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ASSESSMENT OF MULTIVARIATE ANALYSIS FOR KERNEL YIELD AND YIELD COMPONENT TRAITS IN DROUGHT TOLERANT GROUNDNUT GENOTYPES

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Abstract

Thirty drought tolerant groundnut genotypes were evaluated for their genetic diversity with respect to kernel yield and yield component traits at Agricultural Research Station (ARS), Kadiri. The genotypes were classified into six clusters, based on Mahalanobis D2 statistic. Results on inter-cluster distances revealed maximum diversity between genotypes of cluster I and VI. Intra-cluster distance was highest for cluster IV, indicating the existence of high variability within this cluster. A perusal of the results on cluster means revealed high for pod yield per plant, kernel yield per plant, 100 kernel weight, SPAD Chlorophyll Meter Reading, haulm yield per plant and protein content for cluster I, while high oil content and free proline content and low days to 50 per cent flowering and specific leaf area were for cluster VI. Similarly, high sound mature kernel percentage for cluster III indicated the desirability of genotypes from these clusters for improvement of kernel yield and yield traits. Further, oil content, free proline content and protein content contributing to 94.94per cent of the total genetic divergence need to stressed in selection of parents for hybridization programme.

Key words: D2 analysis, genetic divergence, Mahalanobis, kernel yield, oil content.

Introduction

India ranks first in groundnut cultivated area but occupies second place in production. The productivity of groundnut in India is also low, primarily due to cultivation of the crop mostly under rainfed conditions with frequent dry spells. Therefore, there is an urgent need for development of high yielding drought tolerant varieties in groundnut. In view of severity of the drought, high yielding groundnut varieties with improved performance are being developed. For bringing further improvement in yield and resistance to abiotic stresses, it is essential to know the divergence among genotypes for yield and yield component traits. Studies on genetic divergence among cultivars are essential for planning efficient and successful hybridization programme. By using biometric techniques such as multivariate analysis based on Mahalanobis D2 statistic, it has now become possible to quantify the degree of genetic divergence amongst biological populations and to assess relative contribution of various attributes to total divergence. Genetic diversity studies also determine the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. Hence, the present study was undertaken to classify and understand the nature and magnitude of genetic diversity among the groundnut genotypes using Mahalanobis D2 statistic by Mahalanobis (1936).

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Materials and Methods

Experimental material for the present investigation comprised of 30 drought tolerant groundnut genotypes developed at Agricultural Research Station, Kadiri of Acharya N.G. Ranga Agricultural University. These genotypes were sown during *kharif* 2015 at Agricultural Research Station, Kadiri of Ananthapuram District in Andhra Pradesh state. Each genotype was sown in continuous two row plots of 5m row length at a spacing of 30cm between rows and 10cm between plants within the row in Randomized Block Design with two replications. The crop was raised under rainfed conditions and all recommended practices were followed to raise a

healthy crop. Observations were recorded on yield, physiological and quality traits, namely, days to 50 per cent flowering, pods per plant, pod yield per plant, sound mature kernel per cent, kernel yield per plant, 100 kernel weight, SPAD chlorophyll meter reading, specific leaf area, haulm yield per plant, oil content, protein content and free proline content. The observations were recorded from five randomly selected plants for each genotype, in each replication, while observations on days to 50 per cent flowering, oil, protein and free proline content were recorded on plot basis. The data thus obtained were analyzed using Mahalanobis D2 statistic developed by Mahalanobis (1936) and the genotypes were grouped into different clusters according to Tocher's method.

Results and Discussion

Analysis of variance revealed highly significant differences for all traits studied indicating the existence of sufficient variability for effective selection. Further, the 30 drought tolerant genotypes studied were grouped into six clusters (table 1), based on the relative magnitude of D2 values. Among the six clusters, cluster IV consisted of maximum genotypes (10), while cluster II had six genotypes, cluster I, III, and V had four genotypes and clusters VI with two genotypes, indicates the presence of maximum degree of divergence and genetic heterogeneity among the cultivars. The findings are in conformity with the reports of (Suneetha *et al.,* 2012).

An analysis of inter and intra-cluster distances (table 2) revealed maximum inter-cluster distance between clusters I and VI (891.47) followed by II and VI (794.14); III and VI (648.33); II and IV (632.57) and II and V (631.51) indicating that genotypes from these clusters were highly divergent meriting their consideration in selection for hybridization. Similar greater diversity between genotypes from different clusters based on their inter cluster distance has also been reported earlier in the crop (Kumar *et al.*, 2012) and (Dharani *et al.*, 2017). Minimum inter-cluster distance was observed between the clusters V and VI (242.25) indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be minimum for cluster V (91.06) and maximum for cluster IV (204.32). The genotypes included in cluster IV, exhibiting maximum intra-cluster distance, are inferred to be more divergent than those in other clusters.

A perusal of the results on cluster means for yield and yield component traits (table 3) revealed considerable differences between the clusters for all yield component traits under study. High number of pod yield per plant, kernel yield per plant, 100 kernel weight, SPAD

Table 1: Distribution of 30 groundnut genotypes into different clusters.

Cluster No.	No. of genotypes	Name of the genotypes
I	4	K1847, K1882, K1886,K1535
II	6	K1718, K1725, K1877, K1878, K1884, K2047
III	4	K1717, K1799, K1801, K1802
IV	10	K1800, K1805, K1811, K1812, K1813, K1814, K1815, Dharani, K-9, Kadiri-Harithandhra
V	4	K1719, K1848, K1879, K1899
VI	2	K1809, Anantha

Table 2: Average inter and intra cluster distances for 30 groundnut genotypes.

Clusters	I	II	III	IV	V	VI
I	100.53	279.72	358.07	463.91	470.21	891.47
II		121.90	280.82	632.57	631.51	794.14
III			128.47	306.58	575.17	648.33
IV				204.32	316.95	447.94
V					91.06	242.25
VI						126.89

Table 3: Cluster means for different yield and yield component traits in 30 groundnut genotypes.

Traits /Cluster Means	I	II	III	IV	V	VI
Days to 50% flowering	29.533	29.333	28.714	29.333	29.333	28.083
Pods per plant	17.827	17.820	16.033	16.300	19.321	18.642
Pod yield per plant	14.091	13.570	13.068	10.827	12.271	12.225
Sound mature kernel per cent	80.033	80.333	82.952	79.917	82.143	82.208
Kernel yield per plant	8.903	8.409	8.406	6.482	7.956	7.677
100 kernel weight	34.174	32.596	32.796	30.728	30.386	30.787
SPAD chlorophyll meter reading	45.460	43.310	45.750	42.233	42.031	42.313
Specific leaf area	171.560	168.793	173.812	176.830	151.675	143.652
Haulm yield per plant	12.920	12.066	12.438	11.643	9.208	10.060
Oil content	45.497	44.470	45.629	47.525	47.593	47.837
Protein content	24.850	24.083	25.395	25.217	23.562	23.108
Free proline content	1.287	1.663	1.755	1.602	1.438	1.808

Table 4: Relative contribution of characters studied towards genetic divergence in groundnut.

Source	Times Ranked 1st	Contribution %	Mean
Days to 50% flowering	0	0.01	29.056
Pods per plant	0	0.01	17.763
Pod yield per plant	0	0.01	12.875
Sound mature kernel per cent	0	0.01	81.539
Kernel yield per plant	0	0.01	8.159
100 kernel weight	6	1.38	32.024
SPAD chlorophyll meter reading	0	0.01	43.734
Specific leaf area	16	3.68	163.615
Haulm yield per plant	0	0.01	11.333
Oil content	193	44.37	46.293
Protein content	84	19.31	24.341
Free proline content	136	31.26	1.585

chlorophyll meter reading, haulm yield per plant and protein contentwere noticed for the monogenotypic cluster I, comprising of K1847, K1882, K1886 and K1535 genotypes. However, oil content and free proline content were more for cluster VI and low days to 50 per cent flowering and specific leaf area. In similarly, high pods per plant was noticed for cluster V; high sound mature kernel percentage was observed for cluster III, indicating the importance of selection of genotypes from the corresponding clusters in hybridization programmes for effecting improvement of the respective traits. Hybridization of categorized to cluster I with cluster VI exhibiting high pod yield per plant, kernel yield per plant, 100 kernel weight,SPAD chlorophyll meter reading, haulm yield per plant and protein content is predicted to result in desirable and diverse combinations with high kernel yield per plant, pod yield per plant, 100 kernel weight in addition to high oil content and free proline content and low days to 50 per cent flowering and specific leaf area for early maturity varieties and drought tolerant genotypes for high kernel and oil content. Similarly, hybridization between genotypes of cluster I and III are predicted to result in diverse combinations exhibiting superior sound mature kernel percentage, pod yield per plant, kernel yield per plant, 100 kernel weight, SPAD chlorophyll meter reading, haulm yield per plant and protein content. Crossing of genotypes from cluster I with those from cluster V are expected to result in highly diverse genotypes with high pod per plant, pod yield per plant, kernel yield per plant, 100 kernel weight, SPAD chlorophyll meter reading, haulm yield per plant and protein content.

Information on the relative contribution of various plant characters towards divergence has also been reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations (Suneetha *et al.,* 2012). In the present study, oil content (44.37), followed by free proline content (31.26), protein content (19.31) and 100 kernel weight (1.38) contributed maximum towards the total divergence (Table 4). Similar results were reported earlier for oil content by (Sonone and Thaware, 2009) and (Dharani *et al.,* 2017) and for protein content by (Mukri *et al.,* 2014; Venkateswarlu *et al.,* 2011, Dharani *et al.,* 2017 and Nirmala *et al*., 2013) and (Dharani *et al.,* 2017) for 100 kernel weight. Contribution of the remaining characters to total divergence was, however, relatively low. Therefore, oil content, free proline content and protein content contributing to 94.94 per cent of the total divergence need to be stressed in selection ofparents for hybridization.

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