

Analysis of Diversity in Groundnut (*Arachis hypogaea* L.)

II. Spreading Group

by

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In a hybridisation programme, varieties obtained from different geographic and ecological regions are being utilised with the assumption of their natural diversity and desirable improvement is expected in their progenies. The validity of this assumption depends upon the association between geographic and genetic diversity.

Mahalanobis's D^2 -Statistic based on multivariate analysis measures the amount of genetic diversity in given populations in respect of characters considered together. Genetic diversity has been studied by Murty and Pavate (1962) in *Nicotiana tabacum* L., Murty and Qadri (1966) in brown *sarson* Arunachalam and Jawahar Ram (1967) in Sorghum, Murty and Tiwari (1967) in *Pennisetum typhoides* Burm., Anand and Murty (1968) in linseed, Singh and Bains (1968) and Singh and Gupta (1968) in cotton. Sandhu and Sangha (unpub.) had found a fairly high degree of genetic diversity in a group of 27 varieties of bunch groundnut. The object of this paper is to study the genetic divergence in another group of 27 varieties using D^2 -statistic to determine whether it is related to geographic divergence.

Material and Methods: The material for the present study comprised 27 groundnut (*Arachis hypogaea* L.) varieties with spreading growth habit and was taken from the germplasm collection maintained at the Punjab Agricultural University, Ludhiana. Details regarding the mode of origin and distinguishing characters of these varieties are given in Table 2. The experiment was conducted at the Punjab Agricultural University, Research Farm, Ludhiana during *kharif*, 1966 and was laid out in randomized block design with four replications. The spacing given was 60 cm between rows and 30 cm within rows of 6 m length.

Five plants were chosen at random among the 20 effective plants for each plot in each replication. Detailed observations were made on these five plants throughout the season and among the many characters studied six variables, namely, X_1 pod yield (gm), X_2 number of primary branches, X_3 number of secondary branches, X_4 number of fruiting nodes per secondary branch, X_5 number of pods and X_6 100-kernel weight (gm) have been made use of in the present study.

Plot means based on the above samples were used for statistical analysis. The D^2 between two populations was estimated by the method as described by

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Rao (1952). The uncorrelated variables were obtained by the pivotal condensation of the common dispersion matrix and the mean values (X) were transformed with standardised uncorrelated (Y) variables.

Results: The data obtained for each character were subjected to routine analysis and the results showed that varieties differed highly significantly in regard to all the characters under study except for number of secondary branches which were significant (Table 1).

TABLE 1. Estimates of varietal variances

Source of variation	df	X_1	X_2	X_3	X_4	X_5	X_6
Blocks	3	360.46	41.28	43.04	4.17	521.06	8.58
Varieties	26	264.634**	6.243**	16.379*	0.480**	354.023**	511.382**
Error	78	102.700	2.095	8.190	0.141	100.288	4.559

* Significant ($P = .05$) ** Highly significant ($P = .01$)

The transformed standardised uncorrelated means (y 's) obtained from the correlated values (x 's) as described under materials and methods are presented in Table 2 using the following relationships of x 's and y 's:

$$y_1 = .06147 x_1$$

$$y_2 = .02919 x_1 + .44299 x_2$$

$$y_3 = -.00648 x_1 - .21626 x_2 + .27672 x_3$$

$$y_4 = .01173 x_1 - .00668 x_2 + .03613 x_3 + 1.48082 x_4$$

$$y_5 = -.03946 x_1 - .04315 x_2 - .16920 x_3 + .25757 x_4 + .07322 x_5$$

$$y_6 = -.11463 x_1 - .06973 x_2 + .11136 x_3 + .35886 x_4 + .08447 x_5 + .10232 x_6$$

The actual values of D^2 corresponding to the 351 possible comparisons taking two varieties at a time were computed. The relative contribution of each character was ranked from 1 to 6 depending on its magnitude. The highest contributor was 100-kernel weight (23.9 per cent) followed by number of pods (19.3 per cent), secondary branches (15.7 per cent) primary branches (15.1 per cent), pod yield (13.1 per cent) and fruiting nodes per secondary branch (12.9 per cent). This showed that 100-kernel weight contributed most to the divergence, whereas pod yield and fruiting nodes per secondary branch had the least effect.

After computing the individual D^2 values, the 27 varieties were formed into 7 clusters such that the varieties within the cluster were having a smaller D^2 among themselves than those from groups belonging to two different clusters (Table 3).

TABLE 2. Original means (\bar{x}) and the mean values of uncorrelated linear combinations of characters (\bar{y})

S. No.	Variety	Origin	\bar{x}_1	\bar{x}_2	\bar{x}_3	\bar{x}_4	\bar{x}_5	\bar{x}_6	\bar{y}_1	\bar{y}_2	\bar{y}_3	\bar{y}_4	\bar{y}_5	\bar{y}_6
1.	E 6	India	40.58	11.50	21.05	2.73	44.65	54.40	2.49	6.28	3.08	5.20	-1.69	7.21
2.	E 8	"	35.18	10.70	24.90	1.98	40.95	49.45	2.16	5.77	4.35	4.17	-2.55	7.22
3.	No. 89	Senegal	42.85	10.05	21.60	2.40	35.65	71.73	2.63	5.70	3.53	4.77	-2.55	8.00
4.	Fengman	China	42.08	9.40	22.50	2.18	42.90	53.65	2.59	5.39	3.92	4.47	-2.17	6.92
5.	Che-tse-hau-Seng	"	46.60	11.45	25.85	2.75	46.65	44.43	2.86	6.43	4.38	5.48	-2.58	6.21
6.	R 7.1.1	Sudan	43.80	11.50	22.65	2.58	45.55	53.93	2.69	6.37	3.50	5.08	-2.06	6.99
7.	R 7.1.3	"	49.35	10.15	24.60	3.00	37.30	74.88	3.03	5.94	4.29	5.84	-3.04	8.26
8.	R 7.24.4	"	28.10	10.65	25.30	2.63	39.75	37.38	1.73	5.54	4.52	5.07	-2.26	6.98
9.	R 7.4.1	"	52.75	9.55	24.65	3.03	46.15	67.38	3.24	5.77	4.41	5.93	-2.50	7.91
10.	R 7.47.2	"	32.75	12.65	26.55	2.60	61.15	35.98	2.01	6.56	4.40	5.11	-1.18	8.10
11.	R 7.47.4	"	39.83	11.60	29.70	2.30	52.90	40.10	2.45	6.30	5.45	4.87	-2.63	7.33
12.	R 7.47.7	"	41.78	12.45	26.90	2.48	64.60	39.03	2.57	6.73	4.48	5.05	-1.37	7.68
13.	S. A. Jumbo	S. Africa	31.55	13.25	22.95	2.60	23.65	67.83	1.94	6.79	3.28	4.96	-4.30	7.89
14.	Gangapuri	India	34.75	10.75	24.90	2.70	36.50	48.25	2.14	5.78	4.34	5.23	-2.68	7.03
15.	F 13	C. Africa	35.73	10.90	25.05	2.23	35.85	42.93	2.20	5.87	4.34	4.55	-2.92	6.15
16.	F 14	"	40.03	9.00	22.75	2.85	39.55	57.30	2.46	5.16	4.09	5.45	-2.19	7.54
17.	A 16	E. Africa	38.45	11.25	26.00	2.63	51.15	47.70	2.36	6.11	4.51	5.21	-1.98	5.24
18.	Solaumn	S. Africa	39.80	10.75	23.70	2.63	45.40	45.10	2.45	5.92	3.98	5.15	-2.04	6.72
19.	Oswanabad	India	36.23	10.10	21.60	2.58	43.45	47.93	2.23	5.53	3.56	4.96	-1.67	7.05
20.	Cochine	"	33.18	9.50	25.25	2.53	50.80	37.85	2.04	5.18	4.72	4.98	-1.62	7.42
21.	94 FDCEO 14	E. Africa	44.20	11.40	26.70	2.68	57.80	43.95	2.72	6.34	4.64	5.38	-1.83	7.45
22.	EC 7585	Australia	48.23	10.25	22.40	2.38	50.80	54.60	2.96	5.95	3.67	4.83	-1.80	6.98
23.	T 25	India	56.30	9.30	23.05	2.98	49.90	61.60	3.46	5.76	4.00	5.84	-2.10	7.05
24.	T 99	"	39.95	9.45	22.45	2.45	35.70	65.80	2.46	5.35	3.91	4.84	-2.54	7.89
25.	<i>Arachis monticola</i>	U.S.A.	14.75	12.65	24.20	3.80	26.30	36.83	0.91	6.03	3.87	6.59	-2.32	7.48
26.	Bambara	India	39.35	8.00	21.70	3.03	38.10	59.28	2.42	4.69	4.02	5.68	-2.00	7.72
27.	PG No. 1	"	43.45	10.00	23.65	2.55	45.05	57.05	2.67	5.70	4.10	5.07	-2.19	7.51
	General mean		39.69	10.67	24.17	2.64	44.01	51.71						

Group I and II consisted of one population each from Africa and U. S. A. respectively. Group III had two varieties, one from China and the other from Africa. Group IV and V included four varieties each, of which two were from India and the other two from Africa. Group VI consisted of seven varieties, two of which belong to India, three to Africa and one each to China and Australia. Group VII was the largest group with eight varieties four each from India and Africa.

The groups and their mutual relationship were graphically brought out and the square root of the average D^2 (Table 3), has been used to denote the distance. This is an approximate measure of the group divergences. Clusters IV, V, VI and VII were quite close to each other. Groups I, II and III were at the corners of the triangle, III was farthest away from I. Cluster II was nearly equidistant from I and III. Intra-group variation was almost parallel within the clusters.

TABLE 3. *Intra-and inter-cluster average D^2*

I	II	III	IV	V	VI	VII
...	8.7243	11.3932	8.7060	9.4083	7.7375	7.7272
	2.953	3.375	2.950	3.067	2.781	2.779
	...	8.3543	6.3516	5.9675	6.4143	6.0558
		2.890	2.520	2.442	2.532	2.460
		1.7506	6.3016	5.2457	4.0314	4.2926
		1.323	2.510	2.290	2.007	2.071
			2.1286	3.3280	3.3140	3.6211
			1.459	1.824	1.820	1.902
				1.3557	2.3787	2.8762
				1.164	1.542	1.695
					1.2174	2.5428
					1.103	1.594
						2.1550
						1.468

Lower values in each cell represent D.

The average intra-cluster D^2 was split into its components to determine relative contribution of the 6 characters to the total divergence (Table 4). The 100 kernel weight contributed maximum to total divergence in clusters III, VI and VII; primary branches in cluster IV and number of pods in group V. The least contribution in almost all the groups was that of fruting nodes per secondary branch.

TABLE 4. Components of intra-cluster D^2 in groundnut

Cluster No.	D_1^2	D_2^2	D_3^2	D_4^2	D_5^2	D_6^2	Total divergence
I	Only one variety in this cluster						
II	Only one variety in this cluster						
III	.2510	.1066	.0189	.0711	.3642	.9388	1.7506
IV	.4027	.6524	.0831	.0223	.4496	.5185	2.1286
V	.2119	.4106	.1015	.0454	.4158	.1705	1.3557
VI	.1044	.2664	.1807	.1292	.1935	.3432	1.2174
VII	.1285	.4325	.4382	.3153	.3180	.5225	2.1550

1=Pod yield, 2=Number of primary branches, 3=Secondary branches, 4=Fructing nodes per secondary branch, 5=Number of pods, 6=100-kernel weight.

The intra-cluster group means for 6 characters are presented in Table 5. Group IV had highest pod yield coupled with bold seed size but least primary branches. Cluster I was unique in having boldest seed size but very low pod yield. Similarly, group II had maximum fructing nodes per secondary branch but lowest pod yield. There was a little variation between groups in respect of secondary branches.

Discussion: The multivariate analysis using Mahalanobis's D^2 -statistic revealed the amount of divergence among spreading groundnut varieties. 100-kernal weight and number of pods were found to contribute maximum towards divergence. Sangha and Sandhu (unpub.) found in the same set of varieties a negative and highly significant genotypic correlation between these two traits. An effective compromise between these characters which show considerable divergence will offer good scope in improving pod yield which had positive genotypic correlation with them.

The relative importance of the components contributing towards divergence can be judged by comparing the group means of the characters (Table 5). The distances between clusters I and II, I and III and II and III were found to be maximum. Group I had boldest seed size but minimum number of pods, lower pod yield and a few fructing nodes for secondary branch. Contrary to this, cluster II had maximum fructing nodes per secondary branch but smallest seed size, lowest pod yield and a few pods per plant. Group III had high pod yield and number of pods but small seed size. The intra-cluster average D^2 revealed that in group III, VI and VII, 100-kernel weight had maximum contribution towards divergence. Primary branches in group IV and number of pods in V had maximum effect. This showed that the forces of differentiation appear to be different at inter-and intra-cluster levels. Similar results have been reported by Sandhu and Sangha (unpub.) in groundnut and by Murty and Tiwari (1967) in *Pennisetum typhoides*.

TABLE 5. Intra-cluster group means for six characters in groundnut

Cluster No.	\bar{x}_1	\bar{x}_2	\bar{x}_3	\bar{x}_4	\bar{x}_5	\bar{x}_6
I	31.55	13.25	22.95	2.60	23.65	67.83
II	14.75	12.65	24.20	3.80	26.30	36.83
III	42.53	11.35	25.93	2.69	48.90	46.07
IV	49.44	9.25	23.50	3.01	42.86	65.79
V	40.55	11.63	25.95	2.58	57.15	44.00
VI	41.94	10.51	22.21	2.50	44.06	54.49
VII	35.84	10.32	25.04	2.46	41.50	47.38

The pattern in which different varieties form different clusters did not follow their geographical distribution rather it was fairly at random. This suggests that forces other than geographical separation are also responsible for this diversity. A possible reason for this might be as that improvement in pod yield is considered an ultimate aim in breeding groundnut. Attempts in achieving this goal have always been made by manipulating its main components e. g. number of pods, 100-kernel weight, in such a way that other quality characters such as shelling percentage and oil content are not effected adversely. This unilateral selection adopted in various countries might have similar effect and thus varieties evolved under similar conditions will group together irrespective of their geographic isolation.

Varieties obtained from India and Sudan were distributed in 4 out of 7 clusters showing maximum divergence which can provide better parents in a hybridisation programme.

Summary: A group of 27 spreading groundnut varieties was assessed for genetic diversity using multivariate analysis. The varieties differed highly significantly in five and significantly in one character. The varieties were grouped into 7 tentative clusters according to their closeness from each other. Genetic divergence was not found to be related with geographic diversity and varieties from different sources entered in different clusters. 100-kernel weight and number of pods were the important characters contributing towards divergence. The forces of differentiation were different at inter-and intra-cluster levels.

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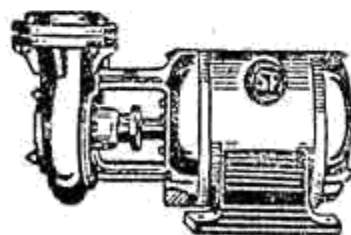
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