Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Assessment of genetic diversity for kernel yield and quantitative traits in drought tolerant groundnut genotypes

K. Venkatesh, A. Prasanna Rajesh, T. Srinivas* and P.Umamaheswari
Department of Genetics and Plant Breeding,
Agricultural College, Mahanandi- 518 502, Andhra Pradesh, India
Email: srinivat68@gmail.com

(Received: June 2015; Accepted: August 2015)

Abstract
Fifty drought tolerant groundnut genotypes of groundnut were evaluated for their genetic diversity with regards to kernel yield and yield attributing characters. The genotypes were classified into nine clusters, based on Mahalanobis D^2 statistic. Geographical origin, habit group and genetic diversity were observed to be unrelated, as genotypes from the same centre and habit group were grouped into different clusters. Results on inter-cluster distances revealed maximum diversity between genotypes of cluster VI and VIII. Intra-cluster distance was maximum for cluster VIII, indicating the existence of high variability within the cluster. A perusal of the results on cluster means revealed high pod yield per plant, kernel yield per plant, pods per plant, filled pods per plant and kernels per plant for cluster IX, while 100 kernel weight and specific leaf area (SLA) at 60 DAS were more for cluster VIII , indicating the desirability of genotypes from these clusters for improvement of respective traits. Further, 100 kernel weight and haulm yield per plant together had accounted for 92.25 per cent of the total genetic divergence indicating their importance in the choice of parents for hybridization programmes.
Key words: D^2 analysis, genetic divergence, groundnut, kernel yield, physiological characters yield components

Introduction

Groundnut (*Arachis hypogaea* L.) is one of the most important oil seed crops of India and contributes to about 30 per cent of the total domestic vegetable oil supply. Andhra Pradesh is one of the major groundnut growing states with an area of 14.99 lakh ha under *kharif* and 2.66 lakh ha under *rabi* and *summer* situations. In *kharif* season, groundnut is mainly cultivated under rainfed conditions. Major constraints in *kharif* production are abiotic stresses, namely, drought and low light in addition to biotic stresses, namely, late leaf spot, rust, sucking insects and leaf webber. Keeping these constraints in view, high yielding groundnut varieties with improved performance in rainfed situation have been bred and released in Andhra Pradesh from time to time. For bringing about further improvement in yield of groundnut under rainfed situation, it is essential to know the extent of diversity among the released and pre-release and germplasm groundnut cultures. In this direction studies on genetic divergence among the identified drought tolerant groundnut genotypes are essential for planning an efficient and successful hybridization programme, since the cross involving genetically diverse parents is likely to produce high heterotic effects and also more variability in the segregating generations for effective selections (Arunachalam, 1981 and Venkateswarlu *et al*., 2011). Further, biometric techniques such as

multivariate analysis based on Mahalanobis's D^2 statistic (Mahalanobis, 1936) quantifies the degree of genetic divergence amongst biological populations and assesses the relative contribution of various attributes to total divergence. Genetic diversity studies also help to determine the inherent potential of a cross for heterosis and frequency of the desirable recombinants in advanced generations. In this context, the present study was undertaken to classify and understand the nature and magnitude of genetic diversity among the released and pre-release drought tolerant groundnut genotypes of Agricultural Research Station, Kadiri of Andhra Pradesh state using Mahalanobis D^2 statistic.

Materials and methods

Experimental material for the present investigation comprised of 50 drought tolerant groundnut genotypes screened for drought tolerance from 2010-2013 at Agricultural Research Station, Kadiri of Acharya N. G. Ranga Agricultural University (Annual Reports, 2010-2013). The 50 genotypes studied comprised of 13 were from ICRISAT, one from Tirupathi and 36 from Kadiri. Among these, Dharani from Regional Agricultural Research

Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Station, Tirupathi; and Kadiri 4, Kadiri 6, Kadiri 9, Kadiri Harithandhra (KH), Anantha and Vemana from Kadiri are released as drought tolerant varieties. These genotypes were sown during *kharif*' 2014 in a randomized block design with three replications at the PG Block of College Farm, Agricultural College, Mahanandi. Seeds of each genotype were sown in two-rows of 6m length at spacing of 30cm between rows and 10cm between the plants within the row. All recommended practices were followed to raise a healthy crop. Observations were recorded on days to maturity, plant height, pods per plant, filled pods per plant, kernels per plant, sound mature kernel per cent, 100 kernel weight, pod yield per plant, kernel yield per plant, shelling per cent, SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) and haulm yield per plant. Observations for all the above traits were recorded from five randomly selected plants for each genotype, in each replication, except for days to maturity which was recorded based on all plants of the genotype. The data obtained was then subjected to standard statistical procedures. Genetic diversity in the material was analyzed using Mahalanobis D^2 statistic (Rao, 1952) and the varieties were grouped into different clusters according to Tocher's method.

Results and discussion

Analysis of variance (Table 1) revealed highly significant differences for all quantitative characters studied indicating the existence of sufficient variability for effective selection. Further, the 50 genotypes studied were grouped into nine clusters (Table 2), based on the relative magnitude of D^2 values. Among the nine clusters, cluster I consisted of maximum genotypes (26), representing collections from Kadiri, ICRISAT, and Tirupati groundnut breeding research stations of Andhra Pradesh, while cluster III had nine collections from Kadiri, cluster IV had seven collections from ICRISAT and Kadiri, cluster VIII had three collections from Kadiri, The clusters II, V, VI, VII and IX were however, with single genotype from Kadiri. The mode of distribution of genotypes from different geographical regions into various clusters was at random indicating that geographic diversity and genetic diversity are not related. Genotypes chosen from the same eco-geographic region were observed to be present in different clusters as well as in the same cluster, while genotypes from diverse geographical regions were included in the same cluster. The findings are in conformity with the reports of Kumar *et al* (2012). The production of greater diversity by genetic drift and selection, compared to that produced by geography was also observed in the present study. Genotypes from Kadiri were observed to be distributed over all the nine clusters while, genotypes from diverse geographical regions of the state were placed in the same cluster (clusters I and IV). The results are in agreement with the reports of Kumar *et al* (2012). A further, classification of the genotypes in each cluster based on habit group also revealed the distribution of genotypes to be at random indicating that habit group and genetic diversity were also not related. Genotypes from the same habit group were observed to be present in different clusters (clusters I, II, III, IV, VIII, IX for the Virginia habit group and clusters I, IV, V, VI and VII for the Spanish bunch habit group) as well as in the same cluster (cluster I and IV).

An analysis of the inter and intra-cluster distances (Table 3) revealed maximum inter-cluster distance between clusters VI and VIII (6041.01) followed by I and VIII (4324.52); IV and VIII (4255.95) and VIII and IX (2897.6) indicating that genotypes from these clusters were highly divergent meriting their consideration in selection for hybridization. Similar greater diversity between genotypes from different clusters based on their inter cluster distance has also been reported earlier in the crop (Kumar *et al.*, 2012). Minimum inter-cluster distance was observed between the clusters, V and VII (110.81) indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be minimum for cluster I (12.72) and maximum for cluster VIII (272.27), while it was zero for clusters II, V, VI, VII and IX as they included only single genotype. The genotypes included in cluster VIII, exhibiting maximum intra-cluster distance, are inferred to be more divergent than those in other clusters.

A perusal of the results on cluster means for yield and yield components (Table 4) revealed considerable differences between the clusters for all characters under study. High number of pods per plant, filled pods per plant, kernels per plant, pod yield per plant, kernel yield per plant and haulm yield per plant were noticed for the monogenotypic cluster IX, comprising of K1847 genotype. However, 100 kernel weight and SLA were more for cluster VIII. In contrast, high SMK and early maturity was noticed for cluster VII; low plant height and high shelling per cent was observed for

DOI : 10.5958/0975-928X.2016.00004.1

cluster V; and high SCMR was recorded for cluster VI, indicating the importance of selection of genotypes from the corresponding clusters in hybridization programmes for effecting improvement of the respective traits. Hybridization of K1847 categorized to cluster IX with K1879 of cluster VIII exhibiting high 100 kernel weight (48.78) is predicted to result in desirable and diverse combinations with high kernel yield and pod yields in addition to high 100 kernel weight. Similarly, hybridization between genotypes of cluster V and VIII are predicted to result in diverse combinations exhibiting superior shelling per cent, 100 kernel weight and SLA in addition to low plant height. Crossing of genotypes from cluster VI with those from cluster VIII are expected to result in highly diverse genotypes with high 100 kernel weight, SLA and SCMR, while hybridization of genotypes from cluster VII and cluster VIII are assumed to result in early maturing genotypes with high 100 kernel weight, SMK and SLA.

Information on the relative contribution of various plant characters towards divergence has also been reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations (Suneetha *et al.,* 2012). In the present study, 100 kernel weight contributed maximum (58.78%), followed by haulm yield per plant (33.47%) towards the total divergence (Table 5). Similar results were reported earlier (Venkateswarlu *et al.,* 2011) for 100 kernel weight and haulm yield per plant (Dashora and Nagda, 2004). Contribution of the remaining characters to total divergence was, however, relatively low. Therefore, 100 kernel weight and haulm yield per plant contributing to 92.25 per cent of the total divergence need to be stressed in selection of parents for hybridization.

References

Annual Report 2010. Genetrics and Plant Breeding Discipline, Agricultural Research Station, Kadiri, Acharya N.G. Ranga Agricultural University pp. 50-57.

Annual Report 2011. Genetrics and Plant Breeding Discipline, Agricultural Research Station, Kadiri, Acharya N.G. Ranga Agricultural University pp. 52-59.

Annual Report 2012. Genetrics and Plant Breeding Discipline, Agricultural Research Station, Kadiri, Acharya N.G. Ranga Agricultural University pp. 56-65.

Annual Report 2013. Genetrics and Plant Breeding Discipline, Agricultural Research Station, Kadiri, Acharya N.G. Ranga Agricultural University pp. 48-59.

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

Dashora, A. and Nagda, A.K. 2004. National symposium: Enhancing productivity of groundnut for sustaining of food and nutritional security, Oct.11-13, NRCG, Junagadh pp : 39-41.

Kumar, R.D., Reddi sekhar, M., Raja Reddy, K and Ismail, S. 2012. Comparision of cluster formation by mahalanobis D^2 and metroglyph analysis in groundnut (*Arachis hypogaea* L.). *Int. J. App. Bio. Pharmaceutical Tech*. 3 : 395-399.

Mahalanobis, P. C. 1936. A statistical study at Chinese head measurement. J. Asiatic Soc. Bengal 25 : 301: 77.

Rao, C. R. V. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc New York pp: 236-72.

Suneetha, N., Vasanthi, R.P., Sudhakar, P. and Raja Reddy, K. 2012. Genetic diversity analysis among released and pre-release cultures in groundnut. *Leg. Res.* 36 : 208 – 213.

Venkateswarlu, O., Sudhakar, B. V. G., Sekhar, M. R. and Sukhakar, P. 2011. Genetic divergence in confectionary types of groundnut (*Arachis hypogaea* L.). *Leg. Res.* 34 : 1-7. 13

Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Table 1. Analysis of variance (ANOVA) for yield, yield components and physiological characters in drought tolerant groundnut genotypes

Source of variation	degrees of freedom	Mean squares												
		Days to maturity	Plant height (cm)	Pods per plant	Filled pods per plant	Kernels per plant	Sound mature kernel (%)	100 kernel weight (g)	Pod yield per plant (g)	Shelling (%)	SPAD chloroph-yll meter reading (SCMR)	Specific leaf area (SLA)	Haulm yield per plant (g)	Kernel yield per plant (g)
Replications	2	0.8	18.9	42.6	13.4	35.00	88.9	0.8	10.0	9.1	0.7	122.4	0.3	1.6
Genotypes	49	17.9**	34.4**	147.9**	64.0**	204.7**	222.2**	532.8**	222.1**	174.7**	43.4**	3336.6**	190.2**	60.2**
Error	98	0.9	11.4	69.3	23.8	88.2	117.0	0.5	40.1	50.5	1.1	268.1	0.8	0.8

*, ** Significant at 5% and 1% levels, respectively

Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Table 2. Distribution of groundnut genotypes into different clusters based on genetic divergence

Cluster number	Number of Genotypes	Genotypes	Source	Habit Group
I	26	K1454, K1535, K1812, K1814, K2034, K2040, K2038, K2157, K1802,K2159, K1809, K1805, K2033, Kadiri6, Dharani, Kadiri9, K2031, K1815, K2042, K1813, K1848, K1834, Kadiri4, K1789, K2035, K1811.	Kadiri, ICRISAT and Tirupati	Spanish Bunch and Virginia
II	1	K1884	Kadiri	Virginia
III	9	K1878, K1741, K1886, K1725, K1717, K1877, K1718, K1721, K1719.	Kadiri	Virginia
IV	7	K1801, K1800, K1799, K2160,K2158, K1787, K2047	ICRISAT, Kadiri	Spanish Bunch and Virginia
V	1	Vemana	Kadiri	Spanish Bunch
VI	1	Kadiri Harithandhra	Kadiri	Spanish Bunch
VII	1	Anantha	Kadiri	Spanish Bunch
VIII	3	K1899, K1882, K1879.	Kadiri	Virginia
IX	1	K1847	Kadiri	Virginia

Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Table 3. Average inter and intra-cluster distances for groundnut genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	162.1 (12.7)	296.2 (17.2)	1348.1 (36.7)	524.9 (22.9)	558.0 (23.6)	309.8 (17.6)	383.1 (19.5)	4324.5 (65.7)	1290.0 (35.9)
II		0.0	578.1 (24.1)	419.3 (20.5)	260.3 (16.1)	845.3 (29.1)	125.6 (11.2)	2685.4 (51.8)	645.0 (25.4)
III			211.0 (14.5)	1634.9 (40.4)	385.2 (19.6)	2269.0 (47.6)	463.3 (21.5)	1131.7 (33.6)	1355.8 (36.8)
IV				207.0 (14.4)	1190.3 (34.5)	974.3 (31.2)	756.7 (27.5)	4255.9 (65.2)	480.1 (21.9)
V					0.0	1027.4 (32.1)	110.8 (10.5)	2320.1 (48.2)	1548.9 (39.4)
VI						0.0	799.8 (28.3)	6041.0 (77.7)	2269.9 (47.6)
VII							0.0	2506.1 (50.1)	1076.3 (32.8)
VIII								272.2 (16.5)	2897.6 (53.8)
IX									0.0

Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Table 4. Cluster means for kernel yield and yield attributing traits in groundnut genotypes

Clusters	Days to maturity	Plant height	Pods per plant	Filled pods per plant	Kernels per plant	Sound Mature Kernel (%)	100 kernel weight	Pod Yield per plant	Kernel Yield per plant	Shelling (%)	SPAD Chlorophyll meter reading	Specific leaf area	Haulm Yield per plant
I	109.0	34.0	28.7	23.7	47.8	81.1	39.6	30.2	18.4	62.5	44.6	177.5	20.2
II	108.0	29.8	28.3	22.9	42.5	75.3	47.7	29.1	20.1	68.8	41.6	150.1	26.2
III	108.7	32.8	24.2	20.5	42.0	79.1	62.6	36.0	22.4	62.5	40.1	165.3	21.8
IV	110.0	36.8	25.6	21.3	41.4	78.0	39.4	29.0	18.0	62.5	45.2	191.2	35.8
V	108.7	29.8	16.2	12.7	25.5	82.0	52.7	14.4	10.4	73.3	41.9	147.7	14.2
VI	108.0	33.6	21.3	17.4	41.3	85.7	33.3	26.4	15.8	60.4	51.5	127.1	13.2
VII	106.7	40.3	24.0	20.4	44.2	89.1	51.4	31.4	21.5	68.5	47.8	148.3	19.1
VIII	108.3	32.7	25.2	22.0	43.4	78.4	82.1	46.1	31.0	66.5	37.1	205.5	29.1
IX	115.3	41.0	61.4	33.2	58.7	83.8	49.4	47.8	31.3	65.5	42.2	179.4	46.0

Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI : 10.5958/0975-928X.2016.00004.1

Table 5. Relative contribution of characters studied towards genetic divergence in groundnut

Character	Times Ranked 1st	Contribution (%)
1. Days to maturity	6	0.49
2. Plant height (cm)	1	0.08
3. Pods per plant	0	0.00
4. Filled pods per plant	1	0.08
5. Kernels per plant	0	0.00
6. Sound mature kernels (%)	0	0.00
7. 100 kernel weight	720	58.78
8. Pod yield per plant (g)	5	0.41
9. Kernel yield per plant (g)	1	0.08
10. Shelling %	6	0.49
11. SPAD Chlorophyll Meter Reading (SCMR) at 60 DAS	51	4.16
12. Specific leaf area at 60 DAS	24	1.96
13. Haulm yield per plant (g)	410	33.47