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Analysis of genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes collected from various parts of India

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Abstract

During *kharif*, the genetic diversity among 144 genotypes for 13 characters was measured by employing D^2 statistic. The 144 groundnut genotypes were grouped under 16 clusters. Among 16 clusters, cluster IV was the largest which comprising of 24 genotypes followed by clusters I and II with 22 genotypes in each, cluster III and VII comprising 15 genotypes, cluster IV (14), VI (12), VII (7) and X (6) genotypes. The rest of clusters had shown solitary in nature. The average D^2 values of inter cluster distances, showed maximum distance between Cluster-XI and XVI (241.24) followed by inter cluster distance (223.43) between IV and XVI. It indicates that crossing between these clusters helps in production of transgressive segregates or better recombinants. The clusters were ranked based on the overall score across 13 traits. Accordingly, cluster-V was superior which indicates the presence of most promising genotypes in them. Each character had their own contribution to total divergence where, the haulm yield and oil percentage had maximum contribution of 33.39% and 30.99% respectively to the divergence of genotypes.

Keywords: D^2 statistics, groundnut, solitary clusters, cluster distance and percent of contribution

Introduction

The cultivated groundnut is allotetraploid ($2n=4x=40$) in nature. Obviously allopolyploidy crops have complex genome. This may leads to more diversity in groundnut genotypes. Genetic divergence in the population, especially in respect of the character in which improvement is sought for, is a pre requisite for successful plant breeding work. Genetic divergence and genetic variability are playing vital role in successful breeding programme. Analysis of genetic diversity within and between groups of genotypes is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. Several methods have been advocated by various workers to estimate the genetic divergence in crop plants (Murthy and Quandri, 1966; Bhat, 1970 and Hussaini, 1973) [8, 5, 6]. Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) [9] is a unique tool for discriminating population considering a set of parameters together rather than infusing from indices based on morphological similarities and phylogenetic relationships.

Material and Method

The present investigation was initiated during *kharif* 2015 at Main Agriculture Research Station (MARS), University of Agriculture Sciences, Raichur, India. The experimental material for the present study comprised of 144 groundnut genotypes which are derived from different institutes, university and research stations of India. The genotypes were collected from across India which consists of released varieties, pipeline varieties, advance breeding lines and germplasm lines. For quantifying the diversity in 144 groundnut genotypes for 13 quantitative characters and their fitness was assessed using the concept of Mahalanobis (1936) [7] D^2 statistic. Genetic divergence analysis helps in identify the genetically diverse genotypes for their use in plant breeding programmes.

Result 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) [9].

Group constellation

Based on the D^2 statistics 144 groundnut genotypes were grouped under 16 clusters. The genetic material used in experiment was collected by various locations across India.

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Table 1: Clustering pattern of 144 groundnut (*Arachis hypogaea* L.) genotypes

Clusters	No. of genotypes	Genotypes
I	22	ICGV 07235, CHINTAMANI-2, DH-216, DH-86, Kadiri-6, ICGV 4729, ICGV 97092, ICGV 3102, DTG-15, R-8808, ICGV 13242, ICGV 3343, ICGV 98105, ICGV 00350, TAG-24, TG-72, ICGV 95070, DHARANI, ICGV 07219, ICGV 99233, R-2001-2, TMV-2.
II	22	ICGV 07296, ICGV 07408, ICGV 07395, ICGV 07392, ICGV 00187, ICGV 89178, ICGV 99161, ICGV 07213, ICGV 07406, ICGV 06319, ICGV 07396, ICGV 07405, ICGV 01265, ICGV 07166, DSG-41, ICGV 03042, CHICO, ICGV 07227, ICGV 4955, ICGV 98163, ICGV 07404, TG 67.
III	15	ICGV 96155, ICGV 96153, ICGV 07403, ICGV 05036, MUTANT-3, ICGV 91114, ICGV 02411, ICGV 03397, ICGV 86015, ICGV 97058, ICGV 01361, ICGV 13241, ICGV 07222, ICGV 04018, ICGV 02189
IV	24	G2-52, ICGV 00189, ICGV 06227, ICGV 99160, ICGV 98184, ICGV 00201, ICGV 07270, ICGV 07390, ICGV 02317, GPBD-5, ICGV 93280, ICGV 07273, ICGV 07286, Kadiri-Haritendra, GPBD-4, Somanatha, ICGV 03064, ICGV 99210, TPG-41, S-230, ICGV 00162, TG-36, SEL-01, ICGV 06189
V	14	ICGV 1-13238, ICGV 27X49-12, ICGV 06431, ICGV 07148, KRG-01, ICGV 89104, TG-47, R-2001-3, ICGV 97262, ICGV 96466, ICGV 97182, ICGV 01276, ICGV-99206, ICGV 05193
VI	12	K-9, ICGV 00440, TG-75, TG-80, ICGV 15415, ICGV 3584, M-28-2, ICGV 05184, TG-74, ICGV 04149, TG-37A, TG-51
VII	15	ICGV 05057, ICGV 96172, CS 39, ICGV 01274, M49-M-16, ICGV 00246, ICGV 99052, ICGV 06422, ICGV 99051, ICGV 06423, ICGV 07120, ICGV 07247, ICGV 39X49-81-1, ICGV 02266, ICGV 00247
VIII	7	ICGV 03043, ICGV 99102115, ICGV 95440, ICGV 13245, ICGV 06188, ICGV 02242
IX	1	ICGV-00351
X	6	ICGV 01464, TG 49, ICGV 05198, TDG-39, ICGV 07337, ICGV 9507
XI	1	ICGV 95058
XII	1	TDG-51
XIII	1	ICGV 00343
XIV	1	ICGV 93470
XV	1	ICGV 05141
XVI	1	ICGV 03136

which may lead to more clusters in diverse study. The distribution pattern of genotypes into 16 clusters is presented in table 1. Among 16 clusters, cluster IV was the largest comprising of 24 genotypes followed by clusters I and II with 22 genotypes in each, cluster III and VII comprising 15 genotypes, cluster IV, VI, VII and X consist of 14, 12, 7 and 6 genotypes respectively. The cluster IX, XI, XII, XIII, XIV, XV and XVI are solitary in nature. The formation solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes.

Intra and inter relation of clusters

The average D^2 values of intra and inter cluster distances are given in table 2. Maximum difference among the genotypes within the same cluster was shown by cluster-VIII (85.38) and followed by cluster X (69.21), cluster VII (68.68), cluster VI (62.83), cluster IV (45.57), cluster III (43.83), cluster I (39.38), cluster II (13.3) and cluster V (5.02). Some clusters like IX, XI, XII, XIII, XIV, XV and XVI intra cluster value was zero due to solitary nature.

Cluster-XI and XVI showed maximum inter cluster distance

(241.24) followed by inter cluster distance (223.43) between IV and XVI and the lowest inter cluster distance (36.48) was noticed between cluster-IX and XI, respectively (Table 2). It indicates that crossing between these clusters helps in production of transgressive segregantes or better recombinants. The lowest inter cluster distance (36.48) was noticed between cluster-IX and XI. Dwinedi *et al.* (2001) ^[3] have stated that low diversity in groundnut due to self fertility. Similarly Badigannavar *et al.* (2002) ^[4] also reported relatively low genetic diversity with respect to morphological characters in peanut.

Cluster Means

The cluster means in respect of 13 characters and over all character wise score across the 16 clusters are presented in (Table 3). All the genotypes were spread over 16 clusters and means of each character in each cluster were scored across the cluster for all the 13 characters. Based on the overall score across 13 traits, the clusters were ranked. Accordingly, cluster-V with overall score of 95 across the thirteen characters secured first rank followed

Table 2: Average intra and inter cluster distance of 144 genotypes of groundnut (*Arachis hypogaea* L.)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	39.38	69.52	61.29	58.64	80.66	69.13	103.24	106.77	79.41	130.33	103.98	104.72	123.25	118.01	151.28	197.27
II		13.3	68.72	67.59	107.57	93.44	68.86	109.51	62.48	136.99	92.89	145.53	156.07	147.65	130.89	180.24
III			43.83	84.29	77.56	87.56	84.5	86.47	103	125.03	134.36	99.19	107.31	97.43	108.66	165.48
IV				45.57	95.31	94.29	101.8	115.93	65.86	160.53	82.22	139.25	162.84	149.5	170.31	223.43
V					5.02	120.11	120.46	81.61	137.6	172.75	160.47	92.19	120.37	86.31	144.53	217.45
VI						62.83	127.44	142.24	89.4	101.74	112.45	116.68	122.13	139.2	164.11	181.66
VII							68.68	107.41	102.71	156.45	121.03	161.46	168.09	154.42	109.73	172.24
VIII								85.38	148.74	181.16	174.51	122.5	139.89	106.64	118.72	201.66
IX									0	142.38	36.48	170.62	183.82	185.226	178.16	208.31
X										69.21	169.26	145.57	123.25	163.42	154.21	123.85
XI											0	196.49	213.52	214.45	212.69	241.24
XII												0	53.35	55.07	155.3	194.54
XIII													0	61.63	140.5	162.46
XIV														0	131.9	192.53
XV															0	110.42
XVI																0

Table 3: Cluster mean value for 13 quantitative traits in groundnut genotypes

Clusters	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	Overall score	Rank
I	26(2)	22.75(10)	4.64(15)	115.7(7)	13.32(6)	1.43(8)	71.27(3)	8.33(9)	85.39(9)	37.21(9)	14.71(14)	39.24(10)	11.68(11)	113	11
II	27.93(12)	21.48(6)	5.41(9)	116.84(12)	11.41(12)	1.95(13)	68.79(5)	7.31(13)	85.32(10)	36.38(10)	23.05(5)	41.04(6)	10.65(13)	126	14
III	26.43(5)	25.01(15)	5.93(6)	115.57(6)	13.13(7)	1.73(10)	68.31(6)	8.84(7)	85.47(8)	35.66(11)	20.6(6)	37.17(12)	12.95(9)	108	8
IV	27.31(9)	20.19(3)	5.17(10)	116.08(11)	11.9(11)	1.58(9)	67.11(10)	6.82(14)	82.46(15)	33.03(13)	15.71(11)	41.66(4)	10.16(14)	134	16
V	26.18(4)	22.41(9)	5.46(8)	115.96(8)	16.57(2)	1.75(11)	67.43(7)	9.99(4)	86.75(4)	30.9(15)	17.23(9)	40.58(7)	14.83(7)	95	1
VI	26(3)	20.92(5)	4.96(14)	115.33(5)	12.25(9)	1.33(6)	69.52(4)	8.26(10)	85.88(7)	47.67(3)	14.06(15)	40.32(9)	11.92(10)	100	4
VII	27.67(11)	23.57(13)	6.9(1)	117.63(13)	12.2(10)	1.83(12)	64.26(13)	7.35(12)	83.7(13)	33.18(12)	29.01(3)	40.55(8)	11.48(12)	133	15
VIII	26.43(6)	24.77(14)	6.36(4)	115.14(4)	17.71(1)	2.07(16)	63.27(14)	9.73(5)	86.36(5)	30.41(16)	25.34(4)	42.16(3)	15.4(6)	98	3
IX	28.5(14)	20.35(4)	5(12)	116(9)	8.5(16)	0.5(2)	74.96(1)	6.4(15)	85(11)	40.83(7)	18.39(8)	43.52(2)	8.54(15)	116	12
X	26.5(7)	23.02(11)	5.17(11)	119(14)	9(14)	1.42(7)	67.27(8)	9.23(6)	88.67(2)	60.1(1)	20.25(7)	39(11)	13.74(8)	107	7
XI	27.5(10)	23.4(12)	6.5(2)	116(10)	10.5(13)	1(3)	71.97(2)	5.15(16)	82(16)	41.01(6)	15.88(10)	46.11(1)	7.16(16)	117	13
XII	25.5(1)	19.4(2)	3(16)	115(2)	15(4)	1(4)	48.94(16)	7.97(11)	86(6)	38.04(8)	11.1(16)	32.91(15)	16.29(4)	105	6
XIII	28.5(15)	27.35(16)	5(13)	114(1)	15(5)	0.05(1)	64.81(12)	11.48(2)	84.5(12)	46.83(4)	15.25(13)	34.34(14)	17.72(1)	109	9
XIV	28(13)	22.2(8)	5.5(7)	115(3)	16.5(3)	1(5)	67.26(9)	11.76(1)	87(3)	32.41(14)	15.66(12)	31.72(16)	16.98(3)	97	2
XV	28.5(16)	19.35(1)	6(5)	120(15)	13(8)	2(14)	65.94(11)	11.47(3)	83(14)	41.87(5)	32.13(2)	41.09(5)	17.39(2)	101	5
XVI	27(8)	21.95(7)	6.5(3)	121(16)	9(15)	2(15)	52.41(15)	8.51(8)	89(1)	58.07(2)	36.97(1)	35.28(13)	16.23(5)	109	10

Where,

X₁=Days to 50% flowering

X₂= Plant height (cm)

X₃=No. of Primary branch/plant

X₄= Days to physiological maturity

X₅= No. of mature pods/plant

X₆= No. of immature pods/plant

X₇= Shelling Percentage

X₈= Kernel yield (g/plant)

X₉= Sound Mature Kernel (%)

X₁₀= Hundred Kernel Weight (g)

X₁₁= Haulm Yield (g/plant)

X₁₂= Oil percent

X₁₃= Dry Pod yield (g/plant).

Table 4: Relative contribution of 13 quantitative traits towards divergence in groundnut genotypes

Source	Times Ranked 1 st	Contribution %
Haulm yield (g/plant)	3438	33.39
Oil percentage	3119	30.99
Hundred Kernel Weight (g)	2539	24.66
Dry pod yield (g/plant)	722	7.01
Kernel yield (g/plant)	326	3.17
Plant height (cm)	50	0.49
Days to physiological maturity	30	0.29
Days to 50% flowering	0	0
No. of Primary branches/plant	0	0
No. of mature pods/plant	0	0
No. of immature pods/plant	0	0
Shelling percentage	0	0
Sound Mature Kernel (%)	0	0
Total		100

by cluster-XIV, VIII, VI, XV, XII, X, III, XII and XVI. These clusters were indicating the presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material. With respect to improvement of pod yield and oil content the genotype in cluster XIII (ICGV 00343) and XI (ICGV 95058) could be more valuable.

Contribution of different characters towards divergence

Difference in proportion of contribution of each character to total D^2 statistics was observed and presented in table 4. The haulm yield contributed 33.39 per cent to the total divergence of genotypes followed by oil percentage (30.99%), hundred kernel weight (24.66%), dry pod yield (7.01%), kernel yield (3.17%), plant height (0.49%) and days to maturity (0.29%). Some of the characters like days to 50% flowering, primary branches, number of mature pods, number of immature pods, shelling percentage and sound mature kernels not shown their contribution to total divergence. These observations were in accordance with observations of Singh and Kaur (1993) ^[1] and Foundra *et al.* (2000) ^[2].

Conclusions

The diversity study is prerequisite for hybridization programme. The most of times selecting parents blindly based on phenotypic appearance won't give the satisfactory result. The selections of parents based on intra and inter cluster distance and cluster mean helps in production of transgressive segregantes or better recombinants.

References

1. Singh AJ, Kaur P. Genetic divergence studies in groundnut. *Agric. Sci.* 1993; 18:244-245.
2. Foundra MZ, Harnande R, Lopez L, Ravelo I. Analysis of variability in collected peanut. *Legume, Res.* 2000; 13:9-13.
3. Dwinedi SL, Gurtu S, Chandra W. Assessment of genetic diversity. *Pl. Breed.* 2001; 120:345-349.
4. Badigannavar AM, Kale DM, Murty GS. Genetic bases and diversity in groundnut genotypes. *Pl. Breed.* 2002; 121:348-355.
5. Bhatt GM. Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self pollinated crops. *Australia. J agric Res.* 1970; 21(1):1-7.
6. Hussain SH. Multivariate analysis and group distribution in world collection of *elusine coracana gaertn.* NCSI, Publication, 1973, 81.
7. Mahalanobis PC. On the generalized distance in statistics. *Proc. Natn. Inst. Sci. India.* 1936; 2:49-55.
8. Murthy BR, Quadri ML. Analysis of divergence in some self compatible forms of *Brassica campestris* (L.) Var. Brown sarson. *Indian J. Genet.* 1966; 20:45-48.
9. Rao CR. *Advanced Statistical Methods in Biometric Research.* John Wiley Sons, New York, 1952, 390.