

Research Note

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

R.M. Chavadhari, V.H. Kachhadia, J.H. Vachhani* and Sureshkumar Sharma

Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh-362 001 (Gujarat).

E-mail: jhvachhani@jau.in

(Received: 24 June 2017; Revised: 15 Aug 2017; Accepted: 20 Aug 2017)

Abstract

Divergence analysis among seventy groundnut genotypes using Mahalanobis's D^2 statistic grouped into eleven clusters. The maximum inter-cluster distance (D) was observed between clusters IV and XI ($D=239.0$) followed by clusters VIII and IX ($D=235.65$) and clusters II and VIII ($D=228.02$) indicating that the genotypes of these groups may be more 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 form ideal parents for improvement in groundnut.

Key words

Clusters, genetic divergence, groundnut (*Arachis hypogaea* L.)

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. To a plant breeder, single character is not of much importance as the combined merit of number of desirable traits becomes more important when he/she is concerned with a complex trait like pod yield. Thus, for improving the pod yield, selection of parents based on number of characters having quantitative divergence is required which can be assessed by D^2 -statistic developed by Mahalanobis (1936). The use of Mahalanobis's D^2 statistic for estimating genetic divergence had been emphasized by Murty and Arunachalam (1966), because it permits precise comparison among all the population in given any groups before effecting actual crosses, therefore, the present study was carried out to ascertain the nature and magnitude of genetic divergence among the 70 groundnut genotypes, which will help to plan hybridization programme to develop groundnut varieties with high pod yield and high oil percentage.

Seventy genotypes of groundnut were sown in a Randomized Block Design (RBD) with three replications during summer of 2015. Each genotype was sown in a single row of 2.0 m length with a spacing of 30 x 10 cm. The experiment was surrounded by two guard rows to avoid damage and border effects. The fertilizers were applied at the rate of 25.0 kg N_2 , 50.0 kg P_2O_5 and 50.0 kg K_2O per ha, as it is a recommended dose for summer 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 sixteen characters viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number

of mature pods per plant, sound mature kernels (%), pod yield per plant (g), 100-pod weight (g), kernel yield per plant (g), 100-kernel weight (g), biological yield per plant (g), shelling out-turn (%), harvest index (%) and oil content (%). The data was subjected to analysis of genetic divergence using Mahalanobis (1936) as described by Rao (1952). The significant mean squares due to genotypes suggested the presence of ample variability. The D^2 -values between all possible pairs indicated the presence of greater diversity among the genotypes for all the traits.

Composition of clusters:

In all, 11 clusters were formed from 70 genotypes (Table 1). The largest cluster was cluster I contained 21 genotypes, cluster VI was second largest cluster, which contained 11 genotypes, cluster IX having 9 genotypes, cluster VIII having 8 genotypes, the cluster IV having 7 genotypes, the cluster II having 6 genotypes and cluster XI having 4 genotypes from different geographical regions. On the other hand, remaining clusters; III, V, VII and X possessed only one genotype in each cluster. A wide range of variation for several characters among single as well as multi-genotype clusters was observed. However, the differences were clearer for kernel yield per plant followed by number of mature pods per plant, pod yield per plant and number of branches per plant. These findings are in conformity with those reported earlier in groundnut by Venkataramana *et al.* (2008); Sonone and Thaware (2009); Korat *et al.* (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.

Inter and intra cluster distances (D): The maximum inter-cluster distance ($D=239.0$) was found between clusters IV and XI followed by that between clusters VIII and IX ($D=235.65$), II and VIII ($D=228.02$), II and IV ($D=225.78$), IV and XI ($D=220.91$), VIII and XI ($D=214.78$), IV and X ($D=209.22$), III and IV ($D=198.29$) and IX and XI ($D=186.94$). The minimum inter-cluster distance ($D=37.81$) was found between clusters III and VII. The Intra-cluster distance ranged from 34.73 (Cluster I) to 100.01 (Cluster IX). Intra-cluster distances were lower than the inter-cluster distances showing that the genotypes included within a cluster tended to diverse less from each other. The clustering pattern of genotypes showed that the genotypes of different origins were clubbed into one cluster, whereas the genotypes belonging to same origin were grouped into different clusters indicating that the geographic distribution was not the sole criterion of genetic diversity. This indicated no parallelism between geographic distribution and genetic diversity (Kumar *et al.*, 2011). The earlier findings of Murty and Arunachalam (1966) showed that genetic drift and selection in different environments could cause greater diversity than geographic distance. Further, the free exchange of genotypes among the different regions consequently causes character constellations because of the human interference and genotype may lose its individuality.

Cluster means for various characters: High coefficient of variation was recorded for kernel yield per plant (17.36 %) followed by number of mature pods per plant (16.96%), pod yield per plant (14.45%) and number of branches per plant (12.78%). Low coefficient of variation was noted for days to maturity (2.04%) followed by days to 50% flowering (5.76%) and oil content (7.06%) (Table 3). The cluster VI was best for number of matured pods per plant, pod yield per plant, 100-pod weight and sound mature kernel. The cluster III was best for plant height and shelling out turn. The cluster IV was best for 100-kernel weight. The cluster VII was best for number of branches per plant. The cluster V was the best for days to 50% flowering and days to maturity. Because, it showed the early flowering with early maturity. The cluster VIII had was best for harvest index. The clusters III had desirable value for plant height, because it showed the longer plant height. The cluster IX was best for oil content. The cluster XI was best for kernel yield per plant and biological yield per plant. Therefore, inter crossing of genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rationale improvement for increasing the pod yield in groundnut.

Contribution of various characteristics to total divergence: The analysis of per cent contribution of various characters towards the expression of

total genetic divergence (Table 3) indicated that biological yield followed by kernel yield per plant, harvest index, 100-kernel weight, plant height, number of branches per plant, 100-pod weight, sound mature kernels, number of matured pod per plant and days to 50% flowering contributed maximum towards divergence in the present study. These ten characters accounted for more than 98% of total divergence in the material studied. The earlier findings of Suneetha *et al.* (2013) reported maximum contribution to diversity was by biological yield per plant. 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 resulted 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 IV with the genotypes of cluster XI as well as VIII with IX and II with VIII which may lead to broad spectrum of favorable genetic variability for yield improvement in groundnut.

References

- Arunachalam, V. 1981. Genetic distance in plant breeding. *Indian J. Genet.*, **41**: 226-236.
- Korat, V.P., Kavani, R.H., Pithia, M.S., Savaliya, J.J. and Pansuriya, A.G. 2009. Genetic divergence in groundnut (*Arachis hypogaea* L.). *J. Oilseeds Res.*, **26**(2):148-150.
- Kumar, S.I., Govindaraj, M. and Kumar, V.I. 2011. Estimation of correlation co-efficient and genetic diversity of new advance breeding lines of groundnut (*Arachis hypogaea* L.). *World J. Agric. Sci.*, **6**:547-555.
- Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci. (India)*, **2**:49-55.
- Murty, B.R. and Arunachalam, V. 1966. The nature of divergence in relation to breeding systems in crop plants. *Indian J. Genet.*, **25A**:188-198.
- Rao, C.R. 1952. Advanced Statistical Methods in: *Biometric Research*. John Wiley and Sons, New York, pp: 357-363.
- Sonone, N.G. and Thaware, B.L. 2009. Study on genetic diversity in groundnut. *Ann. Agric. Res.*, **26**:1-4.
- Sonone, N. G.; Thaware, B. L.; Bhave, S. G.; Jadhav, B. B.; Joshi, G. D. and Dhekale, J. S. 2011. Multivariate studies in groundnut (*Arachis hypogaea* L.). *J. Oilseeds Res.*, **28**(1) : 24 -28.
- Suneetha, N., Vasanthi, R.P., Sudhakar, P. and Reddy, K. Raja. 2013. Genetic diversity analysis among released and pre-release cultures in groundnut. *Legume Res.*, **36**(3):208-213.
- Venkataramana, P. 2008. Studies on genetic diversity in groundnut. *Crop Res.*, **31**:56-59.

Table 1. Grouping of 70 genotypes of groundnut in various clusters on the basis of D²-statistic

Cluster	No. of genotypes	Name of the Genotypes	Source
I	21	J-19, JB-FDR-4, J-54, JB(E)-336, JB(E)-554, JB(E)-548, JB-FDR-54, JB(E)-550, GJG-9	Gujarat
		Gangapuri	Madhya Pradesh
		Dh-19	Karnataka
		VRI- 3, ALR-2	Tamil Nadu
		TG-41, TG-26, JL-24	Maharashtra
		USA-86, Robusto	USA
		Vemana, BSR-1	Andhra Pradesh
		Durgapura	Rajasthan
		Jawan	Odisha
		Dh-40	Karnataka
II	6	Rajkot Valencia	Gujarat
		TG-40, TG-3	Maharashtra
		NCAc-995	USA
III	1	JB-FDR-51	Gujarat
IV	7	TG-42, TG-50, JL-839, JL-42, TG-51, J-42	Maharashtra
		NRCG-CS-253	Gujarat
V	1	JB-FSD-459	Gujarat
		JB-FSD-383, JB-FDR-50, J-60	Gujarat
		Kadiri-4	Andhar Pradesh
VI	11	TG-23, TAG-24, TG-71	Maharashtra
		VRI-2	Tamil Nadu
		R-8808	Karnataka
		SG-19	Punjab
		Kishan	Odisha
VII	1	AH-2-4-14-1	Nigeria
VIII	8	JB-FDR-17, JB-FSD-398, J42(TS), Girnar-1, GG-8, GG-7	Gujarat
		CO-2	Tamil Nadu
		K-9251	Andhra Pradesh
IX	9	ALR-1, ALR-3	Tamil Nadu
		ICGV-91040, ICGV-02266, K-1319	Andhra Pradesh
		GG-5	Gujarat
X	1	G-2-52, Dh-221, CTMG-9	Karnataka
		J-53	Gujarat
XI	4	J-11, JB(E)-262	Gujarat
		Tirupati, K-1535	Andhra Pradesh



Table 2. Average inter and intra-cluster distance ($D = \sqrt{D^2}$) values for 70 genotypes groundnut

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	34.73	109.32	59.25	103.92	53.21	72.07	61.55	86.75	118.47	72.51	127.13
II		38.27	117.32	225.78	60.05	132.78	94.69	228.08	146.90	67.13	91.09
III			0.00	198.29	52.79	135.38	37.81	140.27	106.45	39.22	102.83
IV				51.13	184.30	120.27	160.30	102.96	220.91	209.22	239.00
V					0.00	79.39	43.68	156.53	96.70	62.52	121.73
VI						62.71	107.09	119.00	185.52	119.37	185.30
VII							0.00	141.03	109.66	58.77	142.41
VIII								89.39	235.65	154.82	214.78
IX									100.01	157.68	186.94
X										0.00	59.48
XI											73.18



Table 3. Cluster mean for 14 different characters in groundnut

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/ plant	No. of mature pods/ plant	Sound mature kernels (%)	Pod yield/ Plant (g)	100-pod weight (g)	Kernel yield/ plant (g)	100- kernel weight (g)	Biological yield/plant (g)	Shelling out-turn (%)	Harvest index (%)	Oil content (%)
	1	2	3	4	5	6	7	8	9	10	11	12	13	14
I	36.70	117.95	31.23	6.21	11.34	74.94	15.59	100.68	9.09	37.93	42.43	68.96	26.94	48.10
II	37.44	116.85	27.17	6.60	10.94	73.64	14.91	97.94	5.08	41.64	60.38	66.87	19.80	47.54
III	34.80	119.77	40.40	8.33	11.00	68.80	13.42	90.00	10.67	33.20	47.00	72.47	22.19	46.07
IV	33.88	116.70	24.24	6.24	11.10	76.03	16.28	109.5	11.29	56.03	36.24	66.86	30.80	48.03
V	33.67	113.80	30.67	6.67	11.00	73.70	15.22	97.00	4.67	31.00	49.00	68.80	23.72	49.07
VI	36.50	116.10	26.87	7.15	13.36	85.27	17.49	110.3	5.90	37.71	42.12	66.80	29.65	46.93
VII	36.27	116.10	38.73	9.33	6.67	63.40	15.51	96.67	5.23	41.47	46.33	66.63	24.98	47.13
VIII	35.53	117.52	33.26	6.18	12.21	77.28	16.52	106.33	12.19	38.93	34.83	67.28	32.22	48.94
IX	36.08	117.04	30.28	6.58	10.20	72.54	10.12	79.41	7.60	45.81	44.18	64.73	18.24	51.01
X	38.47	120.27	37.67	8.67	10.33	74.80	15.51	109.00	10.30	32.53	56.67	71.03	21.55	47.93
XI	36.45	119.19	30.38	7.42	12.92	77.69	14.64	92.25	14.77	38.50	63.08	68.84	18.83	48.47
Mean	36.15	117.31	29.88	6.62	11.55	76.40	15.20	100.13	8.87	40.98	44.25	67.53	25.94	48.32
S. Em. ±	1.20	1.38	1.37	0.48	1.13	3.53	1.26	4.35	0.88	2.06	2.05	2.83	1.11	1.97
C.V. %	5.76	2.04	7.95	12.78	16.96	8.02	14.45	7.53	17.36	8.70	8.03	7.28	7.42	7.06
Percentage contribution of characters towards total divergence														
No. of times appearing first	23	8	226	126	30	37	1	100	351	261	912	4	332	6
% contribution	0.96	0.33	9.36	5.18	1.24	1.53	0.10	4.14	14.53	10.81	37.76	0.17	13.75	0.26