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Genetic diversity assessment and cluster analysis of morphological yield attributing traits of groundnut (*Arachis hypogaea* L.)

Yashi Singh Tomar, Sushma Tiwari, MK Tripathi and Ravindra Singh Solanki

Abstract

Groundnut (*Arachis hypogaea* L.) is a highly nutritious legume being used for farming globally. The present investigation was conducted for analysing genetic diversity among 59 local groundnut germplasm using Mahalanobis D² statistical analysis for quantify the degree of divergence at genotypic level. Hundred pod weight is positively correlated to hundred kernel weight ($r=0.656$) 1% level of significance and sound mature kernels ($r=0.554$) 1% level of significance. Biological yield is negatively correlated to harvest index ($r= -0.416$) 1% level of significance and Shelling % ($r= -0.281$) 5% level of significance. Based on D² values 59 genotypes were grouped into different seven clusters, in which Cluster I contain maximum number of genotypes *i.e.* 43 followed by seven in cluster II, four in cluster IV, two genotypes are in Cluster V and Cluster III, VI and VII consist of only one genotype each. Average inter cluster values were maximum between cluster II and IV on the basis of analysis. At intra cluster level, maximum values were recorded for cluster IV followed by cluster II, cluster I and then cluster V hence these clusters appeared to be divergent and might have different geographical genetic origin hence could be gainfully utilized in groundnut improvement programme. Cluster mean of 16 morphological characters was seen most extreme in Cluster V, followed by cluster VII and then Cluster VII.

Keywords: Cluster analysis, groundnut, mahalanobis D² Statistics, morphological traits

Introduction

Groundnut (*Arachis hypogaea* L.) locally known as “moongphali” in India was introduced in early 16th century and gained agricultural importance and emerged as major oilseed crop in 19th century in the country. Groundnut is a leguminous cash crop which is highly self-pollinated auto-tetraploid ($2n=4x=40$) with the extent of out crossing in groundnut is very low, reported upto 3.9% only because of very small insects such as ants. This crop groundnut is extensively cultivated in tropical and sub-tropical region originated in South America with a genome size of 2891 Mbp, originated through a single hybridization and polyploidization event (Bhavar *et al.*, 2020) [1]. In Indian subcontinent peanut is obsessively consumed as cooking oil and in various food products. It is valued as an opulent source of energy in form of oil (48-50%) and protein (25-28%) in the kernels. Groundnut is not necessarily a nut but is a legume having remarkable capacity to fix environmental nitrogen through valuable relationship with Rhizobium. It is also a day length insensitive crop thus facilitate it to grow at any latitude where favourable temperature can be achieved hence it is effectively cultivated in more than 110 countries of the world with India being the largest exporter worldwide. Genetic architecture of a population is the result of prolonged natural and artificial selection. The populations from different geographical regions are usually included in hybridization programmes presuming genetic diversity and greater likelihood of recovering promising transgress. Therefore, the information about the nature and magnitude of genetic divergence in a given population is essential for selection of diverse parents which upon hybridization lead to a wide spectrum of gene recombination for quantitatively inherited traits. Among several statistical methods of quantifying genetic divergence, assessment of genetic divergence by the use of D² statistics is useful in choosing parents for any breeding objective.

Correlation studies provide better understanding of yield components which helps the plant breeder during selection (Pramanik *et al.*, 2019; Mishra *et al.*, 2021a, b; Mishra *et al.*, 2022) [9, 6, 7, 8]. Mass selection has been used to improve grain yield in several crops through indirect selection for highly heritable traits which are associated with yield.

A positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneous improvement of both the characters. The evaluation of diversity is important to know the source of genes for particular trait within the available germplasm (Tomooka 1991; Tiwari *et al.*, 2014; Rajpoot *et al.*, 2020; Verma *et al.*, 2021; Yadav *et al.*, 2021) [16, 15, 11, 17, 18]. Groundnut germplasms are one of the best resources to get novel traits and could be applied effectively in breeding programme. It is essential to know the genetic diversity of the existing genotypes to carry out focused crop improvement programme. Therefore, the present work was conducted to estimate the nature and magnitude of genetic diversity present in 59 groundnut germplasm.

Materials and Methods

Plant Material

In present investigation, five check varieties including JGN 3, GPBG4, Sun Oleic 95 R, KDG-128 and Gangapuri and fifty-one groundnut germplasm lines were evaluated during the Kharif 2020 at research farm, Rajmata Vijayraje Scindia Agricultural University, Gwalior (M.P.). Temperature between 25 °C-30 °C suits best for the crop with an average rainfall ranging between 50-75 cm. The experimental field of College of Agriculture, Gwalior is located at 26 13 N latitude, 78 14" E longitude and at an altitude of 211.5 m above the sea level in gird belt. It has hot weather conditions and during summers the temperature rises beyond 45 °C.

Methodology

Morphological Characterization

Sowing of groundnut seeds was done during Kharif 2020 in random block design in two replications with 40 cm x 15 cm (row to row and plant to plant distance). Morphological observations were recorded in 5 random plants from each replications including days to 50% flowering, days to maturity, number (s) of primary branches per plant, fresh weight per plant (gm), plant height (cm), number (s) of pods per plant, pod weight per plant (gm), plant dry weight per plant (gm), dry pod weight per plant (gm), number (s) of kernels per plant, 100- kernel weight (gm), sound mature kernel, shelling percentage, 100-pod weight (gm), biological yield (gm) and harvest Index (%). The coefficient of variation (CV) was computed using SPSS V19 software as well as in excel which was prepared manually along with the computation of coefficient of correlation among all morphological traits at maturity. D² analysis for genetic diversity and to determine Inter-Cluster and Intra-Cluster distances between the clusters and cluster mean along with 3-D plot was done in INDOSTATE software. The statistical distance (Mahalanobis D²) between groundnut genotypes were calculated as the sum of the squares of the difference between any two genotypes evaluated at the same time. Tocher's technique was used for the conversion of correlated mean characters into standard uncorrelated mean to calculate D².

Results and Discussions

Correlation coefficient of morphological traits

Fresh weight of plant is positively correlated to primary branches ($r=0.756$) 1% level of significance, number of pods ($r=0.720$) 1% level of significance, pod weight ($r= 0.804$) 1% level of significance, dry weight of plant ($r= 0.965$) 1% level

of significance, dry pod weight ($r=0.750$) 1% level of significance, number of kernels ($r=0.674$) 1% level of significance and biological yield ($r=0.973$) 1% level of significance. It is negatively correlated to hundred kernel weights ($r= -0.269$) 5% level of significance, harvest Index ($r= -0.438$) 1% level of significance and Shelling Percentage ($r= -0.318$) 5% level of significance. Number of kernels are positively correlated with biological yield ($r=0.715$) 1% level of significance and harvest Index ($r=0.258$) 5% level of significance. Hundred pod weight is positively correlated to hundred kernel weight ($r=0.656$) 1% level of significance and sound mature kernels ($r=0.554$) 1% level of significance. Biological yield is negatively correlated to harvest index ($r= -0.416$) 1% level of significance and Shelling % ($r= -0.281$) 5% level of significance (Table 1).

Genetic Divergence (D² Analysis)

Percent Contribution of individual character towards genetic divergence

Percentage contribution to genetic divergence by sixteen quantitative characters in study is shown in (Table 2). The percentage contribution of individual traits towards the total divergence was highest for Hundred kernel weight (59.21%), followed by Hundred Dry Pod weight (19.17%), Shelling percentage (6.49%), Dry plant weight (4.68%) and Sound mature kernel (4.68%) on the other hand other eleven characters contributed very low or negligible towards divergence.

Inter and intra cluster divergence D²

In the (Table 3) the intra and inter cluster D² mean values are shown. On the basis of D² values 59 groundnut genotypes are being grouped under VII clusters. The range of Intra-cluster distance is 9.09 to 5.33. Cluster IV showed highest intra-cluster value (9.09), followed by cluster II (8.64), Cluster I (8.50) and cluster V showed lowest intra-cluster distance (5.33). Cluster III, VI and VII has shown 0.00 intra-cluster distance. The genotypes of Cluster II and Cluster IV has shown the highest inter cluster distance (27.56), followed by Cluster IV and Cluster VI (25.44), Cluster II and Cluster VII (23.70), Cluster II and Cluster III (23.42), cluster III and Cluster VI (21.83), Cluster II and Cluster V (21.19), Cluster V and Cluster VI (20.36), Cluster IV and Cluster VII (19.66). The lowest inter cluster was between Cluster III and Cluster IV (7.65).

Cluster Mean

The cluster mean of different observed quantitative characters are presented in the (Table 4). For Days to 50% flowering Cluster VI showed maximum mean (26.00) days whereas Cluster VII showed minimum mean of (19.50) days. For Days to maturity Cluster IV showed maximum mean (106.00) days and minimum mean of (98.0) days was observed in Cluster III. Cluster mean for Fresh weight of plants was highest in cluster V (189.25) and lowest in Cluster VII (83.33). Plant height has highest cluster mean in Cluster III (40.06) and lowest cluster mean in Cluster VII (31.39). Primary branching cluster mean was highest for Cluster V (8.00) and lowest for Cluster VII (5.66). Cluster mean for number of pods was highest in Cluster V (30.17) and lowest cluster mean for Cluster VI (13.16), for Pod weight per plant highest cluster mean was in Cluster V (42.67) and lowest mean in Cluster VII (15.16). Cluster mean for dry weight of plant was

observed highest in Cluster V (111.50) and lowest in Cluster VII (52.67), for dry pod weight per plant cluster mean was highest in Cluster V (27.17) and lowest in Cluster VII (9.84). Cluster mean for Number of Kernels per plant is highest in Cluster V (57.33) and lowest in Cluster VI (23.33). Hundred Dry pod weight has highest cluster mean in Cluster V (92.00) and lowest in Cluster IV (36.50), for hundred kernels weight it is highest in Cluster VI (42.50) and lowest in Cluster III (15.50). Cluster mean is highest for sound mature kernel in Cluster II (85.50) and lowest in Cluster IV (57.75), for biological yield cluster mean is highest in Cluster V (138.66) and lowest in Cluster VII (62.50). Cluster mean for harvest index is highest in Cluster VII (48.91) and lowest in Cluster VI (29.64) and Cluster mean for shelling percentage is highest in Cluster VI (83.11) and lowest in Cluster V (20.70).

Grouping of genotypes into various clusters

Distribution of 59 groundnut germplasm into 7 clusters based on divergence analysis is shown in table 5 and fig 1. Cluster I is the largest among them constituting of 43 genotypes,

followed by Cluster II having 7 genotypes, Cluster IV have 4 genotypes, 2 genotypes are in Cluster V and Cluster III, VI and VII consist of only one genotype each. 3D plot, also depicted groupism of groundnut genotypes (fig 2)

Zaman *et al.*, (2010) [20] have studied 34 groundnut genotypes and reported 5 clusters using multivariate analysis for divergence. There are several reports on morphological divergence studies in various crops focused on selection of superior germplasm lines (Choudhary *et al.*, 2021b, c; Yadav *et al.*, 2022; Sahu *et al.*, 2020; Shyam *et al.*, 2021; Rathore *et al.*, 2022; Makwana *et al.*, 2021; Mandloi *et al.*, 2022; Pramanik *et al.*, 2021; Mishra *et al.*, 2022) [2, 3, 19, 13, 14, 12, 4, 5, 10, 8]. In our study, varieties KDG 128, Gangapuri, JGN 3 and GPBD 4 are grouped into Cluster I along with 39 local germplasms and Sun Oleic 95R is in Cluster IV along with Badwani 6, ICGV 13236, Shivpuri local 65 and thus by selecting such parents having high genetic diversity there are greater chances of achieving transgressive segregants. Selected germplasm with diverse character could efficiently be applied in groundnut crop improvement programme.

Table 1: Correlation Coefficient of the Morpho-physiological and biochemical traits of groundnut germplasms

	DF	DM	ELS_30	ELS_45	LLS_75	LLS_85	FW	PHT	PB	NP	PW	DW	DPW	NK	HPW	HKW	MK	BYD	HI	SP	
DF	1	-.079	-.290*	-.392**	-.263*	-.338**	.167	-.048	.315*	.035	.151	.166	.082	.129	-.082	.053	-.250	.158	-.211	.070	
DM		1	-.061	-.061	-.171	-.106	.107	.001	.017	-.008	.056	.033	.173	.021	-.126	-.185	-.096	.061	-.024	-.122	
ELS_30			1	.798**	.511**	.483**	-.277*	.199	-.216	-.170	-.328*	-.224	-.300*	-.283*	-.201	-.070	.168	-.249	.005	.127	
ELS_45				1	.800**	.767**	-.295*	.263*	-.308*	-.133	-.403**	-.227	-.409**	-.269*	-.197	-.100	.069	-.272*	.050	.131	
LLS_75				*	1	.904**	-.317*	.196	-.283*	-.093	-.336**	-.255	-.394**	-.141	-.136	-.054	-.012	-.293*	.158	.165	
LLS_85						1	-.354**	.225	-.346**	-.100	-.344**	-.278*	-.376**	-.121	-.128	-.058	-.032	-.311*	.245	.166	
FW							1	.253	.756**	.720**	.804**	.965**	.750**	.674**	-.043	-.269*	-.114	.973**	-.438**	-.318*	
PHT								1	.085	.220	.040	.266*	.030	.109	.132	.023	.096	.234	-.236	-.102	
PB									1	.503**	.657**	.741**	.599**	.504**	-.103	-.258*	-.115	.752**	-.441**	-.223	
NP						*				1	.841**	.712**	.774**	.921**	.124	-.080	.147	.759**	.139	-.190	
PW											1	.775**	.951**	.834**	.198	-.023	.140	.847**	-.082	-.207	
DW												1	.683**	.668**	-.009	-.225	-.126	.991**	-.470**	-.289*	
DPW													1	.741**	.177	.002	.177	.776**	-.060	-.168	
NK														1	.175	-.089	.131	.715**	.258*	-.224	
HPW															1	.656**	.554**	.025	.062	-.131	
HKW																1	.511**	-.193	.076	.625**	
MK																	1	-.075	.219	.138	
BYD																		1	-.416**	-.281*	
HI																			1	.123	
SP																*					1

** Correlation is significant at the 0.01 level (2-tailed).

* Correlation is significant at the 0.05 level (2-tailed).

DF= Days to 50% Flowering, DM= Days to Maturity, ELS_30= Early leaf spot at 30 DAS, ELS_45= Early leaf spot at 45 days, LLS_75= Late leaf Spot at 75 days, LLS_85= Late leaf spot at 85 days, FW= Fresh weight of plant(gms), PHT=Plant height(cm), PB= primary branches per plants, NP= Number of Pods per plant, PW= pod weight per plant(gms), DW= Dry weight per plant(gms), DPW= Dry Pod weight per plant(gms), NK= number of kernels per plant, HPW= Hundred pod weight(gms), HKW= Hundred kernel weight(gms), MK= sound mature kernels, BYD= biological yield(gms), HI= Harvest Index(%), SP= shelling Percentage

Table 2: Percent Contribution of individual character towards genetic divergence

S.no	Source	Times Ranked 1 st	Contribution %
1	Days to 50% flowering	4	0.23
2	Days to Maturity	12	0.70
3	Fresh weight per plant(gms)	13	0.76
4	Plant height (cm)	10	0.58
5	Primary branches per plant	10	0.58
6	Number of pods per plant	11	0.64
7	Pod weight per plant	7	0.41
8	Dry weight per plant(gms)	80	4.68
9	Dry pod weight per plant(gms)	1	0.06
10	Number of kernels per plant	11	0.64
11	100 dry pod weight(gms)	328	19.17
12	100 kernel weight(gms)	1013	59.21

13	Sound mature kernel	80	4.68
14	Biological yield(gms)	9	0.53
15	Harvest index	11	0.64
16	Shelling %	111	6.49

Table 3: Intra-cluster and Inter-cluster Distance between groundnut germplasm

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	8.50	15.73	11.79	15.92	13.60	15.39	15.57
Cluster II		8.64	23.42	27.56	21.19	15.35	23.70
Cluster III			0.00	7.65	15.82	21.83	16.92
Cluster IV				9.09	19.28	25.44	19.66
Cluster V					5.33	20.36	16.61
Cluster VI						0.00	12.78
Cluster VII							0.00

Table 4: Cluster mean of observed Morphological characters of groundnut

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to 50% flowering	23.70	23.79	22.50	24.63	22.25	26.00	19.50
Days to Maturity	105.73	103.64	98.00	106.00	105.50	101.00	103.00
Fresh weight of plant	163.53	117.57	132.84	160.58	189.25	94.83	83.33
Plant height	38.48	37.49	40.06	35.04	38.97	33.85	31.39
Primary branches	6.66	5.93	7.00	6.71	8.00	6.00	5.66
Number of pods	24.32	16.62	18.83	17.92	30.17	13.16	16.33
Pod weight per plant	31.56	24.88	22.17	21.08	42.67	20.17	15.16
Dry plant weight	97.00	69.64	81.00	91.50	111.50	63.17	52.67
Dry pod weight per plant	22.55	18.14	17.33	15.29	27.17	13.17	9.84
Number of kernels per plant	38.46	27.57	24.17	28.46	57.33	23.33	29.50
100 dry pod weight	65.58	88.07	47.50	36.50	92.00	51.50	39.50
100 kernel weight	27.64	41.79	15.50	12.88	19.00	42.50	30.00
Sound mature kernel	84.12	88.50	77.00	57.75	83.00	75.00	75.50
Biological yield	119.55	87.86	98.33	106.79	138.66	76.33	62.50
Harvest index	35.01	33.02	33.03	33.40	42.39	29.64	49.81
Shelling %	42.39	47.62	32.88	34.93	20.70	83.11	76.06

Table 5: Grouping of groundnut genotypes into cluster based on D² analysis

Cluster no.	No. of genotypes	Name of the Genotypes
Cluster I	43	DHGN-6, DHGN-4, DHGN-5, ICGV-13214, KDG-128, ICGN-13573, ICGN-13520, ICGV-13549, ICGV-13236, DHGN-7, Shivpuri local-82, BTGN-5, Shivpuri local-47, Gangapuri, ICGV-13523, ICGV-9268, GPBD-4, ICGV-1936, DGGN-4, Shivpuri local-75, ICGV-13246, Shivpuri local-39, Shivpuri local-42, Gangapuri, Shivpuri local-37, ICGV, JAGN-1, ICGV-7988, JGN-3, DGGN-6, Dhar-1, ICGV-4927, Bajjatakurd-1, Bajjatakurd-2, ICGV-9249, GPBD-4, ICGV-13562, Shivpuri local-28, ICGV-13245, Shivpuri local-29, BTGN-4, Shivpuri local-6, ICGV-13565
Cluster II	7	ICGV-13520, JCGN-4, Badwani-2, ICGV-9112, DHGN-1, Talun-1, ICGV-13264
Cluster III	1	ICGV-13297
Cluster IV	4	badwani-6, ICGV-13236, Shivpuri local-65, Sunolic Local 95R
Cluster V	2	Shivpuri local-74, ICGV-13574
Cluster VI	1	ICGV-13269
Cluster VII	1	ICGV-6300

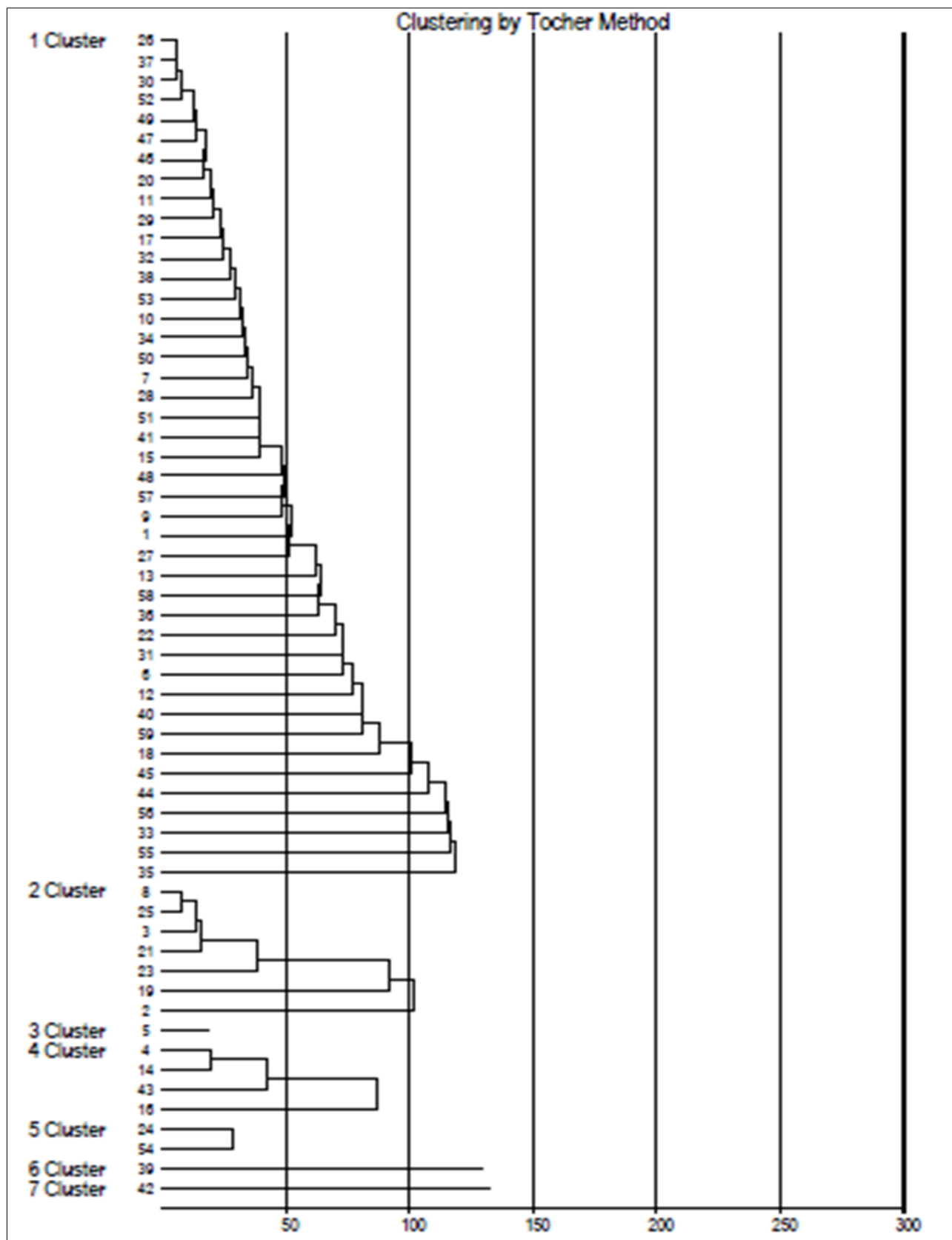


Fig 1: Cluster Diagram of diverse groundnut germplasms based on D² analysis

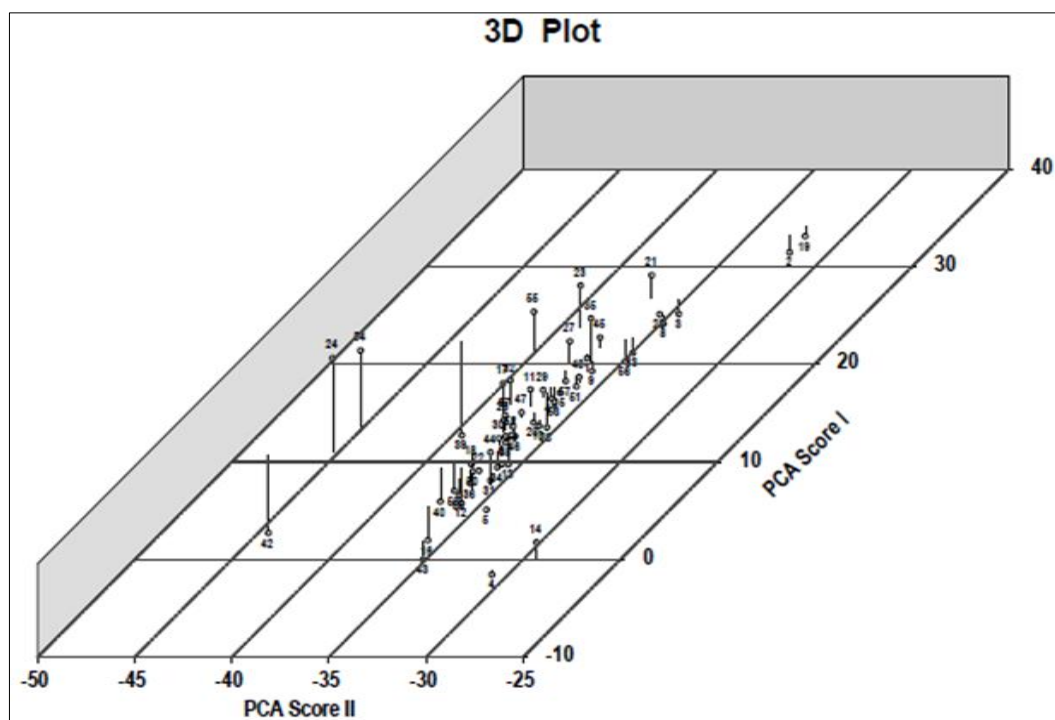


Fig 2: 3-D plot of groundnut genotypes based on D² analysis

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