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Divergence study in groundnut breeding lines

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Abstract
In the present study D^2 analysis was done. The advance breeding lines showed considerable amount of diversity for the morphological traits. On the basis of average D^2, haulm yield per plant contributed maximum divergence followed by pod yield per plant, kernel yield and kernel number per plant. Shelling percent contributed least divergence. All other characters like plant height, number of branches per plant, harvest index, pod number per plant and hundred kernel weights contributed less to D^2 estimates.
On the basis of critical D^2 value (60), 36 genotypes were classified into 10 clusters. Four parents of Spanish groundnut released varieties and their 32 cross derivatives in F6 generation were grouped into ten different clusters. This indicated the large diversity existing in the groundnut varieties giving the opportunity for further improvement in groundnut. Thus recent released varieties contain sufficient diversity. Cluster X, IX and III accommodated ten, eight and four genotypes respectively. Rest of the clusters contains two genotypes each. Cluster X was the largest, accommodating as many as 10 genotypes. The clustering pattern of genotypes showed that the genotypes of different origins/parent were clubbed into one cluster whereas the genotypes belonging to same parent or origin were grouped into different clusters indicating that the new genetic recombination increased genetic diversity giving rise to transgressive segregants. Small intra cluster D^2 value of cluster I, II, IV, V, VI, VII and VIII indicated genotypes within a cluster resemble very close to each other. The genotypes of each cluster belong to same parental origin. Large intra cluster D^2 value of cluster III, IX and X indicated their less divergence. These three clusters also exhibited large inter cluster distance with rest of the clusters. Maximum inter cluster distance was observed between cluster III and cluster X followed by cluster III and cluster IX. Inter cluster distance is the main criterion for selection of genotypes. In this context the genotypes from cluster III, IX and X could be selected as parents for hybridization. Cluster IX showed lowest number of branches per plant, harvest index, number of pods per plant, kernel number per plant and pod yield per plant while cluster X exhibited highest value for haulm yield per plant and hundred kernel yield per plant. Thus OGZ5 may be selected as best parent for cross with AK 12-24 exhibiting high mean value for yield and yield contributing characters for obtaining better recombinants or may be advanced for use as new improved breeding line.

Keywords: Divergence study, groundnut breeding lines, pod yield, segregants

Introduction
Groundnut is an important oil, food, and feed legume crop grown in over world. It covered 24 million ha area worldwide with a total production of 41 million tons in 2012 (FAOSTAT, 2012) [7]. In India, groundnut is cultivated in an area of 4.9 m ha, with production and productivity levels of 5.8 m tons and 1179 kg/ha respectively during 2012. Groundnut is valued as a rich source of energy contributed by oil (48–50%) and protein (25–28%) in the kernels. They provide 564 kcal of energy from 100 g of kernels (*Jambunathan*, 1991).
The cultivated accessions of *Arachis hypogaea* in the gene banks and the advanced breeding lines in the breeding programs are the most frequently used sources of variability in crop improvement programmes. Adequate amount of genetic variability is an important prerequisite for judicious selection of parents. Limited number of parental sources are available for crop improvement programmes, Groundnut genetic resources are available in the gene banks of ICRISAT, National Bureau of Plant Genetic Resources (NBPGR), and Directorate of Groundnut Research (DGR) etc. in India. However, much of the variability is still underexploited in groundnut improvement. Hence, it becomes imperative to ensure genetic diversity of the varieties currently cultivated by the farming community.
Realizing the importance of developing groundnut varieties with high yield, better resistance and superior quality and in the light of the above discussions, efforts were made to evaluate 32 breeding lines along with 4 parental lines during the course of present investigation for the assessment of grouping of test genotypes into different units through D^2 analysis, for their effective use as parents for genetic enhancement of yield.

Materials and Methods

The present "Study on morphometric and molecular variation in groundnut breeding lines." was undertaken in the Department of Plant Breeding and Genetics, College of Agriculture, Orissa University of Agriculture and Technology, Bhubaneswar. The thirty six genotypes were evaluated comprised of 4 parents and their 32 progenies (Table 1). Observations on ten quantitative characters like plant height (cm), number of branches per plant, haulm yield per plant (g), harvest index (%), number of pods per plant, shelling percentage, number of kernels per plant, 100 kernel weight (g), kernel yield per plant (g) and pod yield per plant (g) were recorded from the field trial. Each entry was represented by three rows of 3m length with 3 replications. Based on the genetic divergence the genotypes were grouped into different clusters. It would help in selection of parents for hybridization programme.

Table 1: Plant materials, their source and characters

Variety no	Genotype	Source	Character
1	AK 12-24	Local variety	Well adopted var.
2	TG-26	Local variety	Better grain filling capasity
3	OGX1	AK-12-24 × TG-26	-
4	OGX2	AK-12-24 × TG-26	-
5	OGX3	AK-12-24 × TG-26	-
6	OGX4	AK-12-24 × TG-26	-
7	OGX5	AK-12-24 × TG-26	-
8	R-2001-3	Local variety	Higher number of pod/plant
9	AK-159	Local variety	Large seed and leaf size
10	OGZ1	AK-159 × TG-26	-
11	OGZ2	AK-159 × TG-26	-
12	0GZ3	AK-149 × TG-26	-
13	0GZ4	AK-159 × TG-26	-
14	OGY1	R-2001-3 × TG26	-
15	OGY2	R-2001-3 × TG-26	-
16	OGY3	R-2001-3 × TG-26	-
17	OGY4	R-2001-3× TG-26	-
18	OGY5	R-2001-3 × TG-26	-
19	OGY6	R-2001-3 × TG-26	-
20	OGY7	R-2001-3 × TG-26	-
21	OGY8	R-2001-3 × TG-26	-
22	OGY9	R-2001-3 × TG-26	-
23	OGY10	R-2001-3 × TG-26	-
24	OGY11	R-2001-3 × TG-26	-
25	OGY12	R-2001-3 × TG-26	-
26	OGY13	R-2001-3 × TG-26	-
27	OGY14	R-2001-3 × TG-26	-
28	OGY15	R-2001-3 × TG-26	-
29	OGY16	R-2001-3 × TG-26	-
30	OGY17	R-2001-3 × TG-26	-
31	OGY18	R-2001-3 × TG-26	-
32	OGY19	R-2001-3 × TG-26	-
33	OGY20	R-2001-3 × TG-26	-
34	OGZ5	AK-159 × TG26	-
35	OGZ6	AK-159 × TG26	-
36	OGZ7	AK-159 ×TG26	-

Ten morpho-metric observations were recorded on five consecutive plants in each entry and replications and mean values of 36 entries were used for the analysis of genetic divergence using Mahalonobis's D^2 statitics. Genetic divergence among the 36 genotypes of groundnut of 10 characters also estimated. Genetic divergence (D^2) between any two genotypes is given by the formula. $D^2_p = W_{ij}\, d_i\, d_j$. Where, Wij is the inverse of the common dispersion matrix (W_{ij}), d_i and d_j are the difference in the means of the two genotypes for i^{th} and j^{th} characters.

The computation of D^2 using this formula is complicated and laborious when more number of mutually correlated characters is involved in the divergence analysis. So the characters means were transformed into the set of uncorrelated variable using pivotal condensation of common dispersion matrix following (Rao, 1952). Accordingly all possible D^2 among the 36 genotypes were computed, the relative contribution of individual characters to divergence was assessed by (a) ranking of components D^2 as well as by (b) % contribution to total D^2 over all combinations.

(a) Rank average: In all the D^2 combinations the characters were ranked 1-10 on the basis of their contribution to the D^2. Then rank of each character are summed over all the D^2 combinations to get rank total and then rank average is estimated.

(b) Average D^2: Average contribution to each characters to all the D^2 combinations is worked out.

Grouping of genotypes into different clusters

Tocher's method: Grouping was done by following Tocher (Rao 1952) method. Construction of cluster is to start with 2 most closely related genotypes (having the smallest D^2) and then find a third one which has smaller average D^2 from the first two and so on. At certain stage when it is felt that after adding a particular population, there is a disrupt increase in the average D^2, this population is not added to cluster.

Similarly, construction of second and third and other clusters are formed till all the genotypes are included in one or the other clusters. Cut off value for addition of a genotype / population to a cluster was determined by following method given by Singh and Choudhari (1977). In that the D^2 values of each genotype with all others are to be arranged from the lowest to highest values in matrix form. The highest value of the lowest column is taken as cut off value for deciding on inclusion a genotype in the cluster. After construction of clusters average intra-cluster and inter cluster D^2 value were estimated. Based on the genetic divergence the genotypes were grouped into different clusters. It would help in selection of parents for hybridization programme.

Results and Discussion

D^2 analysis or genetic divergence

The analysis of variance revealed significant differences among the genotypes for all the characters under study there by indicating the presence of ample variability among the genotypes. Chi-squre test indicated that population was divergent. On the basis of magnitude of D^2 values all the 36 genotypes of groundnut for 10 characters, showed that the generalized distance (D^2) between two populations varied from 0.683(OGY2 and OGY10) to 155.419(AK 12-24 and OGZ5) which were indicators of considerable diversity available in the material evaluated. The smallest D^2 estimate (0.683) was observed between OGY2 and OGY10. So these genotypes were much similar in many traits. The largest D^2 estimate (155.419) was obtained between AK 12-24 and OGZ5, which indicated the maximum diversity. In the present study the advance breeding lines showed considerable amount of diversity for the morphological traits. The genetic diversity study among the cultivated groundnut accessions based on morphological trial in one or more seasons was studied by Khote *et al.* (2010), Dolma *et al.* (2010), Venkataravana and Marappa (2010), Sudhir Kumar *et al.* (2010), Upadhyaya *et al.* (2011), Sonone *et al.* (2011) and Suneetha *et al.* (2013). It revealed wide range of D^2 values suggesting the presence of considerable amount of genetic diversity in the genotypes studied which were grouped into several clusters. Genetic relationships among cultivated and wild accessions of groundnut were studied based on microsatellite markers or SSR (Simple Sequence Repeat) revealed that cultivated groundnut presents a relatively reduced variation at the DNA level (Moretzsohn, 2004 and Tang *et al.* 2007).

Relative contributions of 10 characters to D^2 among the genotypes were estimated by number of first rank (table 2). On the basis of average D^2, haulm yield per plant contributed maximum divergence followed by pod yield per plant, kernel yield and kernel number per plant. Shelling percent contributed least divergence. All other characters like plant height, number of branches per plant, harvest index, pod number per plant and hundred kernel weight contributed less to D^2 estimates. Sonone *et al.* (2011) observed contribution of various characters towards the expression of genetic divergence on pooled performance in twelve different environments indicated that pod length (25.6 %), plant height (15.1 %), shelling percent (11.7 %), seed weight (8 %) and number of kernels per plant (7.2 %) contributed maximum (67.5 %) towards total divergence in the material.

Table 2: Relative contribution of each character to genetic divergence

Character	No. of first rank	% Contribution
Plant height (cm)	29	4.6032
No of branches/ plant	28	4.4444
Haulm yield/ plant (g)	162	25.7143
Harvest index (%)	31	4.9206
No. of pods/ plant	53	8.4127
Shelling (%)	9	1.4286
No. of kernels/ plant	80	12.6984
100 kernel weight(g)	54	8.5714
Kernel yield/ plant (g)	82	13.0159
Pod yield/ plant (g)	102	16.1905
Total	630	100

N.B.: Figures in parentheses indicate the order of contribution to divergence

On the basis of critical D^2 value (60), 36 genotypes were classified into 10 clusters (table 3). In the present study, four parents of Spanish groundnut released varieties and their 32 cross derivatives in F_6 generation were grouped into ten different clusters. This indicated the large diversity existing in the groundnut varieties giving the opportunity for further improvement in groundnut. Halward *et al.* (1990) showed in F_3 and F_4 that pod yields in early generations were ineffective in predicting the yield potential of crosses grown in bulk in later generations. Iroume & Knauft (1987) suggested that in F_2, selection among crosses would be advantageous over individual plant selection or within family selection. Selection of genotypes within crosses was the poorest strategy for selection in early generation. Bandyopadhyay *et al.* (1985) opined that with appropriate selection intensities and the use of selection index based on both physiological and yield components, effective selection for yield improvement in groundnut can be made as early as F2 generation.

Table 3: Composition of genetic clusters using D^2 value

Clusters	No. of genotypes	Name of genotypes
I	2	OG Y2, OG Y10
II	2	OG Y12, OG Y15
III	4	AK 12-24, TG 26, OG Y5,OG Y7
IV	2	OG Y13, OG Y 17
V	2	OG Y4, OG Y14
VI	2	R 2001-3, OG Y19
VII	2	OG Y16,OG Y18
VIII	2	OG Y3, OG Y6
IX	8	OG X1,OG X2, OG X3, OG X4, OG X5, AK 159,OG Z1, OG Z4
X	10	OG Z2, OG Z3, OG Y1, OG Y8, OG Y9, OG Y11, OG Y20, OG Z5, OG Z6, OG Z7

Cluster X, IX and III accommodated ten, eight and four genotypes respectively. Rest of the clusters contains two genotypes each. Cluster X was the largest, accommodating as many as 10 genotypes. The clustering pattern of genotypes showed that the genotypes of different origins/parent were clubbed into one cluster whereas the genotypes belonging to

same parent or origin were grouped into different clusters indicating that the new genetic recombination increased genetic diversity giving rise to transgressive segregants.

Table 4: Average intra and inter cluster D^2 values among clusters of groundnut genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	0.683	4.974	29.046	9.263	4.813	11.112	7.100	4.110	36.631	21.371
II		1.233	29.617	5.461	4.043	4.418	2.423	4.480	32.628	24.149
III			48.354	27.675	34.717	35.907	31.784	27.159	41.499	44.782
IV				1.927	6.160	12.432	4.637	6.988	39.270	28.478
V					2.385	11.361	4.434	5.647	42.492	26.040
VI						2.503	7.270	10.472	40.676	32.693
VII							2.514	4.757	34.418	23.812
VIII								2.520	32.933	22.343
IX									21.821	37.886
X										30.301

Small intra cluster D2 value is in table 4. Cluster I, II, IV, V, VI, VII and VIII indicated genotypes within a cluster resemble very close to each other. The genotypes of each belong to same parental origin. Large intra cluster D^2 value of cluster III, IX and X indicated their less divergence. These three clusters also exhibited large inter cluster distance with rest of the clusters. Maximum inter cluster distance was observed between cluster III and cluster X followed by cluster III and cluster IX. Inter cluster distance is the main criterion for selection of genotypes. In this context the genotypes from cluster III, IX and X could be selected as parents for hybridization.

Table 5: Cluster mean of different characters of groundnut

Clusters	Plant height (cm)	No. of branches/ plant	Haulm yield/ plant	Harvest index (%)	No. of pods/ plant	Shelling (%)	No. of kernels/ plant	100 kernel weight (g)	Kernel yield/ plant (g)	Pod yield/ plant (g)
I	16.8	7	7.833	63.062	18.8	73.147	23.467	40.762	9.59	13.267
II	17	7.3	8.733	61.323	17.733	74.265	27.567	36.825	10.278	13.733
III	16.175	5.558	6.867	66.309	15.217	69.924	24.383	37.247	9.106	13.167
IV	15.6	7.1	6.333	69.093	13.9	74.132	28.267	37.017	10.482	14.133
V	16.733	7.833	8.467	60.838	15.867	71.507	24.567	37.397	9.235	12.933
VI	19.467	7.6	10.667	60.515	21.933	73.847	32.7	36.357	11.838	16.067
VII	17.967	7.267	8.567	62.407	15.833	76.615	27.7	38.475	10.703	14
VIII	19.267	6.7	7.333	62.507	15.833	72.96	22.9	37.572	8.5	11.667
IX	16.362	4.771	10.292	52.751	13.313	72.443	20.834	39.144	8.382	11.517
X	17.187	6.457	10.453	57.932	16.383	73.277	21.9	46.508	10.171	13.847

Cluster IX showed lowest number of branches per plant, harvest index, number of pods per plant, kernel number per plant and pod yield per plant while cluster X exhibited highest value for haulm yield per plant and hundred kernel yield per plant (Table 5). Thus OGZ5 may be selected as best parent for cross with AK 12-24 exhibiting high mean value for yield and yield contributing characters for obtaining better recombinants or may be advanced for use as new improved breeding line.

Conclusion

On the basis of magnitude of D^2 values all the 36 genotypes of groundnut for 10 characters, showed that the generalized distance (D^2) between two populations varied from 0.683(OGY2 and OGY10) to 155.419(AK 12-24 and OGZ5) which were indicators of considerable diversity available in the material evaluated. The smallest D^2 estimate (0.683) was observed between OGY2 and OGY10. So these genotypes were much similar in many traits. The largest D^2 estimate (155.419) was obtained between AK 12-24 and OGZ5, which indicated the maximum diversity. In the present study the advance breeding lines showed considerable amount of diversity for the morphological traits.

On the basis of average D^2, haulm yield per plant contributed maximum divergence followed by pod yield per plant, kernel yield and kernel number per plant. Shelling percent contributed least divergence. All other characters like plant height, number of branches per plant, harvest index, pod number per plant and hundred kernel weight contributed less to D^2 estimates.

Four parents of spanish groundnut released varieties and their 32 cross derivatives in F_6 generation were grouped into ten different clusters. This indicated the large diversity existing in the groundnut varieties giving the opportunity for further improvement in groundnut.The progenies of AK 12-24 X TG 26 were grouped into one cluster i.e., cluster X, different from their parent present in cluster III. The progeny OGY19 remained with its parent R2001-3 indicating its similarity with parent. Similarly OGY5 and OGY7 remained with one of their parent TG 26 while OGZ1 and OGZ2 clustered with one of their parent AK-159. Except these genotypes, other progenies remained in different clusters away from their parent. Thus hybridization among the released varieties in groundnut created genetic diversity due to recombination of characters.

Maximum inter cluster distance was observed between cluster III and cluster X followed by cluster III and cluster IX. Inter cluster distance is the main criterion for selection of genotypes. In this context the genotypes from cluster III, IX and X could be selected as parents for hybridization.

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