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Research Note

Genetic diversity for kernel yield and qualitative traits in peanut stem necrosis tolerant groundnut genotypes of Andhra Pradesh

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Abstract
Fifty peanut stem necrosis tolerant groundnut varieties were evaluated for their genetic diversity with respect to kernel yield, yield attributing characters and qualitative traits at Agricultural Research Station (ARS), Kadiri. The genotypes were classified into eight clusters, based on Mahalanobis D^2 statistic. Results on inter-cluster distances revealed maximum diversity between genotypes of cluster IV and VIII. Intra-cluster distance was highest for cluster VIII, 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, haulm yield and 100 kernel weight for cluster II, while days to 50 per cent flowering, number of filled pods per plant, sound mature kernel per cent and protein content were more for cluster IV. Similarly, high SPAD Chlorophyll Meter Reading (SCMR) for cluster V indicated the desirability of genotypes from these clusters for improvement of kernel yield and disease resistance. Further, SCMR at 60 days after sowing, protein content, harvest index per cent and 100 kernel weight accounted for 80.98 per cent of the total genetic divergence indicating their importance in the choice of parents for hybridization programme

Key words
D^2 analysis, genetic divergence, grain yield, quality characters

Groundnut (*Arachis hypogaea* L.) is an important oil and protein producing legume crop and belongs to family *Fabaceae*. India is the largest grower and second producer after China and occupies an area of 44.46 lakh ha with a production of 71.81 lakh tones and yield of 1615 kg/ha (Annual report 2104-15, Directorate of Groundnut Research). In India, Andhra Pradesh occupies third place in production and productivity is very low (1027 kg/ha) against national productivity of 1615 kg/ha and world productivity of 1675.9 kg/ha(Annual report 2014-15, Directorate of Groundnut Research, Junagadh, Gujarat). The low productivity can be attributed to factors *viz.*, erratic rainfall, incidence of pests and diseases in addition to cultivation of low yielding varieties. Peanut stem necrosis disease (PSND) was initially observed as an epidemic resulting in complete death of young groundnut plants occurred during the *kharif*, 2000 in Anantapuramu district of Andhra Pradesh. The disease affected nearly 2.25 lakh ha and the crop losses were estimated to exceed Rs. 3 billion (Reddy *et al.* 2002). In view of severity of the disease, high yielding groundnut varieties with improved performance are being developed. For bringing about further improvement in yield and resistance to biotic stresses, it is essential to know the divergence among germplasm lines for yield, yield components and other quality attributes. Studies on genetic divergence among cultivars are essential for planning 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 according to Tomooka (1991). By using biometric techniques such as multivariate analysis based on Mahalanobis's D^2 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 D^2 statistic by Mahalanobis (1936).

Experimental material for the present investigation comprised of 50 PSND tolerant groundnut genotypes which were evaluated at Agriculture Research Station, Kadiri during *Kharif*' 2015 in a randomized block design with two replications. Seeds were sown in the two-row plots of 5m at spacing of 30 cm between the rows and 10 cm between the plants within the row. All recommended practices were followed to raise a healthy crop. Observations were recorded on days to50 per cent flowering, plant height, number of filled pods per plant, total pods per plant, number of seeds per pod, sound mature kernel per cent, haulm yield per plant, pod yield per plant, kernel yield per plant, shelling per cent, harvest index per cent, 100 kernel weight, SPAD Chlorophyll Meter Reading (SCMR) at 60 days after sowing, oil content, protein content. The observations for all the characters mentioned above were recorded from five randomly selected plants for each genotype in each replication, while observations on days to fifty per cent flowering were recorded on

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plot basis. The data obtained were analyzed using Mahalanobis D^2 statistic developed by Mahalanobis (1936) and the varieties were grouped into different clusters according to Tocher's method.

Genetic diversity is a pre-requisite for a breeding programme to obtain desirable segregants. The evaluation of diversity using Mahalanobis D^2 statistic is more reliable method as it provides a requisite knowledge in respect of characters for initiation of the crossing programme. The high heterotic nature in the F_1 and broader spectrum of variability in succeeding segregating generations mainly depends upon using of more diverse parents (Arunachalam, 1981).

Analysis of variance revealed highly significant differences for all characters studied indicating the existence of sufficient variability for effective selection. Further, the 50 varieties studied were grouped into eight clusters (Table 1) based on the relative magnitude of D^2 values. Among the eight clusters, cluster II consisted of maximum number of varieties (22), cluster I had fifteen, cluster III had eight, while IV, V, VI, VII and VIII were comprised of single variety in each cluster, indicates the presence of maximum degree of divergence and genetic heterogeneity among cultivars (Suneetha *et al.* 2012). The mode of distribution of varieties from the same eco-geographical region was observed to be present in different clusters as well as in the same cluster.

An analysis of the inter and intra cluster distances (Table 2) revealed maximum inter-cluster distances between clusters IV and VIII (307.39) followed by VI and VIII (247.91) and III and V (229.41) followed by clusters III and VII (225.78) indicating that varieties from these clusters were highly divergent and selection of parents for hybridization from these clusters is rewarding. Minimum inter-cluster distance was observed between the clusters, VI and VII (61.07) indicating their close relationship and similarity with regard to the characters studied for most of the varieties in the two clusters. Further, intra-cluster distance was observed to be minimum for cluster I (65.28), followed by cluster II (77.86) and maximum for cluster III (78.11), while it was zero for the monogenotypic clusters, namely, clusters IV, V, VI, VII and VIII as they included single variety. The varieties included in cluster III exhibiting maximum intra-cluster distance inferred to be more divergent than those in other clusters.

A perusal of the results on cluster means for yield and yield components (Table 3) revealed considerable differences between the clusters for all characters under study. The genotypes of cluster II registered highest values for haulm yield per plant, pod yield per plant, kernel yield per plant and 100 kernel weight, whereas the genotypes of cluster III exhibited highest cluster mean for shelling per cent, harvest index and low values for SCMR at 60 DAS. Similarly, genotypes of cluster IV recorded the highest values for days to 50 per cent flowering, number of filled pods per plant, sound mature kernel per cent & protein content and recorded minimum values for plant height and 100 kernel weight. While genotypes of cluster V recorded the highest values for SCMR and minimum values for total pods per plant, kernel yield per plant, shelling per cent and oil content. The genotypes of cluster VI recorded higher values for total pods per plant and number of seeds per pod. The genotypes of cluster VII had high values for plant height, oil content and low values for days to 50 per cent flowering, sound mature kernel per cent, harvest index, indicating the importance of selection of genotypes from the corresponding clusters in hybridization programmes for effective improvement of the respective traits.

Information on the relative contribution of various plant characters towards the divergence also reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations (Suneetha *et al*. 2012). Among all the characters studied, SCMR at 60 DAS contributed the maximum (40.65 %) to the diversity by taking first rank in 498 times, followed by protein content (25.88 %) with 317 times ranked first, harvest index (8.49 %) with 104 times ranked first, oil content % (7.92 %) with 97 times ranked first, 100 kernel weight (5.96 %) with 73 times ranked first, plant height (4.98 %) with 61 times ranked first and number of filled pods per plant per plant (2.04 %) with 25 times ranked first. These characters are contributing to 95.92 per cent of the total divergence need to be stressed in selection of parents for hybridization. However, the remaining characters were contributing less to the total divergence.

Similar results of maximum contribution of SCMR at 60 DAS was reported by Nirmala *et al*. (2013); Mukri *et al*. (2014) for protein content; Venkateswarlu *et al.* (2011) and Kumar et al. (2012) for harvest index per cent; Lakshmidevamma *et al.* (2006), Sonone and Thaware (2009) for oil content; Venkateshwarlu *et al.* (2011) and Nirmala *et al.* (2013) for 100 kernel weight Nadaf *et al.* (1986) and Golakia and Makne (1991) for number of filled pods per plant.

The study revealed the existence of genetic diversity among the varieties studied for different yield contributing traits. The existence of diversity among the varieties was similar to the reports of Kumar *et al.* (2012). Further, hybridization of K1800 groundnut variety with high protein content of cluster IV with 04 x 481-005 groundnut variety of cluster VI is predicted to result in desirable

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recombinants with high yield. Further, hybridization between 03 x 485-024-01 of cluster VI and 04 x 481-005 of cluster VIII is also suggested to generate diversified breeding material.

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Table 1. Distribution of 50 groundnut varieties into different clusters

Cluster No.	No. of Genotypes	Name of Genotype
I	15	03 x 427-088, 03 x 427-107, 03 x 397-031, 03 x 427-091, JL-24, K 1809, K 1650, 03 x 427-109, 04 x 479-002, K 1811, K 1799, K 1535, 03 x 461-019, 03 x 482-036, 04 x 479-005
II	22	K 1577, K 1574, 03 x 485-001, 04 x 477-021-2, 04 x 480-007, K 1563, K 1621, K 1647, K 1643, 04 x 477-030, K 1501, K 1576, 04 x 477-031, K 1715, K 1735, 04 x 477-024-1, K 1717, K 1641, K 1725, 04 x 477-021-1, 04 x 479-012, 04 x 477-018
III	8	03 x 427-082, 03 x 427-094, 03 x 398-067, Anantha, 03 X 427-086, Harithandhra, Kadiri 6, Kadiri 9
IV	1	K 1800
V	1	04 x 477-010
VI	1	03 X 485-024-01
VII	1	04 x 481-023
VIII	1	04 x 481-005

Table 2. Average inter and intra cluster distances for 50 groundnut varieties

Clusters	I	II	III	IV	V	VI	VII	VIII
I	65.28	112.08	122.47	86.33	129.48	86.07	107.70	177.02
II		77.86	206.67	176.81	124.52	115.08	112.83	122.22
III			78.11	184.18	229.41	216.15	225.78	184.53
IV				0.00	214.63	92.12	113.76	307.39
V					0.00	149.35	130.89	151.26
VI						0.00	61.07	247.91
VII							0.00	199.92
VIII								0.00

Table 3. Cluster means for different yield and yield attributing traits in 50 groundnut varieties

Traits /Cluster Means	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	32.37	31.84	32.13	37.50	33.00	34.00	31.00	31.50
Plant height (cm)	20.47	21.37	25.24	19.40	21.65	22.30	26.00	20.85
No of filled pods per plant	13.70	13.68	13.76	16.00	10.80	15.10	10.50	10.40
Total pods per plant	15.53	16.16	15.32	17.00	11.50	20.30	12.70	14.80
No of seeds per pod	1.58	1.58	1.59	1.56	1.58	1.72	1.60	1.54
Sound mature kernels (%)	79.13	78.95	81.50	82.00	80.00	77.00	75.00	81.00
Haulm yield per plant (g)	15.08	19.18	14.20	14.60	14.15	15.08	14.60	12.57
Pod yield per plant (g)	10.73	14.24	9.95	10.11	9.80	10.44	9.74	8.38
Kernel yield per plant (g)	7.11	9.22	6.82	6.84	5.03	6.65	5.74	5.13
Shelling percentage (%)	67.06	65.25	69.07	68.29	51.74	65.07	59.03	60.99
Harvest index (%)	0.55	0.54	0.57	0.52	0.49	0.41	0.31	0.40
100 kernel weight (g)	37.99	42.04	35.33	29.40	38.38	45.83	33.42	29.69
SCMR at 60 DAS	37.96	43.87	31.95	37.55	46.25	41.25	44.15	43.40
Oil content (%)	49.61	50.68	50.46	50.97	42.52	50.87	51.91	51.49
Protein content (%)	31.00	25.84	24.69	39.50	24.50	35.50	35.00	12.50

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

Source	Times Ranked 1st	Contribution %	Mean	Min.	Max.
Days to 50% flowering	15	1.22	32.20	28.50	37.50
Plant height (cm)	61	4.98	21.78	13.90	31.30
No of filled pods per plant	25	2.04	13.59	9.20	20.80
Total pods per plant	1	0.08	15.75	11.50	22.40
No of seeds per pod	3	0.24	1.58	1.44	1.72
Sound mature kernels (%)	1	0.08	79.42	71.00	86.50
Haulm yield per plant (g)	11	0.90	16.65	11.22	27.04
Pod yield per plant (g)	0	0.00	12.04	7.48	20.80
Kernel yield per plant (g)	17	1.39	7.87	5.03	14.25
Shelling percentage (%)	2	0.16	65.98	44.06	79.23
Harvest index (%)	104	8.49	54.00	31.48	70.01
100 kernel weight (g)	73	5.96	39.08	28.32	47.74
SCMR at 60 DAS	498	40.65	40.06	28.85	49.80
Oil content (%)	97	7.92	50.21	42.52	52.99
Protein content (%)	317	25.88	27.56	12.50	39.50