Assessment of Genetic Diversity in Groundnut (*Arachis hypogaea* L.) Genotypes under Konkan condition in Maharashtra

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Abstract

One hundred and twenty one groundnut genotypes were evaluated to assess the genetic diversity. The D^2 values were ranging between 3.5 to 17.7 which suggesting the presence of considerable amount of genetic diversity among the genotypes. All the 121 genotypes were grouped into 7 clusters in which cluster had maximum genotypes (109) followed by remaining all the clusters which exhibited two genotypes each. The maximum intra cluster distance was exhibited by cluster VII (311.6) followed by cluster VI (147.2) and I (80.7) while as maximum inter cluster distance was recorded between cluster VI and VII (22.9), followed by cluster II and VII (22.2), cluster III and VII (19.5), indicating a wide divergence between these clusters. Variance of cluster means revealed that dry pod yield plant^{-1}, number of kernels pod^{-1}, shelling percentage, 100 kernel weight and number of pods plant^{-1} were the main characteristics contributing to divergence. On the basis of intra and inter cluster distances, cluster means and *per se* performance of genotypes *viz.*,Pratap Mungphali 2, TGLPS 3, M III, TG 37 A, TKG Bold, M 548, R 2001-1 and TMV (GN) 13 may be recommended for future breeding programme.

Keywords : Divergence, D^2 statistics, intra and inter cluster, groundnut.

Introduction

Groundnut (*Arachishypogaea* L.) is one of the most important oil seed crops of India and contributes about 30 per cent of the total domestic vegetable oil supply. Maharashtra is one of the major groundnuts growing states with an area of 1.96 lakh hectares with the productivity of 1163 kg ha^{-1} during *kharif* season and 0.71 lakh ha area with 1366 kg ha^{-1} productivity during *rabi* season 2013-14. During *kharif,* in Konkan region, groundnut is grown on 8400 hectares area with the productivity of 1130 kg ha^{-1} while, it is cultivated on more than 5000 ha area with 1827 kg ha^{-1} during *rabi* season. For bringing about a further improvement in yield of groundnut under rainfed situation, it is essential to know the extent of diversity among the released and pre-released varieties and germplasm cultures. In this direction studies on genetic divergence among the identified drought-tolerant groundnut genotypes are essential for planning an efficient and successful hybridization programme, since the cross involving genetically diverse parents is likely to produce high heterotic effects and also more variability in the segregating generations for effective selections (Arunachalam 1981 and Venkateswarlu *et al.* 2011). Further, biometric techniques such as multivariate analysis based on Mahalanobis's D^2 statistic (Mahalanobis 1936) quantify the degree of genetic divergence amongst biological populations and assesses the relative contribution of various attributes to total divergence. Genetic diversity studies also help to determine the inherent potential of a cross for heterosis and frequency of the desirable recombinants in advanced generations. In this context, the present investigationwas undertaken to study the genetic divergence in groundnut germplasm to identify potential genotypes for yield contributing characters which could be utilized in further groundnut improvement programme.

Material and Methods

The experimental material comprised of 121 genotypes of groundnut was obtained from Directorate of Groundnut

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Research, Junagadh (Gujarat). The experimental materials were evaluated during four succeeding seasons from *rabi* 2010-11 to 2012-13 at Agricultural Research Station, Shirgaon, Ratnagiri, Maharashtra, India. The genotypes were grown in two rows of 2 m length with 30 x 10 cm spacing during each season.

All the recommended cultural practices were adapted. The observations were recorded on five randomly selected plants in each genotype for 10 quantitative traits *viz*., days to 50% flowering, number of primary branches plant^{-1}, plant height (cm), number of pods plant^{-1}, number of kernels pod^{-1}, dry pod yield plant^{-1} (g), haulm yield plant^{-1} (g), 100 kernel weight (g), shelling percentage and days to maturity. Genetic diversity in the material was analyzed using Mahalanobis's D^2 statistic (Rao, 1952) and the varieties were grouped into different clusters according to Tocher's method.

Results and Discussion

The analysis of variance exhibited significant differences among 121 genotypes of groundnut for all the ten characters. These 121 genotypes were grouped into seven clusters (Table 1). The cluster I had maximum genotypes i.e. 109, followed by two genotypes each in remaining all the clusters. Based on divergence, existed among groundnut population, Katule *et al.* (1992) grouped groundnut genotypes into 8 clusters. Golakiya and Makne (1991) grouped 24 groundnut genotypes in 6 clusters, Venkatramana et al. (2001) grouped 144 genotypes in 6 clusters, Awatade (2007) grouped 40 genotypes in 7 clusters and Nikam and Thaware (2010) grouped 39 genotypes in 9 clusters in their groundnut crop studies.

In the present investigation, the D^2 values (Table 2) among all possible pairs of 121 genotypes ranged from 3.5 to 17.1 suggesting the presence of considerable amount of genetic diversity. Among the clusters maximum intra cluster distance was recorded within Cluster VII (17.7) followed by cluster VI (12.1) and cluster I (9.0). The maximum inter cluster distance was observed between cluster VI and VII (22.9), followed by cluster II and VII (22.2), cluster III and VII (19.5), indicating wide divergence between these clusters. The criteria used for hybridization using D^2 analysis is the inter cluster distances. Those genotypes included in cluster with maximum inter cluster distance were

Table 1 : Distribution of 121 groundnut genotypes into different cluster.

Cluster No.	No. of genotypes included	Genotypes
I	109	T 28, RSB 87, M 145, TMV 10, BG 2, ICGS 37, ICGS 76, RS 138, VRI 3, GG 20, ICGS 5, B 95, BAU 13, ICGV 86325, M 522, R 8808, HNG 10, LGN 2, R 9251, ALR 3, CSMG 884, BG 3, Punjab 1, Karad 4-11, S 230, M 13, GAUG 10, Chandra, Kadiri 2, M 37, M 197, Chitra, GG 11, Kaushal, UF 70-103, CSMG 84-1, DRG 12, DRG 17, GG 13, Kadiri 71-1, Tirupati 3Sp. Improved, AK 12-24, TMV 2, J 11, SB XI, TMV 7, S 206, Jyothi, DH 3-30, MH 1, JL 24, Co 1, Kisan, KRG 1, TG 17, Co 2, GG 2, DGR 36, DH 8, ICGS 11, SG 84, Girnar 1, ICGS 11, RG 141, Tirupati 1, ICG (FDRS)4, ICG (FDRS)10, ICGS 1, GG 3, ICGV 86590, TAG 24, Tirupati 2, GG 4, K 134, GG 5, ALR 2, GG 7, VG 9521, AK 159, JL 220, MH 2, Gangapuri, GG 6, BAU 19, MA 16,TMV 3,TMV 4,TMV 1, JL 286, BSR 1, OG 52-1,TG 1, Kopergaon,GAUG 1, AK 265, AK 303, CO (GN) 4, DH 4-3, DH 40, DH 86, DH 101, GPBD 4, GG 8, GG 15, GG 21, JL 501, Konkan Gaurav
II	2	R 2001-1, TMV (GN) 13
III	2	SG 99, TPG 41
IV	2	M III, TG 37 A
V	2	*Pratap Mungphali* 1, TG 51
VI	2	*Pratap Mungphali* 2, TGLPS 3
VII	2	TKG Bold, M 548

Table 2 : Intra and Inter cluster distance D^2 (above the diagonal) and D value (below the diagonal) on pooled basis.

Clusters	I	II	III	IV	V	VI	VII	Intra cluster
I		67.5	55.2	77.8	61.6	155.8	361.6	80.7
II	8.2		31.0	85.8	53.5	129.3	494.0	12.1
III	7.4	5.6		25.4	43.4	73.0	382.2	13.1
IV	8.8	9.3	5.0		70.4	72.9	319.0	18.7
V	7.9	7.3	6.6	8.4		161.9	304.3	57.3
VI	12.5	11.4	8.5	8.5	12.7		523.5	147.2
VII	19.0	22.2	19.5	17.9	17.4	22.9		311.6
Intra cluster	9.0	3.5	3.6	4.3	7.6	12.1	17.7	

Table 3 : Intra cluster means for different characters and contribution of character towards genetic divergence of groundnut on pooled environment basis.

Characters	Cluster Means							Contribution (%)
	I	II	III	IV	V	VI	VII	
Days to 50% flowering	36.8	34.3	34.7	35.2	34.2	34.2	37.5	1.7
Primary branches plant^{-1}	3.0	2.6	2.5	2.9	2.6	2.6	3.2	0.3
Plant height (cm)	40.1	38.2	37.3	38.3	37.9	35.4	38.1	2.1
Number of pods plant^{-1}	10.4	10.1	7.8	8.5	7.8	8.3	10.1	0.4
Number of kernels pod^{-1}	1.9	1.9	1.9	2.0	1.9	2.0	2.0	1.6
Dry pod yield plant^{-1} (g)	7.3	5.6	6.3	5.6	5.8	7.4	7.3	0.6
Haulm yield plant^{-1} (g)	6.9	5.3	6.0	5.6	5.6	6.0	7.3	0.1
100 kernel weight (g)	44.5	41.5	47.1	51.8	42.9	53.2	50.2	21.4
Shelling %	70.3	73.7	71.0	70.0	68.2	71.1	57.4	14.2
Days to maturity	101.2	98.3	99.5	101.5	101.8	96.7	111.3	57.5

obviously genetically more divergent. Hence, it would be logical to choose genotypes from these clusters in the future breeding programme. Mahalaxmi *et al.* (2005) observed maximum inter cluster divergence between cluster IV and VII. Maximum inter cluster D^2 values between cluster II and IV in both the environment by Venkatramana *et al.* (2001). Nikam and Thaware (2010) reported maximum inter cluster distance between clusters VI and VII as 23.70 in their study of 38 groundnut genotypes.

The cluster means for different characters (Table 3) showed that cluster-III exhibiting highest mean value for the character dry pod yield plant^{-1} (7.4 g). The genotypes, *Pratap Mungphali* 2 and TGLPS 3were the members of this cluster. The cluster I had less number of days to 50% flowering (34.2), and plant height (34.2 cm). While, cluster V had maximum shelling per cent (73.7) and least days to maturity (98.3) and cluster VII exhibited maximum number of primary branches (7.2) and haulm yield plant^{-1} (7.3 g). The two genotypes *viz*., TKG Bold and DM 548 are the member of this cluster. The cluster I recorded maximum number of pods plant^{-1} (10.4).

Golakia and Makne (1992) observed highest mean for the character kernel yield plant^{-1}, biomass yield plant^{-1} and recovery percentage in cluster III. They reported that genotype for important characters like pod yield plant^{-1}, 100-kernal weight and recovery percentage recorded maximum mean performances were grouped into cluster

II, III and IV. Nikam and Thaware (2010) recorded that cluster II exhibited highest mean value for the characters oil percentage and cluster III had maximum number of pods plant^{-1}. Maximum contribution towards the genetic divergence was in days to maturity (57.5%) followed by 100 kernal weight (g) (21.4%) and shelling percentage (14.2%). Nikam and Thaware (2010) observed maximum genetic divergence days to maturity (113.49) followed by shelling percentage (80.07 %) and oil percentage (45.33 %).

Based on cluster mean and genetic diversity studies, genotypes *viz.,* Pratap Mungphali 2, TGLPS 3 for dry pod yield plant^{-1}, number of kernels pod^{-1}, 100 kernel weight and days to maturity, genotypes M III, TG 37 A, TKG BOLD, M 548 for number of kernels pod^{-1} and R 2001-1, TMV (GN) 13 for shelling percentage were considered as potential parents for breeding programme (Table 4).

Table 4 : Genotypes identified for specific characters.

Genotypes identified	Specific characters
Pratap Mungphali 2, TGLPS 3	Dry pod yield plant^{-1}
M III, TG 37 A, Pratap Mungphali 2, TGLPS 3, TKG Bold, M 548	No. of kernels pod^{-1}
R 2001-1,TMV (GN) 13	Shelling percentage
Pratap Mungphali 2, TGLPS 3	100 kernel weight (g)
Pratap Mungphali 2, TGLPS 3	Days to maturity

Conclusion

121 genotypes of groundnut tested could be grouped into 7 clusters of which cluster I had 109 genotypes. The cluster distance was observed indicating a wide divergence between these clusters. On the basis of intra and inter cluster distances, cluster means and *per se* performance of genotypes *viz.,*Pratap Mungphali 2,TGLPS 3, M III, TG 37 A, TKG Bold, M 548, R 2001-1 and TMV (GN) 13 may be recommended for future breeding programme.

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