Bangladesh J. Pl. Breed. Genet., 23(1): 45-49, 2010

GENETIC DIVERGENCE IN GROUNDNUT (*Arachis hypogaea* L)

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ABSTRACT

Comprising 34 groundnut genotypes an experiment was conducted in a randomized block design with three replication at the Research farm of Regional Agricultural Research Station, BARI, Hathazari, Chittagong during Rabi season (December 2009 to April 2010) for estimation of the multivariate analysis of divergence. The genotypes were grouped into five clusters. Cluster III contained the highest number of genotypes (12) and the cluster II contained the lowest (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 grouped. The highest intra cluster distance was observed in cluster V and the lowest in II. The highest inter cluster distance was observed between the cluster IV and III followed by V and III and the lowest between cluster V and I. Days to 50% flowering, days to maturity, number of branches per plant, number of matured nuts per plant and karnel size were the most important contributors based on the latent vector. But the highest cluster means for matured nuts per plant, 100 karnel weight, 100 nuts weight and yield per plant were obtained from the cluster II. With moderate yield but early maturity varieties were found in cluster IV. Therefore, more emphasis should be given on cluster VI for selecting genotypes as parents for crossing with the genotypes of cluster II and III for getting new recombinants with early maturity and higher yield.

Key Words: Genetic divergence, cluster analysis, D^2 analysis, groundnut (*Arachis hypogaea* L)

INTRODUCTION

Groundnut *(Arachis hypogaea L.)* is an important food, feed and oilseed crop. It is grown in nearly 100 countries of the world. Major groundnut producer countries in the world are China, India, Nigeria, USA, Indonesia and Sudan. The annual production of groundnut in our country is 46533 thousand metric tons from 77336 thousand acres of land during 2008-09 (BBS, 2010). Groundnut is mainly used as a bakery food in our country. But it can be used as a multipurpose crop which also reduces the edible oil food, fodder shortage and leguminous crop for improvement of soil health. Groundnut oil contains 46 and 32 percent of mono unsaturated fatty acids (MUFA) and poly unsaturated fatty acids (PUFA), respectively. Groundnut oil is also used in many preparations like soap making, fuels, cosmetics, shaving cream, leather dressings, furniture cream and lubricants etc. 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 F_1 and broader spectrum of variability

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 34 genotypes of groundnut.

MATERIALS AND METHODS

An experiment comprising 34 groundnut genotypes was conducted in a randomized block design with three replication at the Research farm of Regional Agricultural Research Station, BARI, Hathazari, Chittagong during Rabi season (December 2009 to April 2010). The unit plot size was 9.6 square meter (6 rows with 4 meter length). The row to row and plant to plant spacing were maintained at 40 cm and 10 cm respectively. Recommended fertilizer doses, cultural practices and all plant protection measures were followed to ensure a good crop. The data on 10 morphological characters namely days to 50% flowering, days to pod maturity, plant height (cm), number of branches per plant, number of matured nuts per plant, number of immature nuts per plant, 100 nuts weight (g), 100 karnel weight (g), shelling percentage, and seed yield per plant (g) were recorded. 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 eight characters under study, which revealed the presence of considerable variability among the genotypes. The thirty two genotypes were grouped into five 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 (12) were comprised into cluster III followed by 10 in cluster I. The minimum genotypes (2) comprised into cluster II. The cluster IV and V comprised the BARIchinabadam-8 and Dhaka-1, respectively with the different origin ICRISAT materials which indicated that genotypes of quite different pedigree may fall into the same cluster, due to unidirectional selection pressure that could yield the genotypes, which were genetically closer than their parents. Like wise, it is also true that selection produce genetically diverse genotypes of same pedigree. The genotypes of the common eco-geographic origin or same location included into different clusters without forming a single cluster indicated that geographic diversity was not related to genetic diversity. The similar results were found by Islam e*t al.* (2005).

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.

Table 1. Distribution of groundnut genotypes in different clusters

Cluster no.	No. of Genotypes	No. of population	Groundnut varieties with origin
I	2, 4, 5, 6, 7, 8, 9, 10, 24, 32	10	JX-87015-SL-1(ICRISAT, India), ICGV-99195(ICRISAT, India), Chico(ICRISAT, India), ICGV-94105(ICRISAT, India), ICGV-93416(ICRISAT, India), ICGV-911228(ICRISAT, India), ICGV-86124(ICRISAT, India), ICGV-00298(ICRISAT, India), ICGV-91114-G32(ICRISAT, India), ICGV-96333(ICRISAT, India),
II	1, 3	2	ICGV-97250(VR) (ICRISAT, India), ICGV-90227(ICRISAT, India), ICGV-96215(ICRISAT, India), ICGV-96224(ICRISAT, India), ICGV-95148(ICRISAT, India), ICGV-97119(ICRISAT, India), ICGV-96225(ICRISAT, India), ICGV-96217(ICRISAT, India),
III	11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22	12	ICGV-93416(ICRISAT, India), ICGV-97118(ICRISAT, India), ICGV-95146, ICGV-97115(ICRISAT, India), ICGV-97116(ICRISAT, India), ICGV-95145(ICRISAT, India),
IV	27, 28, 30, 31, 34	5	ICGV-95058(ICRISAT, India), ICGV-9563(ICRISAT, India), ICGV-95070 (ICRISAT, India), ICGV-95090(ICRISAT, India), BARIchinabadam-8 (BARI, Bangladesh)
V	23, 25, 26, 29, 33	5	ICGV-9316-G6(ICRISAT, India), ICGV-88474-G82(ICRISAT, India), ICGV-3479-G37(ICRISAT, India), ICGV-95066, (ICRISAT, India), ICGV-95066(ICRISAT, India), Dhaka-1(BARI, Bangladesh)

Table 2. Intra (Bold) and inter cluster distances (D^2) for 34 groundnut genotypes

Cluster	I	II	III	IV	V
I	**0.028**	6.99	10.73	5.45	4.29
II		**0.000**	6.37	10.19	10.18
III			**0.018**	14.60	13.71
IV				**0.114**	4.65
V					**0.192**

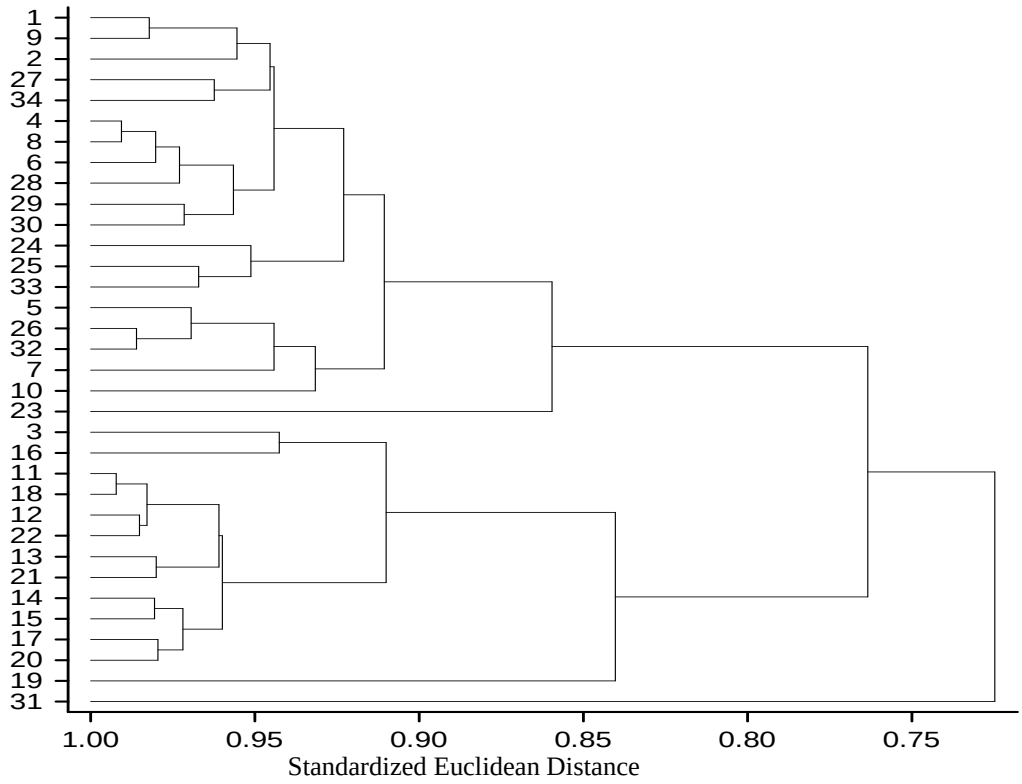

Fig 1. Dendrogram of 34 genotypes of Groundnut (*Arachis hypogaea* L)

Table 3. Cluster mean values of 10 different characters of 34 groundnut genotypes

Characters	I	II	III	IV	V
Days to 50% flowering	36.97	38.33	39.06	37.40	36.87
Days to maturity	168.73	168.83	165.81	165.80	167.13
Plant height	27.65	27.17	24.82	29.36	27.95
No. branches/plant	6.75	7.23	10.81	7.68	5.77
No. mature nuts/plant	20.35	22.10	21.45	18.67	14.12
No. immature nuts/plant	6.99	8.10	8.84	6.40	5.71
100 nuts weight	90.22	108.76	84.18	103.74	74.90
100 karnel wt.	45.94	61.26	50.36	56.91	41.02
Shelling percentage	50.92	56.33	59.82	54.86	54.77
Yield/Plant	10.69	18.30	12.90	12.77	6.39

The maximum inter-cluster distance of 14.60 existed between cluster IV and III followed by 13.71 between cluster V and III and 10.73 between cluster III and I suggesting wide diversity between them and the genotypes in these cluster could be used as parents in hybridization programme for getting transgressive segregates. A two dimension scatter diagram was constructed using component I as "X" axis and component II "Y" axis, reflection the relative position (Fig 1). As per scatter diagram, the genotypes were apparently distributed into five clusters; it was also revealed that the genotypes of cluster IV were more diverse from the genotypes of cluster III and II. The graphical scenario also confirmed the result presented in the Table 1 and Table 2. The lowest inter-cluster distance of 4.29 existed between cluster V and I followed by 4.65 between cluster V and IV indicating a close relationship between the same grouped. The highest intra-cluster distance was observed in cluster V (0.192) and the lowest (0.000) in cluster II (Table 2). Katule *et al*. (1991) worked with groundnut and found the inter and intra cluster values D ranged from 9.50 to 22.20 and 5.18 to 8.45 respectively. On the basis of Euclidean distances dendrogram was formatted (Fig 2.). Different genotypes were grouped into five clusters. Among the clusters it was observed that the genotypes 23(ICGV-9316-G6), 3(ICGV-90227), 16(ICGV-96217), 19(ICGV-95146) and 31(ICGV-95090) were widely separated which might be chosen in hybridization programme for getting the most variability.

Table 4. Relative contributions of the nine characters of 34 groundnuts genotypes to the total divergence

Characters	**Vector-I**	**Vector-II**
Days to flowering	0.03827	0.11685
Days to maturity	0.00889	0.16284
Plant height (cm)	-0.04949	-0.01227
No. of branches/plant	0.19058	-0.02973
No. mature nuts/plant	-0.05279	0.03556
No. immature pods/plant	-0.00244	-0.41554
100 nuts weight (g)	-0.01854	-0.02578
100 karnel weight (g)	0.03046	-0.13696
Yield/Plant (g)	-0.04911	-0.13820

The mean values of cluster II ranked first for maximum nuts per plant (22.10), 100 nuts weight (108.96g) 100 karnel weight (61.26g) and yield per plant (18.30g) and medium plant height (27.17 cm) (Table 3). The mean values of cluster IV ranked top for plant height (29.26 g), branches per plant (7.68), 100 nuts weight (103.74g) and seed yield per plant (12.77g) with early days to maturity (165.80 days). The genotypes from

cluster III contained the shortest plant (24.82 cm) along with earliness in days to maturity (165.81 days) and maximum number of primary branches per plant (10.81) with medium yield per plant (12.90g) (Table 4). Therefore, the genotypes from cluster II, III and IV could be utilized in the hybridization programme for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration.

Contributions of the characters towards divergence are presented in Table 4. The canonical analysis revealed that values in both vectors (Vector I and II) for days to flowering and days to maturity were positive, values in one vectors for branches per plant, mature nuts per plant and 100 karnel weight was positive. Such results indicated that these characters contributed maximum towards total divergence of the genotypes and it was also suggested that attention should be given for these five characters for yield improvement of groundnut. Similar finding was recorded by Reddy and Reddy (1993). Hossain *et al.,* (2003) also recorded the similar results in groundnut where the harvest index contributed maximum towards the total divergence of the genotypes.

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