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Research Paper

Genetic divergence in bunch groundnut (*Arachis hypogaea* L.)

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ABSTRACT

Divergence analysis among fifty groundnut genotypes was carried out using Mahalanobis's D^2 statistic. The genotypes were grouped into thirteen clusters. The maximum inter-cluster distance (D=327.33) was found between clusters III and XIII followed by clusters III and IX (D=267.26) and III and V (D=253.94) indicated that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial difference in the means for important yield contributing characters suggesting that the genotypes belonging to these clusters from ideal parents for improvement in groundnut.

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Key words : Clusters, Genetic divergence, Groundnut

INTRODUCTION

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 statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966) because it permits precise comparison among all the population in given any group before effecting actual crosses.

MATERIALS AND METHODS

Fifty genotypes of groundnut were sown in a Randomized Block Design with three replications during *Kharif* 2009. Each entry was accommodated in a single row of 3.0 m length with a spacing of 45 cm between rows and 10 cm between plants within the row. The fertilizer in the experimental area was applied at the rate of 25.0 kg N and 50.0 kg P_2O_5 ha^{-1} as it is a recommended dose for *Kharif* cultivation of groundnut in the region. All the recommended packages of practices were followed for raising healthy crop. Data were recorded for days to first flower, days to 50% flowering, days to maturity, plant height, primary branches per plant, number of mature pods per plant, number of immature pods per plant, 100-pod weight, 100- kernel weight, shelling out-turn, oil content, protein content, kernel yield per pod, pod yield per plant, biological yield per plant and harvest index. The analysis of genetic divergence using Mahalanobis's D^2 (1936) statistics was carried out as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance revealed that highly significant differences among the genotypes were observed for all the traits except oil content, which indicating the presence of good amount of genetic variability. On the basis of D^2-values, 13 clusters were formed from 50 genotypes. The cluster I was the largest having 23 genotypes followed by cluster II and cluster III having 12 and five genotypes, respectively (Table 1). Cluster IV to XIII included a single genotype and remained solitary. The grouping of genotypes revealed that there was no perfect relationship between genetic diversity and geographical diversity as genotypes

Table 1 : Grouping of 50 genotypes of groundnut in various clusters on the basis of D^2-statistic

Cluster	No. of genotypes	Genotypes	Source/Origin
I	23	JB-HPS-08-1, JB-HPS-08-3, JB-HPS-08-4, JB-HPS-08-5, JB-1135, JB-1140, JB-1153, JB-1165, JB-1174, JB-1176, JB-1184, JB-1191, JB-1198, JB-1199, JB-1201, PBS-30086	Junagadh (Gujarat)
		GG-2, GG-4, GG-6, GG-7	Released Varieties of Gujarat
		VG-17	Vridhachalam, (Tamil Nadu)
		AG-2006-15	Anand (Gujarat)
		ICGV-95386	ICRISAT, Hyderabad
		TAG-24, TG-37A, TPG-41	BARC, Trombay (Maharashtra)
II	12	JB-HPS-08-6, JB-1155, JB-1168, JB-1169, JB-1175	Junagadh (Gujarat)
		JL-501	Jalgaon (Maharashtra)
		TVG-0004	Tindivanam, (Tamil Nadu)
		Dh-209	UAS, Dharwad
		GG-3	Released Variety of Gujarat
III	5	JB-1136, JB-1197, JB-1202	Junagadh (Gujarat)
		TG-67	BARC, Trombay (Maharashtra)
		RG-452	Durgapura, Jaipur
IV	1	JL-24	Jalgaon (Maharashtra)
V	1	GG-5	Released Variety of Gujarat
VI	1	JB-HPS-08-9	Junagadh (Gujarat)
VII	1	AK-159	PKV, Akola (Maharashtra)
VIII	1	JB-1177	Junagadh (Gujarat)
IX	1	AG-2006-10	Anand (Gujarat)
X	1	TG-26	BARC, Trombay (Maharashtra)
XI	1	PBS-30051	DGR(NRCG), Junagadh
XII	1	GG-8	Released Variety of Gujarat
XIII	1	JB-1196	Junagadh (Gujarat)

Table 2 : Average and intra and inter-cluster ($D=\sqrt{D^2}$) value for 50 genotypes of bunch groundnut

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	41.25	71.02	180.19	56.59	55.01	59.36	69.94	57.99	83.36	135.27	85.75	123.05	179.54
II		70.13	173.24	70.50	77.46	85.13	92.06	104.18	91.36	124.59	106.56	143.10	173.24
III			52.21	241.31	253.94	208.62	243.21	220.45	267.26	100.06	78.18	80.49	327.33
IV				0.00	24.12	100.38	26.44	80.60	38.96	134.14	144.66	159.21	155.32
V					0.00	94.60	39.57	67.74	64.56	169.76	150.38	169.12	186.52
VI						0.00	114.20	103.91	101.50	201.50	106.83	198.46	248.00
VII							0.00	73.53	47.58	101.07	151.39	175.66	216.61
VIII								0.00	124.37	155.10	110.35	144.89	129.13
IX									0.00	146.05	159.74	192.54	184.59
X										0.00	102.67	93.11	252.21
XI											0.00	54.07	228.17
XII												0.00	229.29
XIII													0.00

from different geographical origin were included in one cluster. The maximum inter-cluster distance (D=327.33) was found between clusters III and XIII carrying one genotype each followed by that between clusters III and IX (D=267.26) and III and V (D=253.94). The minimum inter-cluster distance was observed between clusters IV and V (D=24.12). The intra-cluster distance ranged from 41.25 to 70.13, the maximum being in cluster II (70.13). The minimum intra-cluster distance was found in cluster I (41.25) (Table 2). The genotypes belonging to the clusters

Table 3: Cluster means for 16 characters in 50 genotypes of bunch groundnut

Clusters	Days to 1st flower	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant	No. of mature pods /plant	No. of immature pods/ plant	100 pod weight (g)	100 kernel weight (g)	Shelling out turn (%)	Oil content (%)	Protein content (%)	Kernel yield/ plant (g)	Pod yield/ plant (g)	Biological yield/plant	Harvest index (%)
I	28.97	33.36	116.19	30.79	4.56	7.75	4.74	97.16	48.21	73.20	47.00	29.23	5.01	6.83	14.37	48.54
II	31.00	34.97	118.94	27.25	4.71	9.88	5.39	86.70	46.88	65.15	48.06	27.96	6.06	9.36	15.77	62.35
III	28.20	32.47	116.00	27.19	4.49	19.25	4.45	102.51	50.92	82.97	47.39	27.01	12.01	14.49	18.55	79.65
IV	31.00	36.00	120.33	25.53	4.20	6.67	4.53	93.70	35.33	67.44	46.57	32.04	4.53	7.01	14.71	47.33
V	32.33	35.67	119.00	34.93	4.20	6.53	4.40	76.90	29.72	62.60	45.27	31.22	3.48	5.73	15.30	41.71
VI	31.33	33.67	117.33	25.67	3.87	5.33	3.40	128.75	62.07	59.63	49.34	26.58	4.15	6.93	10.90	63.87
VII	29.67	32.67	117.33	22.67	4.00	6.33	4.20	76.95	27.35	59.34	44.23	29.54	3.30	5.59	16.08	34.78
VIII	26.00	30.67	113.33	35.20	5.13	6.40	3.93	83.94	42.80	51.55	47.69	29.71	4.33	8.33	16.82	48.63
IX	30.67	36.00	120.33	22.00	5.07	6.00	3.80	100.34	35.35	71.81	50.41	26.55	4.00	5.56	19.44	28.87
X	27.00	30.33	112.00	17.33	3.73	15.87	4.93	62.19	33.53	80.68	46.99	27.13	8.28	10.44	19.72	52.59
XI	27.00	30.33	112.00	31.60	4.67	14.07	5.93	127.31	46.90	77.37	48.70	25.31	8.74	11.39	14.55	79.82
XII	26.00	32.67	116.00	31.00	4.80	17.60	5.07	101.83	41.82	71.93	47.21	30.20	7.52	10.57	15.01	72.59
XIII	26.67	35.67	119.00	35.87	5.13	9.20	4.53	108.97	54.71	48.48	46.66	31.27	6.93	14.20	28.31	50.28
Mean	28.91	33.42	116.75	28.23	4.50	10.07	4.56	95.94	42.74	67.09	47.35	28.75	6.03	8.96	16.89	54.69
S.E.	0.59	0.65	1.49	1.64	0.46	0.67	0.46	6.66	2.77	5.32	1.56	1.04	0.60	0.63	1.31	5.39
C.V.%	3.46	3.32	2.21	9.79	17.61	11.89	16.62	12.14	10.26	13.04	5.72	6.31	17.13	12.71	14.43	16.76
Percentage contribution of characters towards total divergence																
No. of times appearing first	85.00	36.00	5.00	45.00	0.00	427.00	2.00	94.00	156.00	25.00	13.00	44.00	21.00	83.00	71.00	18.00
% contribution	15.10	2.94	0.41	3.67	0.00	34.86	0.16	7.67	12.73	2.04	1.06	3.59	1.71	6.78	5.80	1.47

separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates (Table 3). The primary branches per plant, kernel yield per plant, harvest index, number of immature pods per plant, biological yield per plant, shelling out-turn contributed maximum towards the total genetic divergence. The analysis of the per cent contribution of various characters towards the total genetic divergence indicated that number of mature pods per plant, days to first flower, 100-kernel weight, 100-pod weight, pod yield per plant and biological yield per plant contributed maximum towards the divergence (Table 3). They accounted for more than 83% towards the total divergence in the material studied. Bases on high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster I and II with the genotypes of cluster XIII, which may lead to broad spectrum of favourable genetic variability for yield improvement in groundnut.

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