Legume Res., **33** (2) : 124 - 127, 2010

AGRICULTURAL RESEARCH COMMUNICATION CENTRE
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GENETIC DIVERGENCE OF NEW GERMPLASM AND ADVANCED BREEDING LINES OF GROUNDNUT (*ARACHIS HYPOGAEA* L.) STUDIED UNDER LATE *KHARIF* SITUATION

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ABSTRACT

Analysis of genetic divergence of sixty four genotypes (39 new germplasm accessions and 25 advanced breeding lines) of groundnut revealed wide range of D^2 values ranging between 4.52 and 27.75 suggesting the presence of considerable amount of genetic diversity in the genotypes studied, which were grouped in to seven clusters where, cluster VII (28) was the largest followed by cluster I (24) and cluster VI (4). Maximum inter cluster distance was recorded between IV and VI representing wide divergence among these clusters. On the basis of inter-cluster distance and cluster means the genotypes viz., ICGV-05033, ICGV-05052, PAFRGVT-58, GG-20×ICGV-91114, ICGX-020063-F_2-B_1-SSD-P20-B_1, ICGX-020055-F_2-SSD-P37-B_1 were widely diverse therefore may be considered for future breeding programmes.

Key words: Genetic divergence, Cluster.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is the premier oilseed crop of India. In Southern Karnataka, groundnut occupies nearly 4.0 lac hectares, where the late onset of monsoon rains is the limiting factor responsible for low productivity (697 kg/ha). The presently cultivated varieties in this region (TMV-2, JL-24) are low yielding and not suitable for late *kharif* (July-Aug) sowings. Hence, there is a need for introduction of newer genetic material in the future breeding programmes to evolve high yielding varieties suitable for late *kharif* situations in Southern Karnataka.

A broad spectrum of variability in segregating generations can be generated by crossing genetically diverse parents. Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations of yield in desirable transgressive segregants in advanced generations. For this, precise information about the extent of genetic divergence is very crucial. Genetic diversity between population or genotypes indicates the difference in gene frequencies and any measure of genetic divergence must reflect these differences. Phenotypic diversity is usually considered as an indication of underlying genetic differences. To assess the diversity in the population of diverse origin, usually two important methods *viz.*, Mahalanobis D^2 and Canonical analysis were employed. Mahalanobis generalized distance technique considers the variation produced by any character and the consequent effect that it bears on the other characters. Hence, in the present study, 64 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 and Smith, 1936).

MATERIAL AND METHODS

The material for the present investigation comprised of 64 genotypes (39 new germplasm accessions and 25 advanced breeding lines) of groundnut grown in 8×8 simple lattice design with two replications as per Cochran and Cox (1957) during *kharif* 2006 (August) in the field unit of All India Coordinated Research Project (AICRP) on Groundnut, Agricultural Research Station,

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Chintamani, representing Southern Karnataka. Each replication consisted of eight sub-blocks with eight genotypes in each sub block. Entries and sub blocks were randomized. Each genotype was grown in one row of two meter length. A spacing of 45 cm between row and 15 cm between plants with a population of twenty plants per row was maintained. Observations were recorded on ten randomly selected plants in each genotype within the replication for fourteen characters, *viz.*, plant height, branches per plant, days to 50% flowering, days to maturity, matured pods per plant, pod yield per plant, kernel yield per plant, shelling percentage, 100-kernel weight, sound mature kernel per cent, harvest index, oil content, oil yield per plant and specific leaf area. Multivariate analysis was done as per Mahalanobis D^2 statistic (1936) and as described by Rao (1952) and genotypes were grouped in to different clusters following Tocher's method described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters studied. The per cent contribution of fourteen quantitative characters towards genetic divergence was presented in the Table 1. It has shown that no single character alone had greater contribution to total divergence. Nevertheless, relatively maximum contribution was by specific leaf area (27.67%) followed by kernel yield per plant (21.72%) and Oil content (15.32%). Contribution to the total divergence was least by pod yield per plant (1.09%). In accordance with the results Vijay sekhar *et al*. (2005) reported little contribution of pod yield per plant towards genetic divergence.

Based on magnitude of D^2 values, 64 genotypes were grouped into seven clusters (Table 2). Cluster VII was the largest with maximum number of genotypes (28) followed by cluster I (24). Cluster II, III, IV and V comprised two genotypes each and cluster VI constituted four genotypes. The estimates of intra and inter cluster distances represented by D^2 values have been given in Table 3. D^2 values between all possible pairs of 64 genotypes ranged between 4.52 and 27.75, which showed the presence of considerable amount of diversity in the material under study. The maximum intra cluster distance was recorded for cluster VI (19.14) followed by cluster VII (17.91) and cluster I (15.49) revealing substantial diversity within the cluster. However the lowest intra cluster distance was observed in cluster II indicating that the strains of this cluster resemble one another genetically and appeared to have evolved from common gene pool. Maximum inter cluster values were observed between IV and VI (27.75) which indicated the maximum divergence between the genotypes included in these clusters suggesting formation of desirable recombinants by way of intermating between the genotypes from these clusters.

The mean values of each cluster for all the fourteen characters are given in Table 4. It could be seen that clusters differ with respect to mean expression of various characters and this reflects that the clusters formed are very distinct. The genotypes included under cluster VII showed high mean values for the characters pod yield per plant, shelling percentage, kernel yield per plant, oil content and oil yield per plant while clusters IV showed lower values for

Table 1: Contribution of various characters towards total divergence

S. No.	Character	Contribution (%)
1	Plant height (cm)	7.83
2	Branches/plant	1.24
3	Days to 50% Flowering	4.66
4	Days to maturity	3.67
5	Matured pods/plant (g)	2.28
6	Pod yield/plant (g)	1.09
7	Kernel yield/plant (g)	21.72
8	Shelling percentage	2.03
9	100 kernel weight (g)	1.73
10	Sound mature kernel (%)	1.98
11	Harvest index (%)	4.41
12	Oil content (%)	15.32
13	Oil yield/plant (g)	4.31
14	Specific leaf area (cm^2/g)	27.67
	Total	100

Table 2: Distribution of 64 Groundnut genotypes into different clusters

Cluster No.	Number of genotypes	Accession Number/name
I	24	ICGV 88145, ICGV 89104, ICGV 1337, ICGV 89322, ICGV 00350, ICGV 01354, ICGV 87846, ICGV 02322, ICGV 99210, ICGV 05089, ICGV 05090, ICGV 05094, ICGV 05099, ICGV 05100, ICGV 05103, ICGV 04071, ICGV 02409, ICGV 04096, ICGV 02099, ICGV 02063, ICGV 05049, ICGV 03042, ICGX-020063-F2-B1-SSD-P18-B1, ICGX-020063-F2B1-SSD-P13-B1
II	2	ICGX-040038-F2-SSD, TKG19A X K3
III	2	ICGX-020063-F2-B1-SSD-P20-B1,ICGX-020055-F2-SSD-SSD-P37 B1
IV	2	JL-24, VRI-2
V	2	TAG-24 X ICGS-76, PBS 11039 X NRCG 4839
VI	4	ICGV 05033, ICGV 05052, PAFRGVT-58, GG-20 X ICGV 91114
VII	28	ICGV 03037, ICGV 03016, ICGV 03010, ICGV 03157, PAFRGVT 60, ICGX-020063-F2-B1-SSD-P12-B1, ICGX-020063-F2-B1-SSD-P11-B1, ICGX-020063-F2-B1-SSD-P18-B1, ICGX-020063-F2-B1-SSD-P16-B1,ICGX-030043-F2-SSD-SSD-P2, ICGV 86301 X TAG 24, ICGX-020063-F2-B1-SSD-P18-B2, ICGX-020063-F2-B1-SSD-P15-B1, ICGX-020058-F2-SSD-SSD-P7-B1, CO-3 X JAL-31, PBS111039 X TAG-24, ICGV 86031 X TAG-24 XCSMG 84-1, ICGX-020063-F2-B1-SSD-P19-B1, JAL-18 X ALR-2, GG-2 XICGV 91114, JAL-31 X CO-3, ICGV-92267, ICGV-86031, TMV-2, Narayani, ICGV-91114, CTMG-1, GPBD-4.

Table 3: Average Intra and Inter cluster distances among seven clusters formed by 64 genotypes of groundnut

Cluster	I	II	III	IV	V	VI	VII
I	15.49	16.65	13.81	18.01	15.15	20.86	17.02
II		4.52	10.97	23.19	7.97	16.42	17.00
III			5.56	20.45	10.42	16.09	14.46
IV				5.60	22.53	27.75	19.82
V					5.84	17.51	17.10
VI						19.14	21.11
VII							17.91

Table 4 : Mean values of seven clusters of groundnut for 14 quantitative characters

Cluster No.	Plant height	Branches /plant	Days to 50% flowering	Days to maturity	Matured pods /plant	Pod yield / plant	Kernel yield /plant	Shelling (%)	100-kernel weight	Sound mature kernel (%)	Harvest index	Oil content (%)	Oil yield /plant	Specific leaf area
I	26.49	7.38	37.67	112.90	16.90	15.10	10.45	69.39	26.99	68.13	33.89	44.34	4.66	113.45
II	25.63	5.85	38.50	116.75	13.75	13.25	10.65	80.37	35.43	75.50	39.09	45.75	4.87	115.45
III	26.10	8.75	39.75	106.50	16.50	14.63	11.10	75.91	25.73	66.25	31.30	45.70	5.08	116.40
IV	21.50	4.20	36.25	108.25	14.25	12.63	7.85	62.31	37.00	75.50	27.88	42.58	3.35	160.20
V	22.45	7.50	39.75	119.75	12.75	13.00	10.33	79.41	28.03	68.50	34.73	46.60	4.81	119.65
VI	29.38	8.58	36.88	109.75	17.25	17.23	13.61	78.90	28.73	70.75	33.08	47.23	6.47	96.99
VII	27.62	7.28	37.34	110.82	16.36	14.90	10.66	72.11	28.81	71.38	30.46	44.73	4.76	126.47

all the above characters. The genotypes from these clusters may be used as parents to recombine these characters. Here, it is worthy to mention that in calculating cluster means, the superiority of a particular genotype in respect of a given character get diluted by other genotypes that are related and grouped in the same cluster which are inferior or intermediary for that character in question. Hence, apart from selecting lines from clusters which have high inter cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence in respect to a character of interest.

The instances of grouping of genotypes of different origin or geographic origin in the same cluster observed. This suggests no relation between genetic and geographic diversity. Such lack of relationship between genetic and geographic diversity may be attributed to genetic drifts and selection in different environments that may cause greater genetic diversity than geographical distance (Arunachalam *et al.*, 1981). Therefore, the

choice of suitable diverse parents selected on the basis of genetic divergence analysis would be more rewarding than the choice made on the basis of geographic diversity. This finding is in agreement with Gan *et al.* (1985), Katule *et al.* (1992), Nayak and Patra (1997) and Venkataravana *et al.* (2000).

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