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RESEARCH ARTICLE

Genetic Diversity for Yield and Water Use Efficiency related Traits in Groundnut (*Arachis hypogaea* L.)

K Gangadhara, AL Rathnakumar, PP Thirumalaisamy, BC Ajay and HK Gor
ICAR-Directorate of Groundnut Research, Junagadh–362001, Gujarat, India

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Cluster analysis using Mahalnobis D^2 was performed using 97 groundnut diverse genotypes for 14 yield contributing and water use efficiency related traits. The genotypes were grouped into twelve clusters based on D^2 statistic. Cluster II was the largest with 54 genotypes followed by cluster I with 33 genotypes and remaining ten clusters had one genotype each. The inter cluster D^2 values revealed maximum divergence between cluster VI and cluster III (1736), followed by cluster XII and cluster III (1622); cluster VI and cluster X11 (1389); cluster IX and cluster XI (1171) and cluster XI and cluster II (1041). It was observed that plant height was the largest contributor (65%) towards genetic divergence followed by days to maturity (10%) and secondary branches per plant (10%), SPAD Chlorophyll Meter Reading (SCMR; 4.3%) kernel length and hundred pod weight (1.2%) and Specific Leaf Area (SLA; 0.06%) contributed the least for divergence. Estimates of GCV and PCV were high for plant height, primary and secondary branches and pod yield per plant indicating higher genetic variation present in the genotypes studied. High heritability coupled with high genetic advance as per cent of mean was observed for days to fifty per cent flowering, secondary branches per plant, hundred pod and kernel weight, kernel length and, SCMR. SLA exhibited moderate estimates of heritability and genetic advance as per cent of mean.

Key Words: Divergence, Germplasm, Yield, Water use efficiency

Introduction

Groundnut is oilseed legume crop grown mainly by small and marginal farmers in arid and semi arid tropical areas. It covers an area of 53 lakh hectares and production of 91 lakh tonnes with productivity of 1731 kg/ha in India (FAOSTAT, 2017). In spite of having largest groundnut area in the world, its production and productivity levels are low in India because maximum area (75%) is rain fed condition. Hence, the crop is frequently subjected to drought stresses of different duration, intensities and timing.

Use of genetic resources has been limited in groundnut breeding programs, resulting in a narrow genetic base of cultivars (Upadhyaya *et al*., 2005). Characterising groundnut germplasm for agronomically superior traits is currently a major part of groundnut breeding efforts across the globe. Therefore identification of trait specific broad based germplasm and pyramiding of novel gene combinations in breeding population is important breeding strategy to address the complex nature of water deficit stresses. The Mahalanobis D^2 analysis followed by cluster analysis using Tocher's method is the rational criteria to assess the divergence and identifying diverse parents for hybridization. In the present study, efforts have been made to assess the genetic diversity in a set of 97 groundnut genotypes based on yield and surrogate traits of water use efficiency.

Materials and Methods

Ninety seven diverse groundnut genotypes consisting of released varieties of India and germplasm accessions obtained from Genetic Resources Section of ICAR-DGR, Junagadh (Table 1) including 4 checks were planted in the Randomized Complete Block Design (RCBD) with two replications at the Experimental plots of ICAR-Directorate of Groundnut Research (DGR) Station, Junagadh, Gujarat, India during *kharif*-2017. ICAR-DGR is situated between 21.49° N latitude and 70.44°E longitude at an elevation of 107 meters above mean sea level. Recommended agronomic practices were followed to raise crop. Each genotype was sown in a single row of 3m length and with a spacing of 60×10 cm. The observations on days to first flowering, days to 50% plants flowering, plant height, number of primary and secondary branches per plant, days to

**Author for Correspondence: Email- Gangadhara.K1@icar.gov.in*

Table 1. List of 97 groundnut genotypes used for diversity study

S.No.	Genotype	Origin	S.No.	Genotype	Origin	S.No.	Genotype	Origin	S.No.	Genotype	Origin
1	NRCG 6780	AUSTRALIA	25	NRCG 14487	UNKNOWN	49	GG 2	INDIA	73	SB XI	INDIA
2	NRCG 17277	BRAZIL	26	NRCG 14412	USA	50	GG 3	INDIA	74	SG 99	INDIA
3	NRCG 14507	EQUDOR	27	NRCG 14386	CHINA	51	GG 6	INDIA	75	Spanish Improved	INDIA
4	Gangapuri	INDIA	28	NRCG 14309	HONDURAS	52	GG 8	INDIA	76	TAG 24	INDIA
5	NRCG 14345	INDONESIA	29	GG 12	INDIA	53	Girnar 1	INDIA	77	TG 38	INDIA
6	NRCG 14379	SUDAN	30	GJG 17	INDIA	54	Girnar 3	INDIA	78	TG 51	INDIA
7	NRCG 14435	USA	31	Kaushal	INDIA	55	GJG 9	INDIA	79	TLG 45	INDIA
8	NRCG 14491	CAMAROON	32	M 13	INDIA	56	GJG 31	INDIA	80	TMV 9	INDIA
9	GG 20	INDIA	33	NRCG 14467	INDIA	57	GPBD 4	INDIA	81	TPG 41	INDIA
10	Girnar 2	INDIA	34	Somnath	INDIA	58	ICGV 91114	INDIA	82	VRI (Gn)-6	INDIA
11	HNG 10	INDIA	35	NRCG 14475	UNKNOWN	59	J 11	INDIA	83	VRI 2	INDIA
12	HNG 69	INDIA	36	NRCG 734	USA	60	JGN 23	INDIA	84	VRI 3	INDIA
13	ICGS 76	INDIA	37	Sun oleic	USA	61	JGN 3	INDIA	85	NRCG 14477	INDONESIA
14	Kadiri 3	INDIA	38	NRCG 14368	ARG	62	JL 220	INDIA	86	NRCG 14456	TANZANIA
15	LGN 2	INDIA	39	NRCG 14472	BURMA	63	JL 24	INDIA	87	NRCG 1439	TAIWAN
16	M 522	INDIA	40	NRCG 10983	CENTRAL AFRICAN REPUBLIC	64	JL 501	INDIA	88	NRCG 14405	UNKNOWN
17	NRCG 14457	INDIA	41	NRCG 14485	CONGO	65	Kadiri 6	INDIA	89	NRCG 14326	UNKNOWN
18	NRCG 2615	INDIA	42	GG 7	INDIA	66	Kadiri 9	INDIA	90	NRCG 7627	UNKNOWN
19	R 8808	INDIA	43	TG 26	INDIA	67	NRCG 10620	INDIA	91	NRCG 8763	UNKNOWN
20	R 9251	INDIA	44	TG 37 A	INDIA	68	NRCG 14343	INDIA	92	NRCG 14336	USA
21	TG 39	INDIA	45	AK 159	INDIA	69	NRCG 14350	INDIA	93	NRCG 14501	USA
22	TGLPS 3	INDIA	46	AK-12-24	INDIA	70	NRCG 14474	INDIA	94	NRCG 14407	ZIM
23	NRCG 14463	KOREA	47	Dh 101	INDIA	71	R 2001-2	INDIA	95	NRCG 14424	ZIM
24	NRCG 12431	SENEGAL	48	DH 86	INDIA	72	S 206	INDIA	96	NRCG 14473	ZIM
									97	NRCG 17284	INDIA

maturity, hundred pod and kernel weight, kernel width, kernel length, pod yield per plant and late leaf spot incidence were recorded on a five random plants from each genotype.

The surrogate traits of water use efficiency, SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) were measured at 60 days after planting. SCMR was recorded at 60 days after sowing by collecting the second to third leaves from the top of the main stem of each plant and transported to a laboratory soon fresh weight was recorded. SCMR was measured immediately by a Minolta handheld portable SCMR meter (SPAD-502 plus Minolta, Tokyo, Japan), using four leaflets per sample and care was taken to ensure that the SPAD meter sensor fully covered the leaf lamina, avoiding any interference from veins and midribs. The same samples were further measured for leaf area, using a leaf area meter (LI 3100C Area meter, LI COR Inc., USA). The modified 1-9 point scale to late leaf spot as given by Subba Rao *et al.* (1990) was used for late leaf spot (LLS) screening under the natural condition. The analysis of genetic divergence was carried out using Mahalanobi's (1936) D^2 statistic and clustering of genotypes was done as per Tocher (Rao, 1952) using Indostat software package. Genotypic and phenotypic coefficients of variation were worked out as per the method suggested by Burton and De Vane (1953), heritability and genetic advance were calculated according to Johnson (1955) and Robinson *et al.* (1949).

Results and Discussion

Genetic improvement in groundnut crop depends on extent of genetic variability for yield and its components, resistance/tolerance to biotic and abiotic stresses. Judicious selection of parents for hybridization based on

genetic divergence between genotypes using D^2 statistics proves to be useful tool. The present investigation aims to determine the magnitude and extent of variability and extent of divergence among genotypes for 14 different traits including two surrogate traits of water use efficiency.

Variability and genetic parameters

The analysis of variance (Table 2) for different traits exhibited significant differences among the genotypes for all the traits studied which indicates that considerable genetic variability is available in the genotypes studied. This genetic variation enables selection of desired genotypes for improvement in desired direction. First flowering ranged from 21 to 33 days and 50 per cent flowering ranged from 23 to 37 days. Plant height was in the range of 25 to 69 cm. Primary and secondary branches per plant were between 3 to 8 and 1 to 24 respectively. Hundred pod weight ranged from 35 to 108 g and hundred kernel weight ranged from 15 to 48 g. Kernel shape which is decided by kernel length and kernel width ranged from 10 to 17 mm and 6 to 8 mm respectively. Pod yield per plant was as low as 2 g to as high as 18 g per plant (Table 3). The two surrogate traits of water use efficiency *viz.,* SPAD cholorophyll meter reading (SCMR) ranged between 19 and 39 and specific leaf area (SLA) ranged from 155 to 259 $cm^2\ g^{-1}$. Range of disease score for late leaf spot indicated that the genotypes fell between tolerance (recorded a disease score of 5) to susceptibility (recorded a disease score of 8). Most of the genotypes studied matured early (92 to 106 days) irrespective of botanical groups. It may be due to shortening of life cycle to escape end-of-season drought that prevailed during *kharif* 2017.

Selection efficiency mainly depends on the magnitude of genetic variability for quantitative traits. An assessment of heritable and non-heritable components of the total variability decide breeding procedure to be adopted. The nature and magnitude of variation for individual traits was assessed by phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (Table 3). High GCV and PCV estimates were observed for plant height, primary and secondary branches per plant and pod yield per plant indicating the higher genetic variation observed in the genotypes. Higher estimates of GCV and PCV for these traits were not uncommon in groundnut and have already been well documented (Sudha *et al.,* 2012; Sunday and Omalayo 2013).

Four other traits, days to first and fifty per cent flowering, kernel length, SPAD chlorophyll meter reading and reaction to late leaf spot incidence were exhibited moderate estimates of GCV and PCV. Moderate estimates for days to first flowering (Patel, 2017); days to fifty per cent flowering (Sunday and Omalayo, 2013); SCMR (Yamunara, 2015 and Savita, 2012) and reaction to late leaf spot incidence (Vishnuvardhan *et al.,* 2012) have already been reported in groundnut. Low GCV and PCV estimates were observed for days to maturity (Zaman *et al*., 2011) and kernel width which indicate the existence of low variability for these traits in the genotypes studied.

Table 2. Analysis of variance for yield and water use efficiency related traits in groundnut

S. No.	Character	Source of Variation (Mean sum of squares)			CV
		Replication (df=1)	Genotypes (df=96)	Error (df=96)	
1	Plant height (cm)	0.6237	198.49***	0.70	1.98
2	Primary branches per plant	0.0463	0.0463***	0.23	10.45
3	Secondary branches per plant	5.2783**	32.478***	0.74	16.6
4	Late leaf spot (LLS) incidence	1.3195*	1.6429***	0.21	6.3
5	Days to maturity	4.0412***	10.018***	0.29	0.5
6	Days to first flowering	1.4896	17.126***	3.45	7.3
7	Days to 50% flowering	0.3298	26.001***	4.75	7.8
8	SPAD chlorophyll meter reading	17.460*	39.686***	2.87	5.7
9	Specific leaf area ($cm^2\ g^{-1}$)	135.98	993.47***	337	9.0
10	Hundred pod weight (g)	791.73***	394.65***	55.8	10.7
11	Hundred kernel weight (g)	211.58***	70.582***	9.06	10.5
12	Kernel width (cm)	2.7505***	0.3997***	0.13	4.77
13	Kernel length (cm)	0.0561	5.4695***	0.76	6.47
14	Pod yield per plant (g)	15.164	28.708***	8.33	32.4

Table 3. Genetic parameters for yield and water use efficiency related traits in groundnut

S.No.	Particulars	Minimum	Maximum	Mean	σ^2_g	σ^2_p	GCV (%)	PCV (%)	$h^2_{(BS)}$	GA	GAM
1	Plant height (cm)	25	69.5	42.09	98.9	99.5	23.62	23.7	99.3	20.4	48.5
2	Primary branches per plant	3	8	4.62	1.04	1.27	22.1	24.45	81.7	1.9	41.2
3	Secondary branches per plant	1	24	5.14	15.87	16.6	77.44	79.21	95.6	8.0	155.9
4	Late leaf spot (LLS) incidence	5	8	7.16	0.719	0.92	11.83	13.41	77.8	1.5	21.5
5	Days to maturity	92	106	96.03	4.86	5.15	2.297	2.36	94.4	4.4	4.6
6	Days to first flowering	21	33	25.14	6.83	10.28	10.39	12.75	66.5	4.4	17.5
7	Days to 50% flowering	23	37	27.75	10.62	15.37	11.47	14.12	96.1	5.6	20.1
8	SPAD chlorophyll meter reading	19.3	40.0	29.58	18.4	21.27	14.5	15.95	86.5	8.2	27.8
9	Specific leaf area ($cm^2\ g^{-1}$)	155.5	259.4	202.60	328	665.4	8.937	12.73	49.3	26.2	12.9
10	Hundred pod weight (g)	35.5	108.6	69.60	196.4	225.2	18.67	21.73	75.2	23.3	33.4
11	Hundred kernel weight (g)	15.9	48.0	28.44	30.76	39.8	19.49	22.18	77.3	10.0	35.3
12	Kernel width (mm)	6.4	8.65	7.64	0.133	0.26	4.779	6.753	50.1	0.5	7.0
13	Kernel length (mm)	10.1	17.75	13.40	2.356	3.11	11.41	13.122	75.7	2.8	20.5
14	Pod yield per plant (g)	2.1	18.51	8.90	10.187	18.52	35.82	48.311	55	4.9	54.7

σ^2 g – Genetic variance | σ^2 p - Phenotypic variance | $h^2_{(BS)}$ - Heritability in broad sense
GCV (%) - Genotypic coefficient of variation | PCV (%) -Phenotypic coefficient of variation | GAM- Genetic advance as per cent of mean

Heritability estimates along with genetic advance estimates would be more useful in predicting effectiveness of selection. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, primary and secondary branches per plant, days to fifty per cent flowering, hundred pod and kernel weight, kernel length, SPAD chlorophyll meter reading and reaction to late leaf incidence suggesting role of additive gene effects and scope for simple phenotypic selection. Sudha *et al.* (2012), Vishnuvardhan *et al*. (2012), Rao *et al.* (2012) and Sunday and Omalayo (2013) have also advocated selection of these traits for genetic improvement. The traits *viz*., days to first flowering exhibited high heritability with moderate genetic advance as per cent of mean (Zongo *et al*., 2017). Specific leaf area (SLA) had moderate heritability and genetic advance as per cent of mean indicating role of environment in the inheritance of these traits. Pod yield per plant showed moderate heritability coupled with high genetic advance as per cent of mean. Two traits, kernel width (with moderate heritability and low genetic advance as per cent of mean) and days to maturity (high heritability with low genetic advance as per cent of mean) exhibited non-additive effects indicating less usefulness of these traits for direct selection. These results are in accordance with the findings of Vishnuvardhan *et al*. (2012) for days to maturity, Shreya *et al.* (2014) for specific leaf area and Kavera (2008) for pod yield per plant.

Correlation analysis

Days to first and fifty per cent flowering, hundred pod and kernel weight, kernel width and length and SPAD Chlorophyll meter reading (SCMR) were correlated significant positively with pod yield per plant, whereas the relationship of plant height and specific leaf area (SLA) with pod yield was negative and significant (Table 4). High SCMR indicates higher unit chlorophyll efficiency and higher photosynthesis rate and which in turn results in higher pod yield (Nageswara Rao *et al.,* 2001). The surrogate traits of water use efficiency, SPAD chlorophyll meter reading and specific leaf area correlated negatively to each other (Nageswara Rao *et al.,* 2001 and Upadhyaya, 2005). SPAD chlorophyll meter reading correlated positively with flowering and productive traits. Hence SCMR can be a more reliable trait for enhanced WUE and yield traits (Kalariya *et al.,* 2017).

Diversity analysis

The D^2 statistic is more useful tool to determine divergence among populations in terms of generalized group distance. Following the procedure of Tocher (Rao,1952) and by treating the estimated D^2 values as the square of the generalized distance, 97 genotypes studied were grouped into twelve clusters (Table 5, Fig. 1). Cluster II was the largest with 54 genotypes followed by cluster I with 33 genotypes. Remaining ten clusters had one genotype each. Interestingly it has been observed that the 13 genotypes in both the large clusters

Table 4. Phenotypic correlation coefficients of yield and water use efficiency related traits in groundnut

Trait	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1	-0.128	-0.179	-0.032	-0.143	-.312**	-.326**	-.417**	0.216*	-.207*	-.260*	-.226*	-.409**	-.331**
X2		1	0.196	-0.096	0.022	0.139	0.129	0.118	-0.18	0.037	0.028	0.148	0.094	0.188
X3			1	-.210*	0.250*	0.288**	.330**	0.134	-0.177	-0.176	-0.187	-0.047	0.008	0.085
X4				1	-0.175	-0.077	-0.058	.247*	-0.224*	0.13	0.186	0.029	0.109	0.169
X5					1	.201*	0.232*	0.007	0.032	-0.013	-0.071	-0.173	0.155	-0.024
X6						1	0.957**	0.439**	-0.355**	0.043	-0.029	-0.049	0.270**	0.287**
X7							1	0.445**	-0.370**	0.063	-0.023	-0.043	0.288**	0.290**
X8								1	-0.689**	0.347**	0.405**	0.343**	0.544**	0.536**
X9									1	-0.297**	-0.332**	-0.255*	-.383**	-0.409**
X10										1	0.890**	0.533**	0.734**	0.538**
X11											1	0.691**	0.692**	0.558**
X12												1	0.375**	0.467**
X13													1	0.559**
X14														1

*significance at 0.05%; ** Significance at 0.01%

X1- Plant height (cm) X2- Primary branches per plant X3- Secondary branches per plant X4-Late leaf spot incidence
X5- Days to maturity X6- Days to first flowering X7- Days to 50% flowering X8-SPAD chlorophyll meter reading
X9- Specific leaf area (cm^2 g^{-1}) X10- Hundred pod weight (g) X11- Hundred kernel weight (g) X12- Kernel width (mm)
X13- Kernel length (mm) X14- Pod yield per plant (g)

Table 5. Distribution of 97 genotypes of groundnut among the 12 clusters on the basis of D^2 analysis

Cluster	No. of genotypes	Grouped genotypes
I	33	AK 159, Dh 101, Gangapuri, Girnar 1, Girnar 2, Girnar 3, GJG 09, HNG 69, JGN 23, JL 220, JL 501, Kadiri 3, Kadiri 6, R 2001-2, Somnath, Spanish Improved, TG 38, TG 39, DH 86, TG 26, NRCG 10983, NRCG 12431, NRCG 14326, NRCG 14336, NRCG 14345, NRCG 14379, NRCG 14386, NRCG 14407, NRCG 14424, NRCG 14463, NRCG 14474, NRCG 14487, NRCG 14507
II	54	AK-12-24, GG 2, GG 3, GG 6, GG 8, GG 20, GJG 17, GPBD 4, HNG 10, ICGV 91114, J 11, JGN 3, JL 24, Kadiri 9, Kaushal, LGN 2, M 13, M 522, R 8808, S 206, SB XI, SG 99, Sun oleic, TG 51, TGLPS 3, TLG 45, TPG 41, VRI (Gn)-6, VRI 3, GG 7, TAG 24, TG 37 A, TMV 9, NRCG 734, NRCG 1439, NRCG 2615, NRCG 6780, NRCG 7627, NRCG 8763, NRCG 10620, NRCG 14309, NRCG 14368, NRCG 14405, NRCG 14412, NRCG 14435, NRCG 14456, NRCG 14457, NRCG 14467, NRCG 14473, NRCG 14477, NRCG 14485, NRCG 14501, NRCG 17277, NRCG 17284
III	1	VRI 2
IV	1	GG 12
V	1	R 9251
VI	1	NRCG 14472
VII	1	ICGS 76
VIII	1	NRCG 14491
IX	1	NRCG 14475
X	1	NRCG 14350
XI	1	NRCG 14343
XII	1	GJG 31

had either JL 24 or Robut 33-1 genetic background in their pedigree. Similarly genotypes M 13, TG 26, TAG 24, GAUG 10, J 11, Girnar 1, TMV 10 and BARC-1 have been used in the development of 22 genotypes in cluster I, II and VI. Four in each cluster of I and II were direct selections from local land races/germplasm.

D^2 values between clusters revealed maximum divergence between cluster VI and cluster III, followed by cluster XII and cluster-III; cluster VI and cluster X11; cluster IX and cluster XI and between cluster XI and cluster II (Table 6). Larger inter-cluster distance between these clusters suggests considerable diversity between genotypes of these clusters. The minimum divergence between cluster VIII and cluster V (12) followed by cluster V and cluster IV (42) indicates the close relationship among the genotypes included in these two clusters.

The per cent contribution of each character (Table 8**)** indicated that plant height was the largest contributor (65.98%) towards divergence. This is because the

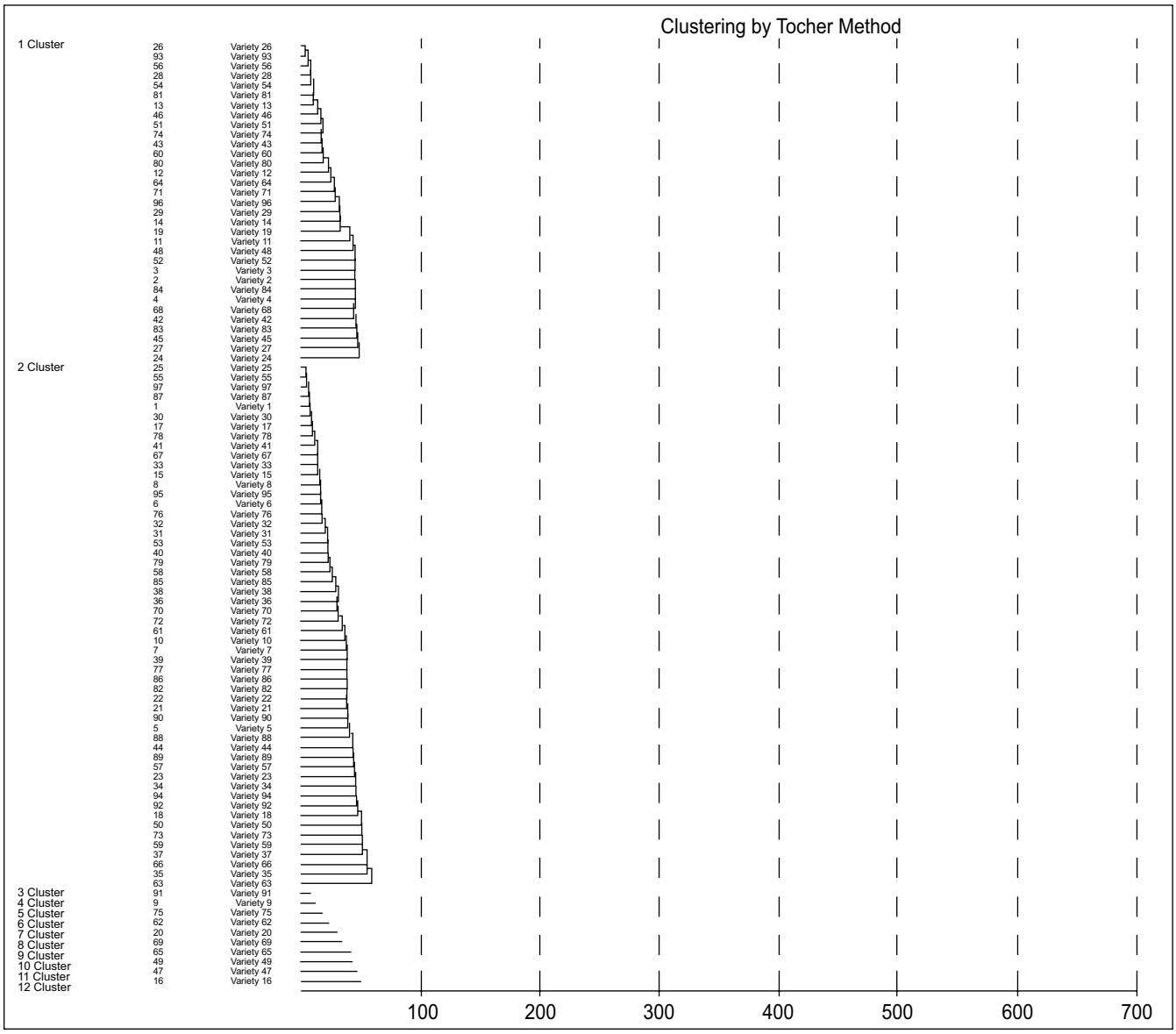

Fig. 1. Dendrogram showing 12 clusters of groundnut genotypes based on Tocher's method

Table 6. Intra and inter cluster distances among 12 clusters constructed based on Toucher's method

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	101.36											
II	320.41	105.41										
III	684.68	181.61	0.00									
IV	146.04	202.18	463.14	0.00								
V	216.01	203.32	447.09	42.48	0.00							
VI	332.84	1041.27	1736.22	568.03	713.84	0.00						
VII	304.67	368.53	711.18	133.76	77.18	729.37	0.00					
VIII	166.48	342.2	698.39	86.03	12.36	442.92	212.67	0.00				
IX	501.25	366.17	579.34	459.93	450.33	1171.21	626.48	619.7	0.00			
X	195.03	286.44	617.03	160.33	235.49	546.7	352.19	208.52	263.63	0.00		
XI	344.19	931.81	1622.04	473.28	578.74	182.03	585.51	431.72	702.5	358.72	0.00	
XII	636.84	384.84	577.65	395.03	325.28	1388.9	447.64	613.63	192.3	303.37	880.54	0.00

genotypes studied belonged to all the four botanical groups of groundnut which vary greatly in their heights. The other traits *viz.,* days to maturity (10.22%), secondary branches per plant (10.09 %), SPAD chlorophyll meter reading (4.3%), primary branches per plant, hundred kernel weight (1.57%), disease score of late leaf spot (1.16%), kernel length (1.18%), hundred pod weight (1.14%), pod yield per plant (0.34%), kernel width (0.34%) and days to fifty per cent flowering (0.6%) contributed less to the divergence.

It is observed that 97 genotypes from different geographical origin representing diverse agro-climatic conditions were distributed at random among the clusters formed based on their genetic distance. The absence of relationship between genetic diversity and geographical diversity may be attributed to forces other than geographical origin such as exchange of breeding material, genetic drift, variations, natural and artificial selection are responsible for diversity (Murthy and Arunachalam, 1966 and Sheriff and Shivashankar, 1992).The genotypes with high mean performances for different traits studied in diverse clusters (II, III, VI, VII and IX) may serve as potential donors in hybridization programme.

Table 7. Cluster means of twelve clusters for yield and water use efficiency related traits of groundnut

Cluster	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X 12	X 13	X 14
I	51.58	4.3	3.55	7.1	95.0	23.83	25.88	27.50	210.00	66.53	27.05	7.59	12.58	7.42
II	35.45	4.79	5.27	7.2	96.0	25.98	28.91	30.97	199.27	71.49	29.24	7.70	13.88	9.99
III	25.0	4.0	2.0	7.0	95.0	26.0	29.0	35.00	183.09	108.6	48.02	8.65	17.75	12.74
IV	45.5	4.0	4.5	7.5	100.0	22.5	26.0	33.50	160.35	108.4	42.30	8.10	15.40	15.93
V	43.5	4.5	5.0	8.0	102.0	21.5	24.0	28.05	211.05	71.31	33.54	7.55	14.80	4.83
VI	69.5	5.5	1.5	7.5	94.0	23.5	25.0	24.30	210.50	49.82	20.99	7.30	11.45	4.18
VII	47.0	4.5	4.5	5.5	106.0	24.5	26.5	26.15	236.68	39.13	18.18	7.10	11.80	5.90
VIII	49.5	4.0	3.5	7.5	99.0	24.0	25.0	23.55	213.13	94.24	27.45	6.35	16.55	2.97
IX	38.5	4.0	24.0	6.0	94.0	23.5	25.5	26.70	201.74	54.21	22.00	7.65	11.15	4.48
X	47.5	7.0	14.0	5.0	96.0	30.5	35.0	34.30	164.59	67.62	16.63	7.35	16.30	7.26
XI	65.5	4.0	15.0	7.0	97.0	25.5	30.5	26.65	208.35	54.90	21.11	7.20	10.25	3.40
XII	35.5	6.5	23.5	7.5	101.0	28.5	30.5	32.20	175.91	55.70	27.51	8.00	14.30	18.1

X1- Plant height (cm) X2- Primary branches per plant X3- Secondary branches per plant X4-Late leaf spot incidence
X5- Days to maturity X6- Days to first flowering X7- Days to 50% flowering X8-SPAD chlorophyll meter reading
X9- Specific leaf area (cm^2 g^{-1}) X10- Hundred pod weight (g) X11- Hundred kernel weight (g) X12- Kernel width (mm)
X13- Kernel length (mm) X14- Pod yield per plant (g)

Table 8. Relative contribution (%) of individual trait to the genetic divergence

S.No.	Source	Times ranked 1st	Contribution (%)
1	Plant height (cm)	3072	65.98
2	Primary branches per plant	139	2.99
3	Secondary branches per plant	470	10.09
4	Late leaf spot (LLS) incidence	54	1.16
5	Days to maturity	476	10.22
6	Days to first flowering	28	0.6
7	Days to 50% flowering	1	0.02
8	SPAD chlorophyll meter reading	200	4.3
9	Specific leaf area (cm^2 g^{-1})	3	0.06
10	Hundred pod weight (g)	53	1.14
11	Hundred kernel weight (g)	73	1.57
12	Kernel width (cm)	16	0.34
13	Kernel length (cm)	55	1.18
14	Pod yield per plant (g)	16	0.34

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