



Cluster Analysis of Groundnut (*Arachis hypogaea* L.) Genotypes in Ethiopia

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Key words: Cluster mean, divergent genotypes, Grain yield, parents of hybridization

Abstract: Genetic variation is a tool improving yield, wider adaptation, selection of parents for hybridization, desirable quality, pest and disease resistance. This study was planned to investigate Phenotypic diversity of groundnut genotypes based on cluster analysis. The crop was sown during 2015 growing season in Ethiopia. The result of cluster analysis based on average linkage of 16 groundnut genotypes assessed for 12 agromorphological traits was shown that Baha Jidu, Shulamith, Oldhale (local variety) and Baha gudo genotypes were found to be divergent while the most similar genotypes were NC-343 and Roba belonging to cluster I; followed by Tole-1 and Tole-2 (cluster 2), Fetene and Werer 961(cluster7). The cluster mean analysis, for agromorphological traits has shown that genotypes in clusters 1, 2, 5, 6, 9 & 10 including NC-343, Roba, Manipeter, Werer-962, Tole-1, Tole-2, Behajidu, shulamith, Fetene, Werer-961 and Beha gudo can be used as parents in hybridization program for grain yield improvement.

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INTRODUCTION

Arachis hypogaea L. commonly called groundnut or peanut is a member of the family Fabaceae is a major source of food, edible oil, feed, digestible proteins, vitamins, minerals, phytosterols, fuel, cosmetics and green manuring crop for improvement of soil fertility^[1,2]. Information on the nature and degree of genetic diversity helps plant breeders in choosing the diverse parents for hybridization. One of the issues with breeding projects based on hybridization is to estimate the relationship between parents before initiating the crossing^[3].

Cluster analysis groups genotypes based on similarities and differences in their traits. It minimizes homogeneity within group variance and maximizes heterogeneity between group variances. It is also helpful for parental selection in the breeding program and crop

modeling^[4]. Grouping variables is important because it can reveal information about the variables such as outliers, dimensionality, or previously unnoticed interesting relationships. In clusters, the differences among items is indicated by some sort of distance. Some common measurements of distance between two multivariate data vectors include ordinary Euclidean distance or Mahalanobis distance. Euclidean distance can theoretically estimate the genetic distance between parents to maximize the transgressive segregation^[5,6].

An agglomerative hierarchical clustering method which is the most commonly used clustering approach, begins with each variable as its own cluster. It then successively merges the most similar clusters together until the entire set of data becomes one group^[1]. Various agglomerative hierarchical cluster analysis have been used to explore genetic diversity of which UPGMA

(unweighted pair grouping based on arithmetic mean) and Ward's methods are the most popular approaches. The UPGMA is the most valid method in accordance with the relationship of family based on their genetic material^[7]. The objective of the present study was to observe the genetic variability among different genotypes of groundnut by using cluster analyses, so that, the genotypes possessing traits that could be used for improvement of grain yield in groundnut cultivars and identify traits that contribute for improvement of grain yield.

MATERIALS AND METHODS

The experimental materials consisted of fifteen groundnut genotypes obtained from Werer Agricultural Research Center, Ethiopia and a local check variety. The field experiment was conducted in four locations Ethiopia, in a Randomized Complete Block Design (RCBD) in three replications. Data were recorded for twelve agromorphological traits including plant height (PH, cm), number of mature pods per plant (NMP), number of primary branches per plant (NBP), above ground biomass per plant (AGBP, g), pod weight per plant (PWP, g), number of seeds per plant (NSP), seed weight per plant (SWP, g), shell percentage (SHP%), 100 seed weight (100 SW,g), Harvest index (HI%), number of seeds per pod (NSPOD), grain yield per hectare (GY, kg/ha).

Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes^[8]. UPGMA clustering method was performed to obtain dendrogram and sort genotypes and traits into clusters. All statistical analysis was carried out based on twelve agro-morphological traits Microsoft excel program and Genes software VS 2016.6.0^[9].

RESULTS AND DISCUSSION

The Euclidean distances matrix (D) (Table 1) was worked out for 16 groundnut genotypes evaluated for 12 agromorphological traits. The distance matrix was used to study genetic diversity among the genotypes based on principal component analysis and clustering methods. The most divergent genotype pairs were those having greater D while the most similar were those having less D. The most similar groups were formed between NC-343 and Roba (D = 0.91); between Tole-1 and Tole-2 (D = 1.31) and also between Fetene and Werer-961 (D = 1.57). Such pairs for comparing similarity standards are not recommended for use in breeding programs for hybridization. Since they avoid restriction in genetic variability and derail the gains to be obtained by selection. On the other hand, the most divergent pairs were between Werer-963 and Roba (D = 7.40), between Tole-1 and Sedi (D = 7.25), between Werer-963 and NC-343 (D = 7.01).

The large divergence, in principle, allows to recommend the crossing among such pairs of genotypes in order to maximize heterosis and increase possibility of segregants in advanced generations^[10]. In the present study, genetic divergence of groundnut genotypes through distance matrix based on Euclidean distance (D) revealed that there was small range of genetic diversity from 0.91 (between NC-343 and Roba) to 7.40 (between Werer-963 and Roba). This finding was in accordance with Showemimo^[11] who reported estimates of the generalized Mahalanobis distance (D²) clearly indicated that the pairs of genotypes are more divergent and more similar genetically.

The dendrogram for the clustering of groundnut genotypes evaluated for 12 agromorphological traits was shown in Fig. 1. The cutting point for the dendrogram (Fig. 1) was determined at a mean plus standard deviation distance, that was found to be 4.57, based on which 4 clusters were obtained (Table 2). Those varieties in same cluster do not significantly different from one another. Thus, they belonged to the same group or cluster. The first cluster constituted 10 varieties that have shown nonsignificant above average performance for grain yield and most of the studied traits except for SHP, HI and NSPOD. Thus, they can be used for improvement of GY, since these varieties have shown above average performance for grain yield and its component traits. The second cluster consisted of only one variety that has shown nonsignificant above average performance for only PWP. The third cluster consisted of two varieties with non-significant above average performance for PH, SHP, HI and NSPOD, indicating that such varieties were less important for GY improvement. The fourth cluster consisted of three varieties that have shown significant and above average performance for SHP and HI but non-significant above average for SWP, 100SW, NSPOD and GY indicating that such varieties could be used for improvement of GY. These findings were in accordance with previous work by Makinde and Ariyo^[12] who studied divergence of groundnut genotypes based on agromorphological traits and Canteli *et al.*^[13] cluster analysis of soybean.

As suggested by Vieira *et al.*^[14] clusters formed by one single individual suggest that those individuals are the most divergent in relation to the rest. Accordingly in this study, the cluster analysis based on average linkage (UPGMA) of 16 groundnut genotypes, measured for 12 agromorphological traits (Fig. 1) was shown that Shulamith (cluster 2) was found to be distinct while the most similar varieties were NC-343 and Roba belonging to cluster 1; followed by Tole-1 and Tole-2 (cluster 1), Fetene and Werer-961 (cluster 4). Abreu *et al.*^[15] suggested the knowledge of genetic divergence allows inferences to be made about the specific combination capacity before carrying out the crossings, resulting in a

Table 1: Range and mean Euclidean distances of 16 groundnut genotypes evaluated for 12 agromorphological traits

Variety	Minimum	Maximum	Mean	SD	CV
NC-343	0.91 (NC-343 & Roba)	7.01 (NC-343 & Werer-963)	3.96	4.31	1.09
Behagudo	3.83 (Behagudo & Fetene)	6.94 (Behagudo & Behajidu)	5.39*	2.20	0.41
Behajidu	2.59 (Behajidu & NC-343)	7.15 (Behajidu & Werer-963)	4.87	3.22	0.66
Bulki	2.12 (Bulki & Lote)	5.93 (Bulki & Behagudo)	4.03	2.69	0.67
Fetene	1.57 (Fetene & Werer-961)	6.25 (Fetene & Oldhale)	3.91	3.31	0.85
Lote	2.12 (Lote & Bulki)	5.52 (Lote & Werer-963)	3.82*	2.40	0.63
Manipeter	1.93 (Manipeter & Werer-962)	6.84 (manipeter & Werer-963)	4.39	3.47	0.79
Oldhale	2.64 (Oldhale & Bulki)	6.53 (Oldhale & Behagudo)	4.59	2.75	0.60
Roba	0.91 (Roba & NC-343)	7.40 (Roba & Werer-963)	4.16	4.59	1.10
Sedi	2.81 (Sedi & Werer-963)	7.25 (Sedi & Tole-1)	5.03*	3.14	0.62
Shulamith	4.01 (Shulamith & Bulki)	6.51 (Shulamith & Behajidu)	5.26	1.77	0.34
Tole-1	1.31 (Tole-1 & Tole-2)	7.25 (Tole-1 & Sedi)	4.28	4.20	0.98
Tole-2	1.31 (Tole-2 & Tole-1)	6.42 (Tole-2 & Sedi)	3.87*	3.61	0.93
Werer-961	1.57 (Werer-961 & Fetene)	6.67 (Werer-961 & Tole-1)	4.12	3.61	0.88
Werer-962	1.88 (Werer-962 & Roba)	6.26 (Werer-962 & Sedi)	4.07	3.10	0.76
Werer-963	2.81 (Werer-963 & Sedi)	7.40 (Werer-963 & Roba)	5.11*	3.25	0.64
Overall	2.15	6.71	4.43	0.54	0.12

Table 2: Relative contribution of each trait to clusters with the average of traits for each cluster (above number) and the difference between each cluster mean with the total mean (below number)

Cluster	M & MD	PH	NMP	NBP	AGBP	PWP	SWP	NSP	SHP	100 SW	HI	NSPOD	GY
1	CM	30.96	46.36	13.37	81.32	42.19	36.09	68.37	60.51	56.73	23.87	1.48	3312.21
	MDF	1.41	4.56	1.95	13.64	2.11	2.41	1.83	-1.07	1.25	-2.75	-0.11	156.08
2	CM	21.46	38.29	9.52	61.5	44.45	23.20	57.71	54.47	49.53	22.85	1.53	2693.58
	MDF	-8.09	-3.51	-1.91	-6.18	4.36	-10.48	-8.84	-7.11	-5.95	-3.76	-0.05	-462.54
3	CM	31.36	28.44	6.31	46.83	30.04	26.45	62.51	62.14	46.58	27.56	2.00	2269.63
	MDF	1.81	-13.4	-5.12	-20.85	-10.05	-7.23	-4.03	0.57	-8.90	0.95	0.41	-886.50
4	CM	26.33	36.69	8.98	38.16	38.32	33.97	66.09	67.13	59.22	36.39	1.69	3381.03
	MDF	-3.22	-5.11	-2.45	-29.52	-1.77	0.29	-0.45	5.56	3.74	9.78	0.10	224.90
	GM	29.55	41.8	11.43	67.68	40.08	33.68	66.55	61.58	55.48	26.61	1.59	3156.13
	SD	3.37	8.43	3.19	19.82	6.94	5.24	7.39	4.39	13.49	5.99	0.19	535.06

M: mean; CM: cluster mean; MDF: mean difference; GM: grand mean; SD: standard deviation; PH: plant height; NMP: number of mature pods per plant; NBP: number of primary branches per plant; AGBP: above ground biomass per plant; PWP: pod weight per plant; SWP: seed weight per plant; NSP: number of seeds per plant; SHP: shelling percent; 100 SW: 100 seed weight; HI: harvest index; NSPOD: number of seeds per pod; GY: grain yield (kg/ha)

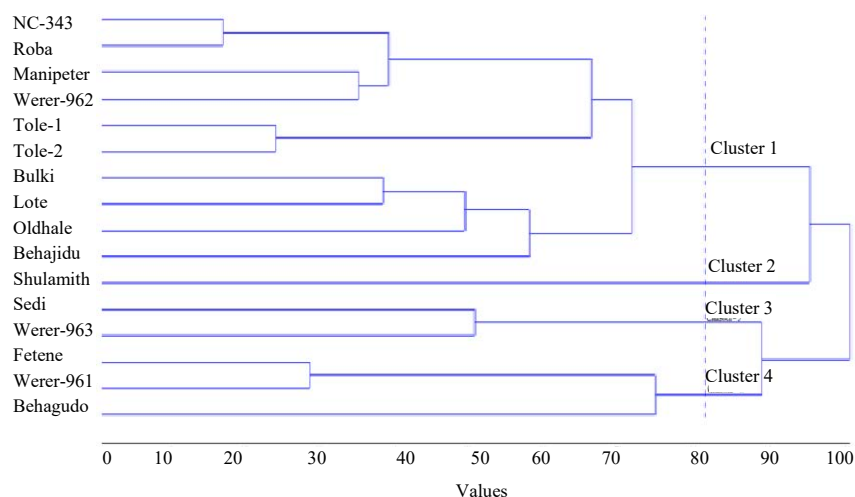


Fig. 1: Dendrogram based on UPGMA for 16 groundnut genotypes

greater chance of identifying and recovering more promising combinations among the segregating populations. Accordingly, on the basis of the results obtained from the present study, various degrees of genetic divergences were observed. It is evident as more

number of cluster formed by the 16 groundnut varieties and high range of values of intercluster distance which exhibit high degree of genetic diversity and thus, may be utilized under inter varietal hybridization program.

CONCLUSION

Among 16 groundnut genotypes evaluated for 12 morphometric traits 11 genotypes including NC-343, Roba, Werer-962, Manipeter, Tole-1, Tole-2, Behajidu, Shulamith, Fetene, Werer-963 and Behagudo are considered to be promising for improvement of grain yield. Of 12 metric traits pod weight per plant (PWP), seed weight per plant (SWP) and 100 seed weight (100 SW) were found to be equally important to make selection for grain yield trait. Eleven out of twelve metric traits including SWP, AGBP, PWP, 100SW, NBP, PH, NMP, NCSP, NSPOD, SHP and Hi were contributed significantly for grouping of genotypes into clusters.

Authors' contributions: Zekeria Yusuf: field experiment, data collection and analysis; Habtamu Zeleke: initiation and design of the study; Arno Hugo; acquisition of data and doing the laboratory phase; Wassu Mohammed and Shimelis Hussein: Analysis and interpretation of data. All authors contributed to drafting the article and revising it critically for important intellectual content.

Conflict of interest: The authors declare no conflict of interest.

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