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Genetic Diversity Analysis Based on Drought Resistance and Water Use Efficiency Traits in Groundnut (*Arachis hypogaea* L.)

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ABSTRACT

Divergence was studied among 32 genotypes based on data of physiological and yield attributes in groundnut. The analysis of variance indicated significant differences among genotypes for all the attributes studied. Thirty two genotypes were grouped into seven clusters. The cluster size varied from one to 14. The highest inter-cluster distance was recorded between cluster III and VII among which cluster III had five genotypes and cluster VII had single genotype. Crosses between these genotypes would be more rewarding. Based on intra and inter cluster distances and cluster means, parents were identified for further breeding programmes for isolation of useful transgressive segregants.

Key words: *Groundnut, Physiological, Yield attributes and Divergence.*

INTRODUCTION

Groundnut is not only a major oilseed crop but also an important food crop in India. India groundnut occupies an area of 40.68 lakh ha with production of 66.15 lakh tonnes and productivity of 1626 kg ha^{-1} in *Kharif* season. In *rabi-summer,* it is being grown in 8.39 lakh ha with production of 16 lakh tonnes with productivity of 1909 kg ha^{-1}. In Andhra Pradesh, in *Kharif* season, it is cultivated in an area of 6.48 lakh ha with production of 8 lakh tonnes and productivity of 1238 kg ha^{-1}. In *rabi* season,it is cultivated in 0.90 lakh ha with production of 2.07 lakh tonnes and productivity of 2300 kg ha^{-1}[1].

Over two thirds of the global peanut production occurs in rainfed regions where erratic and insufficient rainfall is a major constraint. Drought of various intensities and duration severely limits peanut productivity. Although some agronomic interventions to conserve soil moisture and enhance water use efficiency (WUE) are available, developing groundnut varieties tolerant to drought and efficient in water use offers the best long term and cost effective solution to the uncertainty of availability of water .Various characters *viz.,* high SCMR (SPAD Chlorophyll Meter Reading), low SLA, high RWC, deep root system have been reported to be involved in drought resistance and water use efficiency mechanism.

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With this background, the present study was planned to study the diversity for drought and WUE traits among genotypes consisting of advanced breeding lines, lines from AICRP system and state MLT.

The Mahalanobis D^2 statistic has been used to quantify the degree of divergence among a set of genotypes[2,8,11]. This statistical tool gives information on the divergent parental genotypes to be used in a breeding programme. By Mahalanobis generalized distance estimated by D^2 statistic[7] estimation of degree of divergence between biological populations and computation of relevant contributions of different components to total divergence is done.

MATERIAL AND METHODS

Experimental material used for this study consisted of 32 genotypes of groundnut. They were sown in Randomized Complete Block Design with four replications at Regional Agricultural Research Station, Tirupati during *kharif*, 2017. Each genotype was sown in two rows of 5 m length with a spacing of 30 x 10 cm. Recommended dose of chemical fertilizers @ of 20 kg N, 40 kg P_2O_5 and 40 kg K_2O per hectare in the form of urea, single super phosphate and murate of potash were applied before sowing. Gypsum @ 500 kg ha^{-1} was applied at flowering stage. In each genotype, five competitive plants were selected at random to record observations on the characters, SCMR at 60 DAS, SLA at 60 DAS (cm^2 g^{-1}), root length(cm), root dry mass(g), plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant, 100 seed weight (g), shelling percentage (%),harvest index (%) and pod yield per plant (g). For LAI at 60 and 80 DAS, LAD at 80 DAS (dm^2 day), angle (^{0}) between main axis and primary branches at 60 and 80 DAS three plants were selected at random. Data were subjected for analysis of variance[10] and D^2 analysis and grouping of the genotypes into different clusters was done by using Tocher's method as described by Rao[12] and Singh and Chaudhary[3].

RESULTS AND DISCUSSION

The thirty two genotypes of groundnut were grouped into seven clusters based on D^2 value (Table 1). Cluster I had maximum number of 14 genotypes, whereas cluster II comprised seven genotypes, cluster III had five genotypes, cluster IV had three genotypes, while cluster V, VI and VII had one genotype each. Constellation of genotypes into different clusters based on physiological, yield and yield attributes was at random. Clustering in twenty two genotypes by Makinde and Ariyo[6], did not follow any pattern. The genotypes from different sources were grouped together while some genotypes from the same source were separated into eight different groups. Vasanthi *et al.*[13], reported that clustering pattern was according to the objective for which they were bred. Zaman *et al.*[15], and Islam *et al.*[5], reported that genotypes of quite different pedigree and/or genotypes of common geographic origin or bred at same location were grouped into different clusters.

The inter-cluster distance (Table 2) were larger than the intra-cluster distance which indicated that greater diversity among the genotypes of distant group[15]. Maximum intra-cluster D^2 (112.90) and D (10.62) distances were recorded by cluster I while minimum distance was noticed in clusters V, VI and VII as they had single genotype each. Inter-cluster average D^2 values ranged from 238.78 to 3316.04. Maximum inter-cluster D^2 value was observed between cluster III and VII (3316.04). Hence the genotypes from these clusters may be utilized as parents for hybridization which would result in high heterotic expression for physiological and yield components and wider segregation in filial generations. By using such genotypes as parents in hybridization programme, superior recombinants can be obtained. Similar inferences were also suggested by Golakia and Makne[4], Vijayasekhar[14] in groundnut. While minimum inter-cluster D^2 value was found between II and V (238.78) indicating that most of the characters had similar values in these clusters.

The cluster mean value (Table 3) for SCMR at 60 DAS was maximum in cluster II (45.12) and minimum in cluster V (40.13). Cluster VI had maximum SLA at 60 DAS (207.67) while cluster I had minimum SLA at 60 DAS (179.32). Mean values of LAI at 60 DAS ranged from 2.92 (cluster I) to 3.88 (cluster VII). LAI at 80 DAS ranged from 2.29 in cluster V to 5.65 in cluster VI. Cluster VI had maximum mean (290.98) for LAD at 80 DAS and it was minimum in cluster IV (163.24). Mean values of angle between main axis and primary branches at 60 DAS was from 48.67 (cluster VII) to 84 (cluster III).

Angle between main axis and primary branches at 80 DAS was highest in cluster III (85.41) and lowest in cluster VII (48.67). Cluster V and cluster VI showed maximum root length (10.83) whereas in cluster VII it was low (9.70). Mean root dry mass was minimum (0.55) in cluster V and maximum (0.74) in cluster VI. Maximum number of primary branches per plant was identified in cluster VII (7.30) whereas the value was minimum in cluster V (3.75). Cluster VII exhibited maximum number of secondary branches per plant (4.45) and cluster V showed minimum number of secondary branches per plant (0.10).

Plant height ranged from 60.60 (cluster VI) to 38.48 (cluster VII). Number of pegs per plant was maximum in cluster VII (39.70) and minimum in clusters V (20.63). Cluster VI had maximum number of mature pods per plant (24.33) while cluster III had minimum number of mature pods per plant (11.25). Number of immature pods per plant ranged from7.65 in cluster VII to 2.07 in cluster III. Shelling percentage was maximum in cluster V (71.50) and minimum in cluster VI (64.75). Highest 100-seed weight was found cluster III (39.45) while it was lowest in cluster VI (32). Mean value of harvest index ranged from 32.00 (cluster IV) to 47.64 (cluster VII). Pod yield per plant was maximum in cluster VII (17.90) whereas it was minimum in cluster IV (8.90). Intercrossing of the genotypes from these clusters would be useful to generate a wide range of variability for effective selection. Major emphasis has been given by many earlier workers[13,9] on cluster means for selecting the best parents for crossing programme.

Among all the characters studied, angle between main axis and primary branches at 60 DAS contributed maximum (72.58%) to the diversity by taking first rank 360 times (Table 4), followed by plant height (6.85%) ranking 34 times first, LAI at 80 DAS (5.44%) with 27 times ranking first and angle between main axis and primary branches at 80 DAS (5.44%) with ranking 27 times first. The characters, number of secondary branches per plant, LAI at 60 DAS, SLA at 60 DAS, harvest index, shelling percentage, number of primary branches per plant, SCMR at 60 DAS, number of mature pods per plant, number of immature pods per plant and 100-seed weight contributed 3.43, 2.02, 1.41, 1.01, 0.6, 0.4, 0.2, 0.2, 0.2 and 0.2 per cent respectively to the total genetic divergence. On contrary, LAD at 80 DAS, number of pegs per plant and pod yield per plant did not contribute towards genetic divergence. Vasanthi *et al.*[13], studied genetic diversity among 29 genotypes based on ten physiological attributes- LAD, LAI. CGR, NAR, SLA, SCMR, seedling vigour index, germination percentage, harvest index and pod yield per plant. LAD at 54 DAS contributed maximum (34.48%) followed by LAI at 72 DAS (20.20%), LAD at 72 DAS (12.81%), CGR at 72 DAS (12.32%), CGR at 54 DAS (8.37%), harvest index (4.68%) and SLA at 72 DAS (3.21%).

Table 1: Distribution of 32 genotypes of groundnut in different clusters (Tocher's method)

Cluster	Number of Genotypes	Genotypes
I	14	TCGS-1694, TCGS-1696, ALG-06-320, K 1789, TCGS-1630, R 2001-2, R-2001-3-1, R 2001-3, TCGS-1616, K 1847, ICG 86325, K1805, TCGS-1073, K 9
II	7	TCGS-1097, GG 20, K 1725, TCGS-1157, K. Anantha, K 6, J 89
III	5	R-2001-2-1, K 1811,Dharani, ICGS 76, GG 16
IV	3	TCGS-1622, K. Harithandra, GPBD-4
V	1	Narayani
VI	1	TCGS-1653
VII	1	SG 99

Table 2: Average intra and inter cluster D^2 and D values in 32 genotypes of Groundnut

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	**112.90** **(10.63)**	363.62 (19.07)	454.29 (21.31)	1050.3 (32.41)	304.55 (17.45)	304.12 (17.44)	1612.33 40.15)
Cluster 2		**102.86** **(10.14)**	1312.14 (36.22)	317.86 (17.83)	238.78 (15.45)	793.22 (28.16)	686.1 26.19)
Cluster 3			**93.76** **(9.68)**	2539.13 (50.39)	986.94 (31.42)	401.63 (20.04)	3316.04 (57.59)
Cluster 4				**111.91** **(10.58)**	611.9 (24.74)	1569.09 (39.61)	320.29 (17.90)
Cluster 5					**0.00** **(0.00)**	575.34 (23.99)	1152.37 (33.95)
Cluster 6						**0.00** **(0.00)**	2047.55 (45.25)
Cluster 7							**0.00** **(0.00)**

Figures in parenthesis indicate D values
Figures in bold indicate intra-cluster D^2 values

Table 3: Relative contribution of physiological, yield and yield attributes to genetic diversity in 32 groundnut Genotypes

Sl. No.	**Characters**	**Times ranked first**	**Contribution (%)**
1.	SCMR at 60 DAS	1	0.20
2.	SLA at 60 DAS	7	1.41
3.	LAI at 60 DAS	10	2.02
4.	LAI at 80 DAS	27	5.44
5.	LAD at 80 DAS	0	0.00
6.	Angle between main axis and primary branches at 60 DAS	360	72.58
7.	Angle between main axis and primary branches at 80 DAS	27	5.44
8.	Root length	0	0.00
9.	Root dry mass	0	0.00
10.	Number of Primary Branches per plant	2	0.40
11.	Number of secondary Branches per plant	17	3.43
12.	Plant height	34	6.85
13.	Number of pegs per plant	0	0.00
14.	Number of mature pods per plant	1	0.20
15.	Number of immature pods per plant	1	0.20
16.	Shelling percentage	3	0.60
17.	100-seed weight	1	0.20
18.	Harvest index	5	1.01
19.	Pod yield per plant	0	0.00

Table 4: Cluster means for physiological,yield and yield attributes in 32 groundnut genotypes (Mahalanobis's D^2 method)

Clus-ter No.	**SCMR**	**SLA**	**LAI 60**	**LAI 80**	**LAD**	**Angle 60**	**Angle 80**	**RL**	**RDM**	**PB**	**SB**	**PH**	**PP**	**MP**	**IP**	**SP**	**100 SW**	**HI**	**PYP**
I	44.36	179.32	2.92	2.84	173.80	72.30	73.53	10.38	0.59	4.78	0.82	46.09	24.68	15.34	2.57	70.50	34.80	45.70	10.96
II	45.12	181.74	2.95	2.60	166.52	61.80	64.49	10.02	0.61	4.85	1.02	41.07	21.66	12.46	2.51	70.64	37.71	43.88	10.80
III	43.18	191.48	3.26	3.22	190.92	84.00	85.41	10.25	0.61	4.91	1.00	47.38	20.99	11.25	2.07	69.90	39.45	41.98	10.02
IV	42.59	195.93	3.30	2.53	163.24	52.28	54.03	10.38	0.71	4.75	0.58	46.33	21.39	12.28	2.60	69.83	32.17	38.00	8.90
V	40.13	197.87	3.66	2.29	178.75	61.58	76.25	10.83	0.55	3.75	0.10	55.10	20.63	12.50	2.50	71.50	34.75	41.88	9.70
VI	42.78	207.67	3.50	5.65	290.98	75.00	76.00	10.83	0.74	4.61	1.10	60.60	30.10	24.33	2.95	64.75	32.00	40.16	12.90
VII	44.10	184.97	3.88	3.63	230.89	48.67	50.88	9.70	0.72	7.30	4.45	38.48	39.70	22.45	7.65	68.50	38.00	47.64	17.90

SCMR- SPAD chlorophyll metre reading at 60 DAS; SLA - Specific leaf area at 60 DAS **($cm^2\ g^{-1}$)**; LAI 60 -Leaf area index at 60 DAS; LAI 80 - Leaf area index at 80 DAS; LAD - Leaf area duration at 80 DAS(dm^2 day); Angle 60 - Angle between main axis and first two primary branches at 60 DAS (^{0}); Angle 80 - Angle between main axis and first two primary branches at 80 DAS (^{0}); RL- Root length (cms); RDM- Root dry mass (g); PB- Number of primary branches per plant; SB- Number of secondary branches per plant; PH= Plant height (cms); PP- Number of pegs per plant; MP- Number of mature pods per plant; IP- Number of immature pods per plant; SP- Shelling percentage (%); 100 SW- 100 seed weight (g); HI- Harvesr index (%); PYP- Pod yield per plant (g)

CONCLUSION

From the above discussion, it is suggested that the character with maximum contribution towards divergence should be given importance in selection of parents for hybridization programme. Considering the cluster distances and cluster means in the present investigation, emphasis should be given to crosses between genotypes belonging to cluster VII and cluster III; cluster VII and cluster III in order to get transgressive segregants for physiological, yield and yield parameters since these genotypes showed maximum diversity among themselves with desirable yield parameters. Similarly, the crosses between genotypes in cluster VII and cluster I could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance.

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