VARIATION IN THE MORPHOLOGICAL, BIOCHEMICAL, AND MOLECULAR CHARACTERISTICS OF SOME YAM (*Dioscorea alata* L.) GENOTYPES IN WEST AFRICA

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ABSTRACT

Dioscorea alata is a species belonging to the genus *Dioscorea*. It's also known as water yam, or purple yam. Its tubers are usually white-fleshed but occasionally possess a varying degree of pigments due to their high anthocyanin presence. Morphological, biochemical, and molecular studies have been conducted on *Dioscorea alata* in other regions however, limited information is available on landraces cultivated in West Africa.

The research was carried out to determine the level of variation present in 100 genotypes of *Dioscorea alata* species. One hundred *D. alata* accessions collected from eight different countries of West Africa by Genetic Resources Centre, IITA were used in this study. This study showed that certain morphological, biochemical, and molecular traits delineated the accessions effectively. It helps to understand the level of diversity within *alata* genotypes available in West Africa which in turn underwrites the effective conservation and utilization of the yam genetic resources for breeding purposes.

INTRODUCTION

Dioscorea alata is a very important tuberous plant. Out of the total world production of yam, about 70 % is produced in Nigeria and the rest are from Côte d'Ivoire, Ghana, Benin, Togo and Cameroon (FAO, 2002).

Morphological characterization is one of the major steps in genetic diversity study as it serves as a powerful tool in the classification of cultivars and understanding their taxonomic status (Norman *et al.*, 2011).

The purple colour found in purple yam shows presence of anthocyanin. These antioxidant compounds help in protecting cells from the toxic effects produced by free radicals thereby contributing to disease prevention.

Using markers through the DArT sequence is considered to be a good choice for analyzing molecular diversity in purple yams because of their high reproducibility, high efficiency, and polymorphism. (Ellegren H. 2002). Genetic diversity is an important requirement for a successful breeding program.

Variation in *Dioscorea alata* germplasm is critical for Genetic improvement in yam. Mignouna *et al.* (2002) reported that genetic erosion can be controlled by the collection and characterization of existing germplasms for diversity studies and crop improvement

OBJECTIVES
- To characterize 100 *D. alata* accessions using morphological descriptors and DArTseq SNP Markers.
- To determine the level of morphological, biochemical and molecular variation present in 100 genotypes of D *alata*.
- To determine the quantity of anthocyanin present in the 100 *D. alata* accessions.

METHODS AND MATERIALS

Location and experimental site
The experiment was conducted in the experimental field of the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. Ibadan is situated at the northern fringe of the tropical forest with (longitude 3° 89'E, latitude 7° 49'N and Altitude of 239.34m above sea level).

Morphological Characterization of 100 *Dioscorea* genotypes
Morphological characterization was conducted by measuring morphological characters from five healthy plants. The traits measured and data collection procedure used was based on those presented in the International Plant Genetic Resources Institute's descriptor list for *Dioscorea* spp.(Yam) (IPGRI/ IITA, 1997).

Biochemical characterization (Anthocyanin quantification) of 100 *Dioscorea alata* accessions
100 accessions of *Dioscorea alata* was worked on. Anthocyanin was extracted from the upper and lower part of the tubers of 3 plants belonging to each accession and replicated twice to make a total of 600 samples. Anthocyanin content was determined through an extraction protocol that was developed by following the PH differential method described by Harbone (1999)

Molecular Characterization of *Dioscorea alata* using DArTseq technology.
The DNA of 100 alata genotypes were extracted at Bioscience Laboratory and sent to Australia for DArT analysis.

Statistical Analysis
The Principal Component Analysis (PCA) was performed to analyse the level of variation contributed by various variables or characters using Statistical Analyses Software (SAS) version 9.4. PRINTCOMP procedure. Clustering analysis was done by constructing a dendrogram through the same software

RESULT AND DISCUSSION

The yam descriptor list (IPGRI/ IITA, 1997) was sufficient in the characterization and assessment of variation among the 100 *Dioscorea alata* accessions. Morphological polymorphism exhibited by the qualitative and quantitative traits used in this study confirm that the selected descriptors are suitable for assessing variation in yam diversity. The number of leaves, Petiole length, Leaf length, Leaf width, and Tuber size accounted for the majority of the morphological variation observed. The first 3 principal components (PC1 - PC3) accounted for 74.8% of the total variation.

There is a significant difference in the anthocyanin content present in different tubers belonging to the same genotypes. However, there is no significant difference in anthocyanin present in the upper and lower part of the tubers. This indicates that there is a uniform distribution of the pigment to all parts of the tuber which is affirmed by Srivichai and Parichat (2020) whose research showed that the purple pigment in the variety KKFCRC yam tuber was evenly distributed in the flesh throughout their age. DArTseq cladogram classified the 100 *alata* accessions into three major clusters. Cluster A consists of 48 genotypes, Cluster B has 24, while Cluster C consists of 22 genotypes respectively. These clusters were characterized by accessions from differing countries.

CONCLUSIONS

This research elaborates on the presence of abundant polymorphism in *Dioscorea alata* genotypes originating from West Africa.

The result from the DArTseq and anthocyanin quantification help expose other variations existing among the accessions at the molecular and biochemical level which the morphological analysis could not reveal.

Grouping the genotypes into 4 and 3 clusters through PCA clusters formation and DArT cladogram respectively, helped in recognizing parents with unique traits for future improvement programs and conservation. It also described the level of similarity and dissimilarity among the genotypes being studied. These purple accessions can subsequently be propagated to improve yam nutrients which can, in turn, contribute to food security.

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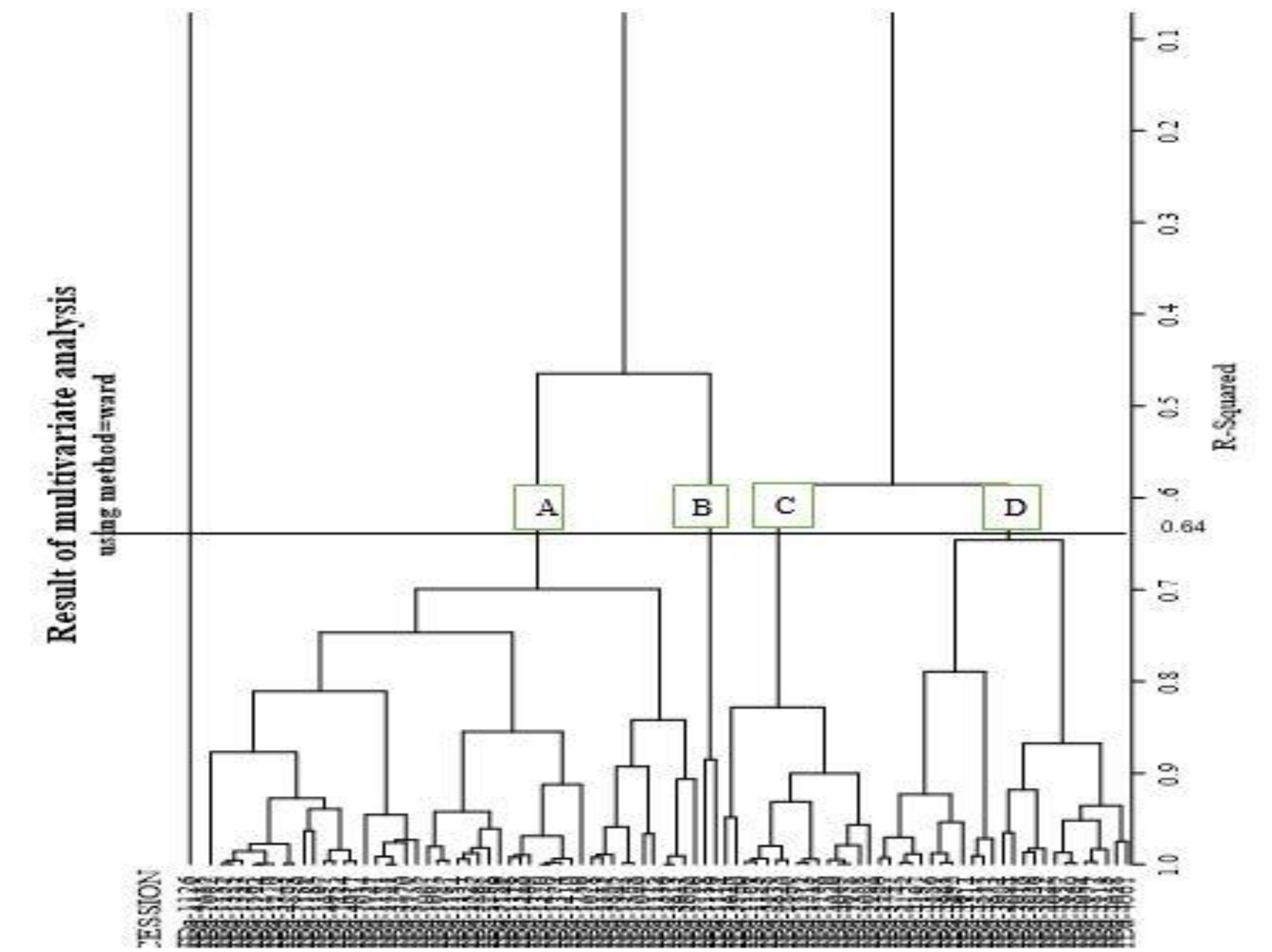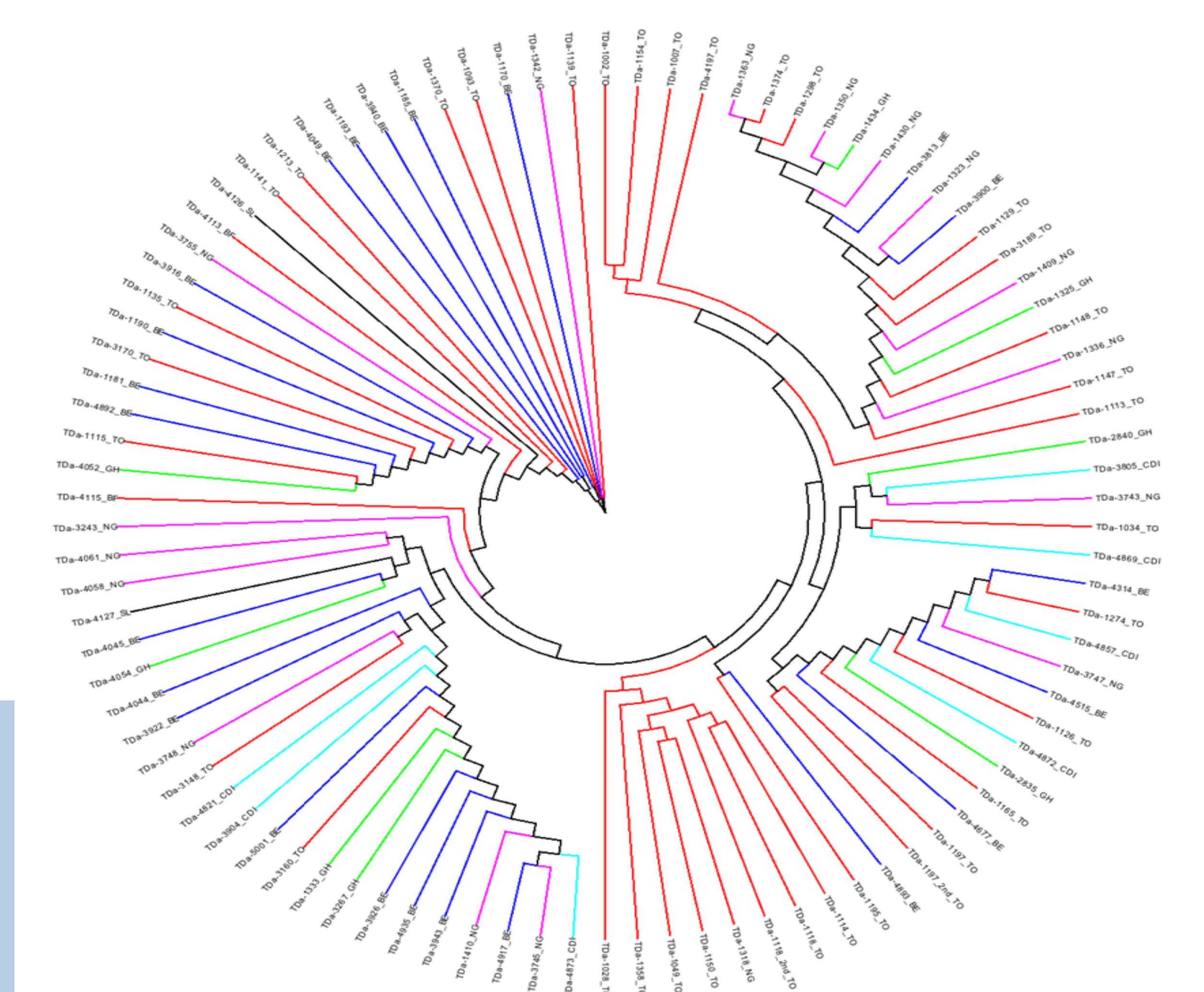

Dendrogram showing the clusters formed based on the quantitative morphological traits.
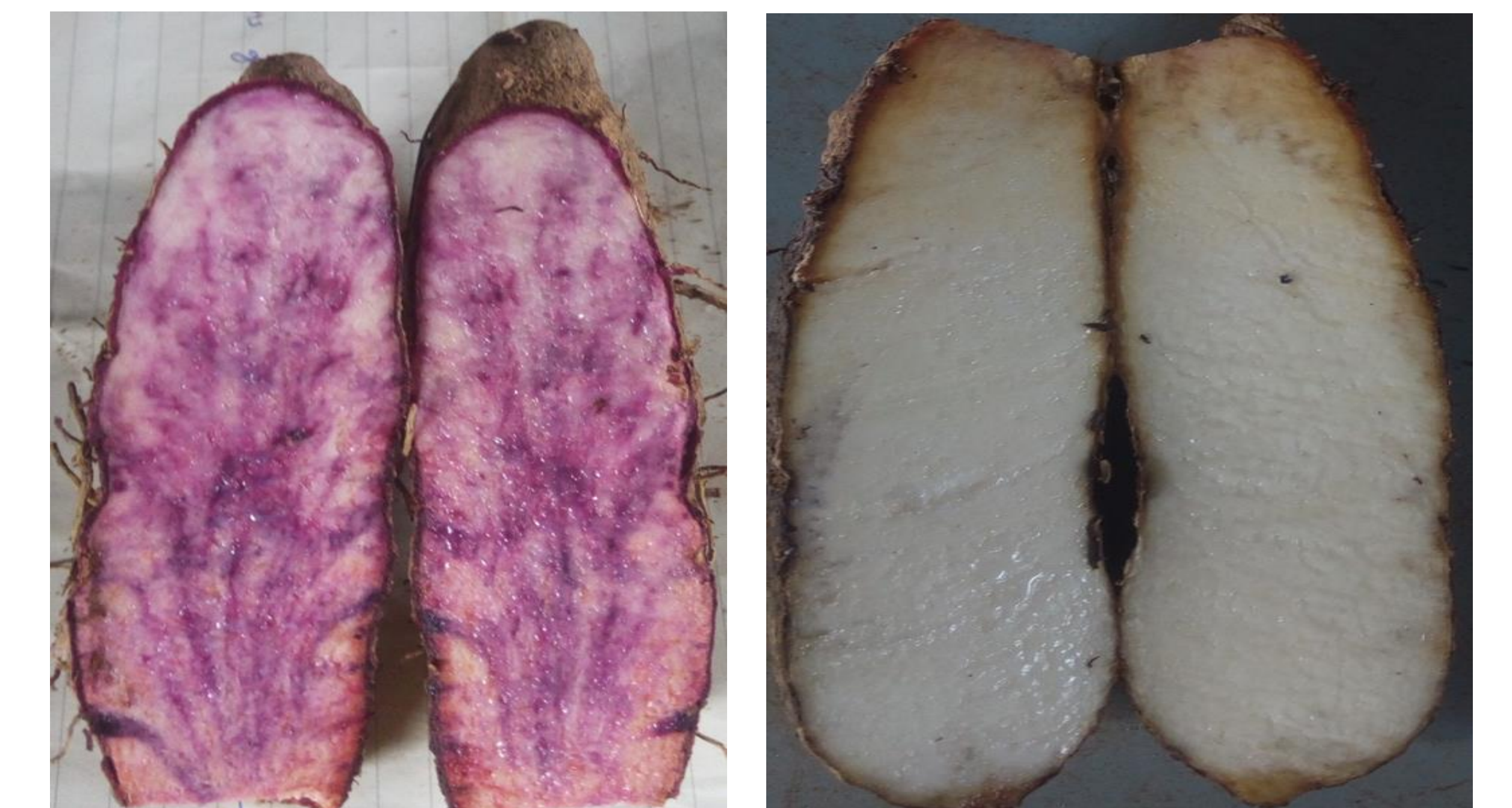
TDa 1049 accession (purple)   TDa 1007 accession (White)

Cladogram showing Cluster Formation and Genetic Distance between the Yam Accessions.