Genetic divergence in ground nut (*Arachis hypogaea* L.)

Satyenrda Singh Raghuwanshi, V. H. Kachhadia, J. H. Vachhani*, L. L. Jivani and M. B. Patel
Main Oilseeds Research Station, JAU, Junagadh-362 001 (Gujarat).
E-mail:jhvachhani@jau.in

(Received: July 2015; Accepted: September 2015)

Abstract

Divergence analysis among fifty groundnut genotypes using Mahalanobis's D^2 statistic grouped into twenty-seven clusters. The maximum inter-cluster distance was found between clusters XXVII and XVIII (D=22.53) followed by clusters XXVI and XVIII (D=20.79) and XXVII and XXIII (D=20.63) 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 form ideal parents for improvement in groundnut.

Keywords: 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 statistics 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 50 groundnut genotypes, which will help to plan hybridization programme to develop groundnut varieties with high pod yield and high oil percentage.

Fifty genotypes of groundnut were sown in a Randomized Block Design (RBD) with three replications during summer 2014. Each genotype was sown in a single row of 3.0 m length with a spacing of 45 x 15 cm. The experiment was surrounded by two guard rows to avoid damage and border effects. The fertilizers was applied at the rate of 25.0 kg N_2 ha^{-1} and 50.0 kg P_2O_5 ha^{-1} 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, number of primary branches per plant, number of mature pods per plant, sound mature kernel, pod yield per plant, 100-pod weight, kernel yield per plant, 100-kernel weight, biological yield per plant, shelling out-turn, harvest index, oil content and protein 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 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.

Composition of clusters:

In all 27 clusters were formed from 50 genotypes (Table 1). The cluster I contained 16 genotypes while cluster V contained 9 genotypes from different geographical regions. Remaining clusters 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 clear for protein content followed by oil content, 100-pod weight, 100-kernal weight, biological yield per plant and kernel yield per plant. The present findings are in conformity with studies in groundnut (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.

Inter and intra cluster distances ($D=\sqrt{D^2}$):

The maximum inter-cluster distance varied from 5.68 (cluster III and IV) to 22.53 (cluster XXVII and XVIII), which indicates considerable diversity among the genotypes evaluated whereas the lowest inter-cluster distance (D=5.68) was found between clusters IV and III (Table 2). The Intra-cluster distance ranged from 9.09 (cluster I) to 9.88 (cluster V). 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 (15.06 %) followed by number of mature pods per plant (13.54 %), pod yield per plant (13.48%) and harvest index (10.18%) while it was low for days to maturity (1.38%) followed by oil content (2.38%) and days to 50% flowering (3.21%) (Table 3). The cluster XXVII was the best for pod yield per plant, 100-pod weight, kernel yield per plant, 100-kernel weight and harvest index (Table 3). The cluster XXV was best for biological yield per plant. The cluster XXIII was best for oil content. The cluster XIX was best for number of primary branches per plant. The cluster XVIII was best for shelling out-turn. Clusters XIV, XVII and XVIII were best for days to 50% flowering while cluster XVII is best for days to maturity. The cluster XVI was best for sound mature kernels. The cluster XXI had desirable value for plant height because it showed the longer plant height. The cluster IV was the best for number of mature pods per plant. The cluster III was the best for protein content. Therefore, intercrossing 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 number of primary branches per plant followed by biological yield per plant, days to maturity, number of mature pods per plant, 100-kernel weight, days to 50% flowering, oil content, 100-pod weight, plant height, harvest index and kernel yield per plant contributed maximum (98%) towards divergence in the present study. The earlier findings of Suneetha *et al*. (2013) reported maximum contribution to diversity was by harvest index while; minimum contribution was by number of mature pods 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 result 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 XXVII with the genotypes of cluster XVIII as well as XXVI and XVIII and XXVII and XXIII, which may lead to broad spectrum of favorable genetic variability for yield improvement in groundnut.

Table 1. Grouping of 50 genotypes of groundnut in various clusters on the basis of D^2– statistic

Cluster	No. of genotypes	Name of the Genotypes	Source
I	16	Rajkot Valencia, C-124, 1025, Samarala, AH-25, SB-XI	India
		28-204	Benin
		U 4-4-2	Sierra Leone
		US-9	Argentina
		Russian International-2	Surinam
		Porte Alegre	Brazil
		Ah-7091	South Africa
		Ah-7158	Cuba
		EC-37483	Australia
		PI-337409	Argentina
		C-123	India
II	1	U 4-4-8	South Africa
III	1	EC-16681	Not available
IV	1	GG-7	India
V	9	GG-2, GG-5, GJG-9, S-227, JL-24 (Spanish group), RS-66	India
		B-1	Uganda
		U 4-7-14	Sudan
		EC-38603	United States
VI	1	Osmanabad	India
VII	1	NCAc-749	United States
VIII	1	GJG-31	India
IX	1	C-45	India
X	1	Ah-6990	Not available
XI	1	EC-76446	Uganda
XII	1	PB-148	Not available
XIII	1	Kadiri-3	India
XIV	1	ND 1-1	India
XV	1	NG-268	India
XVI	1	JL-501	India
XVII	1	NCAc-2718	United States
XVIII	1	WCG-156	Brazil
XIX	1	M-13	India
XX	1	Mixture	Not available
XXI	1	NCAc-2751	United States
XXII	1	BH 5-3-2	India
XXIII	1	88/6/7	United States
XXIV	1	C-41	India
XXV	1	NCAc-12	United States
XXVI	1	VAR-154	China
XXVII	1	TPG-41	India

Table 2. Average inter and intra–cluster distance$\left(\mathbf{D} = \sqrt{\mathbf{D^2}}\right)$ values for 50 genotypes of groundnut

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XXII	XXIII	XXIV	XXV	XXVI	XXVII
I	9.09	11.26	10.76	11.44	11.28	10.42	12.47	14.67	10.89	11.62	11.65	12.38	11.77	10.49	11.08	13.95	11.56	13.13	13.41	10.84	12.38	14.84	14.40	14.76	12.49	16.39	18.40
II		0.00	10.05	10.08	13.18	8.08	14.73	14.09	10.08	7.45	14.74	12.30	9.62	11.26	10.46	15.64	15.36	8.25	16.17	11.19	9.64	8.36	9.42	9.05	11.55	16.04	16.14
III			0.00	5.68	10.42	11.70	15.57	6.40	14.97	9.62	12.78	7.11	7.13	7.35	9.10	9.28	10.83	15.18	15.29	12.59	9.97	14.83	16.28	12.90	13.57	12.26	14.63
IV				0.00	9.38	12.91	1700	9.50	15.13	12.10	13.17	10.02	10.24	8.49	11.72	11.08	12.63	15.49	14.65	15.37	10.99	16.18	17.67	15.37	14.10	15.05	16.25
V					9.88	14.30	15.68	13.30	14.35	14.41	12.87	12.90	12.18	12.32	12.40	12.71	12.89	17.55	13.25	15.55	13.68	18.61	18.80	17.37	14.95	16.84	17.04
VI						0.00	15.54	16.75	10.20	8.92	16.81	12.63	11.82	13.19	9.87	17.56	15.71	8.53	18.93	8.82	13.32	11.42	9.72	12.30	8.79	18.35	20.07
VII							0.00	17.05	10.47	13.96	10.36	14.31	12.78	14.06	15.71	13.92	11.28	15.66	10.94	13.30	14.71	15.36	13.45	13.11	18.72	16.19	18.34
VIII								0.00	18.29	12.33	13.84	9.25	8.72	9.24	12.37	7.60	11.64	19.33	15.78	16.21	12.35	18.34	19.41	14.51	17.63	9.71	12.98
IX									0.00	13.06	14.70	16.13	13.34	14.92	13.58	17.33	15.90	10.45	13.99	12.69	15.36	13.62	10.90	12.14	12.05	18.78	19.26
X										0.00	13.68	10.09	7.60	9.68	8.54	14.03	12.26	11.79	16.50	7.80	7.98	9.24	9.06	8.64	12.55	12.54	14.63
XI											0.00	12.85	13.51	9.68	16.03	11.23	8.48	17.21	9.72	13.39	11.36	16.70	16.89	16.99	19.38	15.23	18.77
XII												0.00	7.41	9.26	12.28	8.98	10.50	16.12	16.82	13.33	11.52	14.75	15.50	12.71	17.17	13.34	17.06
XIII													0.00	10.20	8.66	9.02	10.77	15.34	14.71	12.02	10.49	13.54	13.40	8.48	14.30	10.69	11.47
XIV														0.00	11.89	10.02	7.64	14.30	12.79	12.29	10.12	14.35	15.65	14.14	14.76	10.93	15.91
XV															0.00	14.81	12.80	15.11	15.46	10.98	11.23	14.42	14.94	12.26	8.74	12.33	12.44
XVI																0.00	8.52	20.35	13.76	16.19	14.54	19.78	19.26	15.68	19.59	11.54	15.24
XVII																	0.00	18.07	10.62	12.83	12.87	17.77	17.46	16.11	17.19	10.52	15.76
XVIII																		0.00	19.39	11.79	14.41	8.10	8.89	12.63	13.45	20.79	22.53
XIX																			0.00	17.72	14.62	19.29	19.70	17.65	18.14	14.14	15.16
XX																				0.00	11.94	12.16	9.59	13.19	13.42	16.61	19.30
XXI																					0.00	10.28	13.88	12.07	15.71	14.00	15.60
XXII																						0.00	8.43	9.16	16.14	18.34	19.87
XXIII																							0.00	9.63	15.65	19.20	20.63
XXIV																								0.00	15.43	14.25	14.72
XXV																									0.00	17.62	18.30
XXVI																										0.00	10.24
XXVII																											0.00

Table 3. Cluster mean for 15 different characters in groundnut

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary 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 (%)	Protein content (%)
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
I	34.65	112.48	29.21	4.34	12.82	86.98	12.03	95.19	7.98	38.36	55.24	67.90	21.65	50.41	27.16
II	37.67	120.33	34.81	3.60	16.07	88.59	16.10	100.25	11.36	42.87	54.30	70.52	29.61	50.48	27.55
III	37.33	109.00	28.00	4.07	17.20	88.23	15.77	91.68	11.16	38.66	42.97	70.82	36.58	47.17	28.78
IV	37.00	109.67	34.93	4.20	20.33	86.68	17.99	88.88	12.31	40.53	52.85	68.31	34.46	46.98	28.17
V	38.11	108.78	31.48	4.73	17.33	89.89	17.07	95.28	11.76	42.13	62.45	68.78	26.57	49.94	27.64
VI	36.00	115.33	28.59	3.00	13.27	87.64	11.08	83.43	7.32	34.97	58.80	65.94	18.85	51.55	25.92
VII	34.33	121.00	25.51	5.33	9.73	90.76	9.51	96.62	6.10	41.20	41.74	64.31	22.76	52.52	23.76
VIII	39.00	108.33	26.88	4.40	18.47	94.17	18.67	101.07	12.55	42.61	39.74	67.06	46.86	46.89	28.10
IX	35.33	124.00	28.85	4.40	14.20	89.84	12.74	89.15	8.46	42.83	66.64	66.66	19.11	53.11	26.64
X	37.33	114.67	30.88	3.27	12.93	94.16	14.50	112.35	9.08	41.44	46.06	63.06	31.56	52.65	26.23
XI	34.33	112.00	34.06	5.53	9.47	88.90	10.82	112.85	6.80	36.90	39.89	64.08	27.10	50.55	27.65
XII	39.67	107.67	27.53	4.07	10.80	90.10	8.45	72.40	5.13	32.09	29.07	65.57	29.13	50.33	26.24
XIII	40.00	113.00	26.00	4.07	17.27	91.59	16.09	93.46	11.32	42.43	43.29	70.38	36.81	52.99	26.30
XIV	32.00	110.33	33.91	4.07	12.13	93.79	12.73	98.75	8.04	38.94	37.22	66.42	34.51	48.92	28.49
XV	37.33	110.33	25.62	3.33	14.40	91.81	16.66	115.80	11.54	50.68	58.01	69.26	29.35	50.67	26.02
XVI	38.00	108.33	27.02	5.13	19.27	94.48	16.63	82.78	11.42	35.45	38.54	71.72	43.03	51.27	25.60
XVII	32.00	107.33	28.95	4.67	11.33	91.79	11.44	101.06	7.73	39.47	36.07	67.58	31.71	52.37	24.71
XVIII	32.00	124.00	34.66	3.33	9.80	91.12	8.44	84.63	6.13	35.26	46.85	72.86	17.96	50.16	28.63
XIX	33.00	115.33	34.09	5.60	11.53	87.39	14.54	121.27	9.70	55.85	52.29	66.70	27.77	51.61	25.77
XX	34.00	114.67	26.23	3.60	12.20	89.67	13.63	111.87	9.13	32.44	51.10	66.99	26.66	52.05	26.25
XXI	38.33	112.67	35.29	4.13	11.27	85.55	12.60	130.49	7.73	46.63	38.77	61.95	28.94	48.59	28.09
XXII	36.33	123.00	34.76	3.40	6.20	88.24	6.72	108.64	4.63	42.44	31.01	69.03	21.59	50.28	28.01
XXIII	36.33	125.33	31.15	3.33	12.53	92.15	12.36	98.56	7.80	35.49	50.78	62.93	24.33	54.40	24.09
XXIV	39.67	123.33	26.68	3.73	13.80	90.86	13.06	97.12	8.32	46.39	38.30	69.14	34.03	52.51	26.62
XXV	33.67	113.33	28.68	2.80	16.27	86.60	15.28	103.54	10.27	49.33	73.41	67.36	22.71	52.10	27.89
XXVI	35.33	110.33	28.25	4.00	12.00	92.69	14.69	121.35	10.45	54.32	32.36	71.21	45.42	52.01	24.04
XXVII	39.67	115.00	27.20	4.13	19.27	88.69	26.10	135.37	18.52	65.39	51.89	70.85	50.22	53.21	26.57
Mean	36.06	112.94	29.99	4.26	14.06	89.12	13.85	98.68	9.33	41.15	51.95	67.92	27.13	50.63	26.99
S.Em. ±	0.67	0.90	0.95	0.11	1.10	3.99	1.08	3.52	0.81	1.37	2.49	1.77	1.59	0.70	0.70
C.V.%	3.21	1.38	5.48	4.54	13.54	7.77	13.48	6.19	15.06	5.76	8.30	4.52	10.18	2.38	4.47

Table 4. Percentage contribution of characters towards total divergence

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**
No. of times appearing first	60	210	31	281	125	8	24	32	3	102	257	4	26	60	2
% contribution	4.90	17.14	2.53	22.94	10.20	0.65	1.96	2.61	0.24	8.33	20.98	0.33	2.12	4.90	0.16

References

Arunachalam, V. 1981. Genetic distances in plant breeding. *Indian J. Genet*., **41**: 226-236.

Dashora A. and Nagda, A. K. 2004. Paper presented in the National Symposium on "Enhancing Productivity of Groundnut for Sustaining Food and Nutritional Security" held at NRCG Junagadh during October 11-12, 2004.

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.

Odedra, R. K.; Dobariya, K. L.; Jivani, L. L.; Ponkia,H. P. and Khanpara, M. D. 2008. Genetic divergence in groundnut (*Arachis hypogaea* L.). *Intl. J. Bioscience Reporter*, **6**: 277-281.

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. *Annl. 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.

Sumathi, P. and Muralidharan, V. 2008. Genetic divergence analysis in some bold seeded genotypes of groundnut (*Arachis hypogaea* L.). *J. Oilseeds Res*., **25**: 1-3.

Suneetha, N.; Vasanthi, R. P.; Sudhakar, P.; Reddy, K. Raja (2013). Genetic diversity analysis among released and pre-release cultures in groundnut. *Legume Res*., **36**(3):208-213.