnut centres were studied for genetic divergence analysis utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2value) groundnut accessions were grouped into 16 clusters. Of the 16 clusters formed, cluster I was the largest with 47 accessions followed by cluster II with 10 accessions. Test weight, days to maturity and oil content were the most potential traits contributing to the total divergence. Cluster XI and XVI had maximum inter-cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Cluster XII has genotype with most favorable characters and hence can be involved as potential parent for development of superior genotypes.

Key words: *Arachis hypogaea*, Clusters, Divergence, Groundnut, D^2 technique

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop of India. The information on genetic diversity in a crop is essential in order to have breeding programmes for higher yield potentials. Choosing genetically diverse parents will enables the expansion of genetic base and development of superior types. In this regard, Mahalanobis (1936) generalized distance (D^2) technique has been extensively used to measure the genetic divergence in breeding programmes. Intercrossing between more divergent parents is expected to generate a broad spectrum of variability and selection can be adopted in the segregating generations. Hence, an attempt was made the magnitude of genetic divergence in groundnut accessions and to identify genetically divergent parents, which can be utilized in hybridization programmes.

Materials and Methods

Eighty-one genotypes of groundnut representing different parts of India were grown in 9 x 9 simple lattice design with two replications at GKVK Farm, University of Agricultural Sciences, Bangalore. Observations were recorded on five randomly chosen plants in each replication for 13 quantitative characters. The mean values were transformed into uncorrelated linear functions using Mahalanobis group distance (D^2) analysis [Rao, 1952]. The D^2 values corresponding to all possible pairs of genotypes were calculated to determine group constellations. 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).

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Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Based on relative magnitude of values, all the genotypes were grouped into 16 clusters (Table1) Among the 16 clusters, cluster I was the largest having 47 genotypes followed by cluster II with 10 genotypes.

Table 1. Distribution of 81 Groundnut genotypes into different clusters

Cluster no	No of genotypes	Accession Name/ Number
I	47	J-41, J-46, Dh-88, JL-24-2, K-1240, J-39, J-45, JSSP-7, J-42, JL-24, J-47, ICGS-30, TVG-9363, K-1257, ICGV-86325, AK-135, SAMRAT, TNAU-97, Dh-55, AK-107, JL-286, R-8806, Dh-87, AK-159, K-134, VRI-2, IC-1224, R-9214, VG-9521, TMV-2, Dh-53B, J-40, K-134 x D-8-29, ICGV-92242, OG-931, TNAU-325, J-48, Bagepalli Local, TG-36B, TAG-24, Dh-10 x R-847259, R-9217, TG-37C, TG-26, HNG-35, J-38, KGN-20
II	10	VG-9516, CSMG-919, Dh-53A, VG-9513, KGN-35, JL-274, ALG-75, Dh-56, ICGV-23, SB-11
III	1	JSSP-28
IV	4	M-335, JSSP-30, ICGS-76, JSSP-15
V	5	JSSP-13, RG-369, JSSP-29, TG-37D, TNAU-281
VI	1	LGN-1
VII	2	VG-9711, JSSP-17
VIII	3	ICGV-86590, ICGV-86532, JL-24-B
IX	1	J-54
X	1	TG-37F
XI	1	R-9248
XII	1	JSSP-18
XIII	1	Dh-992
XIV	1	JSSP-16
XV	1	TNAU-269
XVI	1	M-13

Ten clusters were found to be solitary with one genotype each. The clustering pattern of genotypes from different centres was of random nature. The tendency of genotypes from different centres to group together in one cluster may be due to similarity in requirements and selection approach followed under domestic cultivation. The results are in accordance with the findings of Nadaf *et al.* (1986), Katule *et al.* (1992), Nayak and Patra (1997) and Venkataravana *et al.* (2000).

Another feature that came to light was that genotypes from the same centre were placed in separate clusters indicating wide diversity among genotypes originating from the same place. The clustering pattern, thus failed to indicate any relationship between the genetic divergence and the centres of development of these accessions. Similar results were obtained by Katule *et al.* (1992), Nayak and Patra (1997) and Venkataravana *et al.* (2000).

The intra and inter cluster D^2 values among the 16 clusters are presented in Table 2. Cluster VIII had the maximum intracluster distance of 69.2 followed by cluster II with a distance of 66.5. Ten clusters, which were solitary, had no intra cluster distances. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or segregants. A general notion exists that the larger the divergence higher will be the variability generated in the segregating generation. In this context, inter-cluster distances were worked out considering 13 quantitative characters. The inter-cluster distance was the maximum between clusters XI and XVI (1117.5) followed by cluster X with XVI (901.4). The minimum inter-cluster distance was between the VI and XI (60.8). Hence, the genotypes included in the cluster VI, X, XI and XVI may be selected for more effective crossing programme and should result in wide spectrum of variability to operate selection in segregating populations.

The per cent contribution of each character in grouping the genotypes was worked out and presented in Table 3. Since each genotype produced 80 combinations with all the genotypes, 3240 D^2 values were obtained. Based on these D^2 values, per cent contribution of different characters towards divergence was obtained. Test weight ranked first i.e., 1337 times with a maximum contribution of 41.27 per cent to the total divergence followed by days to maturity (21.11%) and oil content (11.67%). These characters can be given greater

Table 2. Intra-cluster (diagonal) and inter-cluster distances for 16 clusters in groundnut

Clusters I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**56.15**	169.52	115.33	214.15	317.59	102.17	208.2	119.99	114.85	118.83	175.22	210.63	188.02	362.86	278.05	605.11
	(7.493)	(13.02)	(10.739)	(14.634)	(17.821)	(10.108)	(14.429)	(10.954)	(10.717)	(10.901)	(13.237)	(14.513)	(13.712)	(19.049)	(16.675)	(24.599)
II		**66.5**	210.77	248.9	168.79	119.7	140.49	157.75	148.18	298.22	271.85	246.24	111.87	443.01	320.23	446.86
		(8.156)	(14.518)	(15.777)	(12.992)	(10.941)	(11.853)	(12.56)	(12.173)	(17.269)	(16.488)	(15.692)	(10.577)	(21.048)	(17.895)	(21.139)
III			**0.000**	193.66	333.17	204.03	284.19	137.17	190.19	143.07	230.95	302.66	191.43	352.91	308.04	706.07
				(13.916)	(18.253)	(14.284)	(16.858)	(11.712)	(13.817)	(11.961)	(15.197)	(17.397)	(13.836)	(18.786)	(17.551)	(26.572)
IV				**51.37**	192.82	361.3	106.15	292.03	191.05	346.03	553.71	131.24	281.03	100.02	168.56	324.68
				(7.167)	(13.886)	(19.008)	(10.303)	(17.089)	(13.822)	(18.602)	(23.531)	(11.456)	(16.764)	(10.001)	(12.983)	(18.019)
V					**52.1**	385.4	138.6	266.57	141.47	564.68	661.67	178.28	318.23	248.54	173.03	170.22
					(7.218)	(19.632)	(11.773)	(16.327)	(11.894)	(23.763)	(25.723)	(13.352)	(17.839)	(15.765)	(13.154)	(13.047)
VI						**0.000**	253.16	124.9	211.03	129.96	60.81	312.58	81.59	609.79	465.52	733.49
							(15.911)	(11.176)	(14.527)	(11.4)	(7.798)	(17.68)	(9.033)	(24.694)	(21.576)	(27.083)
VII							**36.9**	279.09	170.56	378.96	477.03	135.79	226.02	193.82	179.18	265.27
							(6.075)	(16.706)	(13.060)	(19.467)	(21.841)	(11.653)	(15.034)	(13.922)	(13.386)	(16.287)
VIII								**69.21**	149.06	190.27	214.83	250.08	169.65	421.36	289.85	553.61
								(8.319)	(12.209)	(13.794)	(14.657)	(15.814)	(13.025)	(20.527)	(17.025)	(23.529)
IX									**0.000**	297.7	389.39	132.69	291.08	276.32	163.41	362.14
										(17.254)	(19.733)	(11.519)	(17.061)	(16.623)	(12.783)	(19.03)
X										**0.000**	106.63	380.17	201.89	561.03	497.69	901.44
											(10.326)	(19.498)	(14.209)	(23.686)	(22.309)	(30.024)
XI											**0.000**	546.25	173.37	857.2	684.82	1117.56
												(23.372)	(13.167)	(29.278)	(26.169)	(33.43)
XII												**0.000**	333.9	138.79	143.4	231.92
													(18.273)	(11.781)	(11.975)	(15.229)
XIII													**0.000**	562.83	489.07	641.96
														(23.724)	(22.115)	(25.337)
XIV														**0.000**	93.01	254.95
															(9.644)	(15.967)
XV															**0.000**	253.89
																(15.934)
XVI																**0.000**

* Parenthesis : D value

** Outside the Parenthesis : D^2 value

Table 3. Percentage contribution of each character towards genetic divergence in groundnut

Characters	Times Ranked first	Contribution (%)
Days to 50 % Flowering	225	6.94
Days to maturity	684	21.11
Plant height	247	7.62
No. of Branches/plant	13	0.40
No. of pegs/plant	28	0.86
No. of matured pods/plant	16	0.49
No. of immature pods/plant	35	1.08
Pod yield per plant	24	0.74
Kernel yield	10	0.31
Shelling %	197	6.08
Test weight	1337	41.27
Oil content	378	11.67
Oil yield/plant	46	1.42
TOTAL	3240	100

importance in selection of potential parents for hybridization.

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters (Table 4). Cluster XI, which was solitary with one genotype (R-9248) was relatively early with maximum number of mature pods, but recorded lowest test weight, where as, cluster XVI again a solitary cluster with one entry (M 13) was late maturing with less number of mature pods and very high test weight. Crossing between these two genotypes appeared to be most promising to combine the desirable characters. Cluster XII, with one genotype

Table 4. Mean values for 13 quantitative characters of 16 clusters in groundnut

Cluster No.	Day to 50% flower-ing	Days to maturity	Plant Height (cm)	Number of bran-ches / plant	No. of pegs / plant	No.of mature pods/ plant	No. of immature pods / plant	Pod yield /plant(g)	Kernel yield/ plant (g)	Shelling (%)	Test weight (g)	Oil content (%)	Oil yield/ plant (g)
I	36	110	35.90	9.0	32	21	11	20.43	15.96	78.59	41.58	44.49	7.08
II	39	121	37.10	7.0	29	21	8	21.45	16.26	75.90	46.23	42.44	6.89
III	41	109	29.10	12.0	34	22	13	18.15	13.04	71.81	42.00	41.90	5.45
IV	43	113	33.78	10.0	32	19	12	21.88	16.74	76.41	56.13	43.53	7.22
V	41	121	38.68	7.0	29	19	11	22.60	16.69	73.93	58.90	34.84	5.82
VI	36	116	41.10	6.0	28	22	6	20.85	15.90	76.31	35.25	48.10	7.65
VII	40	120	36.65	8.0	29	21	8	21.40	16.75	78.41	55.50	47.26	7.93
VIII	36	112	37.72	6.0	31	19	12	22.93	15.55	67.77	41.25	41.36	6.38
IX	36	113	36.40	7.0	28	20	18	20.95	17.15	81.96	50.75	34.61	5.88
X	36	109	30.80	8.0	32	19	13	14.25	10.45	73.31	34.25	52.52	5.49
XI	35	113	36.30	7.0	37	28	10	20.75	15.50	74.83	27.00	51.18	7.93
XII	38	111	45.50	11.0	39	28	11	31.40	24.00	76.33	55.25	39.48	9.46
XIII	44	120	31.60	5.0	28	20	8	21.10	14.60	70.92	38.75	47.69	6.97
XIV	40	109	32.90	11.0	35	22	13	26.80	19.45	72.47	64.25	42.03	8.17
XV	37	110	35.30	7.0	40	23	12	24.65	17.85	72.45	59.75	39.59	7.07
XVI	39	120	43.50	6.0	36	17	19	30.50	18.65	73.12	67.25	36.20	6.72

(JSSP-18) was highly promising since it was comparatively early with tall growth habit, maximum pod yield, kernel yield and oil yield. Shelling percentage and test weight was also relatively high. Therefore, it is available to select this genotype for various desirable characters. Similarly the genotypes can be involved as potential parents for various desirable characters.

References

1. Katule BK, MV Thombre, AD Dumbre and BB Pawar (1992) Genetic diversity in bunch groundnut. *J. Maharashtra Agric. Univ.* **17(2):** 302-303.
2. Mahalanobis PC (1936) On the general distance in statistics. In: *Proc. Nat. Acad. Sci.* (Indian) **12**: 49-55.
3. Nadaf HL, AF Habib and JV Goud (1986) Analysis of genetic diversity in bunch groundnut. *J. Oilseeds Res.* **3**: 37-45.
4. Nayak PK and GJ Patra (1997) Genetic divergence in a collection of groundnut germplasm. *Environment and Ecology*, **15(2):** 249-254.
5. Rao CR (1952) *Advanced statistical methods in Biometric Research.* John Wiley and Sons, Inc., Newyork, pp.357-363.
6. Venkataravana P, RA Sheriff, RS Kulkarni, V Shankaranarayana, and PS Fathima (2000) Genetic divergence in groundnut (*Arachis hypogaea* L.) *Mysore J. Agri. Sci.* **34**: 125-129.