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Assessment of genetic diversity in groundnut (*Arachis hypogaea* L.) genotypes under semi-arid condition of Rajasthan

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Abstract
A set of forty five groundnut genotypes were assessed the genetic diversity during kharif season of 2019 using Mahalanobis D^2 statistics. Among the characters studies, the biological yield per plant (g) contributed highest percentage towards the total genetic divergence. The groundnut genotypes were grouped into 8 clusters. Among these 8 clusters, cluster I had maximum number of genotypes 17 followed by cluster II with 11 genotypes, cluster III with 9 genotypes, cluster IV with 3 genotype, cluster VI with 2 genotypes and the remaining clusters (V, VII, VIII) were solitary cluster consisting of only one genotype. Cluster II had the maximum intra cluster distance followed by cluster IV. The maximum inter-cluster distance was found between cluster I and VI followed by cluster II and VI. Cluster VI (RG 584, RG 604) showed the highest cluster mean for kernel yield per plant (g), pods per plant, dry pod weight per plant (g), biological yield per plant (g) and harvest index (%). Hybridization between genotypes of cluster I and VI followed by cluster II and VI could yield better segregants.

Keywords: Cluster mean, genetic diversity, groundnut, hybridization, mahalanobis D^2 statistic

Introduction
Groundnut is one of the most important oilseed crops of India which is native to Brazil. It is annual, herbaceous, allotetraploid legume with 2n = 40 chromosomes and belongs to the family Leguminosae (Fabaceae). Groundnut is highly autogamy crop and has cleistogamous flowers (Korat *et al*. 2010) [2]. Groundnut is known as a "wonder legume" for its flowering, pegging and pod formation pattern (Boraiah *et al*., 2012) [3]. Groundnut is utilized for different purposes like seed (kernel) consume directly raw, roasted and boiled into confections; oil used for edible and industrial purpose; Haulm used as animal fodder or in green manuring; roots being legume add the nitrogen (100-152 kg ha-1N) and organic matter to soil. The composition of groundnut kernel is high quality edible oil (44-56%), protein (22-30%), carbohydrates (10-25%), vitamins (E, K, and B complex) and minerals such as Ca, P, Mg, Zn and Fe (Nigam, 2014) [4]. In India, it is grown over in area of 48.10 lakh hectares with total production of 66.9 lakh metric tonnes (Anonymous, 2019) [1]. Assessment of genetic diversity is essential for the planning an effective breeding programme (Reddy *et al.*, 2018) [5]. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization. Keeping the above in view, the present investigation was undertaken to identify the best performing genotypes of groundnut based on metric traits.

Material and Methods
The experimental material consisted of 45 groundnut genotypes including released varieties representing diversity in adaptability and variability in characters and geographical origin. These materials were evaluated in randomized block design (RBD) with 3 replications at Research Farm of S.K.N. College of Agriculture Jobner, Jaipur (Rajasthan) during *kharif* 2019 to identify diversity among them. Each genotype was sown in a plot of 4.0 m x 0.80 m accommodating two rows spaced at 40 cm apart and plant to plant distance of 15 cm. All the recommended agronomic package of practices was followed for raising of healthy crop. Five plants per genotype per replication were randomly selected for recording the observations at appropriate stages of crop growth on characters *viz.* pods per plant, dry pod yield per plant, shelling percentage, solid mature kernel, biological yield per plant, harvest index and kernel yield per plant. The observations on days to 50 per cent flowering, days to maturity and 100-kernel weight were recorded on plot basis.

The data were analyzed according to Mahalanobis D^2 statistic (Mahalanobis, 1936) [66] and first suggested by Rao (1952) [7] for the assessment of genetic diversity in plant breeding. Grouping of 45 genotypes of groundnut into eight different clusters were performed by Tocher's method (Rao, 1952) [7]. The methods of Singh and Chaudhary (1985) [8] were used for calculating the intra and inter cluster distances.

Results and Discussion

In the present investigation, 45 groundnut genotypes were grouped into 8 clusters by using Tocher's method which indicates the presence of maximum divergence for further crop improvement programme (Table 1). Among these 8 clusters, cluster I had maximum number of genotypes 17 followed by cluster II with 11 genotypes, cluster III with 9 genotype, cluster IV with 3 genotypes, cluster VI with 2 genotypes and the remaining clusters; (V, VII, VIII) were solitary cluster consisting of only one genotype. Similar finding were obtained by Garjapa *et al.* (2005) [9] and Dolma *et al*. (2010) [10].

The intra and inter-cluster distance (Table 2, Fig 1) ranged from 0.00 (clusters V, VII, VIII) to 52.78 (cluster II). Cluster II had the maximum intra cluster distance (52.78) followed by cluster IV (48.16), cluster III (45.32) and cluster VI (37.86). This indicates that genotypes present in these cluster had wider variation among themselve. The maximum inter-cluster distance (394.99) was found between cluster I and VI followed by cluster II and VI (340.03), cluster IV and VI (271.46) and V and VI (264.77) suggesting that the genotypes belonging to these clusters are diverse, Hence the hybridization between genotypes of these clusters may create more variability in segregating population. The smallest inter-cluster distance (58.88) was found between I and II followed by clusters IV and V (60.65), cluster IV and VIII (65.86) and cluster I and V (70.70) indicating that the genotypes belonging them are less diverse and constitute similar genotypic makeup. Same results were obtained by Dolma *et al*. (2010) [10] and Zaman *et al.* (2010) [12].

Based on mean performance of different quantitative characters (Table 3) for various clusters revealed that genotypes present in cluster III (24.29 days) was early for days to 50% flowering followed by cluster V (24.33 days). Genotypes in cluster V (113.33 days) was observed early maturity followed by cluster III (113.74 days). The number of pods per plant had highest cluster mean value of 38.16 was observed in cluster VI followed by cluster VII (28.33). The cluster VI had superior performance for dry pod weight per plant (33.66g) followed by cluster VII (26.33g). The maximum mean value for shelling (%) was recorded in cluster III (67.92%) followed by cluster VII (67.66%). Cluster VIII possessed the maximum mean value for solid mature kernel percentage (87.66%) followed by cluster I (86.25%). The maximum mean value of 100-kerenl weight (g) was observed in cluster VIII (72.06) followed by cluster VII (66.50). The clusters VI showed highest mean value for biological yield per plant (91.25g) followed by cluster VII (84.93g). The maximum mean value for harvest index (%) was recorded in cluster VI (37.00) followed by cluster I (35.01). The cluster VI had maximum mean value for kernel yield per plant (21.80) followed by cluster VII (17.83). Therefore crosses between members of clusters having high inter cluster distance along with high mean value for important characters are likely to be highly rewarding (Rajalakshmi *et al*., 2020) [11].

The per cent contribution of individual trait towards genetic divergence by all the ten traits (Table 4) showed that the character biological yield per plant had highest per cent contribution (35.86%) towards total genetic divergence followed 100-kernel weight (27.68%), days to maturity (8.69%), solid mature kernel and kernel yield per plant (8.28%) whereas, the lowest contribution towards total genetic divergence was found for harvest index (0.20%).

In conclusion, the extent of genetic divergence was observed among 45 genotypes of groundnut. On the basis of the above analysis it can be concluded that selection of parents, based on biological yield per plant (g) will be effective as it contributed more to divergence. Cluster VI (RG 584, RG 604) can used to improve kernel yield per plant (g), pods per plant, dry pod weight per plant (g), biological yield per plant (g) and harvest index (%). Genotypes RG 625 is a desirable parent with early maturity. Genotypes in cluster I (RG 425, NRCG 12312, GG 20, TAG 24, ICG 3746, HNG 69, RG 623, RG 559-3, TG 22, RG 639, HNG 10, UTKARSH, GG 21, RG578, GIRNAR 2, ICGV 6119, RG 382) and VI (RG 584, RG 604) had more genetic diversity followed by cluster II (PUNJAB 1, ICGV 86590, T 28, HNG 123, RG 633, ICGV 6052, RG 510, MH 1, CSMG 2003-19, RG 614, RG 575-1) and VI(RG 584, RG 604). Hence, crossing between these genotypes will be generate more variation in segregating population which can be help for improve the groundnut.

Table 1: Distribution of 45 groundnut genotypes into different clusters

Cluster No.	Name of Genotypes	Number of Genotype
I	RG 425, NRCG 12312, GG 20, TAG 24, ICG 3746, HNG69, RG 623, RG 559-3, TG 22, RG 639, HNG 10, UTKARSH, GG 21, RG578, GIRNAR 2, ICGV 6119, RG 382	17
II	PUNJAB 1, ICGV 86590, T 28, HNG 123, RG 633, ICGV 6052, RG 510, MH 1, CSMG 2003-19, RG 614, RG 575-1	11
III	TPG 41, ICG 115-1, RG 643, SC 28, DGR 7, ICG 350, RG 628, RG 420-1, RRCG 95195	9
IV	RG 632, RG 633-1, RG 642-1	3
V	RG 625	1
VI	RG 584, RG 604	2
VII	RG 644	1
VIII	RG 642	1

Table 2: Average intra (bold) and inter-cluster D^2 values for eight clusters

Cluster	I	II	III	IV	V	VI	VII	VIII
I	32.49	58.88	134.70	92.60	70.70	394.99	229.98	198.10
II		52.78	125.35	79.64	100.21	340.03	229.53	174.03
III			45.32	112.69	82.95	121.01	70.78	141.74
IV				48.16	60.65	271.46	131.52	65.86
V					0.00	264.77	87.35	78.57
VI						37.86	85.10	227.22
VII							0.00	93.31
VIII								0.00

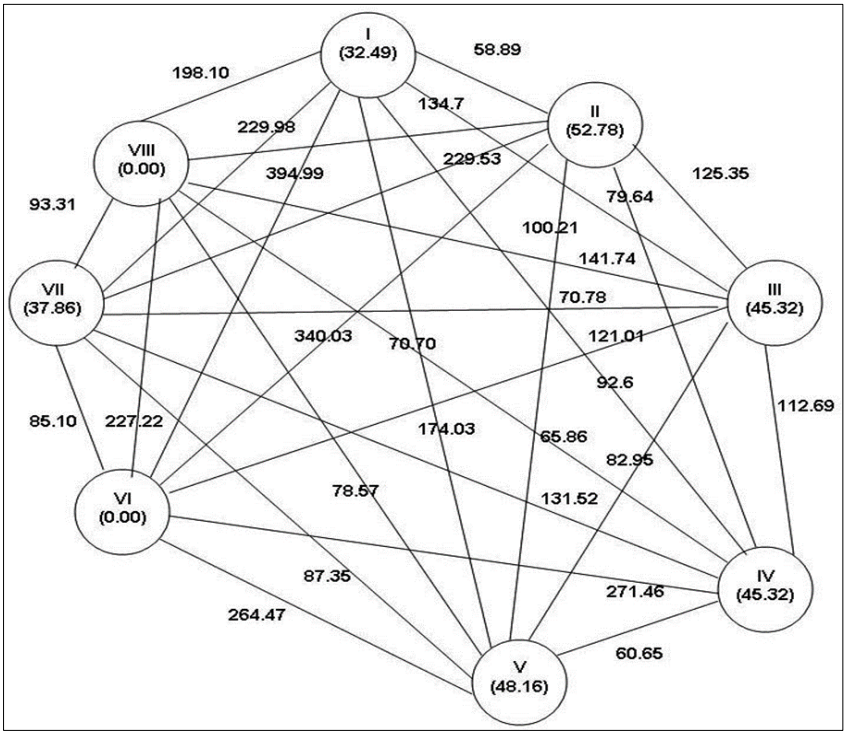

Fig 1: Relative disposition of clusters showing average intra and inter distance in genetic divergence

Table 3: Mean performance of characters in various clusters

Cluster Number	Days to 50% flowering	Days to maturity	Pods per plant	Dry pod weight per plant (g)	Shelling (%)	Solid mature kernel (%)	100-Kernel weight (g)	Biological yield per plant (g)	Harvest Index (%)	Kernel yield per plant (g)
I	25.11	114.82	14.90	12.76	66.09	86.25	52.80	36.32	35.01	8.44
II	27.45	121.42	17.69	14.87	64.63	83.93	45.59	43.18	34.70	9.62
III	24.29	113.74	25.81	22.51	67.92	85.22	49.66	66.25	34.30	15.30
IV	29.22	126.00	20.77	17.55	64.77	75.88	60.58	57.97	30.73	11.44
V	24.33	113.33	19.00	15.66	63.00	85.33	65.20	61.96	25.23	9.86
VI	25.66	115.83	38.16	33.66	64.66	82.00	49.23	91.25	37.00	21.80
VII	25.00	114.00	28.33	26.33	67.66	77.00	66.50	84.93	31.00	17.83
VIII	30.00	129.00	23.33	20.33	62.66	87.66	72.06	79.60	25.56	12.73

Table 4: Contribution of various traits towards divergence in groundnut

S. No	Traits	Number of times ranked first	Contribution (%)
1.	Days to 50% flowering	17	1.72
2.	Days to maturity	86	8.69
3.	Pods per plant	60	6.06
4.	Dry pod weight per plant (g)	6	0.60
5.	Shelling (%)	26	2.63
6.	Solid mature kernel (%)	82	8.28
7.	100-kernel weight (g)	274	27.68
8.	Biological yield per plant (g)	355	35.86
9.	Harvest Index (%)	2	0.20
10.	Kernel yield per plant (g)	82	8.28
Total		990	100

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