



Research Note

Genetic divergence in Virginia groundnut (*Arachis hypogaea* L.)

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Abstract

Divergence analysis among sixty groundnut genotypes was carried out using Mahalanobis's D^2 -statistic. The genotypes were grouped into thirteen clusters. The maximum inter-cluster distance ($D=36.51$) was found between clusters III and V followed by clusters IV and V ($D=32.67$) and II and IV ($D=24.21$) indicated that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters suggesting that the genotypes belonging to these clusters from ideal parents for yield improvement in groundnut.

Keywords

Groundnut, Clusters, genetic divergence

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. Genetic improvement mainly depends upon the amount of genetic variability present in the population. The use of Mahalanobis's D^2 -statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966) because it permits precise comparison among all the population in given any group before effecting actual crosses.

Sixty genotypes of groundnut were sown in a Randomized Block Design (RBD) with three replications during *kharif* 2013. Each genotype was accommodated in a single row of 3.0 m length with a spacing of 60 cm between rows and 15 cm between plants within the row. The experiment was surrounded by two guard rows to avoid damage and border effects. The fertilizers in the experimental area was applied at the rate of 12.5 kg N_2 ha^{-1} and 25.0 kg P_2O_5 ha^{-1} as it is a recommended dose for *kharif* cultivation of groundnut in the region. Other recommended agronomical practices in vogue were followed for reaping good crop. Data were recorded on randomly selected five plants from each genotype and average value was used for the statistical analysis for fifteen characters *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of mature pods per plant, 100-pod weight, 100-kernel weight, sound mature kernel (%), shelling out-turn, biological yield per plant harvest index, kernel yield per plant, pod yield per plant, oil content and protein content. The data subjected to different statistical analysis *viz.*, Analysis of genetic divergence using Mahalanobis's (1936) D^2 -statistic was carried out as described by Rao (1952).

The significant mean squares due to genotypes suggested the preface of ample variability. The D^2 -values between all possible pairs indicated the presence of greater diversity among the genotypes for all the traits.

Grouping of the genotypes was carried-out by following Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller D^2 -values among themselves than those from groups belonging to different clusters. In the present study, D^2 -statistic estimated on 60 genotypes of groundnut for 15 characters showed that the generalized distance ($\sqrt{D^2}$) between two populations varied from 11.05 to 36.51, which was an indicator of considerable diversity available in the material evaluated. On the basis of D^2 -values, 5 clusters were formed from 60 genotypes. The composition of cluster is given in Table 1 and clustering pattern is shown in Table 3. The cluster I was the largest having 39 genotypes from different geographical regions comprising 19 from Junagadh (Gujarat), 1 from Zimbabwe, 2 from Nigeria, 1 from SKRAU, Durgapura (Rajasthan), 11 from Andhra Pradesh, 2 from Tanzania, 1 from Paraguay and 2 their source of origin was not available. The cluster II was the second largest which contained 12 genotypes of which, 8 were from Junagadh (Gujarat) and 4 were from Maharashtra. Cluster III had 7 genotypes, 4 from Gujarat, 2 from Andhra Pradesh and 1 from Maharashtra. Cluster IV having 1 genotype from Junagadh (Gujarat) and Cluster V also having 1 genotype from Andhra Pradesh.

The inter and intra cluster distance values are given in Table 2. The maximum inter-cluster distance found between clusters V and III ($D=36.51$) carrying one genotype and seven genotypes, respectively followed by that between clusters IV and V ($D=32.67$) and III and II

($D=27.92$). The minimum inter-cluster distance ($D=11.05$) found between cluster IV and III. The Intra-cluster distance ranged from 12.56 (cluster I) to 16.43 (cluster II). The clusters IV to V contained single genotype and therefore, their intra-cluster distance was zero. In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. The cluster means for 15 characters are presented in Table 4. The coefficient of variation (CV %) was calculated for all the attributes. High coefficient of variation was recorded for number of mature pods per plant (14.18 %) followed by harvest index (13.58 %), number of primary branches per plant (12.74%), kernel yield per plant (12.25%), plant height (11.38%) and pod yield per plant (11.99%). Low coefficient of variation was noted for protein content (1.01%) followed by oil content (1.04%) and days to maturity (2.03%). Greater range of mean values among the clusters was recorded for different traits. The cluster V revealed maximum values for 100-kernal weight (74.16g), sound mature kernels (98.06%), shelling out turn (72.31%), harvest index (40.59%), kernel yield per plant (11.15g), pod yield per plant (15.46g) and protein content (30.62%). The cluster IV had high mean values for days to 50% flowering (37.00). The cluster III had high mean values for days to maturity (116.67) and oil content (52.13%). The cluster II exhibited maximum values for number of primary branches per plant (5.55), number of mature pod per plant (15.40), 100 pod weight (109.58g) and biological yield per plant (43.61g). The cluster I showed maximum values for plant height (37.20cm).

The analysis of per cent contribution of various characters towards the repression of total genetic divergence indicated that protein content (42.82%) followed by oil content (22.60%), 100-pod weight (19.72 %), 100-kernal weight (7.06%), biological yield per plant (3.79%) and kernel yield per plant (1.02%) contributed maximum towards divergence in the present study (Table-4). These seven characters accounted for more than 97% of total divergence in the material studied. Hence, it is advisable to attempt crossing of these genotypes selecting as divergent parents based on these seven characters, which may lead to broad spectrum of favourable genetic variability for yield improvement in groundnut. The present findings are in conformity with those reported earlier in groundnut by (Dashora and Nagda, 2004; Odedra *et al.*, 2008; Sumathi and Muralidharan, 2008; Sonone and Thaware, 2009; Kumar *et al.*, 2011 and Sonone *et al.*, 2011). The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high

values of any cluster can be used in hybridization programme for further selection and improvement.

It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, in the present investigation, based on high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster V with the genotypes of clusters III and IV as well as genotypes from cluster III with II, which may lead to broad spectrum of favorable genetic variability for yield improvement in groundnut.

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Table 1. Grouping of 60 genotypes of Virginia groundnut in various clusters on the basis of D²-statistic

Cluster	No. of genotypes	Name of the genotypes	Origin
I	39	GG-13, GJG-HPS-1, JSSP-20, JSSP-24, JSSP-25, JSSP-29, JSSP-31, JSSP-33, JSSP-34, JSSP-45, JSSP-HPS-21, JSSP-HPS-28, JVB-134, JVB-153, JVB-170, JVB-244, JVR-309, JSP-46, JSP-HPS-130	Junagadh (Gujarat)
		ICGV-97045, ICGV-97047, ICGV-97049, ICGV-97057, ICGVI-97058, ICGV-97061, ICGV-98397, ICGV-98462, ICGV-98404, ICGV-98426	ICRISAT (Andhra Pradesh)
		AP-80-225	Andhra Pradesh
		NAN-130, NAN-182	Nigeria
		RG-39	Durgapur (Rajasthan)
		RCM-449-7-1	Paraguay
		TGR-1596	Zimbabwe
		TZA-39, EC-146615	Tanzania
		CC-12, CIRR-9402	Not available
II	12	GG-11, GG-12, GG-14, JSSP-32, JSP-38, JSP-22, JSP-24, JSSP-30	Junagadh (Gujarat)
		JL-220	Jalgaon (Maharashtra)
		TCG-1559, TCG-1530, TCG-1556	BARC (Maharashtra)
III	7	ICGV-98432, ICGV-98439	ICRISAT (Andhra Pradesh)
		JSSP-14, JSP-43, JVB-136, JSP-30	Junagadh (Gujarat)
		TCG-1527	BARC (Maharashtra)
IV	1	JVB-144	Junagadh (Gujarat)
V	1	ICGV-98412	ICRISAT (Andhra Pradesh)

Table 2. Average intra and inter-cluster ($D = \sqrt{D^2}$) values (diagonal) for 60 genotypes of Virginia groundnut

Clusters	I	II	III	IV	V
I	12.56	16.94	22.22	15.65	24.04
II		16.43	27.92	22.97	24.21
III			13.57	11.05	36.51
IV				0.00	32.67
V					0.00

Table 3. Source and clustering pattern of 60 genotypes of Virginia groundnut

Source	I	II	III	IV	V	Total number of genotypes
Andhra Pradesh	11	-	2	-	1	14
Gujarat	19	8	4	1	-	32
Maharashtra		4	1	-	-	5
Nigeria	2	-	-	-	-	2
Paraguay	1	-	-	-	-	1
Rajasthan	1	-	-	-	-	1
Tanzania	2	-	-	-	-	2
Zimbabwe	1	-	-	-	-	1
Not available	2	-	-	-	-	2



Table 4: Cluster means for 15 characters in 60 genotypes of Virginia groundnut

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of mature pods /plant	100-pod weight (g)	100-kernel weight (g)	Sound mature kernel (%)	Shelling out-turn (%)	Biological yield/plant (g)	Harvest index (%)	Kernel yield /plant (g)	Pod yield/ plant (g)	Oil content (%)	Protein content (%)	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
I	33.76	115.17	37.20	5.24	14.66	93.02	39.42	90.45	63.96	40.29	33.13	8.39	13.13	47.66	28.20	
II	34.69	116.06	36.49	5.55	15.40	109.5	35.96	90.28	64.49	43.61	31.84	8.85	13.68	46.30	29.74	
III	34.57	116.67	32.97	5.18	13.75	103.4	38.27	95.03	59.58	38.39	35.83	8.26	13.72	52.13	25.54	
IV	37.00	114.33	26.89	5.14	11.27	95.76	33.49	92.16	63.61	36.55	31.93	7.41	11.63	51.46	26.83	
V	32.33	116.00	36.46	4.36	10.30	92.92	74.16	98.06	72.31	38.37	40.59	11.15	15.46	46.33	30.62	
Mean	34.07	115.52	36.38	5.28	14.57	97.59	39.08	91.11	63.69	40.64	33.29	8.50	13.32	47.95	28.22	
S. Em.±	4.06	2.03	11.38	12.74	14.18	3.97	5.43	3.19	6.43	6.92	13.58	12.25	11.99	1.04	1.01	
C.V.%	0.80	1.35	2.39	0.39	1.19	2.24	1.23	1.68	2.36	1.62	2.61	0.60	0.92	0.29	0.16	
Percentage contribution of characters towards total divergence																
No. of times appearing first	16	4	2	2	0.0	349	125	21	6	67	2	18	0.0	400	758	
% contribution	0.90	0.23	0.11	0.11	0.0	19.72	7.06	1.19	0.34	3.79	0.11	1.02	0.0	22.6	42.82	