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D^2 ANALYSIS IN VIRGINIA RUNNER GROUNDNUT GENOTYPES

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ABSTRACT

Analysis of genetic diversity using Mahalanobis' D^2 statistic was carried out in 35 genotypes of virginia runner groundnut. These genotypes were grouped into seven clusters. Cluster I had the maximum number of genotypes. The analysis further indicated that the genotypes of common geographic origin or same location were grouped into different clusters which suggested a lack of relationship between genetic and geographic diversity. The intra- and intercluster average D^2 values indicated maximum statistical distance between clusters II and VII, followed by clusters VI and VII. Cluster VII recorded highest mean kernel yield/plant, pod yield/plant, biomass yield/plant and recovery percentage.

Key words: Cluster, ecogeographical regions, pod yield, genetic variability, diverse parents, groundnut.

It is an established fact that genetically diverse parents are likely to throw desirable segregates and/or to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F_1 and broad spectrum variability in segregating generations [1]. Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. If the parents are identified on the basis of divergence analysis, the resulting recombinants through hybridization would be more promising. The information on this aspect particularly in the subspecific group of groundnut is scanty and, therefore, the present experiment was undertaken.

MATERIALS AND METHODS

The experimental material included 25 genotypes received from ICRISAT, Hyderabad, and 10 advanced fixed genotypes developed through hybridization at the Department of Genetics and Plant Breeding, Parbhani. These 35 genotypes were sown in randomized block

design with three replications in 5-m long rows spaced at 45 cm, maintaining the distance between plants 15 cm. All the recommended packages of practices were followed to raise a good crop. Five competitive plants from the row of each experimental plot were randomly chosen to record observations on 16 quantitative traits.

The genetic divergence analysis was carried out using Mahalanobis' D^2 statistic. The genotypes were grouped into clusters by the Tocher's method as described by Rao [2, 3].

RESULTS AND DISCUSSION

The wilks' test revealed highly significant differences for all the characters. The 35 genotypes were grouped into seven clusters on the basis of D^2 values (Table 1). The distribution pattern of genotypes into clusters indicated that cluster I was the largest containing 25 genotypes, followed by clusters III with 3 genotypes. Three clusters (IV, VI and VII) had a single variety each. The genotypes included in the largest cluster I originated from different ecogeographical regions of the world. This indicated that the geographic distribution and genetic divergence did not follow the same trend. Similar reports of noncorresponding genetic diversity and geographic diversity have appeared earlier [4–8]. Likewise, the genotypes of common geographic origin or same location were grouped in different clusters.

The intra- and intercluster average D^2 values (Table 2) indicated that geographical distribution could not be related to spatial pattern of the clusters. Cluster II and VII showed

Table 1. Clustering pattern of 35 virginia groundnut genotypes

Cluster	No. of genotypes	Genotypes (origin)
I	25	1) 57-95 (Venezuela), 2) Beladi Runner (Sudan), 3) 58-244-1 (Ivory Coast), 4) VRR 640 (India), 5) A 16 (Zaire), 6) VRR 633 (India), 7) Robusto (USA), 8) AH 288 (India), 9) Dixie Runner (USA), 10) 58-198 (Senegal), 14) ERB-1 (Zimbabwe), 15) HR 198 (India), 16) NCAC 17714 (USA), 18) MK 374 (Nigeria), 21) Robut-33-1 (India), 22) HR-100 (India), 24 (Florispan (USA), 27) PBNG-25 (Parbhani, M.S.), 28) PBNG-28 (Parbhani, M.S.), 29) PBNG-29 (Parbhani, M.S.), 31) PBNG-6 (Parbhani, M.S.), 32) PBNG-26B (Parbhani, M.S.), 33) PBNG-27 (Parbhani, M.S.), 34) CS-30 x CS-11 (India), 35) ICGS-11 (India)
II	2	25) PBNG-8 (Parbhani, M.S.), 26) PBNG-26A (Parbhani, M.S.)
III	3	11) M-13 (India), 13) 1357-10 (USA), 30) PBNG-7 (Parbhani, M.S.)
IV	1	12) Chulimbana (Zambia)
V	2	19) Tifton 8-1 (USA), 23) Makulu red (Zimbabwe)
VI	1	20) NC1 (USA)
VII	1	17) 71-202 (Senegal)

Table 2. Intra- and intercluster distance (D^2) for 35 virginia groundnut genotypes

Clusters	I	II	III	IV	V	VI	VII
I	**23.3**	40.4	26.6	29.6	30.1	40.3	40.3
II		**13.0**	35.6	41.7	35.0	31.4	50.3
III			**20.3**	31.2	28.3	28.1	43.5
IV				**00.0**	30.9	37.2	43.3
V					**17.0**	27.8	24.5
VI						**00.0**	44.2
VII							**00.0**

maximum divergence between them (50.3), followed cluster VI and VII (44.2) and cluster III and VII (43.5). Minimum divergence was observed between clusters V and VII (24.5), followed by clusters I and III (26.6). Cluster I (23.3), followed by cluster III (20.3) and cluster V (17.0) had the highest intracluster D value. Cluster II showed divergence (13.0) among its two constituents. However, clusters IV, VI and VII had no intracluster distance (0) as they were represented by a single genotype each. The hybrid derivatives developed at the Agricultural College, Parbhani were distributed in clusters I, II and III. These results suggested that the genetic drift and selection could cause greater diversity than geographical distance.

Cluster means of 16 characters for 35 genotypes are given in Table 3. Differences in cluster means existed for almost all the characters except number of primary branches, undeveloped pods/plant, and oil percentage. Further, amongst the single- variety clusters too, means were variable to the same extent as among the remaining ones. Cluster II had low mean values for days to 50% flowering (28.8) and days to maturity (122.5). The low mean number of days to maturity was associated with cluster VII. This indicated a grouping of early maturing genotypes in these clusters. The mean number of primary branches per plant was highest in cluster III (8.64). Cluster VII had the highest mean number of secondary branches per plant (16.5), followed by cluster VI (14.9) and cluster V (13.9). Clusters IV and VII had low mean number of aerial pegs per plant, i.e. 15.4 and 17.0, respectively. Number of developed pods per plant was highest in cluster VII (33.1), followed by cluster V (32.1). The superiority of this important character was distinct in genotypes like Tifton 8-1, Makulu red and No. 71-202. Cluster VII was superior as evidenced by the highest mean kernel yield/plant (15.0) but had very low shelling percentage (61.9). Cluster mean for shelling percentage was high in cluster I. The maximum shelling percentage was observed in genotype PBNG-29. Cluster VI had fairly high (52.4 g) 100-kernel weight, followed by cluster III (40.5) and cluster II (40.1). Cluster VII recorded the highest mean recovery percentage

Table 3. Cluster means for sixteen characters in 35 virginia groundnut genotypes

Character	Character means in different clusters						
	I	II	III	IV	V	VI	VII
Main stem height (cm)	25.8	30.9	23.1	39.6	29.7	32.7	26.5
Days to 50% flowering	32.5	28.8	34.0	36.0	33.7	30.3	34.7
Number of primary branches/plant	7.3	7.9	8.8	7.7	7.4	7.9	7.5
Number of secondary branches/plant	12.6	12.2	10.9	9.5	13.9	14.9	16.5
Number of aerial pegs/plant	14.4	45.6	19.9	15.4	22.1	23.9	17.0
No. of developed pods/plant	20.4	22.9	18.3	8.5	32.1	19.5	33.1
No. of undeveloped pods/plant	7.1	7.4	7.9	7.7	11.6	6.8	5.3
Kernel yield/plant (g)	9.4	14.3	9.8	3.7	14.0	11.7	15.0
Shelling percentage	64.7	61.5	59.9	53.1	59.6	58.2	61.9
100-kernel weight (g)	30.4	40.1	40.5	33.7	37.5	52.4	34.1
Days to maturity	128.4	122.5	134.8	134.3	129.5	130.0	126.3
Harvest index (%)	28.1	37.6	31.8	12.9	27.0	28.8	22.3
Oil percentage	49.7	50.5	49.6	48.1	49.7	50.5	49.5
Recovery %	48.8	29.9	40.1	26.8	48.8	39.3	61.2
Biomass yield/plant (g)	52.5	62.3	52.0	53.0	86.3	69.6	109.0
Pod yield/plant (g)	14.6	23.4	16.5	6.9	23.4	20.0	24.4

(61.2), biomass yield/plant (109.0) and pod yield per plant (24.4), but Cluster IV had low mean values for these characters. For harvest index and oil percentage, cluster II (37.6 and 50.5) was the best. It could be concluded that the high yielding genotypes coupled with other desirable characters like early maturity, recovery percentage etc. could be selected as parents for hybridization programme from clusters I, V and VII. The genotypes Tifton 8-1, Makulu red, No. 71-202 and PBNG-25 are promising parents for hybridization. However, only one genotype from each cluster should be used in a diallel crossing programme to determine the combining ability of these genotypes for yield and its components. Murty and Arunachalam [9] reached similar conclusions in linseed.

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