# Principal Components and Cluster Analysis of Open Pollinated Tomato (*Solanum lycopersicum* L.) Accessions Using Quantitative Descriptors

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## Abstract

Principal Components and Cluster Analysis were carried out using quantitative descriptors with the aim to analyze the genetic diversity and to identify similar accessions with phylogenetic relationship. Tomato accessions were sourced from; National Centre for Genetic Resources and Biotechnology Ibadan, Agrotropic limited Jos and local farmers in Benue State were planted in the field at the Research and Teaching farm of University of Agriculture Makurdi, in a Randomized Complete Block design with 3 replicates. 18 morphological characters were studied according to set standard by International Plant Genetic Resources Institute tomato descriptor and data were subjected to ANOVA at 95% probability level, significant differences among accession were detected using New Duncan's Multiple Range Test. Analysis of Variance revealed significant variations for 17 out of the 18 quantitative characters studied among tomato accessions, with the first five principal components accounting for 78% of the total variation among the accessions, revealing vine length and yield of plots per hectare as distinguished traits. The 17 traits were thus useful for characterization and based on them, clustered analysis grouped the tomato accessions into 3 clusters based on Euclidean correlation coefficient distance and two pairs of duplicates (NGB-00713, NGB-00731, NGB-00722, NGB-00721, NGB-00724, NGB-00725 and NGB-00726) were identical and accessions (Rio-Grande, Apaa, Atumba and Gambo) were also identified to be similar accessions thereby reducing the total number of accessions to 13. The results obtained in this study revealed common phylogenetic relationships among the accessions.

## 1. Introduction

Tomato (Solanum lycopersicum L) is an important vegetable crop of the family solanaceae, which is consumed nearly in every household in Nigeria [6] owing to its high nutritive value and an excellent source of vitamin A and C [10]. According to Atnafua and Endashaw [1], characterization may be defined as the scoring of characters that can be easily detected and have high heritability based on the form and structure of the organism, especially their external form and is carried out on a representative population of an accession using a list of descriptors for the species. Morphological characterization which also refers to characterizing

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visually detectable variability including form and structure of plants, it defines the characteristics of varieties for their protection and registration as recognized conservation varieties [4, 3] primarily for their botanical and taxonomical classification. It assesses both quantitative and qualitative traits as an essential source of genetic progress and is performed with conventional highly heritable morphological descriptors based on seedling, plant, inflorescence, flower, fruit, and agronomic traits [5, 13, 3]. Morphological characterization examines structures of different plants of the same or different species, then draws comparisons and formulates ideas about similarities [2]. When similar structures in different species are believed to exist and develop as a result of common, inherited genetic pathways, those structures are termed homologous [2]. Local varieties often lack proper typification and characterization, which makes difficult in identifying specific and objective distinctive characteristics for defining cultivar groups, which are established on the basis of defined similarity [11]. Genetic diversity in many crop plants including cultivated tomato is generally low due to the processes of domestication and continued selection [12, 7]. In obtaining heterotic hybrids, parental is considered as an important factor [7] and multivariate analysis is useful in quantifying the degree of divergence among biological population at genotypic level. Principal component analysis (PCA) which reveals the pattern of character variation among individual genotypes and cluster analysis tend to group the individual genotypes base on their characters similarity and differences are used. This necessitated this research with the aim of characterizing these open-pollinated tomato accessions based on their quantitative traits for genetic diversity and to identify accessions with common phylogenetic relationships.

# 2. Materials and Methods

## 2.1. Experimental Site

This experiment was carried out at the Teaching and Research farm, University of Agriculture Makurdi (Latitude 07 degrees North, Longitude 08 degrees East. 98m above sea level).

## 2.2. Sample Collection and Location

A total of 22 tomato accessions were obtained from these locations: National Centre for Genetic Resources and Biotechnology (NACGRAB) Ibadan, Agritropic Limited Jos and Local farmers in Benue state as revealed in table 1.

**Table 1.** Sourced of Accessions and Code used in this study.

| Accessions | Code in this study | Sourced |
|---|---|---|
| NGB-00711 | $G_1$ | NACGRAB, Ibadan |
| NGB-00713 | $G_2$ | NACGRAB, Ibadan |
| NGB-00721 | $G_3$ | NACGRAB, Ibadan |
| NGB-00722 | $G_4$ | NACGRAB, Ibadan |
| NGB-00724 | $G_5$ | NACGRAB, Ibadan |
| NGB-00725 | $G_6$ | NACGRAB, Ibadan |
| NGB-00726 | $G_7$ | NACGRAB, Ibadan |
| NGB-00732 | $G_8$ | NACGRAB, Ibadan |
| Roma VF | $G_9$ | Agrotropic Ltd Jos |
| UC82-B | $G_{10}$ | Agrotropic Ltd, Jos |
| Rio-grande | $G_{11}$ | Agrotropic Ltd, Jos |
| Atumba | $G_{12}$ | Farmers in Benue |
| Roma savanna | $G_{13}$ | Agrotropic Ltd, Jos |
| Tropimech | $G_{14}$ | Agrotropic Ltd, Jos |
| Dereka | $G_{15}$ | Farmers in Benue |
| Cerel | $G_{16}$ | Farmers in Benue |
| Mngishim | $G_{17}$ | Farmers in Benue |
| Apaa | $G_{18}$ | Farmers in Benue |
| Ishase | $G_{19}$ | Farmers in Benue |
| Akeakpev | $G_{20}$ | Farmers in Benue |
| Kal | $G_{21}$ | Farmers in Benue |
| Gambo | $G_{22}$ | Farmers in Benue |

## 2.3. Experimental Design

The field layout was arranged in a Randomized complete Block design with three replicates for the characterization and estimation of fruit yield of the accessions. Area of a plot within a block was $2.73m^2$ (2.73m by 1.00m)

## 2.4. Planting

Three weeks old seedlings were transplanted from the nursery to the field and irrigation was done on alternate days.

## 2.5. Weeding

This was done twice before termination of the experiment using small hoe.

## 2.6. Morphological Characterization of Tomato Accessions

Accessions were characterized based on International Plant Genetic Resources Institute [5] tomato descriptors.

## 2.7. Quantitative Data Analysis

Experiment was terminated 3 months after transplanting and data were subjected to analysis of variance at 95% probability level and significant differences among accessions were detected using New Duncan's Multiple Range Test (NDMRT). The principal component analysis (PCA) and Cluster analysis using Unweighted Pair Group Method and Arithmetic Average (UPGMA) were used to classify the tomato accessions using Minitab version 17.1 Software.

Fruit yield of accessions were estimated in kilogram per

hectare (Kg/ha) using this formula.

$$\text{Fruit yield (Kg/ha)} = \frac{fruits\ weight}{are\ in\ m^2} \times 1000$$

# 3. Results and Discussion

The results for the variability of measured traits as revealed by analysis of variance (Table 2) and mean separation (Table 3 and 4) indicated strongly that traits with P-values (<.0.05) were discriminatory and were important in distinguishing the accessions. Out of the 18 quantitative traits considered in this study, 17 were useful as morphological markers, except for the primary leaf width thereby suggesting that this trait could not entirely distinguish the tomato genotypes used., this observation is contrary to the findings by Figas et al. [3] who observed significant different in primary leaf width from the collection of 69 local varieties of tomato. Result also revealed that, vine length of NGB-00711 and NGB-00713 are significantly the same but different from the rest of the accessions. Tropimech has the highest yield of plots per hectare (744.200kg/ha) and significantly different from the rest of the genotypes, followed by NGB-00713 (724.930kg/ha), Mngishim (622.08kg/ha) and Roma VF (519.344kg/ha) which were significantly different among themselves but higher than the rest of the accessions.

Principal component analysis was able to capture 100% characters of the accessions at the 18th principal component. The first five principal components identified accounted for 78% of the total variations among the accessions as revealed in Table 5. The first Principal Component accounted for 27.3%, the second principal component accounted for 17.7%, the third principal component accounted for 15.2% while the forth Principal Component accounted for 10.4% and the fifth principal component accounted for 7.0% of the 18 traits analyzed. The first Principal Component with reference to its high value (27.3%) was positively associated with traits such as Primary leaf width, Stem internode length, Petal length, Stamen length, Sepal length, Highest number of truss per plant, Fruit weight, Fruit width, Fruit length, Size of locule, Number of seed per fruit, 1000-seed weight, Number of fruit per cluster, Yield of plots per hectare and Pedicel length and negatively associated with vine length which is the only distinguished traits among the accessions. The second Principal Component was positively associated with Primary leaf width, Primary leaf length, Stem internode Length, Petal length, Stamen length, Fruit width, Size of locule, Number of locules and 1000-seed weight and vein length, sepal length, fruit weight, yield of plots per hectare where the distinguishes traits among the accessions. The third Principal Component was positively associated with all the traits except Fruit width, Fruit weight, Size of locule, Yield of plots

per hectare and 1000-seed weight while the forth Principal Component was negatively associated with traits such as Stamen length, Sepal length, Highest number of truss per plant and Fruit weight and Yield of plots per hectare. The fifth principal component was positively associated with the Primary leaf width, Vine Length, Sepal length, highest number of truss per plant, Fruit weight, Number of seeds per fruit, Number of fruit per cluster, Pedicel length and 1000-Seed Weight. Positive Eigen values accounted for similarities across the components while negative Eigen Values accounted for dissimilarities across the components (Table 5).

This result revealed that, vine length and yield of plots per hectare are among the features that shows dissimilarities across the accessions and thus, can be used as important traits for hybridization programs. According to Mohammadi and Prasanna [8], Principal Component Analysis of morphological data is a powerful tool for classification and grouping of local tomato accessions.

From the hierarchical cluster analysis, the accessions were grouped into three (3) clusters based on their average linkage and the Euclidean test (Figure 1). Clusters I and II had a total of 18 accessions which are from the same source while cluster III consisted of 4 accessions. Cluster I was made up of 8 accessions (NGB-00711, NGB-00713, NGB-00731, NGB-00722, NGB-00721, NGB-00724, NGB-00725 and NGB-00726) that had the same traits related to mature leaf shape and size such as: General Petal length, Sepal length, Stamen length, Number of fruit per cluster and highest number of truss per plant. Cluster I showed 90% similarity among the accessions in that cluster.

Cluster II had a total of 10 accessions (Roma VF, Roma-Savanna, Dereka, Rio-Grande, Apaa, Ishase, Atumba, Gambo, Cerel and Kal) which showed 80% similarities. Cluster III had a total of four accessions (UC82-B, Akeakpev, Mngishim and Tropimech) and showed approximately 89% similarity. The dendrogram also revealed that accessions NGB-00713, NGB-00731, NGB-00722, NGB-00721, NGB-00724, NGB-00725 and NGB-00726 were identical and accessions Rio-Grande, Apaa, Atumba and Gambo were also found to be similar and may be two sets of duplicates based on their morphological traits. This reduced the total number of accessions to 13. Kaanjo et al. [6] used the same tomato accessions for characterization using Simple Sequence Repeat Markers, and the dendrogram classified the genotypes into 5 groups namely; group 1 (NGB-00711, NGB-00721, Atumba and Dereka), group 2 (NGB-00724 and Ishase), group 3 (NGB00713, UC82-B, Rio-grande, Cerel, Mngishim, and Kal), group 4 (NGB-00725, NGB-00726, NGB-00732, Roma VF, Roman, and Tropimech) and group 5 (NGB-00722, Apaa, Akeakpev and Gambo). This reduces the total number of genotypes to 5 based on their genetic similarities and suggests phylogenetic relationships among the

accessions. This clearly shows that, molecular markers are effective tool for characterizing the variability that is not detectable by simple visual observation and assessment of genetic diversity within and between populations [9] and characterization of germplasm and detection of duplicates.

NGB-00711 and Tropimech have patterns that were very different and not closely linked with the rest of the accessions.

**Table 2.** Mean Values among Accessions for the Quantitative Descriptors for which are Significant Different at P< 0.05, according to New Duncan's Multiple Range Test.

| Variable | N | Mean | SE. Mean | St. Dev. | Var. | Coef. Var. | P. Value |
|---|---|---|---|---|---|---|---|
| LW | 66 | 0.580 | 0.069 | 0.558 | 0.311 | 96.080 | 0.470$^{ns}$ |
| LL | 66 | 1.938 | 0.023 | 0.184 | 0.034 | 9.480 | 0.000* |
| IL | 66 | 3.883 | 0.182 | 1.482 | 2.196 | 38.160 | 0.000* |
| VL | 66 | 68.640 | 2.720 | 22.100 | 488.540 | 32.200 | 0.000* |
| SML | 66 | 0.726 | 0.015 | 0.122 | 0.015 | 16.800 | 0.004* |
| SL | 66 | 0.964 | 0.029 | 0.231 | 0.053 | 23.990 | 0.000* |
| HPP | 66 | 17.480 | 1.000 | 8.120 | 65.950 | 46.440 | 0.000* |
| FW | 66 | 30.620 | 3.160 | 25.68 | 659.300 | 83.850 | 0.000* |
| FL | 66 | 5.229 | 0.691 | 5.6140 | 31.518 | 107.370 | 0.000* |
| FWW | 66 | 3.485 | 0.115 | 0.933 | 0.870 | 26.760 | 0.000* |
| SLL | 66 | 1.997 | 0.072 | 0.582 | 0.339 | 29.150 | 0.000* |
| SPL | 66 | 69.820 | 3.070 | 24.910 | 620.460 | 35.680 | 0.021* |
| PDL | 66 | 0.773 | 0.026 | 0.208 | 0.043 | 26.920 | 0.000* |
| NL | 66 | 2.939 | 0.154 | 1.251 | 1.566 | 42.570 | 0.000* |
| PL | 66 | 1.162 | 0.019 | 0.157 | 0.025 | 13.480 | 0.000* |
| 1000SW | 66 | 2.474 | 0.046 | 0.371 | 0.137 | 14.980 | 0.000* |
| FPC | 66 | 3.917 | 0.124 | 1.008 | 1.017 | 25.740 | 0.000* |
| YPH | 66 | 277.100 | 28.300 | 229.700 | 52752.100 | 82.88 0 | 0.000* |

* Significant different at P<0.05 and ns Not significant
Key: LW=Primary leaf width, LL= Primary leaf length, IL= Stem internode length, VL=Vine length, SML=Stamen length, PL=Petal length, SL=Sepal length, HPP=Highest no. of truss per plant, FW=Fruit weight, FL=Fruit length, FWW=Fruit width, SLL=Size of locules, SPL=No. of seed per fruit, 1000SW=1000-Seed weight, FPC=No of fruit per cluster, YPH=Yield of plots per hectare, PDL=Pedicel length and NL= Number of locules.

**Table 3.** Mean Separation for each Genotype for the Quantitative Descriptors for which Significant (P<0.05) Differences according to New Duncan's Multiple Range Test.

| Variable | LW (cm) | LL (cm) | IL (cm) | VL (cm) | SML (cm) | SL (cm) | HPP | FW (g) | FL (cm) |
|---|---|---|---|---|---|---|---|---|---|
| $G_1$ | 0.467$^a$ | 1.900$^{ab}$ | 3.167$^{defg}$ | 112.000$^a$ | 0.700$^{ab}$ | 0.567$^f$ | 19.000$^{efg}$ | 3.967$^f$ | 2.330$^b$ |
| $G_2$ | 0.433$^a$ | 1.800$^b$ | 2.900$^{efg}$ | 120.000$^a$ | 0.467$^b$ | 0.766$^{def}$ | 18.000$^{efgh}$ | 21.833$^{cdef}$ | 5.100$^{ab}$ |
| $G_3$ | 0.600$^a$ | 2.100$^{ab}$ | 2.700$^{fg}$ | 98.000$^b$ | 0.667$^{ab}$ | 1.067$^{abcde}$ | 8.000$^{jk}$ | 11.300$^{def}$ | 3.000$^{ab}$ |
| $G_4$ | 0.467$^a$ | 1.733$^b$ | 3.167$^{defg}$ | 65.000$^{de}$ | 0.633$^{ab}$ | .767$^{cdef}$ | 8.000$^{jk}$ | 16.767$^{cdef}$ | 3.333$^{ab}$ |
| $G_5$ | 0.633$^a$ | 2.300$^a$ | 3.267$^{defg}$ | 99.500$^b$ | 0.800$^a$ | 0.767$^{cdef}$ | 4.000$^k$ | 16.500$^{cdef}$ | 3.900$^{ab}$ |
| $G_6$ | 0.533$^a$ | 1.833$^b$ | 3.667$^{defg}$ | 66.500$^{de}$ | 0.733$^{ab}$ | 1.033$^{abcde}$ | 15.000$^{ghi}$ | 4.400$^f$ | 1.933$^b$ |
| $G_7$ | 0.467$^a$ | 1.800$^b$ | 2.967$^{defg}$ | 69.500$^{cde}$ | 0.633$^{ab}$ | 0.667$^{ef}$ | 19.000$^{efg}$ | 5.300$^{ef}$ | 2.000$^b$ |
| $G_8$ | 0.467$^a$ | 1.967$^{ab}$ | 3.267$^{defg}$ | 74.000$^{cd}$ | 0.633$^{ab}$ | 0.967$^{abcdef}$ | 11.000$^{ij}$ | 19.867$^{cdef}$ | 2.733$^{ab}$ |
| $G_9$ | 2.000$^a$ | 1.800$^b$ | 6.767$^{ab}$ | 62.000$^{ef}$ | 0.833$^a$ | 1.067$^{abcde}$ | .000$^{hij}$ | 43.767$^{bcd}$ | 8.733$^{ab}$ |
| $G_{10}$ | 0.567$^a$ | 1.867$^b$ | 3.000$^{defg}$ | 38.000$^h$ | 0.800$^a$ | 0.733$^{def}$ | 14.000$^{ghi}$ | 60.800$^b$ | 5.067$^{ab}$ |
| $G_{11}$ | 0.567$^a$ | 2.033$^{ab}$ | 3.267$^{defg}$ | 41.000$^h$ | 0.833$^a$ | 1.067$^{abcde}$ | 13.000$^{hij}$ | 33.567$^{bcdef}$ | 4.500$^{ab}$ |
| $G_{12}$ | 0.500$^a$ | 1.933$^{ab}$ | 5.267$^{bc}$ | 53.000$^{fg}$ | 0.733$^{ab}$ | 1.233$^{ab}$ | 13.000$^{hij}$ | 16.500$^{cdef}$ | 5.833$^{ab}$ |
| $G_{13}$ | 0.467$^a$ | 2.000$^{ab}$ | 3.767$^{cdefg}$ | 60.000$^{ef}$ | 0.767$^{ab}$ | 1.200$^{abc}$ | 11.000$^{ij}$ | 30.700$^{bcdef}$ | 4.233$^{ab}$ |
| $G_{14}$ | 0.533$^a$ | 1.767$^b$ | 0.467$^{fg}$ | 44.000$^{gh}$ | 0.733$^{ab}$ | 0.933$^{abcdef}$ | 19.000$^{efg}$ | 116.367$^a$ | 5.367$^{ab}$ |
| $G_{15}$ | 0.533$^a$ | 2.000$^{ab}$ | 7.267$^a$ | 80.000$^c$ | 0.800$^a$ | 1.133$^{abcd}$ | 18.000$^{efgh}$ | 40.900$^{bcd}$ | 5.400$^{ab}$ |
| $G_{16}$ | 0.633$^a$ | 2.300$^a$ | 6.900$^a$ | 69.000$^{cde}$ | 0.800$^a$ | 0.967$^{abcdef}$ | 31.000$^b$ | 21.333$^{cdef}$ | 4.333$^{ab}$ |
| $G_{17}$ | 0.500$^a$ | 1.967$^{ab}$ | 2.400$^g$ | 40.000$^h$ | 0.833$^a$ | 1.133$^{abcd}$ | 27.000$^{bc}$ | 51.367$^{bc}$ | 19.200$^a$ |
| $G_{18}$ | 0.533$^a$ | 2.000$^{ab}$ | 4.467$^{cd}$ | 59.000$^{ef}$ | 0.733$^{ab}$ | 1.000$^{abcdef}$ | 21.000$^{def}$ | 39.400$^{bcde}$ | 4.067$^{ab}$ |
| $G_{19}$ | 0.467$^a$ | 1.867$^b$ | 4.000$^{cdef}$ | 53.000$^{fg}$ | 0.833$^{ab}$ | 1.000$^{abcdef}$ | 26.000$^{bcd}$ | 33.067$^{bcdef}$ | 7.133$^{ab}$ |
| $G_{20}$ | 0.433$^a$ | 1.900$^{ab}$ | 2.367$^g$ | 68.667$^{cde}$ | 0.635$^{ab}$ | 1.367$^a$ | 39.000$^a$ | 29.967$^{bcdef}$ | 6.800$^{ab}$ |
| $G_{21}$ | 0.433$^a$ | 1.833$^b$ | 4.400$^{cde}$ | 74.000$^{cd}$ | 0.667$^{ab}$ | 0.867$^{bcdef}$ | 22.000$^{cde}$ | 28.200$^{bcdef}$ | 4.367$^{ab}$ |
| $G_{22}$ | 0.533$^a$ | 1.933$^{ab}$ | 4.000$^{cdef}$ | 64.000$^{def}$ | 0.700$^{ab}$ | 0.967$^{abcdef}$ | 16.000$^{fgh}$ | 27.800$^{bcdef}$ | 5.667$^{ab}$ |

Each value is a mean of 3 replicates. Means within columns separated by different letters are significantly different
Key: LW=Primary leaf width, LL= Primary leaf length, IL= Stem internode length, VL=Vine length, SML=Stamen length, SL=Sepal length, HPP=Highest number of truss per plant, FW=Fruit weight and FL=Fruit length

**Table 4.** Mean Separations for each Genotype for the Quantitative Descriptors for which Significant (P<0.05) Differences according to New Duncan's Multiple Range Test.

| Variable | FWW (cm) | SLL | SPL | 1000SW (g) | PDL (cm) | NL | PL (cm) | FPC | YPH (kg/h) |
|---|---|---|---|---|---|---|---|---|---|
| $G_1$ | 1.600$^h$ | 1.300$^c$ | 27.667$^b$ | 1.800$^j$ | 0.633$^{fgh}$ | 2.000$^f$ | 1.233$^{bcd}$ | 4.033$^c$ | 16.110$^s$ |
| $G_2$ | 3.267$^{ef}$ | 2.100$^{abc}$ | 94.667$^{ab}$ | 2.700$^{def}$ | 0.733$^{defg}$ | 2.000$^f$ | 0.800$^f$ | 5.030$^b$ | 724.930$^b$ |
| $G_3$ | 2.867$^{efg}$ | 1.733$^{bc}$ | 72.667$^{ab}$ | 2.500$^{fg}$ | 0.733$^{defg}$ | 3.000$^{de}$ | 1.233$^{bcd}$ | 3.003$^d$ | 4.990$^u$ |
| $G_4$ | 3.433$^{de}$ | 2.000$^{abc}$ | 55.667$^{ab}$ | 2.300$^{gh}$ | 0.567$^{gh}$ | 3.000$^{de}$ | 1.067$^{de}$ | 3.030$^d$ | 235.540$^j$ |
| $G_5$ | 3.033$^{efg}$ | 1.900$^{abc}$ | 70.000$^{ab}$ | 2.900$^{abcd}$ | 0.606$^{fgh}$ | 2.000$^f$ | 1.167$^{bcde}$ | 1.003$^e$ | 28.050$^s$ |
| $G_6$ | 2.467$^{fgh}$ | 1.567$^{bc}$ | 49.333$^{ab}$ | 2.100$^{hi}$ | 0.500$^h$ | 2.000$^f$ | 1.100$^{de}$ | 2.997$^d$ | 2.190$^v$ |
| $G_7$ | 2.267$^{gh}$ | 1.567$^{bc}$ | 44.333$^{ab}$ | 3.000$^{ab}$ | 0.767$^{cdefg}$ | 2.000$^f$ | 1.133$^{cde}$ | 6.030$^a$ | 39.370$^q$ |
| $G_8$ | 3.633$^{cde}$ | 1.667$^{bc}$ | 58.667$^{ab}$ | 3.017$^a$ | 0.667$^{efgh}$ | 3.000$^{de}$ | 1.167$^{bcde}$ | 4.998$^b$ | 189.260$^o$ |
| $G_9$ | 4.667$^{ab}$ | 2.333$^{abc}$ | 69.333$^{ab}$ | 2.983$^{abc}$ | 1.033$^b$ | 2.000$^f$ | 1.133$^{cde}$ | 4.003$^c$ | 519.344$^d$ |
| $G_{10}$ | 4.233$^{bcd}$ | 3.267$^a$ | 63.333$^{ab}$ | 2.600$^{ef}$ | 0.900$^{bcd}$ | 2.000$^f$ | 1.167$^{bcde}$ | 4.007$^c$ | 470.580$^f$ |
| $G_{11}$ | 3.500$^{de}$ | 2.633$^{abc}$ | 60.333$^{ab}$ | 2.797$^{cde}$ |  | 2.000$^f$ | 1.333$^{ab}$ | 3.000$^d$ | 101.390$^p$ |
| $G_{12}$ | 3.067$^{efg}$ | 1.767$^{bc}$ | 74.667$^{ab}$ | 2.200$^{hi}$ | 0.733$^{defg}$ | 3.000$^{de}$ | 1.000$^e$ | 3.998$^c$ | 207.200$^m$ |
| $G_{13}$ | 3.533$^{de}$ | 2.033$^{abc}$ | 68.667$^{ab}$ | 2.900$^{abcd}$ | 0.967$^{bc}$ | 3.000$^{de}$ | 1.467$^a$ | 5.033$^b$ | 39.190$^p$ |
| $G_{14}$ | 5.033$^{ab}$ | 2.833$^{ab}$ | 57.000$^{ab}$ | 2.800$^{bcde}$ | 0.867$^{bcde}$ | 2.000$^f$ | 1.167$^{bcde}$ | 4.003$^c$ | 744.200$^a$ |
| $G_{15}$ | 4.467$^{abc}$ | 2.167$^{abc}$ | 75.333$^{ab}$ | 2.300$^{gh}$ | 0.767$^{cdefg}$ | 7.000$^a$ | 1.233$^{bcd}$ | 3.997$^c$ | 201.922$^n$ |
| $G_{16}$ | 3.167$^{efg}$ | 2.000$^{abc}$ | 67.333$^{ab}$ | 2.300$^{gh}$ | 0.767$^{cdefg}$ | 3.000$^{de}$ | 1.133$^{cde}$ | 4.003$^c$ | 223.610$^l$ |
| $G_{17}$ | 5.333$^a$ | 1.633$^{bc}$ | 87.000$^{ab}$ | 2.030$^i$ | 0.767$^{cdef}$ | 4.667$^b$ | 1.167$^{bcde}$ | 5.003$^b$ | 622.080$^c$ |
| $G_{18}$ | 4.533$^{abc}$ | 2.000$^{abc}$ | 86.333$^{ab}$ | 2.300$^{gh}$ | 0.667$^{efgh}$ | 4.333$^{bc}$ | 1.300$^{abc}$ | 3.003$^d$ | 387.870$^g$ |
| $G_{19}$ | 3.033$^{efg}$ | 1.733$^{bc}$ | 68.000$^{ab}$ | 2.000$^{ig}$ | 0.833$^{bcdef}$ | 2.667$^{ef}$ | 1.133$^{cde}$ | 4.007$^c$ | 231.960$^k$ |
| $G_{20}$ | 2.833$^{efg}$ | 1.700$^{bc}$ | 99.667$^a$ | 2.100$^{hi}$ | 1.333$^a$ | 3.667$^{cd}$ | 1.133$^{cde}$ | 4.000$^c$ | 259.080$^j$ |
| $G_{21}$ | 3.400$^{de}$ | 2.400$^{abc}$ | 85.667$^{ab}$ | 2.200$^{hi}$ | 0.700$^{defgh}$ | 3.333$^{de}$ | 1.167$^{bcde}$ | 3.998$^c$ | 472.910$^e$ |
| $G_{22}$ | 3.300$^{ef}$ | 1.600$^{bc}$ | 100.333$^a$ | 2.600$^{ef}$ | 0.700$^{defg}$ | 3.000$^{de}$ | 1.133$^{cde}$ | 4.003$^c$ | 374.732$^h$ |

Each value is a mean of 3 replicates. Means within columns separated by different letters are significantly different
Key: FWW=Fruit width, SLL=Size of locules, SPL=No. of seed per fruit, 1000SW=1000-Seed weight, PDL=Pedicel length and NL= No of locules, PL=Petal length, FPC=No of fruit per cluster and YPH=Yield of plots per hectare.

**Table 5.** Magnitude of Variability among the Morphological Characters represented on the first five Principal Components of PCA.

| Variable | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| LW | 0.014 | 0.514 | 0.249 | 0.055 | 0.131 |
| LL | -0.061 | 0.360 | 0.521 | 0.043 | -0.305 |
| IL | 0.223 | 0.132 | 0.331 | 0.336 | -0.712 |
| PL | 0.123 | 0.022 | 0.443 | 0.234 | -0.890 |
| VL | -0.357 | -0.109 | 0.114 | 0.398 | 0.221 |
| SML | 0.064 | 0.347 | 0.112 | -0.551 | -0.066 |
| SL | 0.318 | -0.021 | 0.380 | -0.165 | 0.019 |
| HPP | 0.192 | -0.405 | 0.268 | -0.209 | 0.064 |
| FW | 0.431 | -0.060 | -0.158 | -0.164 | 0.271 |
| FL | 0.412 | -0.133 | 0.071 | 0.315 | -0.147 |
| FWW | 0.420 | 0.146 | -0.151 | 0.043 | -0.020 |
| SLL | 0.301 | 0.266 | -0.353 | 0.133 | -0.045 |
| SPL | 0.297 | -0.176 | 0.224 | 0.349 | 0.432 |
| 1000SW | 0.033 | 0.384 | -0.296 | 0.287 | 0.203 |
| FPC | 0.103 | -0.298 | 0.160 | 0.306 | 0.002 |
| YPH | 0.315 | -0.250 | -0.197 | -0.177 | -0.251 |
| PDL | 0.311 | -0.082 | 0.132 | 0.030 | 0.535 |
| NL | 0.176 | 0.201 | 0.278 | 0.050 | -0.432 |
| Eigenvalue | 3.554 | 2.295 | 1.358 | 0.951 | 0.555 |
| Proportion | 0.273 | 0.177 | 0.152 | 0.104 | 0.070 |
| Cumulative% | 27.300 | 45.000 | 60.200 | 70.700 | 78.000 |

Key: LW=Primary leaf width, LL= Primary leaf length, IL= Stem internode length, VL=Vine length, SML=Stamen length, PL=Petal length, SL=Sepal length, HPP=Highest number of truss per plant, FW=Fruit weight, FL=Fruit length, FWW=Fruit width, SLL=Size of locules, SPL=No. of seed per fruit, 1000SW=1000-Seed weight, FPC=No of fruit per cluster, YPH=Yield of plots per hectare, PDL=Pedicel length and NL= No of locules
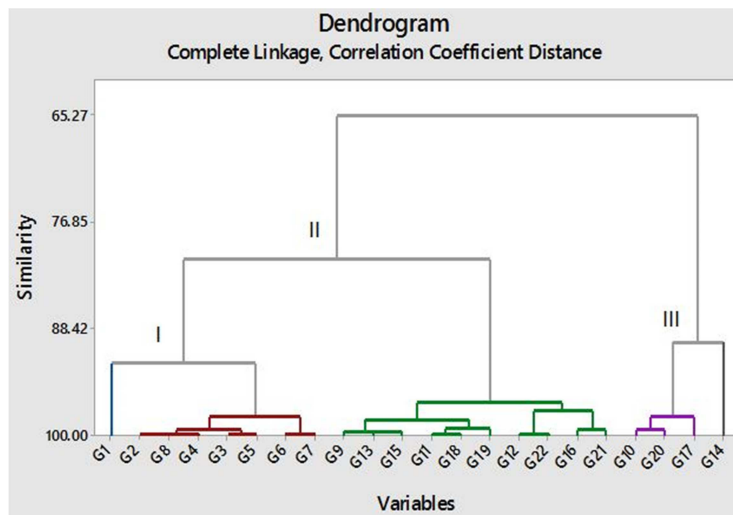
**Figure 1.** Dendrogram showing the distribution of 22 Tomato Accessions based on 18 Morphological Traits.

Legend:  G$_1$=NGB-00711,  G$_2$=NGB-00713,  G$_3$=NGB-00721,  G$_4$=NGB-00722,  G$_5$=NGB-00724,  G$_6$=NGB-00725,  G$_7$=NGB-00726,  G$_8$=NGB-00731, G$_9$=Roma VF, G$_{10}$= UC82-B, G$_{11}$=Rio-Grande, G$_{12}$=Atumba, G$_{13}$=Roma-Savanna, G$_{14}$= Tropimech, G$_{15}$=Dereka, G$_{16}$=Cerel, G$_{17}$=Mngishim, G$_{18}$=Apaa, G$_{19}$=Ishase, G$_{20}$= Akeakpev, G$_{21}$=Kal and G$_{22}$=Gambo

# 4. Conclusion

The result revealed that, vine length and yield of plots per hectare are among the features that shows dissimilarities across the accessions and thus, can be used as important traits for hybridization programs. Accessions; NGB-00713, NGB-00731, NGB-00722, NGB-00721, NGB-00724, NGB-00725 and NGB-00726 were identical and Rio-Grande, Apaa, Atumba and Gambo were also found to be similar and may be two sets of duplicates based on their morphological traits. This reduced the total number of accessions to 13 which shows that, a low phylogenetic relationship existed among the accessions in this study.

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