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Genetic Divergence Studies in Groundnut (*Arachis hypogaea* L.) Germplasm

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ABSTRACT

A field test were carried out on divergence studies against fourty nine groundnut genotypes during *Kharif* season, 2014-15 at Research farm of Agriculture College Navile, Shivamogga The genotypes were grouped into fourteen clusters. Cluster I contained the highest number of genotypes (21) and lowest number in clusters II, V, VII, VIII, IX, X, XI, XII and XIII were solitary with one genotype per cluster. The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity is present among the genotypes of distant grouped. The highest intra cluster distance was observed in cluster IV and lowest in cluster I, The highest inter cluster distance was observed between cluster VI and XII followed by cluster between III and VI, the minimum distance observed between cluster V and VII followed by between clusters VII and X. Pod yield per plant, days to 50 per cent flowering, 100 kernel weight, kernel weight per plant, number of pod bearing nodes were the most important contributors. But the highest cluster means for total number of kernels per plant, number of pod bearing nodes, number of matured pods per plant, karnel weight per plant and pod yield per plant was obtained from the cluster XIV. With moderate yield but early maturity varieties were found in cluster XII.

Key words *Genetic divergence, cluster analysis, D^2 analysis, Arachis hypogaea*

Peanut or groundnut (*Arachis hypogaea* L., $2n = 4x = 40$) is a major oil crop along with soybean and cotton. China, India, and the United States are the leading producers contributing about 70 per cent of the world peanut crop. Groundnut is quick growing; short duration, photo-insensitive and nature enable the plant breeder to raise two crops in a year. Exploitation of the genetic variability in the available germplasm is a prerequisite in the breeding programme for increasing yield and improving quality. Phenotypic diversity is usually considered as an indication of underlying genetic differences. Among all methods, Mahalanobis D^2 statistics is an efficient tool for estimating genetic diversity. Mahalanobis generalized distance technique considers the variation produced by any characters and the consequent effect that it bears on the other characters. Genetic diversity is the pre-requisite for hybridization programme to obtain desirable genotypes. Genetic diversity is very much essential to meet the diverse goals in plant breeding such as for producing cultivars with increased yield (Joshi and Dhawan, 1966), wider adoption, desirable quality and pest resistance (Nevo *et al.,* 1982). Obtaining the high heterotic F1 and broader spectrum of variability 46 in succeeding segregating generations depends upon the using of more diverse parents (Arunachalm, 1981). According to Tomooka, 1991, the evaluation of diversity is important to know the source of genes for particular trait within the available germplasm. So, it is essential to know the genetic diversity of the existing genotypes before undertaking any crop improvement programme. Therefore, the present study was carried out to estimate the nature and magnitude of genetic diversity present in a collection of 49 genotypes of groundnut.

MATERIAL AND METHODS

Field trial were laid out in simple lattice design with two replications carriedout during *kharif* season, 2014-15 at research farm of Agriculture College Navile, Shivamogga, to study the genetic divergence in groundnut germplasm. Each genotype was raised in 4m length with spacing of 30 X 10 cm. All recommended agronomic practices were followed to raise a good healthy crop. Observations were made on five randomly selected plants in each treatment on days to 50 percent flowering, days to maturity, height of main axis (cm), number of primary branches, number of secondary branches, number of nodes on main axis, number of pod bearing nodes, number of mature pods per plant, number of immature pods per plant, total number of kernels per plant, kernel weight per plant, 100

Table 1. Distribution of groundnut genotypes in different clusters

Clusters	No. of entries	Genotypes
I	21	KCG-6, SB-T8, K-6, TMV-2, SB-T13, KCG-2, SB-T11, LOCAL-3, VB-T4, K-9, SB-T15, SB-T17, SB-T12, DH-86, DH-216, SB-T14, LOCAL-2, ICGV-91114, LOCAL-1, DH-245 and DH-246.
II	1	VB-T31
III	3	VB-T18, VB-T7 and VB-T3
IV	7	DH-235, VB, DH-234, ICGV-91115, R-2001-3, SB-T1 and SB-T16,
V	1	VB-T13
VI	7	DH-241, GPBD-4, G2-52, DH-243, SB-T40, DH-247 and GPBD-5
VII	1	VB-T11
VIII	1	DH-101
IX	1	SB-T3
X	1	SB-T2
XI	1	VB-T35
XII	1	VB-T14
XIII	1	SB-T7
XIV	2	SB-T10 and SB-T21

kernel weight, oil content and shelling percentage. The data were recorded on. Genetic diversity were studied following Mahalanobis, 1936 generalized distance (D^2) extended by Rao, 1952. Based on the D^2 values, the studied genotypes were grouped into clusters according to the Tocher's method (Rao, 1952). The methods of Singh and Chauwdhary, 1985 were used for calculating the intra and inter cluster distances. Statistical analyses were carried out by Genstat Discovery edition 3.

RESULTS AND DISCUSSION

The analysis of variance and dispersion showed the highly significant variations among the different genotypes for all the fifteen characters under study, which revealed the presence of considerable variability among the genotypes. The fourty nine genotypes were grouped into fourteen clusters, in such a way that the genotypes within the cluster had smaller D^2 values among themselves than those belonging to different clusters (Table 1). Pattern of distribution of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. The maximum number of genotypes (21) were comprised into cluster I followed by 7 in cluster IV and VI, 3 genotypes in cluster III, 2 genotypes in cluster XIV and remaining clusters II, V, VII, VIII, IX, X, XI, XII and XIII were solitary with one genotype per cluster.

The D^2 analysis showed intra and inter-cluster distance (Table 2). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity is present among the genotypes of distant group. The inter cluster D^2 value was maximum (4319.41) between cluster VI and XII followed by between cluster III and VI with D^2 value of 4280.82 this indicates maximum diversity among the genotypes. The minimum distance observed was 393.80 between cluster V and VII followed by between clusters VII and X with D^2 value of 484.38 which indicate close relationship among the genotypes involved. The intra cluster distance was observed only in clusters I (482.58), III (541.82), IV (787.70), VI (731.78) and XIV (659.40) as remaining five clusters *viz*., II, V, VII, VIII, IX, X, XI, XII and XIII contained only one genotype each. Intra cluster distance was highest in cluster IV (787.70) followed by cluster VI (731.78). This reveals the presence of diverse genotypes within different clusters.

The mean values of cluster XIV ranked first for total number of kernels per plant (108.25), number of pod bearing nodes (72), number of matured pods per plant (62.25), kernel weight per plant (31.25) and pod yield per plant (51.15). The mean values of cluster II ranked top for plant height (32.20 cm), 100 kernels weight (48.50g) and shelling percentage (1.29) with days to maturity (118 days). The genotypes from cluster XII

Table 2. Average intra and inter cluster D^2 values of clusters in Groundnut

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	482.58	847.74	2786.07	996.89	907.31	1295.51	1350.42	1802.28	1349.69	1455.38	2449.53	3108.54	1651.26	2481.49
II		0.00	2576.26	1726.29	1458.69	2453.84	1405.08	2637.50	1224.87	1121.02	3056.29	2821.89	1980.59	3501.95
III			541.82	2302.63	2083.46	4280.82	1270.20	1192.60	2443.73	1876.63	1217.53	1025.38	1262.18	3053.71
IV				787.70	1065.40	1872.44	1208.72	1127.92	1099.16	1392.59	1716.97	2613.65	1751.31	1609.52
V					0.00	1772.13	393.80	1448.39	1128.11	595.47	935.51	1434.08	1272.55	1200.95
VI						731.78	2411.41	2262.42	3511.53	3371.78	3077.20	4319.41	1854.18	3131.69
VII							0.00	1270.17	1013.98	484.38	512.63	566.81	1150.70	1071.54
VIII								0.00	2241.37	2151.71	804.09	2010.59	872.71	2095.12
IX									0.00	456.49	2063.31	2295.01	2941.47	1724.22
X										0.00	1414.44	1166.14	1962.20	1429.75
XI											0.00	613.75	1190.96	1209.78
XII												0.00	1522.29	1832.35
XIII													0.00	2460.46
XIV														659.40

contained the shortest plant (19.70 cm) along with earliness in days to maturity (112.50 days) and maximum number of primary branches per plant (12.50) with medium pod yield per plant (39.40g) (Table 3).

From the divergence study of 49 groundnut germplasms using fifteen quantitative characters, it was found to be the most important character contributing to the divergence (Table 4) is Pod yield per plant. These present finding are inline with the findings of Nadaf *et al.*, 1986; Katule *et al.,* 1992; Khurram *et al.,*2009 and Kumar *et al.*, 2010. Further, Days to 50 per cent flowering, 100 kernel weight, Kernel weight per plant, Number of pod

Table 3. Cluster mean values of different characters of groundnut genotypes

Clusters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
I	29.64	7.52	4.24	13.17	41.95	35.00	6.93	26.29	72.14	19.87	34.07	116.48	30.86	0.76	1.34
II	32.20	9.50	4.00	11.50	33.50	21.00	12.50	21.90	35.50	16.95	48.50	118.00	32.00	0.66	1.29
III	21.93	11.67	18.17	10.83	41.50	32.83	8.67	26.83	59.50	22.12	37.83	117.17	42.33	0.74	1.34
IV	28.51	7.43	6.29	13.93	56.79	48.73	8.00	37.01	87.71	30.47	36.07	116.07	32.93	0.81	1.39
V	24.40	9.50	3.50	10.50	44.50	38.50	6.00	33.40	61.00	18.12	29.50	113.00	34.00	0.87	1.10
VI	28.69	7.57	4.93	16.00	69.50	59.43	10.07	32.07	96.64	22.09	25.50	113.43	30.43	0.78	1.25
VII	27.10	11.50	9.50	12.50	52.00	45.00	7.00	37.70	81.00	22.10	38.50	114.50	36.00	0.65	1.10
VIII	26.30	8.50	5.00	11.00	66.00	53.00	13.00	35.00	100.50	30.50	30.50	118.50	41.00	0.78	1.39
IX	30.10	8.50	4.00	12.50	37.00	34.00	3.00	37.00	57.00	27.28	48.50	119.50	32.00	0.76	1.20
X	27.70	11.00	8.50	11.50	41.50	30.50	11.00	37.40	56.00	23.30	44.00	115.50	34.00	0.87	1.18
XI	21.90	8.00	8.50	11.50	65.00	58.00	7.00	43.20	94.00	25.48	32.00	116.50	41.00	0.80	1.02
XII	19.70	12.50	18.00	10.50	55.00	46.00	9.00	39.40	75.00	21.20	40.50	112.50	40.00	0.80	0.96
XIII	27.50	7.50	18.50	10.50	62.50	43.50	19.00	29.30	76.50	19.50	25.50	116.50	39.00	0.86	1.24
XIV	25.45	10.00	12.00	11.50	72.00	62.25	9.75	51.15	108.25	31.25	29.50	116.75	32.50	0.81	1.08

Where, X_1 = Height of main axis
X_2 = Number of primary branches
X_3 = Number of secondary branches
X_4 = Number of nodes on main axis
X_5 = Number of pod bearing nodes
X_6 = Number of matured pods per plant
X_7 = Number of immatured pods per plant
X_8 = pod yield per plant
X_9 = Total no of kernels per plant
X_{10} = Kernel weight per plant
X_{11} = 100 kernel weight
X_{12} = Days to maturity
X_{13} = Days to 50 percent flowering
X_{14} = Oil content
X_{15} = Shelling percentage

Table 4. Percent contribution of different characters towards diversity in Groundnut

Character	Contribution (in per cent)
Pod yield per plant	30.02
Days to 50 per cent flowering	27.13
100 kernel weight	12.24
Kernel weight per plant	10.37
Number of pod bearing nodes	9.27
Oil content	5.00
Number of matured pods per plant	2.81
Days to maturity	1.28
Shelling per cent	0.85
Height of main axis	0.68
Number of secondary branches	0.26
Number of nodes on main axis	0.09

bearing nodes, Oil content, Number of matured pods per plant, Days to maturity, Shelling per cent, Height of main axis, Number of secondary branches and Number of nodes on main axis. Hence, as these characters are important yield attributing traits which are mainly responsible for increasing pod yield. These observations are in accordance with the findings of Suneetha *et al.,* 2013.

LITERATURE CITED

Arunahalam, V., 1981,Genetic distances in plant breeding. *Indian J. Genet*., **4**: 226-236.

Choudary, M. A. Z., Mia, M.F.U., Afzal. M.A. and Ali, M. M., 1998, Comparative study of D^2 and metro glyph analysis in groundnut. *Thailand*. *J. Agric. Sci*., **31**(3): 436-443.

Joshi, A. H. and Dhawan, N. L., 1966, Genetic improvement of yield with special reference to self-fertilizing crop. *Indian J. Genet. Pl. Breed.,* **26**(A): 101-113.

Katule, B. K., Thombre, M.V., Dumbre, A. D. and Pawar, B. B., 1992, Genetic diversity in bunch groundnut. *J. Maharashtra Agric. Univ*., **17**(2): 302-303.

Khurram, B. A., Nazar. and Malik, S. N., 2009, Estimation of diversity and heritability for quantitative traits in Groundnut (*Arachis hypogaea* L.). *Sarhad J. Agri.*, **14**:575-579.

Kumar, S I., Govindaraj, M. and Kumar. K .V., 2010, *Estimation of Genetic Diversity of New Advanced Breeding Lines of Groundnut (Arachis hypogaea L.). World Journal of Agricultural Sciences,* **6** (5). pp. 547-554.

Mahalonobis, P. C., 1936, A statistical study at chinese head measurement. *Journal of Asiatic Society of Bengal.* **25**: 301-377.

Nadaf, H. L., Habib, A. F. and Goud, J.V., 1986, Analysis of genetic diversity in bunch groundnut. *J. Oilseeds Res*., **3**: 37-45.

Nevo, E. E., Golenberg, A., Beilies, A. H. D., Brown and Zohary, D., 1982, Genetic diversity and Environmental associations of wild wheat, in Israel. *Theory and Applied Genetics.* **62**: 241-254.

Rao, C. R., 1952, Advanced statistical method in biometics research. John Wiley & Sons. New York, USA.

Suneetha, N., Vasanthi , R. P., Sudhakar, P., Reddy, K. and Raja., 2013, Genetic diversity analysis among released and pre-release cultures in groundnut. *Internal. J. plant protec*., **3**: 208-213.

Tomooka, N., 1991, Genetic diversity and landrace differentiation of mungbean, *Vigna radiata* (L) Wilezek and evaluation o its relatives (The subgenus ceratotrophics) as breeding materials. Tech. Bull. Trop. Res. Centre, Japan No. 28. Ministry of Agric. Forestry and Fisheries, Japan 1.

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