

GENETIC DIVERGENCE STUDY IN GROUNDNUT (*Arachis hypogaea* L.)

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ABSTRACT

The genetic divergence measured by Mahalanobis's D^2 statistic grouped sixty genotypes of groundnut into 7 clusters. The clustering pattern of the genotypes did not confirm to the geographical distribution. The lowest intra-cluster distance was in cluster II, III, IV, V, VI and VII, whereas the highest intra-cluster distance was in cluster I. The maximum inter-cluster distance was found between cluster VI and VII. The minimum inter-cluster distance was found between cluster VI and V. The genotypes from cluster VII (TG-26), VI (JB-D-29), V (JB-500), IV (ICGS-44), III (KISHAN) and II (JB-564) could be selected as parents in hybridization programme.

KEY WORDS: D^2 statistic, divergence, groundnut

INTRODUCTION

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. The use of Mahalanobis's D^2 statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966), because it permits precise comparison among all the population given in any group before effecting actual crosses. 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). Genetic

diversity plays a pivotal role in survival and adaptability of a species. When a specific environment changes, slight genetic variation is necessary for it to adapt and survive. A species that has a large degree of genetic diversity among its population will have more variation. The genetic diversity is a crucial factor in determining the success of hybridization programme and its importance in crop improvement has long been recognized by breeder. The more diverse parents within overall limits of fitness, the greater are the chances of heterotic F_1 's and broad spectrum of variability in segregating generation (Arunachalam, 1981 and Falconer, 1989). Therefore, the first step in any crop breeding programme is to assess genetic variability.

MATERIALS AND METHODS

The experiment material consisted of 60 genotypes of groundnut. The study was conducted during *kharif* 2015 at the Krishi Gadh Farm, Junagadh Agricultural University, Junagadh. The soil of experimental site was medium black,

alluvial in origin and medium in organic matter. The climate of the area represents tropical and semi-arid. Sixty genotypes of groundnut were sown in a Randomized Block Design (RBD) with three replications. Each genotype was accommodated in a single row of 3.0 meter length with a spacing of 45 cm between rows and 10 cm between plants within the row. The experiment was surrounded by two guard rows to avoid damage and border effects. The fertilizers in the experimental area was applied at the rate of 12.50 kg/ha N₂ and 25.0 kg/ha P₂O₅, as it is a recommended dose for *kharif* cultivation of groundnut in the region. Other recommended agronomical practices in vogue were followed for reaping good crop. The observations were recorded on five randomly selected plants in each entry and replications, their mean values were used for statistical analysis. The characters studied were days to 50 per cent flowering, days to maturity, plant height (cm), number of secondary branches per plant, number of pods per plant, number of mature pods per plant, sound mature kernels (%), 100- kernel weight (g), kernel yield per plant (g), pod yield per plant (g), shelling out-turn (%), oil content (%), biological yield per plant (g) and harvest index (%).

RESULTS AND DISCUSSION

In the present study, D² statistic estimated on 60 genotypes of groundnut for 14 characters. On the basis of D² values, 7 clusters were formed from 60 genotypes. The cluster I contained 54 genotypes from different origins (Table 1). On the other hand, the clusters II to VII 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. The present findings are in conformity with those reported earlier in groundnut by Siddiquey *et al.* (2006), Odedra *et al.* (2008), Korat *et al.* (2009) 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.

The maximum inter-cluster distance varied from 6.46 (clusters VI and V) to 12.14 (clusters VI and VII), which indicates considerable diversity among the genotypes evaluated (Table 3). The lowest intra-cluster distance were in cluster II, III, IV, V, VI, VII (D=0), because they contains only one genotype, whereas the highest intra-cluster distance was in cluster I (D=5.62). In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, 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 country or origin were grouped into different clusters indicating that the geographic distribution was not the sole criterion of genetic diversity (Table 2). The results obtained in the present study are in accordance to the findings of Korat *et al.* (2009), who also reported that there was no parallelism between geographic distribution and genetic diversity. The earlier findings of Murty and Arunachalam (1966) also stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. Further, the free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality.

The maximum inter-cluster distance (D=12.14) was observed between clusters VI and VII (D=12.14) followed by clusters IV and VI (D=11.99), V and VI (D=11.62), V and VII (D=10.75) and IV and V (D=10.62) (Table 3). The closest proximity was observed between clusters VI and V (D=6.46). The genotypes

belonging to different clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster VII (TG-26), VI (JB-D-29), V (JB-500), IV (ICGS-44), III (KISHAN), II (JB-564) could be selected as parents in hybridization programme using appropriate mating design.

High coefficient of variation was recorded for number of mature pods per plant (17.36%) followed by kernel yield per plant (16.94%), pod yield per plant (16.46%), plant height (14.74%), harvest index (14.23%), number of secondary branches per plant (14.02%), number of pods per plant (13.33%), shelling out-turn (13.19%), 100 kernel weight (12.17%) and oil content (10.16%) while it was low for biological yield per plant (3.48%) followed by days to maturity (4.85%), days to 50 per cent flowering (5.67%) and sound mature kernels (5.92%) (Table 4). In the present study, the cluster III was the best for days to maturity, 100 kernel weight, pod yield per plant and harvest index. The cluster V was best for number of secondary branches per plant, shelling out-turn and oil content. The cluster VI was best value for pod yield per plant, number of mature pods per plant and kernel yield per plant. The cluster II was best for days to 50 per cent flowering and sound mature kernels. The cluster VII possessed desirable values for plant height, because it showed the longer plant height. Therefore, intercrossing of genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rational improvement for increasing the pod yield in groundnut.

The analysis of percent contribution of various characters towards the expression of total genetic divergence indicated that biological yield per plant (24.52) followed by number of pods per plant (21.24), oil content (12.43) and sound mature kernels (10.45) contributed maximum towards divergence in the

present study (Table 4). 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 resulted from high yielding parents with a high genetic diversity.

CONCLUSION

Therefore, in the present investigation based on high yielding genotypes and large inter-cluster distances, it was concluded that the genotypes from cluster VII (TG-26), VI (JB-D-29), V (JB-500), IV (ICGS-44), III (KISHAN) and II (JB-564) could be selected as parents in hybridization programme.

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Table 1: Grouping of 60 genotypes of groundnut in various clusters on the basis of $\sqrt{D^2}$ –statistic

Cluster	No. of Genotypes	Name of the Genotypes	Source
I	54	Girnar 1,GG-5,GG-7, GJG- 9, J-17, J-27, J-42 ,J-48, J-54, JB-325, JB-452, JB-634, JB-668, JB-671, JB-D-31, JB-D-35, JB-D-37, JB-E-414, JB-E-550, JB-E-554,JB-F-DR 4, JB-F-DR 34, JB-F-DR 35, JB-F-DR 49, JB-F-DR 51, JB-F-DR 59,JB-F-SD 383, JB-F-SD 404, JB-HOC 4, JB-HOC 8,JB-T5-456,Gc-400	Gujarat
		TG-3, TG-22, TG-23	Maharashtra
		Dh-20, Dh- 19, Dh-24, Dh-55,KRG 1	Karnataka
		JAWAN	Orissa
		Vemana,ICGS-10, ICGS-25, ICGS-76	Andhra Pradesh
		Gangapuri	Madhya pradesh
		Co-2	Tamil Nadu
		Ec-1697, Ec-21134, Ec-21154	Argentina
		USA 86, PI 337394, NcAc 761, NcAc 995	U.S.A
II	1	JB-564	Gujarat
III	1	Kishan	Orissa
IV	1	ICGS-44	Andhra Pradesh
V	1	JB-500	Gujarat
VI	1	JB-D-29	Gujarat
VII	1	TG-26	Maharashtra

Table 2: Source and clustering pattern of 60 genotypes of groundnut

Source	Clusters							Total Number of Genotypes
	I	II	III	IV	V	VI	VII	
Gujarat	32	1	-	-	1	1	-	35
Maharashtra	3	-	-	-	-	-	1	4
Madhya Pradesh	1	-	-	-	-	-	-	1
Karnataka	5	-	-	-	-	-	-	5
Tamil Nadu	1	-	-	-	-	-	-	1
Andhra Pradesh	4	-	-	1	-	-	-	5
Orissa	1	-	1	-	-	-	-	2
United States of	4	-	-	-	-	-	-	1
Argentina	3	-	-	-	-	-	-	3
Total	54	1	1	1	1	1	1	60

Table 3: Average inter and intra-cluster distance ($D = \sqrt{D^2}$) values for 60 genotypes of Groundnut

Cluster	I	II	III	IV	V	VI	VII
I	5.62	7.06	7.40	8.15	7.59	8.24	10.24
II		0.00	8.14	8.80	9.19	8.37	9.61
III			0.00	10.10	10.62	10.22	10.47
IV				0.00	6.46	11.99	6.81
V					0.00	11.62	10.75
VI						0.00	12.14
VII							0.00

Table 4: Cluster means for 14 different characters in groundnut

Cluster	Days to 50 Per Cent Flowering	Days to Maturity	Plant Height (cm)	No. of Secondary Branches /Plant	No. of Pods/ Plant	Mature Pods/ Plant	Sound Mature Kernels (%)	100- Kernel Weight (g)	Kernel Yield/ Plant (g)	Pod Yield/ Plant (g)	Shelling Out- Turn (%)	Oil Content (%)	Biological Yield/ Plant (g)	Harvest Index (%)
I	27.23	98.68	37.09	3.62	9.72	7.78	83.99	26.48	5.30	10.29	52.54	47.74	29.34	36.97
II	29.67	91.33	38.27	3.60	12.47	9.83	96.03	25.17	5.23	9.83	53.90	42.03	35.77	27.43
III	27.00	105.67	37.37	2.73	10.60	9.80	86.07	32.53	6.23	17.43	54.80	46.97	36.40	49.80
IV	25.67	94.33	42.50	2.87	5.47	4.67	95.77	22.87	4.60	8.17	58.77	46.63	45.43	17.90
V	28.67	94.67	35.13	4.13	6.07	4.87	90.57	22.37	4.17	6.77	72.93	50.50	31.20	20.80
VI	28.33	101.00	35.53	3.80	14.47	10.40	80.47	29.47	9.73	11.03	51.87	46.47	23.10	48.00
VII	28.67	92.00	45.37	2.93	9.67	9.27	89.80	25.37	5.67	12.03	47.50	47.30	59.77	21.77
Mean	27.31	98.46	37.28	3.59	9.72	7.94	84.56	26.45	5.35	10.35	52.64	43.89	47.63	30.26
SEm±	0.89	2.75	3.17	0.29	0.74	0.79	2.89	1.85	0.52	0.98	4.00	2.57	0.95	2.48
C.V%	5.67	4.85	14.74	14.02	13.33	17.36	5.92	12.17	16.94	16.46	13.19	10.16	3.48	14.23
Percentage contribution of characters towards total divergence														
No. of Times Appearing First	38	33	8	104	376	19	185	100	106	76	28	220	434	43
% Contribution	2.15	1.86	0.45	5.88	21.24	1.07	10.45	5.65	5.99	4.29	1.58	12.43	24.52	2.43

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