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Assessment of Genetic Diversity of Bunch Groundnut (*Arachis hypogaea* L.) Genotypes Collected from Various Parts of India

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ABSTRACT

The present study was carried out to assess genetic diversity among 58 genotypes of bunch groundnut using D^2 statistics during *kharif* – 2018 in randomized block design with three replications at the instructional farm, Department of Agronomy, College of Agriculture, Junagadh Agricultural University, Junagadh for thirteen agro-morphological characters *viz.*, days to flowering, days to maturity, plant height, number of primary branches per plant, number of mature pods per plant, pod yield per plant, 100-pod weight, kernel yield per plant, 100-kernel weight, sound mature kernel, biological yield per plant, harvest index and oil content. The 58 groundnut genotypes were grouped under 11 clusters. Among 11 clusters, cluster IV was the largest comprising 18 genotypes, followed by cluster I, comprising 17, Cluster II has 12, cluster III has 4 and cluster V to XI were solitary. The D^2 values for inter-cluster distances, showed maximum between cluster VI and X (19.71), followed by VI and VII (18.77), V and X (18.68), III and V (18.65), V and VII (18.62), II and V (17.86), V and VIII (D = 17.78), III and X (D = 17.43) and VI and VIII (D = 17.20). The clusters were ranked based on the overall score across all thirteen characters. Accordingly, cluster III was the best for days to maturity, number of mature pods per plant (DH-24 and ICGV-0642), pod yield per plant (DH-221 and DH-201), kernel yield per plant and sound mature kernel (DH-55 and AH-34-90). Cluster VIII, X and XI were best for oil content (ICGV-03109 and AK-159), harvest index and biological yield per plant, respectively. Each character had their own contribution toward genetic divergence where, 100 kernel weight and sound mature kernel (%) has a maximum contribution of 23.71% and 23.23%, respectively.

Key words: D^2 statistics, Bunch groundnut, Solitary, Cluster distance and Contribution.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the world's most important legume crop. The word groundnut (*Arachis hypogaea* L.) is derived from the Greek word "*Arachis*" meaning legume and "*hypogaea*" meaning below ground. It is commonly known as peanut, monkey-nut and goobernut. The genus *Arachis* is a member of family Fabaceae (Synonym: Leguminosae), subfamily Papilionoidea, tribe Aeschynomeneae and sub-tribe stylosanthinae. It belongs to the section Arachis and series amphiploidies and the family Fabaceae (Gregory *et al.*, 1980). Southern Bolivia and Northern Argentina are thought to be the centre of origin of this crop (Kochert *et al.*, 1996) and the centre of diversity for this genus includes Western

Brazil, Bolivia, Paraguay, and Northern Argentina. Having the basic chromosome number of x=10 (Stalker, 1991)peanut is an allotetraploid (2n=4x=40). Obviously, allopolyploid crops have complex genome. This may lead to more diversity in groundnut genotypes.

This is widely grown in the tropics and subtropics, being essential to both small and large commercial producers. Groundnut requires 20°C-30°C of temperature and 50 cm to 100 cm of rainfall. Like most other legumes, peanuts harbour symbiotic nitrogen-fixing bacteria in root nodules.This capacity to fix nitrogen means peanuts require less nitrogen-containing fertilizer and can improve soil fertility, making them valuable in crop rotations.

The genetic divergence analysis determines the variation pattern in the collection of genotypes, identify the contributing characters and differentiates the genotypes into different groups that could be used in the improvement programme. Genetic diversity plays an important role because hybrids between lines of diverse genetic backgrounds generally display a greater heterosis than those between closely related parents and may generate broad-spectrum genetic variability in segregating generations (Arunachalam, 1981; Sharma, 1998).Moreover, estimating genetic diversity among genotypes through Mahalanobis' D2 technique is very useful for selecting diverse parents.

MATERIALS AND METHODS

The present investigation was carried out to assess genetic divergence in fifty-eight diverse genotypes of bunch groundnut (*Arachis hypogaea* L.) representing different geographic origins across India. The required quantity of seeds for this experiment have

Table 1: Distribution of fifty-eight groundnut genotypes into the different clusters by Tocher's method

Cluster No.	No. of strain	Genotypes included in the cluster
I	17	DSA-201, AMR-43, C-817, AH-8986, EC-21147, AK-7223, AK-135, EC-21048, EC-1283, AMR-22, ALR-2, EC-21121, AH-8253, AH-8189, ICGV-06050, AH-34-90 and ICGV-91040
II	12	AMR-42, AH-7217, EC-2100-8, 68-135, GG-5, CO-2, AK-400, TCGS-1043, EC-100827, EC-21051, 52-35, ALR-1
III	4	DH-24, DH-221, DH-55 and DH-201
IV	18	EC-1697, AK-5144, ALR-3, GG-3, ICGV-03042, ICGS-11, ICGV-90116, EC-21126, AK-159, FE-ESG-10, ICGV-03109, EC-21057, AH-7220, ICGV-06424, ICGV-05030, ENGEUZM, ICGV-86325 and ICGV-06041
V	1	CUL-1-5-3
VI	1	DH-40
VII	1	GG-7
VIII	1	ICGV-06424
IX	1	AMR-49
X	1	ICGV-89359
XI	1	ICGV-06188

Table 2: Source and clustering pattern for fifty-eight genotypes of bunch groundnut (*kharif*)

Source	ICRISAT, Hyderabad	UAS, Dharwad	PAU, Ludhiana	TNAU, Aliyarnagar	TNAU, Tindivanam	TNAU, Coimbatore	PDKV, Akola	ANGRAU, Tirupati	JAU, Junagadh	Unknown
I	6	-	1	1	4	-	2	-	-	3
II	3	-	-	1	1	1	1	1	1	3
III	-	4	-	-	-	-	-	-	-	-
IV	11	-	-	1	1	-	2	-	1	2
V	-	-	-	-	-	-	-	-	-	1
VI	-	1	-	-	-	-	-	-	-	-
VII	-	-	-	-	-	-	-	-	1	-
VIII	1	-	-	-	-	-	-	-	-	-
IX	-	-	-	-	-	-	-	-	-	1
X	1	-	-	-	-	-	-	-	-	-
XI	1	-	-	-	-	-	-	-	-	-
Total number of genotypes	23	5	1	3	6	1	5	1	3	10

Table 3: Average intra (diagonal) and inter (above diagonal) cluster D values for fifty-eight genotypes of bunch groundnut (*kharif*)

	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8	Group 9	Group 10	Group 11
Group 1	6.75	10.09	9.94	11.20	12.17	10.13	15.36	11.02	11.12	15.37	12.59
Group 2		7.59	9.75	14.56	17.86	16.08	14.26	9.28	15.58	12.96	11.47
Group 3			7.92	14.55	18.65	14.35	16.70	10.26	16.43	17.43	13.04
Group 4				10.37	11.82	11.77	13.28	13.80	11.99	15.27	11.45
Group 5					0.00	9.30	18.62	17.78	8.54	18.68	16.43
Group 6						0.00	18.77	17.20	8.81	19.71	15.30
Group 7							0.00	14.33	15.90	8.63	8.36
Group 8								0.00	15.95	14.14	10.24
Group 9									0.00	16.71	14.41
Group 10										0.00	9.72
Group 11											0.00

Table 4: Cluster means for fourteen characters in bunch groundnut *(kharif)*

	Days to flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of mature pods per plant	Pods yield per plant (g)	100 pods weight (g)	Kernel yield per plant (g)	100 kernel weight(g)	Sound mature kernel (%)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)
Group 1	32.14	104.27	39.18	3.06	9.25	9.92	95.67	7.29	39.10	85.51	22.29	41.43	48.53
Group 2	32.08	102.50	38.53	3.08	8.19	9.36	118.83	6.61	48.94	82.83	21.25	43.61	48.36
Group 3	33.42	102.42	41.17	3.00	11.83	11.92	114.58	8.58	47.33	86.83	30.67	41.00	47.67
Group 4	31.83	100.24	35.07	3.00	9.93	9.80	89.89	7.19	34.81	74.56	26.72	36.33	48.94
Group 5	29.67	103.33	36.00	3.00	6.33	5.33	61.67	3.67	26.67	82.67	19.00	28.67	49.67
Group 6	34.33	107.00	41.00	3.00	8.33	9.00	76.33	6.33	30.67	83.33	29.67	31.00	45.33
Group 7	32.00	99.67	38.00	3.00	10.00	11.00	114.00	7.67	45.33	54.33	23.33	41.00	48.67
Group 8	34.33	100.67	35.00	3.00	9.67	11.33	114.00	8.33	49.33	82.33	32.33	34.67	52.67
Group 9	30.00	113.67	42.00	3.00	7.00	7.67	75.33	5.00	33.00	71.67	26.67	29.00	49.00
Group 10	36.33	102.67	25.67	3.00	6.00	9.33	108.00	7.00	51.00	62.00	12.67	53.67	47.00
Group 11	33.67	96.67	34.33	3.00	7.67	9.33	109.33	6.33	48.00	66.67	33.33	26.00	47.67

Table 5: Contributions of various characters to divergence

Sr. No.	Characters	Times Ranked 1st	Contribution (%)
1	Days to flowering	3	0.18
2	Days to maturity	127	7.68
3	Plant height (cm)	1	0.06
4	No. of primary branches per plant	0	0.00
5	No. of mature pods per plant	137	8.29
6	Pods yield per plant (g)	12	0.73
7	100 pods weight (g)	279	16.88
8	Kernel yield per plant (g)	0	0.00
9	100 kernel weights (g)	392	23.71
10	Sound mature kernel (%)	384	23.23
11	Biological yield per plant (g)	149	9.01
12	Harvest index (%)	2	0.12
13	Oil content (%)	167	10.10

been obtained from the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh and it was sown in *kharif*-2018 at the Instructional Farm, Department of Agronomy, J.A.U., Junagadh.For qualifying the diversity in fifty-eight genotypes for thirteen quantitative genotypes *viz.*, days to flowering, days to maturity, plant height, number of primary branches per plant, number of mature pods per plant, pod yield per plant, 100-pod weight, kernel yield per plant, 100-kernel weight, sound mature kernel, biological yield per plant, harvest index and oil content and their fitness was assessed using the concept of Mahalanobis' (1936) D^2statistics.

RESULTS AND DISCUSSION

The genetic diversity among 144 genotypes for 13 characters was measured by employing D^2 statistic. Based on D^2 values, the genotypes were clustered using Tocher's method as given by Rao (1952). In all, eleven clusters were formed from fifty-eight genotypes. The composition of clusters is given in Table 1 and clustering pattern as accordance to geographical region is shown in Table 2.Among 11 clusters, cluster IV was the largest comprising 18 genotypes, followed by cluster I comprising 17, Cluster II has 12, cluster III has 4 and cluster V to XI were solitary.

It was observed that the maximum intra-cluster distance was found in cluster IV followed by cluster III, cluster II, cluster I and the remaining cluster were solitary. The maximum inter-cluster distance (D = 19.71) was found between clusters VI and X followed by that between clusters VI and VII (D = 18.77), V and X (D = 18.68), III and V (D = 18.65), V and VII (D = 18.62), II and V (D = 17.86), V and VIII (D = 17.78), III and X (D = 17.43) and VI and VIII (D = 17.20). This also suggested that the genetic architecture of the genotypes in one cluster differs substantially from those included in another cluster (Table 3).

The minimum inter-cluster distance (D=8.36)

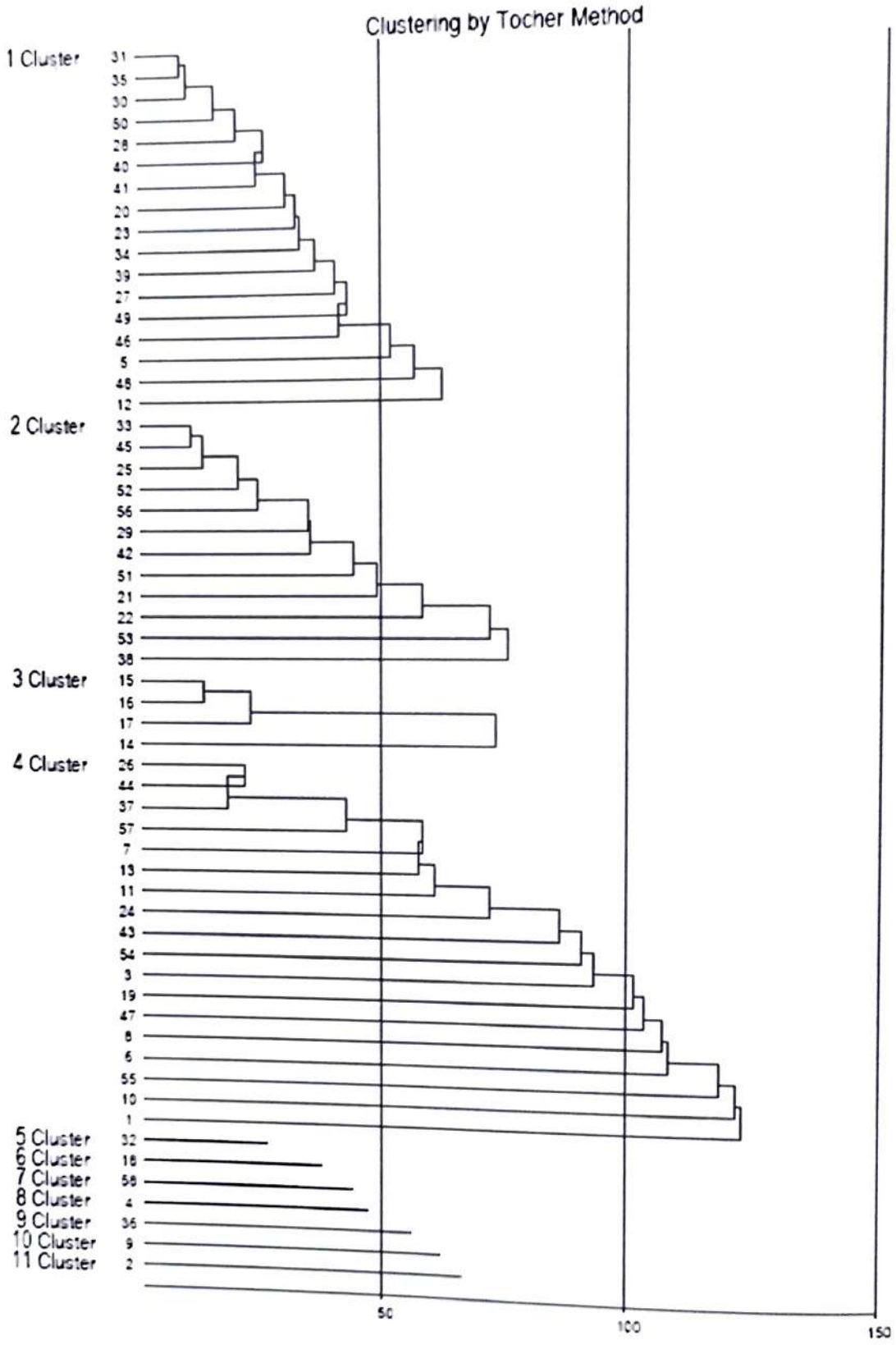

Fig. 1: Cluster diagram representing genetic diversity in studied genotype of bunch groundnut

was found between clusters VII and XI. The lower inter-cluster D values between these clusters suggested that the genetic constitution of the genotypes in these clusters were in close proximity (Table 3).

Based on cluster means of thirteen characters (Table 4), it was observed that the cluster III recorded the highest mean for number of mature pods per plant, pods yield per plant, kernel yield per plant and sound mature kernel.

Percent contribution of various characters for divergence is given in Table 5. Out of thirteen characters studied, the character 100 kernel weight (23.71) contributed the highest for divergence followed by sound mature kernel (23.23), 100 pods weight (16.88), oil content (10.10), biological yield per plant (9.01), number of mature pods per plant (8.29), days to maturity (7.68), pods yield per plant (0.73), days to flowering (0.18), harvest index (0.12) and plant height (0.06) while, number of primary branches per plant (0.00) and kernel yield per plant (0.00) have no contribution. These observations were following observations of Singh and Kaur (1993) and Foundra*et al.* (2000).

Based onthe aforesaid study in present investigation, genotypes DH-221, DH-201, DH-24, ICGV-06424, 68-135, EC-21051, DH-55, AH-34-90, ICGV-03109, AK-159 and 52-35 were found to be superior genotypes for further breeding programme.

CONCLUSION

The diversity study is a prerequisite for the hybridization programme. Most of the time, selecting parents blindly based on phenotypic appearance will not give a satisfactory result. The selections of parents based on intra and inter-cluster distance and cluster mean helps in production of transgressive segregates or better recombinants. According to present divergence study, out of thirteen characters 100 kernel weight, sound mature kernel, 100 pods weight, oil content, biological yield per plant, number of mature pods per plant and days to maturity contributed more than 98% so, we can directly focus on these characters for selection in groundnut.

REFERENCES

Arunachalam, V. (1981). Genetic distance in plant breeding. *Indian J. Genet.*,41: 226-236.

Foundra, M. Z., Harnande, R., Lopez, L., and Ravelo, I. (2000). Analysis of variability in collected peanut. Legume, Res.; 13:9-13.

Gregory, W., Krapovickas, A.andGregory, M.(1980). Structure, variation, evolution and classification in *Arachis. Advances in legume science. Kew, London: Royal Botanic Gardens.*

Kochert, G., Stalker, H. T., Gimenes, M., Galgaro, L., Lopes, C. R.andMoore, K.(1996). RFLP and cytogenetic evidence on the origin and evolution of allotetraploid domesticated peanut, *Arachis hypogaea* (Leguminosae). *American J. of Botany,* 83: 1282-1291.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proc. Nat. Inst. Sci. (India)*2: 49-55.

Rao, C. R. (1952). Advanced Statistical Methods in Biometric Research. *John Wiley Sons, New York*, 390.

Sharma, J. R. (1998). Statistical and Biometrical Techniques in Plant Breeding. *New Age Intern. Limited Publishers, New Delhi.* 432.

Singh, A. J. and Kaur, P. (1993). Genetic divergence studies in groundnut. Agric. Sci.; 18:244-245.

Stalker, H. T.(1991). A new species in section *Arachis* of peanuts with a D genome. *American Journal of Botany.*78: 630–637.