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"Genetic Diversity Study in Bunch Groundnut [*Arachis hypogaea* L.]"

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ABSTRACT:
The present study was carried out to assess genetic divergence in 60 genotypes of bunch groundnut grown in a Randomized Block Design with three replications at the Junagadh Agricultural University, Junagadh during kharif-2020. The observations were recorded on 14 characters viz., days to 50% flowering, days to maturity, number of primary branches per plant, plant height, number of mature pods per plant, pod yield per plant, 100-pod weight, kernel yield per plant, 100-kernel weight, sound mature kernel, shelling out-turn, biological yield per plant, harvest index and oil content. The genetic diversity analysis revealed the formation of seven clusters suggested that the presence of considerable genetic diversity among the 60 genotypes studied. The analysis revealed that maximum contribution to divergence due to number of primary branches per plant followed by oil content, 100-kernel weight and plant height.

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I. Introduction:

Groundnut (*Arachis hypogaea* L.) is one of the world's most important legume crop. The word groundnut (*Arachis hypogaea* L.) is derived from two Greek words "*Arachis*" meaning to legume and "*hypogaea*" meaning below ground, referring to the formation of pods in the soil. Groundnut is commonly known as peanut, monkey-nut, earthnut, manila nut, pinda, kingpin and goober nut. Groundnut is self-pollinated, tetraploid with chromosome number 2n=40. Groundnut is consumed directly as food or snacks, while it is also an important source of vegetable oil. The oil content of the seed varies from 44 to 50 per cent, depending on the varieties and agronomic practices.

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. Therefore, the first step in any crop breeding programme is to assess genetic variability. Yield and yield contributing characters are controlled by polygenes and highly influenced by environment; the exploration of genetic variability in available germplasm is prerequisite. Therefore, evaluation of germplasm to local conditions is very important. The genetic diversity which is the basis of plant breeding produced due to inherent genetic differences in the plant species and is of major interest to the plant breeder. The D^2 statistics measures the degree of diversification and determines the relative proportion of each component character to the total divergence. It helps to measure the force of differentiation at intra-cluster and inter-cluster levels and helps in selection of genetically divergent parents for their exploitation in hybridization programme.

II. MATERIAL AND METHODS

The current study was to assess the genetic diversity analysis in bunch groundnut during *Kharif* 2020-21, the research was conducted at the Main Oilseed Research Station Farm, College of Agriculture, Junagadh Agricultural University, Junagadh. The experimental material consisted of 60 diverse genotypes of groundnut [*Arachis hypogaea* L.]. Each genotype was sown in a single row plot of 3.0 m length with a spacing of 45 cm × 15 cm. Character studied are recorded based on Five competitive plants per genotype in each replication were randomly selected to record observations for different characters (except days to 50% flowering and days to maturity) and their averages were used in the statistical analysis. Days to 50% flowering and days to maturity was measured on plot basis. The observation recorded for 14 characters *viz.*, days to 50% flowering, days to

maturity, number of primary branches per plant, plant height, number of mature pods per plant, pod yield per plant, 100-pod weight, kernel yield per plant, 100-kernel weight, sound mature kernel, shelling out-turn, biological yield per plant, harvest index and oil content.Oil content in seed sample of each genotype was estimated by using Nuclear Infrared Reflectance (NRI). For formation of clusters, the general criteria of grouping as suggested by Tocher were followed in the present study (Rao, 1952). Genetic divergence analysis will be carried out according to the procedure suggested by Mahalanobis (1936)

III. RESULTS AND DISCUSSION:

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 statistic for estimating genetic divergence have been emphasized by many workers, because it permits precise comparison among all the population given in any group before effecting actual crosses. In the present investigation, seven different clusters are made from 60 genotypes which are shown in Table 1.1. The cluster II having largest number of genotypes (24) followed by cluster I (22) and cluster IV (10). On the other hand, cluster III, cluster V, cluster VI and cluster VII are solitary clusters. The intra-cluster distance (D) ranged from 10.03 (cluster-II) to 12.77 (cluster-IV). High intra-cluster distance indicated about the wider genetic diversity among the genotypes which could be used in yield improvement of groundnut. Thus, the genotypes included within a cluster tended to less diverse from one another. The maximum inter-cluster distance was observed between cluster II and V was (D=38.36) followed by cluster V and VII (D=35.98), I and VII (D=35.04) and minimum inter-cluster distance was found between cluster III and VI (D=10.48). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates or to exploit maximum level of hybrid vigour in groundnut.

A wide range of variation for several characters among multi-genotypic clusters was observed. However, the most important trait causing maximum genetic divergence was observed in number of primary branches per plant (68.59 %) and was responsible for differentiating the genotypes studied. Oil content (10.23 %), 100-kernel weight (9.77 %), and plant height (4.07 %) were the next important traits contributed to total genetic divergence. A considerable diversity of 92.66 % was observed due to these four characters. Hence, selection for divergent parents based on these five characters would be useful for heterosis breeding in groundnut. Lakshmidevamma *et al*. (2006), Hampannavar and Khan (2018) and Koraddi *et al*. (2019) were also reported higher diversity due to oil content. On other hand 100-pod weight, number of mature pods per plant, pod yield per plant, biological yield per plant, kernel yield per plant, days to maturity and shelling out-turn also contributed negligible genetic divergence towards the total divergence. Days to 50 % flowering and harvest index not contributed genetic divergence towards the total divergence. Low genetic diversity for these traits in such diverse group of genotypes may also suggest high degree of consistency and moderate to low heritability of these traits.

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption as improved varieties or for hybridization to exploit heterosis breeding. Desirable rating in respect of earliness for days to 50 % flowering (27.33 days) were observed in cluster VII and days to maturity (108.33 days) were observed in cluster III. The cluster VII had highest mean value for 100-pod weight (99.12), plant height (61.27 cm), oil content (49.17 %) and number of primary branches per plant (3). The cluster IV had highest mean value for 100-kernel weight (41.92), biological yield (38.75) pod yield per plant (10.92 g) and kernel yield per plant (7.41 g). The cluster VI had highest mean value for of shelling out-turn (80.45). The cluster I had highest mean value for harvest index (29.25 %). Cluster III had highest mean value for number of mature pods per plant (13.53). Cluster V had highest mean value for sound mature kernel (87.77 %). Therefore, intercrossing of such genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rational improvement for increasing pod yield in groundnut.

REFRENCES

[1]. Hampannavar, M. R. and Khan, H. 2018. Analysis of genetic diversity of groundnut (Arachis hypogaea L.) genotypes collected from various parts of India. J. Pharma. and Phytochem., **7**(2): 1100-1103.

[2]. Korradi, S.; Rao, V. S.; Rani, M. G.; Sreekanth, B.;Kumar, V. M. and Umar, N. 2019. Genetic Diversity Studies in Yield and its Contributing Traits in Groundnut (Arachis hypogaea L.) Genotypes using D^2 Statistics. Int. J. Curr. Microbiol. App. Sci., **8**(6): 32-38.

[3]. Lakshmidevamma, T. N.; Gowda, M. B.; Mahadevu, P. and Lakshmi, G. 2006. Genetic divergence for yield and its component traits in groundnut germplasm. Ind. J. Plant Genet. Resour., **19**(1): 77-79.

[4]. Mahalanobis, P. C. 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci., **2**: 49-55.

[5]. Rao, C. R. 1952. Advanced Statistical Methods in Biometrical Research. John Willey and Sons, New York

Table 1.1 : Grouping of 60 genotypes of bunch groundnut in various clusters on the basis of D^2 statistic

Cluster	No. of genotypes	Name of genotypes
I.	22	K-1578, JSSP-63, RG-559-3, ICGS-1694, HNG-HPS-2, JSSP-13, JVB-143, RTNG-29, K-260, HNG-36, KDG-171, JSSP-50, K-1811, JSSP-65, GJG-22, RG-382, JSSP-49, JSSP-44, RG-391, JSSP-57, RG-632, KISAN
II.	24	PBS-16040, ICGS-5, K-1577, GG-20, JVB-225, RG-390, K-1715, PBS-22059, KDG-213, JSSP-62, JVB-140, RG-438-1, JVB-151, JVB-154, RG-452, KDG-123, K-1574, JVB-139, HNG-163, JVB-155, JVB-137, JSSP-5, K-1813, JSSP-18
III.	1	RG-613
IV.	10	K-1576, K-1725, JVB-202, K-1641, RG-582, KDG-128, JSSP-64, RTNG-53, JSSP-34, HNG-165
V.	1	NcAc-990
VI.	1	RG-438-2
VII.	1	NcAc-761

Table 1.2. : Average intra and inter-cluster distances between seven clusters in bunch groundnut

Cluster No.	I.	II.	III.	V.	V.	VI.	I.
I.	**10.26**	34.10	13.05	18.41	13.08	15.81	35.04
II.		**10.03**	29.85	21.48	38.36	27.86	16.88
III.			**0.00**	15.93	18.37	10.48	34.18
IV.				**12.77**	22.45	16.32	24.14
V.					**0.00**	20.46	35.98
VI.						**0.00**	32.39
VII.							**0.00**

Table 1.3: Contribution of various traits towards total genetic divergence in bunch groundnut

Sr. No	Characters	Time ranked first	Contribution (%)
1.	**Days to 50% flowering**	0	0.00
2.	**Days to maturity**	2	0.11
3.	**Number of primary branches per plant**	1214	68.59
4.	**Plant height (cm)**	72	4.07
5.	**Number of mature pods per plant**	15	0.85
6.	**Pod yield per plant (g)**	10	0.56
7.	**100-pod weight (g)**	38	2.15
8.	**Kernel yield per plant (g)**	5	0.28
9.	**100-kernel weight (g)**	173	9.77
10.	**Sound mature kernel (%)**	52	2.94
11.	**Shelling out-turn (%)**	2	0.11
12.	**Biological yield per plant (g)**	6	0.34
13.	**Harvest index (%)**	0	0.00
14.	**Oil content (%)**	181	10.23

Table 1.4: Cluster mean value of 14 characters in 7 clusters in 60 genotypes of bunch groundnut

Sr. no.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1.	**DFF**	29.80	29.19	28.33	28.83	31.33	30.67	27.33
2.	**DM**	109.74	110.36	108.33	110.57	112.67	110.67	109.33
3.	**NPBP**	2.05	2.97	2.20	2.46	2.00	2.27	3.00
4.	**PH**	34.34	31.82	26.32	37.16	55.82	18.55	61.27
5.	**NMPP**	10.47	11.18	13.53	11.37	7.67	6.80	5.13
6.	**PYP**	10.43	10.20	8.37	10.92	6.53	6.80	9.10
7.	**100-PW**	89.63	86.63	85.17	91.25	87.33	87.90	99.12
8.	**KYP**	6.98	6.91	5.43	7.41	4.15	5.47	5.78
9.	**100-KW**	39.24	38.69	32.70	41.92	35.10	35.01	32.92
10.	**SMK**	83.36	81.54	77.32	80.57	87.77	87.50	83.45
11.	**SOT**	67.09	67.79	64.83	67.59	63.38	80.45	62.81
12.	**BYP**	36.42	35.51	30.61	38.75	34.37	28.05	38.16
13.	**HI**	29.25	29.11	27.68	29.09	19.31	24.73	23.71
14.	**OC**	41.61	41.90	35.71	40.60	41.57	36.03	49.17

ABBREVIATION:

DFF = Days to 50% flowering
DM = Days to maturity
NPBP = Number of primary branches per plant
PH = Plant height
NMPP = Number of mature pods per plant
PYP = Pod yield per plant
100-PW = 100-pod weight
KYP = Kernel yield per plant
100-KW = 100-kernel weight
SMK = Sound mature kernel
SOT = Shelling out-turn
BYP = Biological yield per plant
HI = Harvest index
OC = Oil content