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# Genetic Divergence and Association of Traits Among Groundnut (*Arachis hypogaea* L.) Genotypes in Ethiopia Based on Agromorphological Markers

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**Abstract:** Multivariate analysis was carried out for 16 groundnut genotypes evaluated for 12 agromorphological characters. The crop was sown during2015/16 Ethiopian wet season in four locations in RCBD to study the variability and their interrelationship and divergence pattern based on quantitative traits. The distance matrix was used to study genetic diversity among the genotypes based on principal component analysis, discriminant analysis and clustering methods. Genetic divergence of groundnut genotypes through distance matrix based on Euclidean distance (D) revealed that there was small range of genetic diversity. The Eigen vectors for the first three component loading has shown that the first principal component had high positive component loading from NBP, AGBP, NMP, PWP, SWP as well as GY characters and found to associate with NC 343, Baha jidu, Lote, Manipeter, Roba, Werer 962, Tole1, Tole2 and Oldhale genotypes with high positive PCA1 scores based on Euclidean distance matrix(D). In contrast, PCA2 had high positive component loading from 100SW, PWP as well as GY characters, the associated genotypes are Baha gudo, Fetene, Manipeter, Werer 962 and Werer 961. GY has shown positive loading in all the first three components but the highest positive in component 2 indicating the highest grain yielding genotypes are those that are most positive in second component. The highest positive loading characters in the third component are NSP, SHP, SWP, NMP as well as GY; the associated genotypes were Fetene and Werer 961. On the other hand, high negative PC1 loading was obtained for SHP, HI and NSPOD. High negative loading characters especially in PC1 shows inverse relationship and/or divergence to the rest variables therefore such characters are not mainly recommended for breeding since they have usually low heritability. The dendrogram for Euclidean distance based on genotypic correlation has shown that traits in cluster 2 including PWP, SWP and 100SW were shown positive and nonsignificant correlation with GY. The most similar trait was NBP and AGBP, while NSPOD was the most divergent trait and found to be negatively correlated with GY. Thus, such divergent and negatively correlated trait with yield has no significance in selection so it can be dropped. Those characters in cluster 1 including NBP, AGBP, NMP and NSP were positive but nonsignificantly correlated at genotypic level with GY.

**Keywords:** Groundnut, Discriminant Analysis, Euclidean, Eigen Values, Eigen Vectors, PC

## 1. Introduction

Information on the nature and degree of genetic diversity helps plant breeders in choosing the diverse parents for hybridization (Singh, 2015). For a successful breeding program, the presence of genetic diversity and variability play a vital role. Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, pest and disease resistance. Selection of genetically diverse parents in any breeding program is of immense importance for

successful recombination breeding (Arunachalam, 1981). The genetic divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal, 2003). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. The parent identified on the basis of the divergence analysis would be more promising (Singh *et al*., 2013).

To estimate the genetic diversity either agronomic, morphological, or molecular markers can be used (Silva et al., 2011). Within the available methods for genetic diversity studies, the average Euclidean distance is used as a measure of dissimilarity, which underlies hierarchical clustering methods such as UPGMA (unweighted pair group method with arithmetic mean), nearest neighbor, and the Tocher optimization method (Silva *et al*., 2011; Azevedo*et al.,* 2013). The choice of analysis method to be utilized depends on the desired precision, ease of analysis, and form of obtaining the data and there is no defined parameter of choice for the study of genetic divergence for a group of genotypes (CargneluttiFilho et al., 2008; Cruz et al., 2012). The measure of dissimilarity and together with analysis method used should guarantee the breeder scrutiny in the selection of parents for the crossings. If there is no agreement between the methods used, the choice of parents depends on the method utilized, which requires selection of the most efficient method (CargneluttiFilho et al., 2008).

Statistical analysis quantifies the genetic distance among the selected genotype and reflects the relative contribution of specific traits towards the total divergence. The crosses between parents with suitable genetic divergence are generally the most responsive for yielding the most promising segregants, however satisfactory results are obtained only if the germplasm employed in the cross also present high values for the traits of interest (Prasanna, 2012). The mahalanobis distance ( $D^2$ ) statistics provides a quantitative measure of genetic divergence among populations and assists in classifying genetic stocks into distinct groups which is further helpful for evolving superior genotypes. When breeding for a particular set of growing conditions, it is highly important to know the use of local populations, since in them the relationships among yield components are balanced and in harmony with the effects of the specific climatic and edaphic factors. The principal component analysis (PCA), one of multivariate analysis methods, showed which of the traits were decisive in genotype differentiation (Kovacic, 1994). PCA enables easier understanding of impacts and connections among different traits by finding and explaining them. Several studies on genetic divergence based on agromorphological trait of various crops have been conducted, for example makinde and Ariyo (2010) on groundnut, Singh et al. (2014) on bread wheat, Singh et al. (2013) on onion, Cantelli et al., 2016 on soybean. Even on the same crop, the trait used by researchers and the method of analysis varies. If meticulous effort undertaken multivariate methods can be used as an alternative to modern molecular breeding since the cost for molecular laboratory analysis is ever increasing and difficult to handle with local funds especially in developing countries. Furthermore, no sufficient information is available on genetic divergence of groundnut based on major yield component traits. That is why the present investigation designed to assess the magnitude of genetic diversity among groundnut genotypes and to isolate the diverse ones, with associated yield related traits, according to their genetic affinity for future improvement program.

# 2. Materials and Methods

The experiment was carried out across four locations viz Babile, Fedis, Hirna and Mechara in 2015/16 growing season in Ethiopia under rain fed condition. The experimental materials consist of sixteen groundnut genotypes including locals and varieties which were released by EIAR between 1976 to 2012. The treatment, consists of sixteen groundnut genotypes with three replications in four locations, was planted in a randomized complete block design (RCBD) so that the total number of treatments was being16genotypes x 3 replications x 4 location=192. Each entry was planted in a plot having 2 rows of 3 meter length. The spacing between rows and plants was 60cm and 15cm respectively. Each row had 12 plants. Two seeds were planted in each hole after emergence one of it was removed. The spacing between plots was 1m. The net plot size was 5.4 $m^2$. Following land preparation, groundnut seeds were planted and the treatments were being looked after for recommended agronomic practices including weeding, hoeing, fertilizer application and the necessary plant protection measures.

Data were recorded for 12 agromorphological characters viz. plant height (PH, cm), number of mature pods per plant (NMP), number of 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 (100SW,g), Harvest index (HI%), number of seeds per pod (NSPOD), grain yield per hectare (GY, kg/ha). The pods from entire plot were harvested and immature pods were removed. The mature pods were air dried, cleaned and weighed. The data were recorded on five randomly selected plants in each entry or replication. Random samples of 100 seeds were used to record 100 seed weight. Matured pods per plant were used to estimate shelling percentage according to Misra*et al*. (2000) as: Shelling percent $= \frac{\text{kernel weight(g)}}{\text{pod weight (g)}}$ x100. Harvest index was calculated as HI $= \frac{\text{SWP}}{\text{total dry biomass weight}}$ x100

Genetic diversity was studied using Euclidean distance (D). Trait variability analysis was performed by the discriminant analysis and principal component analysis (PCA) methods, with the number of principal components (Kovacic, 1994). Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes, and the distance measure used was Euclidean distance as the parameter that best reflects the differences existing among the genotypes (Kendall, 1980). Factor

analysis used the covariance matrix of characters (Harman, 1967; Ariyo, 1992) to generate factor loadings and communalities using the method of principal component extraction. The analysis uses the Wilks' lambda as the statistics for entering or removing new variables and thereby identifies the variables that provide the best discrimination among the entries. UPGMA method was performed to obtain dendrogram and sort genotypes into clusters. All statistical analysis was carried out based on twelve agro-morphological characters using SAS 9.2 software SAS Institute (2011) and Gene's software (2006).

# 3. Results and Discussion

### *3.1. Analysis of Genotype Divergence*

The Euclidean distance matrix (D) (Table 1) was worked out for 16 groundnut genotypes evaluated for 12 agromorphological characters. The distance matrix was used to study genetic diversity among the genotypes based on principal component analysis and clustering methods. These distance matrix was found to be more efficient as compared to ordinary principal component and clustering based on trait means since the proportion of eigen values for distance matrix (Table 2) was greater than that of eigen values for cluster analysis directly derived from original data (Table 6). 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 genotypes NC343 and Roba (D=0.23), followed by Tole1 and Tole2 (D=1.31), Fetene and Werer 961 (D=1.57). Such pairs for comparing similarity standards are not recommended for use in breeding programs for hybridization, avoiding restriction in genetic variability, or in order to derail the gains to be obtained by selection. On the other hand, the most divergent pairs were between genotypes werer 963 and Roba (D=7.40), followed by Tole1 and Sedi (D=7.25), Werer 963 and NC343 (D=7.01). The high 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 (Cruz et al., 2014). No previous report on divergence study of groundnut genotypes in Ethiopia.

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 NC343 and Roba) to 7.40 (between Werer 963 and Roba). Showemimo (2004) reported that estimates of the generalized Mahalanobis distance ($D^2$) clearly indicated that the pairs of genotypes are more divergent and more similar genetically.

***Table 1.*** *Euclidean distance (D) measured for 16 groundnut genotypes based on 12 agromorphological characters.*

| gen | NC | Bgud | Bjidu | Bulki | Fet | Lot | Man | Oldh | Roba | Sedi | Shul | Tol1 | Tol2 | W961 | W962 | W963 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NC | | | | | | | | | | | | | | | | |
| Bgud | 5.36 | | | | | | | | | | | | | | | |
| Bjidu | 2.59 | 6.94 | | | | | | | | | | | | | | |
| Bulki | 3.44 | 5.93 | 3.43 | | | | | | | | | | | | | |
| Fet | 4.96 | 3.83 | 6.03 | 4.72 | | | | | | | | | | | | |
| Lot | 2.24 | 5.49 | 2.75 | 2.12 | 4.43 | | | | | | | | | | | |
| Man | 2.52 | 4.21 | 4.07 | 4.77 | 4.44 | 3.14 | | | | | | | | | | |
| Oldh | 3.75 | 6.53 | 3.50 | 2.64 | 6.25 | 2.84 | 5.05 | | | | | | | | | |
| Roba | 0.91 | 5.33 | 3.09 | 4.12 | 4.99 | 2.66 | 2.12 | 4.26 | | | | | | | | |
| Sedi | 6.34 | 5.98 | 6.99 | 4.81 | 4.28 | 5.26 | 6.34 | 5.95 | 6.70 | | | | | | | |
| Shul | 5.66 | 5.27 | 6.51 | 4.01 | 5.28 | 4.64 | 5.95 | 4.61 | 5.90 | 5.94 | | | | | | |
| Tol1 | 4.02 | 4.51 | 5.12 | 4.97 | 5.86 | 3.93 | 3.15 | 4.74 | 4.09 | 7.25 | 5.34 | | | | | |
| Tol2 | 3.81 | 3.97 | 4.83 | 4.65 | 5.19 | 3.73 | 2.99 | 4.43 | 3.88 | 6.42 | 4.88 | 1.31 | | | | |
| W961 | 5.20 | 4.53 | 6.11 | 4.83 | 1.57 | 4.68 | 4.96 | 6.44 | 5.32 | 3.72 | 5.94 | 6.67 | 6.03 | | | |
| W962 | 2.14 | 4.16 | 3.87 | 4.52 | 3.97 | 3.23 | 1.93 | 4.97 | 1.88 | 6.26 | 5.95 | 3.99 | 3.59 | 4.45 | | |
| W963 | 7.01 | 5.83 | 7.15 | 4.92 | 5.06 | 5.52 | 6.84 | 5.71 | 7.40 | 2.81 | 4.82 | 6.62 | 5.93 | 5.01 | 7.04 | |

where NC=NC343, Bgud=Baha gudo, Bjidu=Baha jidu, Bulki=Bulki, Fet=Fetene, Lot=Lote, Man=manipeter, Oldh=Oldhale, Roba=Roba, Sedi=Sedi, Shul=Shulamith, Tol1=Tole1, Tol2=Tole2, W961=Werer 961, W962= Werer 962, W963=Werer 963.

Principal factors were carried out using principal component (PC) method for factor extraction. Differentiation among genotypes occurs in stages, or in other words in different axes of differentiation that accounts for total divergence. Theoretically, many axes of differentiation can be envisaged as there are characters contributing to total variation, but it is not absolutely. It is possible that most of the variation is accounted for by the first two or more axes of differentiation. Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma, 1998). The eigen values are often used to determine how many factors to retain. The sum of the eigen values is usually equal to the number of variables (Singh *et al*., 2013). Accordingly, in the present study the first factor retained the information contained in 7.45 (based on D) of the original variables (Table 2). The proportion of variance explained by each axis was shown that PC1 for D (47%).

Showemimo (2004) reported that estimates of the generalized Mahalanobis distance ($D^2$) clearly indicated that

the pairs of genotypes are more divergent and more similar genetically.

***Table 2.*** *Eigen values and Eigen vectors for correlation matrix based on Euclidean distance (D) for 16 groundnut genotypes evaluated for 12 agromorphological characters.*

| Parameter | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| Eigenvalue | 7.45 | 3.39 | 2.33 | 0.95 | 0.57 |
| Difference | 4.06 | 1.06 | 1.38 | 0.38 | 0.19 |
| Proportion | 0.47 | 0.21 | 0.15 | 0.06 | 0.04 |
| Cumulative | 0.47 | 0.68 | 0.82 | 0.88 | 0.92 |
| NC343 | 0.34 | 0.02 | 0.20 | -0.02 | -0.11 |
| Baha gudo | -0.04 | 0.44 | -0.18 | 0.28 | -0.02 |
| Baha jidu | 0.30 | -0.18 | 0.21 | -0.15 | -0.14 |
| Bulki | 0.13 | -0.4 | 0.20 | 0.35 | 0.30 |
| Fetene | -0.16 | 0.31 | 0.35 | 0.38 | 0.19 |
| Lote | 0.29 | -0.20 | 0.22 | 0.19 | 0.31 |
| Manipeter | 0.30 | 0.26 | 0.05 | -0.03 | 0.08 |
| Oldhale | 0.20 | -0.4 | -0.01 | 0.08 | 0.09 |
| Roba | 0.33 | 0.09 | 0.18 | -0.03 | -0.16 |
| Sedi | -0.30 | -0.08 | 0.22 | -0.2 | 0.34 |
| Shulamith | -0.08 | -0.23 | -0.30 | 0.69 | -0.29 |
| Tole1 | 0.25 | 0.14 | -0.37 | 0.002 | 0.41 |
| Tole2 | 0.24 | 0.16 | -0.38 | 0.03 | 0.46 |
| Werer 961 | -0.19 | 0.23 | 0.43 | 0.23 | 0.17 |
| Werer 962 | 0.29 | 0.26 | 0.18 | 0.04 | -0.08 |
| Werer 963 | -0.31 | -0.17 | -0.04 | -0.14 | 0.29 |

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The coefficients defining the four principal components for 16 groundnut genotype data are given in Table 2. The coefficients are scaled, so that they present correlations between observed variables and derived components. Three principal components, PC1 to PC3, which were extracted from the original data and having eigen values greater than one, and cumulatively they explained 83% based on euclidean distance(D)suggesting these principal component scores might be used to summarize the original 12 variables in any further analysis of the data. According to PCA analysis based on Euclidean distance, the first component has got high positive load from NC 343, Roba, Baha jidu, Lote, Manipeter and Werer 962 genotypes but high negative loading from Werer 963, Sedi and Fetene genotypes. Among them the most divergent genotypes were NC343 or Roba and Werer 963 or Sedi. The second component has got high positive load from Baha gudo, Fetene followed by Manipeter and Werer 962 while highest negative load were from Bulki and Oldhale. The most distinct genotypes being Baha gudo and Bulki or Lote.

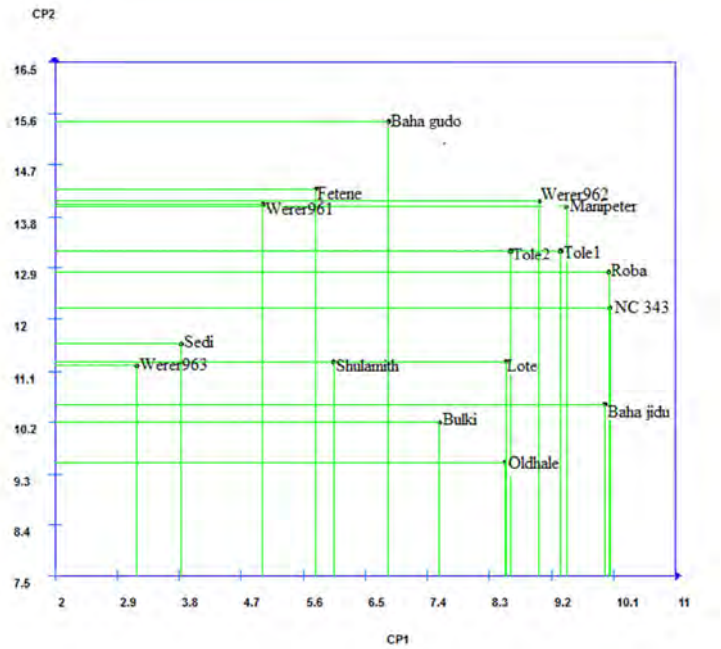


***Figure 1.*** *PCA scores for 16 groundnut genotypes.*

Similarly, the third component has got high positive load from Fetene and Werer 961 while high negative load were from Tole2, Tole1 followed by Shulamith and Baha gudo. Thus, the most distinct genotypes here are Fetene and Tole2.

The result obtained for the plot for PC2*PC1 for D (fig 1). Genotypes that have very close component scores are grouped into same cluster. Similar result was obtained with clustering dendrogram. Jagadev*et al*. (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. According to Chahal and Gosal (2002) characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of some characters rather than small contribution from each character. The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables. Therefore, the above mentioned genotypes with load high positively or negatively contributed more to the diversity and they were the ones that most differentiate the clusters. The cluster analysis based on UPGMA for 16 groundnut genotypes, measured for 12 agromorphological characters (Fig 2) identified 10 clusters. The majority of clusters were formed by a single genotype. Thus, the most distinct genotypes were Oldhale (local variety) in cluster 4, Baha jidu (cluster 5), Shulamith (cluster 6), Sedi(cluster 7), Werer 963 (cluster 8) and Baha gudo (cluster 10). While the most similar genotypes were NC343 and Roba (cluster 1) followed by Tole1 and Tole2 (cluster 2), Fetene and Were 961(cluster 9). All genotypes were distinct at 100% level of similarity. On the basis of results obtained from the present study various degree of genetic divergence was observed. It is evident as more number of cluster formed by the 16 groundnut genotypes and high range of values of intercluster distance. The maximum intercluster distance was observed between NC343 and Baha gudo (Table 3), which exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization program.

***Table 3.*** *Cluster analysis based on UPGMA.*

| Stage | Genotype x | Genotype y | distance | Dissimilarity (%) | Cut point |
|---|---|---|---|---|---|
| 1 | NC343 | Roba | 0.91 | 16.1 | |
| 2 | Tole1 | Tole 2 | 1.31 | 23.2 | 1.5 ns |
| 3 | Fetene | Werer 961 | 1.57 | 27.8 | 1.7 ns |
| 4 | Manipeter | Werer 962 | 1.93 | 34.2 | 2.0 ns |
| 5 | Bulki | Lote | 2.12 | 37.5 | 2.21 ns |
| 6 | Nc343 | Manipeter | 2.17 | 38.3 | 2.3 ns |
| 7 | Bulki | Oldhale | 2.74 | 48.5 | 2.6* |
| 8 | Sedi | Werer 963 | 2.81 | 49.7 | 2.8* |
| 9 | Baha jidu | Bulki | 3.23 | 57.1 | 3.0* |
| 10 | NC 343 | Tole1 | 3.69 | 65.3 | 3.3* |
| 11 | NC 343 | Baha jiddu | 4.00 | 70.9 | 3.6* |
| 12 | Baha gudo | Fetene | 4.18 | 74.0 | 3.9* |
| 13 | Baha gudo | Sedi | 4.98 | 88.1 | 4.3* |
| 14 | NC343 | Shulamith | 5.34 | 94.5 | 4.6* |
| 15 | NC343 | Baha gudo | 5.65 | 100 | 5.0* |

Where, ns= nonsignificant (intracluster distances); * significant (intercluster distances)

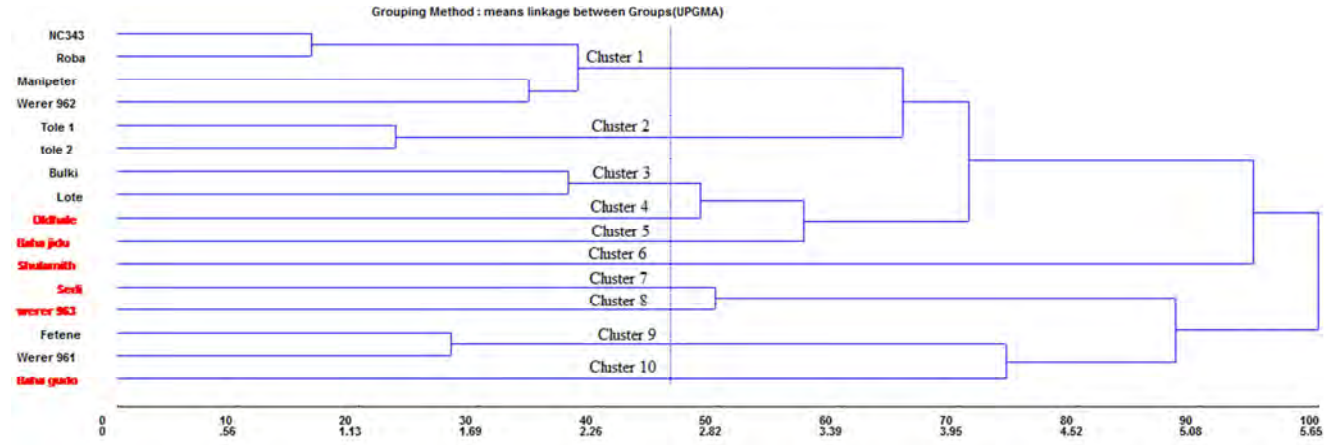


***Figure 2.*** *Clustering based on UPGMA for 16 groundnut genotypes evaluated for 12 agromorphological characters.*

The result obtained from different methods of divergence study was slightly differs from each others. In all methods the dendrogram identifies more subclusters of the major groups at different levels and offers additional opportunity to plant breeders in planning of hybridization programs aimed at crop improvement. The resemblance coefficient between two genotypes is the value at which their branches join. The dendrogram elaborate the relative magnitude of resemblance among the genotypes as well as the clusters. Similar type of result was also found by Garg and Gautam (1997) in their experiment. The result showed that geographical and genetic diversity exhibited no correspondence between them as genotypes from one and different geographic region are grouped together, which might be due to free exchange of genetic material from different regions. Sharma et al. (2002) and Sharma et al. (2008) have also revealed that the pattern of distribution of genotypes within various clusters was random and independent of geographical isolation. So there is no association between the geographical distribution and genetic diversity.

Clustering methods allow for the identification of genotypes genetically that are contrasting for the crosses. The first cluster in a dendrogram is formed by genotypes sharing the greatest similarity (Cruz *et al*., 2014; Cantelli, *et al.,* 2016). Selection of divergent parents should be based on the magnitude of the genetic divergence among genotypes, when the aim is to perform crossings resulting in superior progenies in relation to the traits of interest. Vieira *et al*. (2005) reported that clusters formed by one single individual suggest that those individuals are the most divergent in relation to the rest. According to Abreu *et al*. (2004), knowledge of genetic divergence allows inferences to be made about the specific combination capacity before carrying out the crossings, resulting in a greater chance of identifying and recovering more promising combinations among the segregating populations. Rotili*et al*. (2012) suggested that, compared to the Tocher method, the nearest neighbor method can be used with the objective of evaluating the genetic divergence among corn genotypes.

Vogt et al. (2010) also confirmed that the UPGMA and Tocher optimization methods were in agreement in a study of genetic divergence of sunflowers. Using various clustering methods for processing the data, using different measures of dissimilarity and taking into account the particularities of each method are required for an accurate choice of parents for crossings (CargneluttiFilho*et al*., 2008). Through the use of dendrograms, it is possible to evaluate the formation of clusters and, consequently, to select the genetically most distinct genotypes. The reference information regarding genetic divergence is typically not sufficient for selecting parents for hybridization (Ferreira Júnior*et al.,* 2015). Instead, the reference information should be accompanied by information about the genotype performance in relation to the desirable traits (Cantelli, *et al.,*2016). The ideal strategy is one that combines the results of genetic divergence analyses and the identification of the genotypes carrying the traits that are the target of the breeding program.

***Table 4.*** *Correlation coefficient based on Euclidean distance(D).*

| Gen | NC | Bg | Bj | bul | fet | lot | man | oldh | rob | Sed | shul | tol1 | tol2 | w961 | w962 | w963 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NC | | -0.17 | 0.82** | 0.37 | -0.25 | 0.79** | 0.78** | 0.45 | 0.98** | -0.64** | -0.32 | 0.44 | 0.41 | -0.29 | 0.83** | -0.79** |
| Bg | | | -0.47 | -0.57* | 0.41 | -0.4 | 0.24 | -0.57* | -0.07 | -0.17 | -0.07 | 0.23 | 0.29 | 0.24 | 0.22 | -0.17 |
| Bj | | | | 0.56* | -0.41 | 0.81** | 0.50* | 0.65** | 0.75** | -0.57* | -0.3 | 0.28 | 0.23 | -0.38 | 0.54* | -0.65** |
| Bul | | | | | -0.27 | 0.73** | -0.05 | 0.76** | 0.24 | -0.09 | 0.24 | -0.05 | -0.08 | -0.21 | 0.01 | -0.09 |
| Fet | | | | | | -0.27 | -0.06 | -0.60* | -0.19 | 0.37 | -0.18 | -0.4 | -0.35 | 0.92** | 0.07 | 0.12 |
| Lot | | | | | | | 0.51* | 0.70** | 0.72** | -0.44 | -0.09 | 0.33 | 0.28 | -0.28 | 0.52* | -0.51* |
| Man | | | | | | | | 0.08 | 0.85** | -0.65** | -0.4 | 0.65** | 0.63** | -0.18 | 0.90** | -0.78** |
| ldh | | | | | | | | | 0.35 | -0.37 | 0.17 | 0.21 | 0.18 | -0.57* | 0.07 | -0.27 |
| Roba | | | | | | | | | | -0.66** | -0.35 | 0.47 | 0.44 | -0.25 | 0.88** | -0.82** |
| Sedi | | | | | | | | | | | -0.05 | -0.73** | -0.68** | 0.53* | -0.60* | 0.80** |
| Shul | | | | | | | | | | | | -0.06 | -0.05 | -0.25 | -0.43 | 0.24 |
| tol1 | | | | | | | | | | | | | 0.96** | -0.56* | 0.47 | -0.58* |
| tol2 | | | | | | | | | | | | | | -0.52* | 0.47 | -0.54* |
| w 961 | | | | | | | | | | | | | | | -0.03 | 0.22 |
| w 962 | | | | | | | | | | | | | | | | -0.80** |
| w 963 | | | | | | | | | | | | | | | | |

where NC=NC343, Bg=Baha gudo, Bj=Baha jidu, Bul=Bulki, Fet=Fetene, Lot=Lote, Man=manipeter, Oldh=Oldhale, Rob=Roba, Sed=Sedi, Shul=Shulamith, Tol1=Tole1, Tol2=Tole2, W961=Werer 961, W962= Werer 962, W963=Werer 963.

The correlation coefficient shows significant positive and negative correlations among genotypes with respect evaluated characters. Thus, based on correlation coefficient for euclidean distance measures, the most divergent genotypes were those that do not form significant correlation with most of the other genotypes or those that show significant negative correlation. The correlation coefficient supplements clustering methods by revealing significant relationships in both directions. Based on the result for analysis of correlation coefficient in the present study, the most divergent genotype (Table 4) was shulamith followed by Baha gudo as they didn't form significant correlation with all genotypes except for negative correlation between Baha gudo and bulki based on euclidean distance. Similar result was obtained by clustering. However, the correlation coefficient based on distance matrix has revealed the extent

of association between genotypes. For example, genotypes NC343 and Roba formed cluster since both genotypes have maximum significant correlation but the extent of significant association of these genotypes with those genotypes in the nearest cluster is not shown by clustering dendrogram. Thus, correlation among distance matrix has shown those genotypes having significant positive correlation showing similarity(close relationship) while significant negative correlation in other direction shows dissimilarity or divergence which is important for plant breeders and genetists who are thriving to capture variability to be used for breeding programs.

***Table 5.*** *Euclidean distance for genotypic correlation.*

| trait | PH | NMP | NBP | AGBP | PWP | SWP | NSP | ShP | 100SW | HI | NSPod | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PH | | | | | | | | | | | | |
| NMP | 3.06 | | | | | | | | | | | |
| NBP | 3.7 | 2.40 | | | | | | | | | | |
| AGBP | 3.27 | 2.83 | 1.48 | | | | | | | | | |
| PWP | 5.18 | 4.31 | 2.72 | 3.58 | | | | | | | | |
| SWP | 4.10 | 2.82 | 2.79 | 3.83 | 2.91 | | | | | | | |
| NSP | 2.87 | 2.25 | 4.17 | 4.52 | 5.31 | 3.44 | | | | | | |
| SHP | 5.03 | 5.46 | 6.03 | 6.48 | 5.17 | 4.53 | 4.12 | | | | | |
| 100SW | 5.42 | 5.54 | 4.13 | 4.54 | 2.05 | 4.17 | 5.99 | 4.63 | | | | |
| HI | 5.97 | 6.42 | 6.67 | 7.08 | 5.45 | 5.53 | 5.27 | 1.59 | 4.50 | | | |
| NSPOD | 6.12 | 7.67 | 8.01 | 7.77 | 7.54 | 7.83 | 6.45 | 4.34 | 6.31 | 3.71 | | |
| GY | 5.06 | 4.01 | 3.14 | 4.27 | 1.70 | 1.71 | 4.62 | 4.50 | 2.98 | 5.11 | 7.73 | |

where PH: plant height; NMP: number of mature pods per plant; NBP: number of $1^0$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; 100SW: 100 seed weight; HI: harvest index; NSPOD: number of seeds per pod; GY: grain yield kg/ha.

### *3.2. Character Association*

Euclidean distance based on genotypic correlation (Table 5) above shows the relative genetic distance of each character from grain yield per hectare. The eigen values and eigenvectors for the first five principal components based on genotypic and phenotypic correlations among 12 agromorphological characters were indicated in Table 6. The loading of both genotypes and the associated characters into PCA helps to associate and select genotypes with their corresponding characters (Singh *et al*., 2013). Component loading that contribute high positive or negative to the first axis are responsible for their divergence. Accordingly, the first principal component had high positive component loading from NMP, NBP, AGBP, PWP, SWP as well as GY. These characters correspond to NC343, Baha jidu, Lote, Manipeter, Roba, Werer 962, Tole1, Tole2 and Oldhale genotypes (Table 2)with high positive PCA1 scores based on euclidean distance matrix(D). Usually it is customary to choose one variable from these identified groups. Hence, for PC1 NBP was the best character for selection since it had the largest loading from component ones while NC343 is the best genotype in first component. On the other hand, PCA2 had high positive component loading from 100SW, PWP as well as GY characters, the corresponding genotypes are Baha gudo, Fetene, Manipeter, Werer 962 and Werer 961.100SW being the best character while Baha gudo was the best genotype according to component 2. GY has shown positive loading in all the first three components but the highest positive in component 2 indicating the highest grain yielding genotypes are those that are most positive in second component. The highest positive loading characters in the third component were NSP, SHP, SWP, NMP as well as GY the associated genotypes were Fetene and Werer 961. The best character in third load was NSP while the best genotype was Fetene. On the other hand, high negative PCA1 loading was obtained for SHP, HI and NSPOD. High negative loading characters especially in PC1 shows inverse relationship and/or divergence to the rest variables therefore such characters are not mainly used for breeding since they have usually low heritability. The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables. The characters which load high positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters. Similar finding was reported by Makinde and Ariyo (2010).

***Table 6.*** *Eigen values and Eigen vectors based on Euclidean distance for genotypic and phenotypic correlation matrices.*

| Genotypic | | | | | Phenotypic | | | | | PCA based on original data | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| parameter | pc1 | pc2 | pc3 | pc4 | pc1 | pc2 | pc3 | pc4 | pc5 | PC1 | PC2 | PC3 |
| Eigen value | 6.65 | 3.22 | 1.76 | 0.30 | 5.35 | 2.50 | 1.82 | 1.14 | 0.49 | 4.91 | 2.91 | 2.33 |
| Difference | 3.44 | 1.46 | 1.46 | 0.27 | 2.85 | 0.67 | 0.68 | 0.65 | 0.14 | 1.99 | 0.58 | 1.39 |
| Proportion | 0.56 | 0.27 | 0.15 | 0.03 | 0.45 | 0.21 | 0.15 | 0.10 | 0.04 | 0.41 | 0.24 | 0.19 |
| Cumulative | 0.56 | 0.82 | 0.98 | 0.99 | 0.45 | 0.65 | 0.81 | 0.90 | 0.94 | 0.41 | 0.65 | 0.85 |
| PH | 0.20 | -0.4 | -0.08 | 0.79 | 0.30 | -0.22 | -0.39 | 0.19 | -0.33 | 0.16 | -0.20 | 0.25 |
| NMP | 0.33 | -0.21 | 0.24 | -0.25 | 0.30 | 0.39 | 0.03 | 0.26 | -0.07 | 0.34 | -0.13 | 0.34 |
| NBP | 0.38 | 0.04 | -0.04 | -0.09 | 0.34 | 0.14 | 0.04 | -0.22 | 0.74 | 0.41 | -0.05 | -0.08 |

| Genotypic | | | | | Phenotypic | | | | | PCA based on original data | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AGBP | 0.37 | -0.04 | -0.19 | 0.09 | 0.42 | -0.01 | -0.07 | -0.13 | -0.22 | 0.38 | -0.23 | -0.16 |
| PWP | 0.27 | 0.40 | -0.003 | -0.05 | 0.18 | 0.29 | 0.53 | -0.01 | -0.42 | 0.31 | 0.30 | -0.27 |
| SWP | 0.30 | 0.12 | 0.42 | 0.24 | 0.27 | -0.18 | -0.23 | 0.49 | 0.19 | 0.33 | 0.27 | 0.23 |
| NSP | 0.13 | -0.37 | 0.50 | -0.14 | 0.05 | 0.58 | 0.04 | 0.3 | -0.01 | 0.16 | -0.02 | 0.59 |
| ShP | -0.28 | 0.10 | 0.48 | 0.27 | -0.27 | -0.19 | 0.03 | 0.56 | 0.002 | -0.11 | 0.43 | 0.35 |
| 100SW | 0.08 | 0.52 | -0.17 | 0.30 | 0.12 | -0.45 | 0.43 | -0.15 | -0.12 | 0.14 | 0.36 | -0.41 |
| HI | -0.31 | 0.21 | 0.34 | 0.03 | -0.37 | 0.04 | 0.25 | 0.26 | 0.16 | -0.20 | 0.48 | 0.17 |
| NSPod | -0.38 | -0.04 | -0.05 | 0.22 | -0.4 | 0.17 | -0.08 | -0.14 | -0.04 | -0.39 | 0.07 | 0.05 |
| GY | 0.23 | 0.39 | 0.30 | 0.10 | 0.21 | -0.23 | 0.5 | 0.29 | 0.19 | 0.30 | 0.42 | -0.001 |

where PH: plant height; NMP: number of mature pods per plant; NBP: number of $1^{0}$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; 100SW: 100 seed weight; HI: harvest index; NSPOD: number of seeds per pod; GY: grain yield (kg/ha).

The characters contributed positively to first three principal components could be given due consideration while selecting the best genotypes without losing yield potential. The present investigation provided considerable information useful in genetic improvement of groundnut. In this PCA analysis based on Euclidean distance for genotypic correlation only SWP together with GY have positively contributed to the first three principal components. Thus SWP can be used as the best trait to improve groundnut genotypes. Other characters like 100SW, PWP and NBP were positive for the first two axes so that they can be as best characters next to SWP. These are priori characters for groundnut breeding; however, it doesn't mean that the use of only these characters for breeding. Similar studies should be conducted to confirm it.

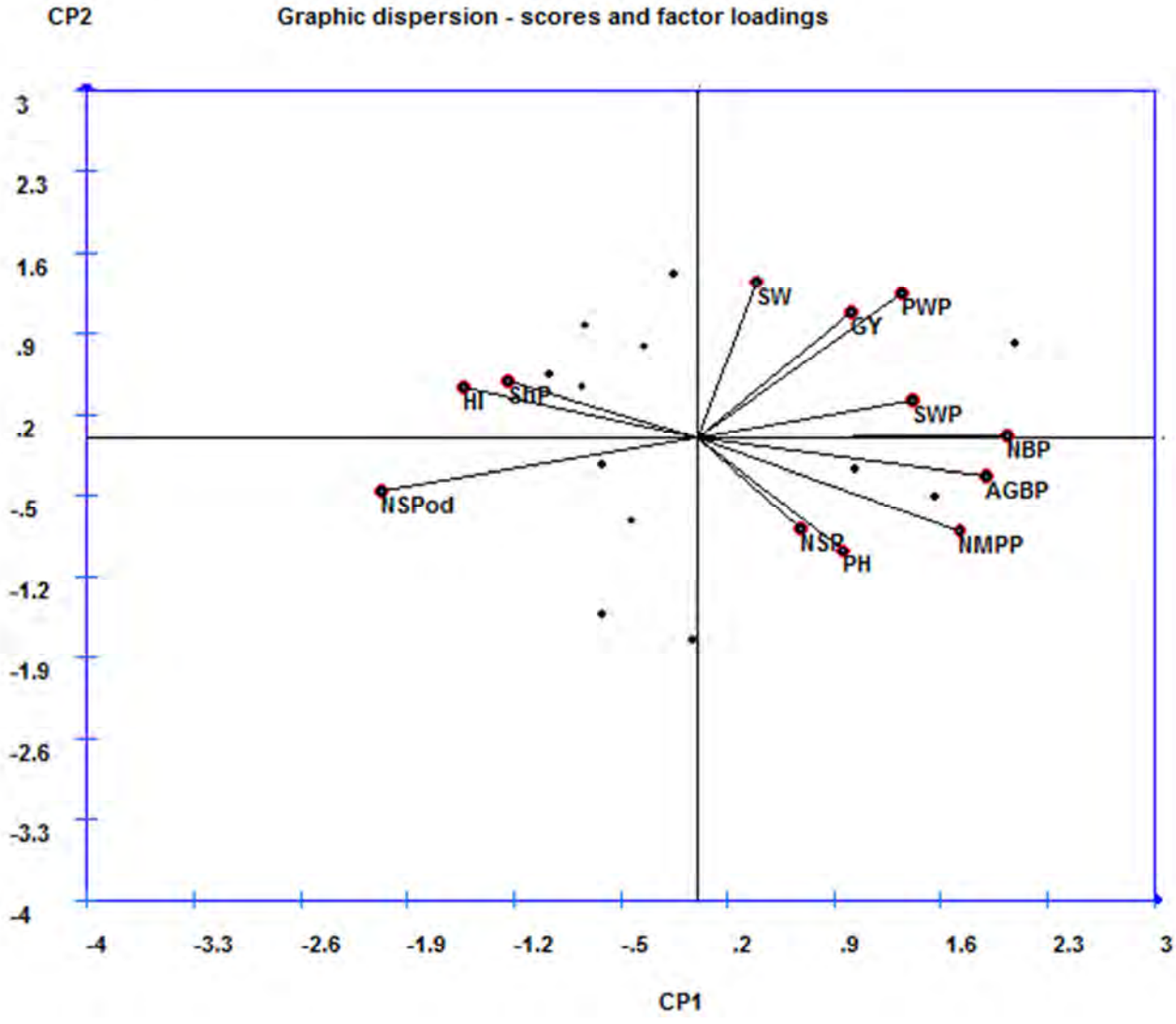


***Figure 3.*** *Principal component analysis for 12 agromorphological characters measured for 16 groundnut genotypes.*

***Table 7.*** *Eigen values for canonical variables and canonical vectors for 12 agromorphological characters evaluated for 16 groundnut genotypes.*

| **Genotypic canonical vectors** | | | | | **Phenotypic canonical vectors** | | | |
|---|---|---|---|---|---|---|---|---|
| parameter | can1 | can2 | can3 | can4 | can1 | can2 | can3 | can4 |
| Eigen value | 3.61 | 2.34 | 1.17 | 0.69 | 3.61 | 2.34 | 1.17 | 0.69 |
| Difference | 1.27 | 1.17 | 0.49 | 0.45 | 1.27 | 1.17 | 0.49 | 0.45 |
| Proportion | 0.42 | 0.27 | 0.14 | 0.08 | 0.42 | 0.27 | 0.14 | 0.08 |
| Cumulative | 0.42 | 0.70 | 0.84 | 0.92 | 0.42 | 0.70 | 0.84 | 0.92 |
| PH | -0.20 | 0.14 | -0.4 | 0.82 | -0.12 | 0.09 | -0.29 | 0.69 |
| NMP | -0.26 | 0.85 | 0.14 | 0.27 | -0.18 | 0.61 | 0.11 | 0.26 |
| NBP | 0.38 | 0.82 | -0.17 | 0.31 | 0.30 | 0.68 | -0.16 | 0.34 |
| AGBP | 0.22 | 0.74 | -0.51 | 0.14 | 0.16 | 0.57 | -0.45 | 0.14 |
| PWP | 0.77 | 0.43 | 0.16 | -0.04 | 0.39 | 0.23 | 0.09 | -0.03 |
| SWP | 0.29 | 0.48 | 0.42 | 0.47 | 0.11 | 0.18 | 0.18 | 0.23 |
| NSP | -0.50 | 0.41 | 0.37 | 0.57 | -0.22 | 0.19 | 0.2 | 0.35 |
| ShP | 0.01 | -0.38 | 0.75 | 0.31 | 0.006 | -0.24 | 0.54 | 0.26 |
| 100 SW | 0.99 | -0.05 | -0.0006 | 0.06 | 0.93 | -0.05 | -0.0007 | 0.07 |
| HI | 0.17 | -0.52 | 0.81 | 0.1 | 0.13 | -0.44 | 0.77 | 0.11 |
| NSPod | -0.17 | -0.95 | -0.04 | 0.07 | -0.13 | -0.78 | -0.04 | 0.07 |
| GY | 0.64 | 0.40 | 0.51 | 0.3 | 0.49 | 0.33 | 0.47 | 0.32 |

Where PH: plant height; NMP: number of mature pods per plant; NBP: number of $1^0$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; 100SW: 100 seed weight; HI: harvest index; NSPod: number of seeds per pod; GY: grain yield kg/ha.

According to PCA analysis based on Euclidean distance for genotypic correlation (Table 7), the first component has got high positive load from NBP, AGBP, NMP, SWP, PWP,GY and PH characters but high negative loading from NSPOD, HI and SHP characters. Among them the most divergent characters were between NBP or AGBP and NSPOD. The second component has got high positive load from 100SW, PWP followed by GY and HI while highest negative load were from NSP and NMP. The most distinct characters being 100SW and NSP. Similarly, the third component has got high positive load from NSP and SHP while negative load were from AGBP. Thus, the most distinct characters here are NSP and AGBP.

Discriminant analysis based on canonical vectors (Table 7) at genotypic and phenotypic levels showed that the first three vector scores greater than one, together accounted for 83% of the variables. GY had highest positive load in can1, showing that most of yield related traits are those that load high positive in this vector including 100SW, PWP, NBP, SWP, AGBP and HI. On the other hand, NSP, NMP, PH, and NSPOD were among high negative load in can1. The result obtained from discriminant analysis was similar with that of PCA for Euclidean distance for genotypic correlation. However, discriminant analysis has shown important yield related traits in the first vector while this is not the case in PCA for Euclidean distance for genotypic correlation. PCA based on Euclidean better than canonical vectors, for associating genotypes with yield related traits.

The proportion of Eigen values (Table 7) for Euclidean distance based on genotypic correlation (56%) is greater than that of proportion of Eigen values for Euclidean distance based on phenotypic correlation (45%). This can be further evidence for superiority of genotypic correlation matrix over phenotypic correlation matrix for breeding and genetic studies of characters.

***Table 8.*** *Clustering agromorphological characters based on Euclidean distance for genotypic correlations.*

| **Stage** | **Genotype x** | **Genotype y** | **Distance** | **Dissimilarity (%)** | **Cut point** |
|---|---|---|---|---|---|
| 1 | NBP | AGBP | 3.63 | 30.28 | |
| 2 | SHP | HI | 4.28 | 35.75 | 4.53 ns |
| 3 | NMP | NSP | 4.72 | 39.41 | 4.89 ns |
| 4 | SWP | GY | 4.94 | 41.23 | 5.11 ns |
| 5 | PWP | SWP | 5.82 | 48.63 | 5.69* |
| 6 | PH | NBP | 6.07 | 50.71 | 6.06* |
| 7 | PWP | 100SW | 6.26 | 52.31 | 6.33 ns |
| 8 | PH | NMP | 6.45 | 53.89 | 6.56 ns |
| 9 | PH | PWP | 7.44 | 62.15 | 7.02* |
| 10 | SHP | NSPOD | 8.18 | 68.32 | 7.55* |
| 11 | PH | SHP | 12.0 | 100 | 9.22* |

where, ns(nonsignificant)=intracluster distance, *significant=intercluster distance; PH: plant height; NMP: number of mature pods per plant; NBP: number of $1^0$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; 100SW: 100 seed weight; HI: harvest index; NSPod: number of seeds per pod; GY: grain yield kg/ha.

The dendrogram for Euclidean distance based on genotypic correlation (fig 4) has shown that traits in cluster 2 including PWP, SWP and 100SW were shown positive and nonsignificant correlation with GY. The most similar trait was NBP and AGBP, while NSPOD was the most divergent trait and found to be negatively correlated with GY. Thus,

such divergent and negatively correlated with yield has no significance in selection so it can be dropped. Those characters in cluster 1 including NBP, AGBP, NMP and NSP were positive but nonsignificantly correlated at genotypic level with GY.

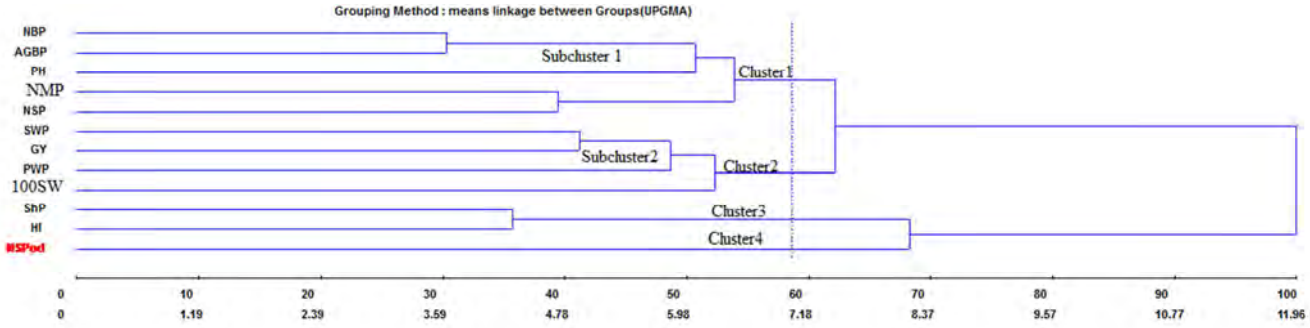


***Figure 4.*** *Dendrograms based on UPGMA for clustering of agromorphological characters for genotypic correlation.*

# 4. Conclusion

The PCA analysis based on distance matrix has found the existence of divergent genotypes to be used for parents in hybridization of groundnut. The component analysis has also identified major yield related traits and their association with divergent genotypes. NBP with GY was the best character for selection whileNC343 is the best genotype selected based on associated traits in first component. In contrast, 100SW and PWP with GY were the best characters; the corresponding best genotypes were Baha gudo in PC2. SWP and GY has shown positive loading in all the first three components but the highest positive for GY in component 2 indicating the highest grain yielding genotypes are those that are most positive in second component. The highest positive loading characters in the third component were NSP with GY the associated best genotype was Fetene. On the other hand, high negative PCA1 loading was obtained for SHP, HI and NSPOD. High negative loading characters especially in PC1 shows inverse relationship and/or divergence to the rest variables therefore such characters are not mainly used for breeding since they have usually low heritability. The present study has well identified yield related traits with respective genotypes and will have significant contribution for future groundnut breeding.

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