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Studies on Genetic Diversity in Groundnut (*Arachis hypogaea* L.) Germplasm

Research Article

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Abstract

Genetics divergence using D^2 analysis of 40 genotypes of groundnut (*Arachis hypogaea* L.) of different geographic origins revealed existence of considerable diversity for eleven quantitative and qualitative characters. The significant treatment mean square indicated adequate variability among the genotype for all characters. The genotypes were grouped into 7 clusters. The clusters VI was the largest containing 12 genotypes each followed by cluster V consisted 7 genotypes, cluster I and cluster VII consisted 6 genotypes, cluster III consisted 4 genotypes, cluster II consisted 3 genotypes and cluster IV consisted 2 genotypes. The diversity among the genotypes measured by intra-cluster & inter cluster distance was adequate for improvement of Groundnut by hybridization and selection. The genotype included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better sergeants in Groundnut.

Keywords: Genetics divergence; D2 Analysis; genetic variability, Groundnut and *Arachis hypogaea* L

Introduction

Groundnut has been the main oilseed crop in India and other developing countries for several decades and will continue to be so in the future. Globally, groundnut (*Arachis hypogaea* L.) production and area during 2011-2012 averaged 6.93 million tonnes and 141.1 million hectare [1] and production of oil seeds in India 30012.2 Thousand tones. In developing countries, the proportion for oil is generally higher than 50%. It is estimated that each 1% increase in oil content would raise the processor's benefit by 7%. The oil content in seed of groundnut cultivars for commercial production is generally around 50%, while some germplasm accessions have been found to contain more than 55% oil. In the western world, most of the groundnut goes into food uses where groundnut butter, roasted groundnut and salted groundnut are preferred food for consumers [2]. There is an increasing need for high protein and low oil groundnut as these traits add to the confectionary quality of groundnuts. High oleate to linoleate (O/L) ratio has been associated with prolonged groundnut shelf life and decreased tendency toward rancidity [3]. High oleate groundnut diet lowers total cholesterol and decreases bad low density lipoprotein (LDL) cholesterol, maintains beneficial high density lipoprotein (HDL) cholesterol, and helps to maintain good flavour [4]. Genetics divergence present in a crop plays an important role in improvement of the crop. It is necessary to utilize useful quantitative traits from diverse genetic sources. The D^2 Analysis provides the means for grouping of genotypes in distinct clusters in order to their relative distance (inter & intra cluster) from each other. Such a study is expected to be useful not only in the choice of the parents for hybridization but also to serve as an index effecting selection. Genetic diversity is the first and foremost need for any crop improvement programme. D^2 Analysis is performed to identify the diverse genotypes for hybridization programme. However, genetic

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gain can be expected only if there is adequate genetic diversity in the present breeding population. Therefore, a study of genetic diversity would held in formulating a rational plant improvement programme through selection or for developing hybrids in groundnut. The concept of $D^{2,}$ as a measure of divergence, was first introduced by Mahalanobis [5] as described by Rao [6]. It is based on third multivariate degree statistical analysis and is self-weighing on the basis of genetic variability. D^2 values between any pair of population account to a measure of genetic divergence than the one which fall into different clusters.

Materials and Methods

The experimental material for the present investigation consisted of 40 genotypes of groundnut obtained from the International Crop Research Institute of Sami Arid Tropic, (Patancheru) Hyderabad, A.P. (India). The present experiment was conducted in randomized block design at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad during *kharif,* 2012. In each replication consisted of two rows of each genotypes with a 1.5 meter row length. Row to row and plant to plant distance 40 x 10 cm. All the recommended agronomic cultural practices and plant protection measure were followed as and when required.

The following eleven quantitative data were recorded on five randomly selected plants from each genotype in each replication for characters were Days to 50% flowering, plant height (cm.), Number of primary branches per plant, Days to maturity, Pod yield per plant (gm.), Pod yield (q/ha.), Sound matured kernel, Seed index(gm.), Shelling percentage, Kernel yield(q/ha.), Kernel uniformity(%). Except Days to 50% flowering & days to maturity recorded on the plot basis. Replication wise data for each character were subjected for analysis of variance [7] and then multivariate analysis of D^2 statistic [5,6]. The genotypes were grouped into different cluster following the ward method. The relative contributions of different characters towards genetic divergence were also worked out.

Results and Discussion

The significant treatment mean square indicated adequate variability among the genotype for all character in Table 1. On the basis of magnitude of D^2 value, 40 genetically diverse genotypes were grouped into 7 clusters [Table 2]. The highest numbers of genotypes were presented in cluster VI which contained 12 entries followed by cluster V which contained 7 entries, Cluster I and cluster VII which contained 12 entries (each cluster having 6 entries). The low number of genotypes were present in cluster III, and cluster II which contained 4, 3, entries respectively. The minimum numbers of genotypes present in cluster number IV which contained 2 entries.

Table 1: Analysis of variance for 11 quantitative characters in groundnut germplasm.

S.No.	Characters	Mean sum of squares		
		Replications df=2	Treatments df=39	Error df=78
1.	Days to 50% flowering	3.71	283.16**	98.28
2.	Plant height 20 days	0.27	3094.37**	69
3.	Plant height 40 days	5.49	7101.08**	62.68
4.	Plant height 60 days	3.88	20972.96**	69.67
5.	Primary branches / plant 20 days	0.01	18.18**	15.77
6.	Primary branches / plant 40 days	0.51	21.81**	15.06
7.	Primary branches / plant 60 days	1.02	49.13**	23.22
8.	Days to maturity	2.31	457.86**	75.68
9.	Pod yield per plant	3.12	2646.4**	100.05
10.	Pod yield	0.52	1082.77**	105.98
11.	Shelling kernel weight	37.76	5526.5**	3934.17
12.	Hundred kernel weight	2.18	3754.37**	37.42
13.	Sound matured kernel	9.80	3227.86**	211.53
14.	Kernel yield	0.48	957.57**	86.87
15.	Kernel uniformity	2.11	10355.12**	72.55

** Significant at 1% level of significance, * Significant at 5% level of significance

Table 2: Distribution of the 40 groundnut genotypes into different clusters.

S. No.	Cluster of numbers	Number of genotypes	Genotypes into different cluster
1	I	6	ICG-6813, ICG-6892, ICG-6993, ICG-7153, ICG-8083, ICG-8490
2	II	3	ICG-6913, ICG-7243, ICG-9037
3	III	4	ICG- 8285, ICG- 8517, ICG-9157, Kaushal
4	IV	2	ICG-118, ICG-188
5	V	7	ICG-7000, ICG-7190, ICG-7906, ICG-8106, ICG-8567, ICG-8760, ICG-9418
6	VI	12	ICG-6888, ICG-7181, ICG-7963, ICG-7969, ICG-9249, ICG-9315, ICG-111, ICG-115, ICG-163, ICG-297, ICG-397, ICG-442
7	VII	6	ICG-36, ICG-76, ICG-81, ICG-332, ICG-334, ICG-437

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Table 3: Cluster mean value of 11 different quantitative characters in groundnut germplasm.

Clusters Characters	I	II	III	IV	V	VI	VII
Days to 50% flowering	26.389	26.042	26.250	26.44	26.33	27.667	26.75
Plant height 20 days	9.608	10.368	16.024	14.784	20.833	19.707	22.929
Plant height 40 days	17.259	19.194	30.608	27.998	33.247	35.101	29.918
Plant height 60 days	32.565	37.311	56.793	53.563	59.984	61.817	58.987
Number of Primary branches per plant 20 days	3.653	2.867	3.400	2.467	3.467	3.150	3.450
Number of Primary branches per plant 40 days	5.203	4.563	4.929	4.900	4.667	4.363	4.250
Number of Primary branches per plant 60 days	6.928	5.733	6.267	6.044	5.711	5.404	5.392
Days to maturity	119.00	119.917	120.625	118.667	117.333	118.250	118.250
Pod yield per plant	15.950	14.926	17.392	20.466	29.22	18.136	11.7936
Pod yield	11.515	10.348	12.365	15.625	15.775	9.513	8.179
Shelling kernel weight	67.711	68.101	65.889	64.758	71.217	65.914	60.500
Hundred kernel weight	32.976	29.985	33.174	42.625	31.161	33.178	32.975
Sound matured kernel	69.167	69.917	72.667	62.667	68.667	69.083	66.417
Kernel yield	9.007	8.140	9.891	13.083	13.091	7.279	5.874
Kernel uniformity	68.611	70.958	64.583	71.444	61.44	73.708	54.33

Table 4: Intra (diagonal) and inter cluster average distance for different quantitative characters in groundnut.

Cluster	I	II	III	IV	V	VI	VII
I	**20.703**	27.752	25.431	43.355	45.380	42.577	**47.071**
II		**19.248**	25.040	37.173	44.179	30.114	36.848
III			**12.648**	30.712	25.436	22.764	29.097
IV				**25.353**	33.612	36.458	**50.937**
V					**14.518**	30.439	43.3701
VI						**15.852**	25.541
VII							**19.733**

Table 5: Percent contribution of different quantitative characters to genetic diversity.

S. No.	Source	Time Ranked 1st	Contribution %
1	Days to 50% flowering	0.00	0.00%
2	Plant height 20 days	8	1.03%
3	Plant height 40 days	53	6.79%
4	Plant height 60 days	334	42.82%
5	Number of Primary branches per plant 20 days	0.00	0.00%
6	Number of Primary branches per plant 40 days	0.00	0.00%
7	Number of Primary branches per plant 60 days	0.00	0.00%
8	Days to maturity	1	0.13%
9	Pod yield per plant	36	4.62%
10	Pod yield	3	0.38%
11	Shelling kernel weight	0.00	0.00%
12	Hundred kernel weight	61	7.82%
13	Sound matured kernel	178	2.18%
14	Kernel yield	0.00	0.00%
15	Kernel uniformity	267	34.23%

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On considering cluster mean in respect of these seven clusters Table 3. Highest cluster mean value was recorded in cluster VI for the characters Days to 50% flowering, plant height 40 days & 60 days, kernel uniformity, in cluster V highest cluster mean for number of primary branches per plant at 20 days, pod yield, shelling kernel weight and kernel yield, highest cluster mean value for days to maturity and sound matured kernel in cluster III, highest cluster mean for number of primary branches per plant in cluster I.

The intra and inter cluster value are presented in Table 4. The highest intra-cluster distance was observed in case of cluster IV (25.353), followed by cluster I and cluster VII. The maximum inter cluster distance was found between cluster IV and VII (50.937), followed by cluster I and cluster VII (47.071) and cluster v and VII (43.3701) exhibited very high inter- cluster distance. The corroborative findings were reported by Singh and Dwivedi [8], Dwevedi and panwar [9], Verma et al. [10] and Peshattiwar et al. [11], Singh et al. [8]. Thus, crossing between the genotypes belonging to cluster pair separated by very high inter-cluster distances, as mentioned above, mat through desirable transgressive segregates which indicated that the genotype belonging to these cluster pairs, with very high inter-cluster distances, may produce desirable transgressive segregates and an opportunity for selection better genotypes in succeeding generations. The result revealed that different genotypes from different source and state were included in different clusters, indicating that genetic diversity and geographic diversity are not related. Emphasis may be given in [Table 5] for improving the characters like hundred kernel weight, pod yield per plant, sound matured kernel and kernel uniformity.

References

1. Agriculture Statistics at glance (2011) Directorate of Economic and Statistic Ministry Government of India.
2. Ahmed EH, Young CT (1982) Composition nutrition and flavors of peanut. Peanut Science and Technology: 655-688.
3. Braddock JS, Sims CA, O'Keefe SF (1995) Flavor and oxidative stability of roasted high oleic acid peanuts. Journal of Food Science 60: 489-493.
4. O'Byrne DJ, Knauft DA, Shireman RB (1997) Low fat monosaturated rich diets containing high oleic peanuts improve serum lipoprotein profiles. Lipids 32: 687-695.
5. Mahalanobis PC (1936) On the generalized distance in statistics. Protection Naionatl. Institute Science. India 2: 49-55.
6. Rao CR (1952) Advanced Statistical Methods In Biometrical Research., John Wiley And Sons, New York, Pp. 357-369.
7. Panse VG, Sukhatme PV (1985) Statistical Method for Agriculture Workers, Indian Council of Agricultural Research. New Delhi, P. 381.
8. Singh SP, Dwivedi VK (2002) New agriculturist 13: 2-7.
9. Dwevedi AN, Panwar IS (2005) Journal of Research Hisar 34: 35-39.
10. Verma AK, Singh PK, Vishwakarma SR, Tripathi RM (2006) Farm Science Journal 15: 32-34.
11. Peshattiwar PD, Ghorpade PB, Dandge MS, Thorat A, Gomase DG (2009) Genetic divergence in duram wheat cultivars. International journal of Agricultural Sciences 5**:** 243-247.

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