RESEARCH PAPER

Genetic variability and divergence studies in groundnut (*Arachis hypogea* Linn.)

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Abstract : Sixty genotypes of groundnut (*Arachis hypogea* L.) were evaluated for the genetic variability and genetic diversity The magnitude of genetic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability and genetic advance as percentage of mean were recorded high for various characters like pod yield per plant, hundred seed mass, harvest index, plant height and shelling per cent. High broad sense heritability estimates were recorded for most of traits *viz.,* hundred seed mass, days to maturity, shelling per cent, pod yield per plant, harvest index, protein per cent indicating that these traits were less influenced by the environment. D^2 analysis indicated existence of wider genetic variability in the population of sixty genotypes which were grouped in twelve clusters, based on their inter clusters distance. The maximum inter-cluster distance (D = 7.044) was found between cluster III and X carrying one and two genotypes from each cluster, respectively followed by that between V and X (D = 6.447) and cluster III and XII (D = 5.943). The minimum inter cluster distance was observed between cluster VII and XI (D = 2.770). The intra-cluster distance (D) ranged from 1.909 to 2.863, the maximum being in cluster V (2.863). The minimum intra-cluster distance (D) was found in cluster II (1.909) which includes eight genotypes. Cluster III showed high genetic divergence with cluster X followed by cluster V.

Key Words : Groundnut, Heritability, Genetic divergence, Variability

INTRODUCTION

Although, India ranks first in area and production of groundnut in the world its average yield is low (1t/ha) in *Kharif* and (2t/ha) in *Rabi* season (Anonymous, 2010). Groundnut is quick growing; short duration, photo-insensitive and nature enable the plant breeder to raise two crops in a year. Exploitation of the genetic variability in the available germplasm is a prerequisite in the breeding programme for increasing yield and improving quality. Phenotypic diversity is usually considered as an indication of underlying genetic differences. Among all methods, Mahalanobis D^2 statistics is an efficient tool for estimating genetic diversity. Mahalanobis generalized distance technique considers the variation

produced by any characters and the consequent effect that it bears on the other characters. Hence, there is a need to study genetic divergence among various cultivars in order to evaluate their usefulness as progenitors in hybridization programme. In the present study, sixty genotypes of groundnut were evaluated for comparing nature and extent of genetic diversity. The importance of this multivariate analysis has been greatly emphasized for assessment of genetic diversity in biological population (Fisher, 1936).

MATERIAL AND METHODS

The present investigation was conducted at Centre for Crop Improvement S.D. Agricultural University,

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Sardarkrushinagar during summer season of 2010-11.Evaluated sixty groundnut genotypes provided by the Centre for Crop Improvement S.D. Agricultural University in a Randomized Block Design with three replications under irrigated condition. Each entry was accommodated in a single row of 3.0 m length with a spacing of 45×15 cm.

Normal recommended cultural practices and plant protection measures were followed.Five competitive plants were randomly selected for recording biometrical measurements on fourteen traits, *viz.,* pod yield per plant, days to 50 per cent flowering, days to maturity, number of branches, plant height, number of kernels per pod, 100 seed weight, harvest index, shelling per cent, oil, protein, total carbohydrate, reducing sugar and sucrose.

The data were subjected to multivariate analysis (Rao, 1952). The original mean values were transformed to normalized variables and all possible D^2 values were calculated. For determining clusters, the criterion suggested by Rao (1952) was followed. After establishing the clusters, the inter-cluster distances were worked out by taking the average of the component genotypes in that cluster. The average of inter-cluster distance was computed taking into consideration all the component D^2 values among the members of the two clusters considered. The square root of D^2 values gave the genetic distance (D) between clusters.

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences between accessions for all the characters. The means, phenotypic and genotypic co-efficients of variation and heritability estimates are presented in Table 1. The highest genotypic co-efficient of variation (GCV) corresponded to pod yield/plant, whereas the lowest one was for oil per cent. The heritability estimates were high for all the characters except for total carbohydrate, reducing sugar and sucrose per cent. The differences between the phenotypic and genotypic co-efficients of variation were low, indicating the little environmental effect on these characters.

The analysis of variance revealed significant differences between the 60 genotypes for all the fourteen characters studied. The aggregate effects of all the fourteen characters were tested by the Wilk's criterion, indicating significant differences between the genotypes. Hence, the analysis of genetic divergence based on D^2 values was considered relevant. The constituents of different clusters with their source are presented in Table 2. Based on D^2 analysis, 60 genotypes were grouped into 12 clusters.

Grouping of the genotypes was carried out by following the Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from groups belonging to different clusters. In all, twelve clusters were formed from 60 genotypes. The composition of clusters is given in Table 2 and clustering pattern is shown in Table 3. The cluster III was the smallest having one genotype ICRISAT-Hyderabad. Cluster II, V, VI, XI contained eight genotypes of ICRISAT-Hyderabad and cluster V also contained two genotypes from Junagadh with cluster VI also contained one genotype from USA. The cluster I and VII had six genotypes of ICRISAT- Hyderabad. The cluster IX and XII had three genotypes. The cluster VIII had five genotypes from ICRISAT-Hyderabad where as cluster IV and X had two genotypes from ICRISAT-Hyderabad. Thus the observed clustering pattern of genotypes was

Sr. No.	Source	GCV	PCV	Heritability (%)	GA	GA (%)
1.	Days to 50% flowering	4.71	5.57	71.60	3.48	8.20
2.	Days to maturity	6.00	6.03	99.20	12.06	12.31
3.	Plant height (cm)	19.15	19.42	97.20	16.79	38.89
4.	Number of branches / plant	11.97	13.53	78.30	1.32	21.81
5.	Number of seeds / pod	9.82	11.28	75.80	0.40	17.69
6.	Pod yield / plant (g)	39.04	39.98	95.30	13.64	78.52
7.	Hundred seed mass (g)	33.23	33.30	99.60	37.91	68.31
8.	Shelling (%)	14.16	14.32	97.80	17.47	28.84
9.	Harvest index (%)	25.96	27.04	92.20	8.61	51.40
10.	Oil (%)	2.52	3.13	64.60	1.96	4.17
11.	Protein(%)	4.55	4.75	91.60	2.98	8.96
12.	Total carbohydrate (%)	3.11	7.38	25.30	0.44	3.83
13.	Reducing sugar (%)	3.95	11.60	11.60	0.06	2.92
14.	Sucrose (%)	4.86	9.34	27.10	0.49	5.21

Table 1: The estimates of genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (%), expected genetic advance and expected genetic advance as percentage of mean for various characters in groundnut

Table 2 : Composition of cluster based on D^2 values of sixty genotypes of groundnut

Cluster	No. of genotypes	Name of genotypes	Origin/Source
I	6	ICGV-93289, ICGV-95440, ICGV-95446, ICGV-95469,ICGV-95492, ICGV-02286	ICRISAT- Hyderabad
II	8	ICGV-02271, ICGV-03157, ICGV-03184, ICGV-01379, ICGV-01433, ICGV-02234, ICGV- 02242, ICGV-01258	ICRISAT- Hyderabad
III	1	ICGV- 97281	ICRISAT- Hyderabad
IV	2	ICGV-02313, ICGV-02240	ICRISAT- Hyderabad
V	8	ICGV-97328, ICGV-01005, ICGV-01015, ICGV-01043, ICGV-1080, ICGV-01105,GG2 , J-11	ICRISAT-Hyderabad Junagadh,Gujarat
VI	8	ICGV-02144, ICGV-03178, ICGV-03179, ICGV-03181, ICGV-01376, ICGV-01395, ICGV-03137, CHICO	ICRISAT- Hyderabad USA.
VII	6	ICGV- 01014, ICGV- 03056, ICGV- 03057, ICGV- 02022, ICGV- 03169, ICGV- 02229	ICRISAT- Hyderabad
VIII	5	ICGV- 01432, ICGV- 01434, ICGV- 01447, ICGV- 02227,ICGV- 03166	ICRISAT- Hyderabad
IX	3	ICGV- 03194, ICGV-03196,ICGV- 03206	ICRISAT- Hyderabad
X	2	ICGV-00371, ICGV- 03207	ICRISAT- Hyderabad
XI	8	ICGV- 01124, ICGV- 99240,ICGV- 99241, ICGV- 99247,ICGV- 99249, ICGV- 00346,ICGV- 00362, ICGV- 00360,	ICRISAT- Hyderabad
XII	3	ICGV- 03187, ICGV- 01369,ICGV- 01393	ICRISAT-Hyderabad

Table 3: Source and clustering pattern of sixty genotypes of groundnut

Cluster	Gujarat Junagadh	Hyderabad ICRISAT	USA	Total
I	0	6	0	6
II	0	8	0	8
III	0	1	0	1
IV	0	2	0	2
V	2	6	0	8
VI	0	7	1	8
VII	0	6	0	6
VIII	0	5	0	5
IX	0	3	0	3
X	0	2	0	2
XI	0	8	0	8
XII	0	3	0	3
Total	2	57	1	60

Table 4: Average inter and intra-cluster distance (D = $\sqrt{D}$) values in groundnut

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	2.559	5.096	3.823	4.829	3.427	5.071	4.447	5.404	4.856	6.152	3.957	5.778
II		1.909	4.873	3.842	4.971	2.484	4.028	2.957	4.168	3.691	3.423	3.667
III			0.000	5.010	4.089	5.624	5.409	5.772	5.907	7.044	4.395	5.943
IV				2.390	5.766	4.574	4.863	4.131	5.228	4.930	3.852	5.407
V					2.863	4.617	3.736	5.099	4.691	6.447	4.117	5.968
VI						2.282	3.155	2.851	3.798	3.663	3.103	3.463
VII							2.089	3.412	4.649	4.920	2.770	4.160
VIII								1.984	5.331	4.759	3.505	5.016
IX									1.926	4.378	4.475	5.631
X										2.275	4.537	3.860
XI											2.016	4.011
XII												2.148

Bold values denote inter cluster distances

S.R. YADAV, **A.H. RATHOD**, A.S. SHINDE, S.S. PATADE, C.N. PATIL **and** P.O. VAGHELA

independent of their origin.

The maximum inter-cluster distance (D = 7.044) was found between cluster III and X carrying one and two genotypes from each cluster, respectively followed by that between V and X (D = 6.447) and cluster III and XII (D= 5.943) (Table 4). The minimum inter cluster distance was observed between cluster VII and XI (D = 2.770). The intra-cluster distance (D ranged from 1.909 to 2.863), the maximum being in cluster V (2.863). The minimum intra-cluster distance (D) was found in cluster II (1.909) which includes eight genotypes. The cluster I had the highest mean values for number of seeds per pod (2.75). The cluster II was better for shelling per cent (68.41). The cluster III got desirable rating in respect of 100-seed weight (102.33) whereas, sucrose per cent (10.17) was higher in cluster IV. The cluster V has highest mean values for pod yield per plant (24.77) and higher oil per cent (47.49) for cluster VI. Protein per cent (34.86) was found to be highest in cluster VII where as in cluster VIII days to 50% flowering (45.27) was desirable. Number of branches per plant (6.98) has better value for cluster XI. Total carbohydrate (12.71) was found to be superior in cluster X and plant height (51.97) for cluster XI. The cluster XII had highest mean values for harvest index (27.35). Murty and Arunachalam (1966) have stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. The absence of parallelism between geographic distribution and genetic diversity in the present study is in accordance to the findings of Nadaf *et al.* (1986), Golakia and Makne (1992), Yadav *et al.* (1991), Kutule *et al.* (1992) and Reddy and Reddy (1993) in groundnut.

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