Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(5): 711-714
Received: 06-07-2018
Accepted: 07-08-2018

NR Tayade
Ph.D. Research scholar Dept. of Agril. Botany, Dr. PDKV, Akola, Maharashtra, India

Ladole MY
Ass. Prof., Oilseed Research Unit, Dr. PDKV, Akola, Maharashtra, India

Nagrale SC
M. Sc. (GPB) Dept. of Agril. Botany, Dr. PDKV, Akola, Maharashtra, India

Walake OB
M.Sc. (GPB) Dept. of Agril. Botany, Dr. PDKV, Akola, Maharashtra, India

Correspondence
NR Tayade
Ph.D. Research scholar Dept. of Agril. Botany, Dr. PDKV, Akola, Maharashtra, India

Assessment of genetic divergence for yield and physiological attributes in groundnut germplasm (*Arachis hypogaea* L.)

NR Tayade, Ladole MY, Nagrale SC and Walake OB

Abstract
Divergence was studied among fifty-two genotypes based on data of thirteen agronomical and three physiological attributes *viz.* leaf area index, chlorophyll content index and canopy temperature. The analysis of variance indicated significant differences among genotypes for all the sixteen attributes studied. The genotypes were grouped into nine clusters. The mode of distribution of genotypes to various clusters was at random suggesting that there is no relationship between geographical distribution and genetic diversity. The cluster size varied from single to 29 genotypes. Plant height (21.87%) followed by pod yield (21.27%) contributed maximum to the total divergence. The highest inter-cluster distance (145.6) was recorded between cluster V (TAG-24) and VIII (AK-14). Crosses between these genotypes would be more rewarding. The diversity among the genotypes measured by intra-cluster & inter cluster distance was adequate for improvement of Groundnut by hybridization and selection. Based on intra and inter-cluster distances and cluster means, parents were identified for further breeding programmes for isolation of useful transgressive segregation.

Keywords: Divergence, groundnut, physiological attributes, clustering pattern

Introduction
Groundnut (*Arachis hypogaea* L.) is the one of the important oilseed crop of India. Economically it is an important oil, food, and feed legume crop grown in over 100 countries. It covered 245.6 lakh ha area worldwide with a total production of 453.08 lakh tonnes and the productivity of 1780 kg/ha in 2014. (Anonymous, 2014) [1]. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. Hence, the present investigation was made to study the genetic divergence in groundnut *(Arachis hypogaea* L.) germplasm to identify potential lines for various yield traits which could be utilized in the hybridization programme to improve yield. Most of the earlier genetic diversity studies are based on morphological and yield attributes. In the present study, diversity was assessed taking a set of physiological attributes that ultimately determine yield.

Materials and methods
The experimental material consisted of fifty-two genotypes of groundnut, evaluated in a randomized block design with three replications during *kharif* 2015 in the experimental farm of Oilseeds Research Unit, Dr. PDKV, Akola. Recommend package of practices for *kharif* groundnut cultivation were followed. Protective irrigation was provided whenever the crop experienced moisture stress. Each genotype was sown in three rows of 5m length with interrow spacing of 30cm and intra-row spacing of 10cm. five plants were taken at random from each genotype in each replication for recording observations. The data on 13 agronomical characters namely days to 50% flowering, days to pod maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, biomass per plant (g), hundred pod weight (g), hundred kernel weight (g), shelling per cent (%), pod yield per plant (g), kernel yield per plant (g), oil content (%) and 3 physiological characters viz. leaf area index, chlorophyll content index and canopy temperature at vegetative, reproductive and harvesting stage were recorded. Genetic diversity were studied using Mahalanobis (1936) [4] generalized distance (D^2) extended by Rao (1952) [5]. Based on the D^2 values, the studied genotypes were grouped into clusters according to the Tocher's method (Rao, 1952) [5]. The methods of Singh and Chaudhary (1985) [6] were used for calculating the intra and inter cluster distances.

Results and discussion
The analysis of variance revealed significant differences among the genotypes for all the traits studied. The fifty-two genotypes were grouped into 9 clusters (Table 1).

Cluster IV was the largest with a maximum number of genotypes (29) followed by cluster I with 16 genotypes. The remaining seven clusters were mono genotypic. The grouping of genotypes revealed that there was no perfect relationship between genetic diversity and geographical diversity as genotypes from different geographical origin were included in one cluster. Lack of correlation between genetic and geographic diversity was also reported by Venkataravana *et al.* (2000) [8] and Sudhir Kumar (2010) [7].

Highest intra-cluster (32.0) distance was observed in cluster IV including 29 genotypes followed by cluster I (20.9) having 16 genotypes. The cluster in which only one genotype was grouped; the intra-cluster distance was zero (D=0) and the cluster was II, III, V, VI, VII, VIII, IX including genotypes AK-265, TG-70, TAG-24, TG-75, ICGV-11, AK-14 and AK-303 respectively. The magnitude of D^2 values indicates substantial diversity for agronomical and physiological attributes among genotypes included in the study. In accordance with above value of intra-cluster distances, cluster showing higher intra-cluster distance, suggested wider diverse genotypes within these clusters and the parents for hybridization can be selected from these clusters.

The maximum average inter-cluster distance was observed between clusters V and VIII (D=145.6), where both the cluster are solitary with the genotypes TAG-24 and AK-14 respectively, followed by cluster VI and VIII including TG-75 and AK-14 in respective clusters (D=126.3), cluster V and IX (D=120.3), cluster VII and cluster IX (D=119.8), cluster IV and IX (D=118.9), cluster VII and VIII (D=116.4) and cluster III and VIII (D=116.3). The lowest average inter-cluster distance was found between cluster III and VI (D=16.1), followed by cluster III and V (D=23.9) (Table 2).

Table 1: Distribution of genotypes in different clusters by Tocher's method

Cluster	Total No. of Genotypes	Genotypes
I	16	Ak-344, AK-360, CO-2, AK-345, AK-359, AK-280, JL-501, PKVG-8, ROBOUT-33-1, AK-358, JL-776, Dh-180, AK-340, TG-68, X0II-2-71, AK-357
II	1	AK-265
III	1	TG-70
IV	29	AK-277, Ah-1, AK-190, Dh-101, AK-147, AK-314, ICGV-06420, AK-327, AK-284, AK-331, AK-206, TG-60, CO-1, GP-201, AK-171, AK-159, AK-34, AKG-18-1, ICGV-76, AK-295, AK-350, AK-174, AK-322, Spancross, AK-355, POL-2, CHICO, TAG-24 (SEL.), AK-329
V	1	TAG-24
VI	1	TG-75
VII	1	ICGV-11
VIII	1	AK-14
IX	1	AK-303

Table 2: Average Intra and Inter-Cluster Distance

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	20.9	33.1	29.2	38.4	31.3	26.1	58.9	91.4	96.4
II		0.0	50.0	37.1	66.6	55.5	77.0	29.1	55.0
III			0.0	51.7	23.9	16.1	43.9	116.3	73.5
IV				32.0	51.8	51.9	56.3	75.3	118.9
V					0.0	26.7	66.4	145.6	120.3
VI						0.0	56.9	126.3	105.1
VII							0.0	116.4	119.8
VIII								0.0	86.8
IX									0.0

Above results revealed that, the inter-cluster distance were larger than the intra-cluster distance which indicated that greater diversity is present among the genotypes of distant group (Zaman *et al.*, 2010) [10]. Those genotypes included in clusters with maximum inter-cluster distance are obviously genetically more divergent. Hence, from the obtained inter-cluster distance result, it would be logical to choose genotypes from these clusters in the breeding programme. On this basis, TAG-24, AK-14, TG-75, AK-303, Chico, ICGV-06420, ICGV-11, TG-70, AK-171 and AK-344 can be selected.

The cluster means for all the sixteen characters is presented in the Table 3. For days to 50 per cent flowering the highest cluster mean was recorded by cluster VII (33.3 days), followed by cluster IX (29.7 days) and cluster I (28.4 days), while cluster VIII (25.7 days) recorded the lowest cluster mean for this character. In case of Days to maturity, cluster VII (120.7 days) recorded the highest mean value, followed by cluster IX (117.6 days) and cluster VIII (111.7 days). Cluster V showed the lowest mean value (106.3 days) for days to maturity. In respect of plant height maximum cluster mean value was noted in cluster VIII (43.3 cm), followed by cluster II (38.9 cm) and cluster IV (36.4 cm). The lowest cluster mean for this character was observed in cluster VII (23.0 cm). Cluster IX showed the highest cluster mean for primary branches per plant (5.0), followed by cluster VII (4.8). The lowest cluster mean for this character was exhibited by cluster VI (3.6). Cluster VII recorded the highest cluster mean (3.27) for number of secondary branches per plant, while cluster II exhibited lowest value (2.0) for this character.

For number of pods per plant cluster V recorded the highest cluster mean value (20.7), followed by cluster I (18.4), while cluster VII give the lowest value (14.8). The highest cluster mean for biomass per cent was observed in cluster IX (49.2 g), followed by cluster VIII (44.3 g) and the lowest mean for biomass per cent was observed in cluster VII (22.8 g). Cluster mean for hundred pod weight was found highest in cluster IX (101.3 g), followed by cluster III (90.7 g) and the lowest mean was observed in cluster V (74.3 g). For hundred kernel weight cluster IX exhibited the highest cluster mean (60.5 g), followed by cluster III (45.3 g). The lowest cluster mean value (33.6 g) was observed in cluster I for the same character. Shelling per cent was found maximum in cluster V (69.7%), while cluster VII (64.2%) exhibited the lowest cluster mean for shelling per cent. In case of pod yield per

plant, cluster IX showed the highest mean value (16.8 g), followed by cluster II (13.0 g) and the lowest cluster mean was recorded in cluster VII (7.7 g). For kernel yield per plant cluster IX showed the highest mean value (12.8 g) and the lowest mean was observed in cluster VII (4.9 g). Cluster II exhibited the highest mean value (49.5%), followed by cluster III (48.3%) for oil content, while cluster IX give the minimum cluster mean (46.0%), followed by cluster VIII (46.8) for oil content.

The highest cluster mean for Leaf Area Index (LAI) at vegetative stage was observed in the cluster VI (0.5) and lowest in the cluster IX (0.3), at reproductive stage cluster V give the highest mean (2.1), while cluster VII showed the lowest mean (0.8). Cluster VII give the highest mean value (2.0), followed by cluster VI (1.9) and cluster V exhibited the lowest cluster mean (1.1) at harvesting stage for the same character.

For chlorophyll Content Index, cluster III gives the highest mean value (45.4), followed by cluster VI (45.2) and cluster IV gives the lowest value (41.1) at vegetative stage and at reproductive stage cluster VI (48.9) give the highest, while cluster IV (44.0) gives the lowest CCI. At harvesting stage cluster VI (47.7) showed the maximum mean value, whereas minimum mean was showed by the cluster VIII (37.7).

Cluster mean for canopy temperature (vegetative stage) was highest in the cluster VIII (40.7 ^{0}c) and found lowest in the cluster IX (32.8 ^{0}c). Cluster VIII has highest mean (31.6 ^{0}c) and cluster III showed lowest (28.2 ^{0}c) mean value at reproductive stage. The highest cluster mean at harvesting stage was found in cluster IX (32.4 ^{0}c), whereas the lowest was recorded in cluster V (28.5 ^{0}c), for the same character.

Relative contribution of characters towards diversity is presented in Table 4. Character plant height ranked first with 290 times and recorded maximum contribution towards total divergence, contributing 21.87 per cent in grouping the genotypes; similar results were obtained for highest contribution of plant height towards total genetic divergence by Bhakal *et al. (*2015) [2]. Pod yield (21.27%) ranked second with 282 times, followed by hundred pod weight (11.76%), Biomass per plant (10.78%), hundred kernel weight (10.26%) and number of pods per plant (5.43%) also gives higher contribution to the total divergence, Venkateswarlu (2011) [9] also recorded the similar results in groundnut where greater contribution of hundred kernel weight was found.

Relatively less contribution was reported by leaf area index (4.3) (Reproductive stage), chlorophyll content index (2.26%) (Harvesting stage), number of secondary branches per plant (2.11%), leaf area index (harvesting), chlorophyll content index (Vegetative) (2.04%) and kernel yield (1.43%). Very less contribution was recorded by leaf area index (0.75%) at vegetative stage, Shelling per cent (0.6%), days to 50 per cent flowering (0.53%), canopy temperature at harvesting (0.38%), number of primary branches per plant (0.3%), days to maturity and Oil content (0.15%) towards genetic divergence. In accordance with these results Sudhir Kumar *et al.* (2010) [7] also reported little contribution of primary and secondary branches per plant towards genetic divergence. From above findings it has been observed that no single character had greater contribution to total divergence. There is zero contribution by canopy temperature at vegetative and reproductive stage towards genetic divergence.

Based on diversity analysis and superiority with respect to agronomical and physiological traits studied, the identified promising genotypes are presented in Table 5.

Table 3: Cluster means for fifty-two genotypes of groundnut

Cluster	Day to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of Secondary Branches per Plant	Number of pods per Plant	Biomass per Plant (g)	Hundred pod Weight (g)	Hundred Kernel Weight (g)	Shelling percent (%)	Pod Yield per Plant
I	28.4	111.2	30.5	4.6	2.2	18.4	32.7	85.8	33.6	65.5	12.8
II	26.3	111.0	38.9	4.6	2.0	16.3	39.2	89.7	38.1	67.0	13.0
III	28.3	110.8	26.2	4.4	2.2	16.6	28.0	90.7	45.9	65.1	11.4
IV	27.7	111.5	36.4	4.5	2.2	15.8	28.5	76.7	34.8	65.7	10.3
V	28.0	106.3	26.9	4.7	2.4	20.7	29.0	74.3	39.7	69.8	12.6
VI	27.3	110.3	27.0	3.6	2.1	18.4	28.8	86.2	36.3	66.3	12.0
VII	33.3	120.7	23.0	4.8	3.3	14.8	22.8	80.9	36.7	64.2	7.7
VIII	25.7	111.7	43.3	4.1	2.0	15.5	44.3	86.2	37.7	64.6	12.2
IX	29.7	117.6	35.9	5.0	2.4	17.4	49.2	101.3	60.5	67.7	16.8

Cluster	Kernel yield per plant	Oil content	Leaf Area Index			Chlorophyll Content Index (g m^{-2})			Canopy Temperature (^{0}C)		
			Vegetative	Reprod.	Harvesting	Vegetative	Reprod.	Harvesting	Vegetative	Reprod.	Harvesting
I	9.5	48.1	0.4	1.4	1.4	42.1	44.8	41.7	35.1	30.3	29.2
II	10.4	49.5	0.3	1.4	1.5	43.5	46.1	41.9	32.9	29.9	28.8
III	8.5	48.3	0.4	1.5	1.4	45.4	46.9	44.4	35.5	28.2	31.1
IV	7.2	48.0	0.4	1.5	1.6	41.1	44.0	40.0	34.6	30.3	29.1
V	9.1	48.0	0.4	2.1	1.1	41.6	46.1	40.7	33.6	28.6	28.5
VI	8.7	47.4	0.5	1.2	1.9	45.2	48.9	47.7	36.4	29.2	31.3
VII	4.9	47.3	0.3	0.8	2.0	44.3	46.7	40.7	35.0	29.4	28.7
VIII	9.0	46.8	0.3	1.4	1.2	43.7	46.1	37.7	40.7	31.6	30.3
IX	12.8	46.0	0.3	1.0	1.8	43.5	44.1	42.9	32.8	29.4	32.4

Table 4: Contribution of various characters towards genetic divergence

S. No.	Character	Times ranked 1st	Contribution percentage
1	Days to 50 per cent flowering	7	0.53%
2	Days to maturity	2	0.15%
3	Plant height (cm)	290	21.87%
4	Number of primary branches per plant	4	0.3%
5	Number of secondary branches per plant	28	2.11%
6	Number of pods per plant	72	5.43%
7	Biomass per plant (cm)	143	10.78%
8	Hundred pod weight (g)	156	11.76%
9	Hundred kernel weight (g)	136	10.26%
10	Shelling per cent (%)	8	0.6%
11	Pod yield per plant (g)	282	21.27%
12	Kernel yield per plant (g)	19	1.43%
13	Oil content (%)	2	0.15%
14.1	Leaf area index (vegetative stage)	10	0.75%
14.2	Leaf area index (reproductive stage)	57	4.3%
14.3	Leaf area index (harvesting stage)	27	2.04%
15.1	Chlorophyll content index (vegetative stage) (g m^{-2})	27	2.04%
15.2	Chlorophyll content index (reproductive stage) (g m^{-2})	21	1.58%
15.3	Chlorophyll content index (harvesting stage) (g m^{-2})	30	2.26%
16.1	Canopy Temperature (vegetative stage) (^{0}C)	0	0.0%
16.2	Canopy Temperature (reproductive stage) (^{0}C)	0	0.0%
16.3	Canopy Temperature (harvesting stage) (^{0}C)	5	0.38%

Table 5: Suggested cross combination

S. No.	Cluster combination	Average inter-cluster distance	Suggested cross combination	Potential traits
1	V × VIII	145.6	TAG-24 x AK-14	TAG -24: Dwarf, early maturing, and high number of pods, high shelling, high oil content, high CCI, LAI and low canopy temperature. AK-14- Early mature, high CCI.
2	VI X VIII	126.3	TG-75 X AK-14	TG-75: Early maturing, dwarf, high pod yield, high CCI and low canopy temperature. AK-14: Early maturity, high CCI.
3	V X IX	120.0	TAG-24 X AK-303	TAG-24: Dwarf, early maturing, high oil and shelling %, high LAI and CCI. AK-303: Bold seeded with high pod and kernel weight.
4	VII X IX Directorate of groundnut research	119.8	ICGV-11 X AK-303	ICGV-11: Medium height, high CCI, LAI and low canopy temperature. AK-303: Bold seeded, High oil and shelling per cent with low canopy temperature.
5	IV X IX	118.9	Chico X AK-303	Chico: Earliest, dwarf, high oil content. AK-303: Bold seeded, high pod and kernel weight.

References

1. Anonymous. Status paper on oilseeds, ministry of agriculture, Govt of India, 2014. Available at: www.nmoop.gov.in.
2. Bhakal M, Lal GS. Studies on Genetic diversity in groundnut (*Arachis hypogaea* L.) germplasm. J of. of Plant Sci. and Res, 2015, 2.
3. Mahalakshmi P, Manivannan N, Muralidharan V. Genetic divergence of groundnut (*Arachis hypogaea* L.) germplasm. Legume Res. 2005; 28(3):220-222.
4. Mahalanobis PC. On the generalized distance in statistics. Proceedings of National Institute of Science, India. 1936; 2:49-55.
5. Rao CR. Advance statistical methods in biometric research Edn. J John Wiley and Sons, New York, 1952.
6. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, 1985, 252.
7. Sudhir K, Govindaraj M, Kumar VK. Estimation of Genetic diversity of new advanced breeding lines of groundnut (*Arachis hypogaea* L.). World J Agric. Sci. 2010; 5(6):547-554.
8. Venkataravana P, Sheriff RA, Kulkarni RS, Shankaranarayana VV, Fathima P. Genetic divergence in groundnut (*Arachis hypogaea* L.). Mysore J agric. Sci. Sci. 2000; 34(2):125-129.
9. Venkateswarlu O, Sudhakar BVG, Reddy M, Sudhakar P. Genetic divergence in confectionary types of groundnut (*Arachis hypogaea* L.). Legume Res. 2011; 34(1):1-7.
10. Zaman MA, Tuhima-Khatum M, Bhuiyan MMH, Yusuf MN. Genetic divergence in groundnut (*Arachis hypogaea* L.). Bangladesh J Pl. Breed. Genet. 2010; 23(1):45-49.