GENETIC DIVERSITY OF AFRICAN YAM (*Dioscorea* spp.) IN NORTH CENTRAL NIGERIA

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ABSTRACT

Yam (*Dioscorea* spp.) are annual crops cultivated for food in tropical and sub-tropical regions of the world. The crops are grown in Nigeria for nutritive, social and economic benefits. In spite all these importance, research on its improvement has been inadequate due to lack of sufficient genetic knowledge of the existing germplasm of the crop. Against this background, a survey and exploration were carried out to collect and characterise the available landraces of the crop germplasm in North-Central Nigeria as well as to identify elite genotypes that could be utilized for further breeding programs. Thus, 50 accessions of yam were randomly collected across the six(6) major cultivating states. The accessions were set on field using a Randomized Completely Block Design (RCBD) with five replicates per accession and morphological features were characterized. Also, analytical evaluation of the nutritional and anti-nutritional properties was conducted using standard procedures. Simple Sequence Repeat (SSR) DNA markers technique was adopted for molecular studies to determine the genetic diversity in the crop. Results showed that the highest number of accessions (21) was recorded in Niger State (NG), followed by Benue (BN) with 19 accessions, Kwara and Nasarawa were with 3 accessions each and the least (2) accessions were obtained from Kogi and FCT, Abuja respectively. Significant differences were obtained ($P < 0.05$) for most of the agro morphological parameters considered. Morphological evaluation showed the highest number of leaves per plant (655.30) from BNr. 063 and the least (34.10) was recorded from NGr. 019. Highest stem length (551.43 cm) was recorded from KGr. 006 and highest auxiliary branch (24.50) was obtained from KGr. 043.Highest yield for tuber length (68.98 cm), tuber breath (31.32 cm) and tuber weight (34.68 kg) were recorded from NGa. 033, BNr. 084 and NGr. 017. Mineral composition indicated that the highest moisture content (16.23 %) and highest carbohydrate content (80.77 %) were recorded in NGr. 023 and BNr. 063 respectively. Highest mineral compositions for sodium (26.22 mg/100g), phosphorus (0.55 mg/100g), potassium (16.90 mg/100g) and Iron (5.24 mg/100g) were recorded in BNr. 071, KGr. 003, NGr. 001 and BNr. 063 respectively. Accession BNr.053 yielded the highest manganese content (2.19 mg/100g) while the highest value for oxalate (10.15 mg/100g), alkaloid (0.08 mg/100g) and flavonoid (4.30 mg/100g) were obtained from BNd. 030. A total of 84 polymorphic reproducible and scorable bands. The six(6) DNA primes used yielded maximum polymorphism of 100% and all the markers produced high polymorphic Information Contents (PIC) range of 0.35-0.55. The UPMA dendrogram group the genotypes into eight (8) clusters based on the species relatedness. The high variability recorded in genotypes for both morphological and nutritional assessment in addition to high molecular and genetic advance recorded provide background information that plant breeders and researchers could exploit for the crop improvement programs of yam in the future.

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ABBREVIATIONS, GLOSSARIES AND SYMBOLS

PGR – Plant Genetic Resources

IPGRI – International Plant Genetic Resources Institute

IITA – International Institute of Tropical Agriculture

SSR – Simple Sequence Repeat

FAOSTAT – Food and Agriculture Organization Corporation Statistical Database

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background to the Study

Yams (*Dioscorea* spp.) are one of domesticated food crop in tropical regions of the world (Food and Agricultural Organization, 2013; International Institute of Tropical Agriculture, 2015 and Garedew, 2017). The crop belongs to the genus *Dioscorea* in the family Dioscoreaceae. The genus contains 600 species with twelve (12) edible and marketable cultivars (Norman *et al*., 2012). Six of these species are indigenous to Africa and form important diet to man and his domesticated animals (Oluwale *et al.*, 2013). Major species strive very well above 20 ^{o}C and required at least 1,000 mm rainfall annually. The growing period of yam varies within 7-9 months depending on the species, and they produce one to three (1-3) large tubers with several smaller ones. The smaller ones are usually used as seed yams (sett) which are sown on mounds or ridges with 2 meter distance between the lines and moulds (Loko *et al*., 2015). Sometimes the seed are planted in trenches or holes filled with organic material.

Nigeria is the highest producer of yam tubers with the total production of 32,318,900 tonnes annually (FAO, 2014; Joyce, 2017). According to Food and Agriculture Organization Statistics (2017), of the 68.13 million tone of the world production of yam, 94.53 % comes from West Africa and 70-76 % of these are produced in Nigeria (Bradshaw, 2010). The most abundant species grown in Nigeria are *Dioscorea rotundata* (white yam), *Dioscorea alata* (water yam), *Dioscorea cayenensis* (yellow yam), *Dioscorea dumetorum* and *Dioscorea hispida* (Nahanga, 2015). The crop is cultivated along the coastal region of rainforest, wood savannah and southern savannah in Nigeria. Major producing areas in North Central Nigeria include Benue, Niger, Federal Capital Territory (FCT) Abuja, Nasarawa, Kogi and Kwara (IITA, 2015). Nigeria has great potentials for yam production that could serve both domestic and export market.

According to FAO (2013), yam tubers are vital in several plans of man; such as diet (Oluwale *et al.,* 2013), energy production (Scarcelli *et al*., 2005), raw materials for starch and pharmaceutical industries (Dutta, 2015), socio-cultural festival among some ethnic groups and small house hold (Nortey, 2012; Jude *et al.*, 2017). Economically, yam has the capacity to alleviate poverty through the provision of employment opportunity in Nigeria and West – Africa sub-region (Asiedu and Sartie, 2010; Olorede and Alabi, 2013). Asides this, some wild species are important source of disogenin and steroidal saponins which are utilized medically in the manufacture of oral contraceptive hormone and cortisome (Islam *et al*., 2008). Alongside with these backgrounds, it is believed that yam play a major role in man life and animals. Consequently, under production of the crop may lead to over-dependent in other food crops which are costlier and not rich in nutritional contents of yam. This may result to nutritional deficiency in consumers and food insecurity in the country.

Besides, plant resources form an integral part of interdependent system that includes physical components and biological community of life (Malik and Singh, 2006). One of the wayto

increase food supply is to plant a good crop variety that is environmental forbearance, tolerance and resistance to pests and diseases. Hence, plant breeders are in search for genetic materials to build new desirable varieties. These genetic materials could only be sourced from the available gene pool; the usefulness of these genetic resources depends on reservoirs of variability present in the gene pool. Thus, the larger the gene pools, the better the chances of finding a desired traits and the smaller the gene pools, the lesser the chances of obtaining desired trait.

These resources are generally referred to as germplasm which constitutes building block of plant breeding FAO (2013). They are heritage to be preserved and use for the benefit of crop restructuring. Plant genetic resources could also be plant itself, seeds, tissues, cells, pollen, vegetative materials or DNA. Indeed they play a vital role in the breeding of new cultivars and development of the existing ones (Ishaq *et al.*, 2004).Furthermore, there are two major sources of plant genetic resources that can be utilized by plant breeders; these are exotic germplasm and indigenous germplasm. The former refers to those genetic resources that exist far away from the native country, while the later are resources that are native to the country.

1.2 Statement of the Research Problem

There have been no deliberate efforts to collect the germplasm of different yam species grown in the North-Central Nigeria, despite the fact that the region falls within the yam producing belt of Nigeria. Maximum production of the crop has been hampered due to biological and environmental factors. The dearth of information on germplasm collection and characterisation of the crop among the researchers is one of the major challenges militating against the improvement of yam in North-Central Nigeria.There has been dwindling in the production of yam in the past years due to poor yield from the available genotypes occasioned by lack of improved varieties that could adapt to the ever changing climatic condition. Unfortunately, no tangible improvement in yam could be made without characterisation of the superior genotypes for the desired traits.

Similarly, lack of adequate knowledge of esixting level of genetic diversity among the genotypes of yams in the North-Central of Nigeria has led to reduced production as well as lack of interest in yam research in the area. Consequently, those genotypes with Low yield have been abandoned by farmers leading to loss of some indigenous genotypes with other desirable traits (Iriondo *et al*., 2008). Furthermore, attempt to resolved the problem of food production have placed more emphasis on increasing the production and productivity of grain crops and little attention is given to yam as one of the staple food crops by the researchers.Furthermore, there is inadequate information on the characterisation of different yam species using nutritional and phytochemical properties. However, no characterisation could be achieved without these types of tests in yam species. To summarize these challenges, and consequent remedy, collection of genotypes among the available genotypes have been considered as one of the promising and foremost options (Pattanashetti *et al*., 2016).

1.3 Justification for the Study

Yam (*Dioscorea* spp.) is considered as a famine food crop. They are unique for their nutritional, medicinal and economic purposes. They form major part of people's diet and cultural values in sub-Saharan Africa in general and in Nigeria in particular. The need for germplasm collection, characterisation, and utilisation of yam species cannot be over-emphasized. These activities will help in identifying the genetic diversity within the crop as well as possible selection of beneficial traits.

Exploitation of variability through germplasm assessment and characterisation study for desirable traits is essential for understanding of the breeding value of the indigenous genotypes and isolation of germplasm line which could be use for the crop improvement programmes. These beneficial traits could be utilised in the development of high yielding varieties that would adapt to biotic streeses. Understanding existing knowledge of the level of genetic diversity

amoung the genotypes could enhance the understanding of selective impact of breeding practices so as to enlarge the genetic base of the crop for better utilization.The Variability study by germplasm assessment of indigenous genotypes with desirable traits is essential for understanding of the breeding value of traditional yam genotypes and selection of germplasm line which could be employed for crop statistical procedures that characterised genetic divergent using the criterion of similarity of dissimilarity based on aggregate effects in classic way. Evaluating genentic variability can be used to group the germplasm without the prior knowledge of area of origin of germplasm groupings (Ogunbodede, 1997). In addition, embarking on molecular rating of genetic variability of the crop germplasm will provide better and detailed knowledge of selecting genetic base to facilitate crop development programmes.

1.4 Aim and Objectives of the Study

1.4.1 Aim

The aim of this study is to evaluate genetic diversity of African yams using agro-morphological, biochemical and molecular characterisations.

1.4.2 Objectives

The objectives of this study are to:

i. Collect and genetically purify the African yam genotypes for further agro-morphological studies.
ii. Determine agro-morphological traits and yield parameters of the yam genotypes.
iii. Quantify biochemical constituents of the African yam genotypes in North-Central Nigeria.
iv. Determine the estent of genetic diversity amoung the yam genotypes using simple sequence repeat (SSR) molecular markers.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and Distribution of Yam

Yams (*Dioscorea* spp.) are annual or perennial tuber and climbing crops belonging to the family Dioscoreaceae. The family has about 600 species grown since 50,000 BC in Africa, Asia, part of South America, the Caribbean and south pacific islands (Cursey, 1967; Jude *et al*., 2017). The crop is believed to have originated in tropical areas of three separated continents. These include Africa (mainly West Africa for *Dioscorea rotundata, Dioscorea cayenensis* and *Dioscorea dumetorum*).South East Asia (for *Dioscorea alata* and *Dioscorea esculenta*) and South America (for *Dioscorea trifida*). The Asiatic yam, *Dioscorea alata* might have originated in tropical Burma and Thailand, *Dioscorea trifida* the south American yam is believed to date back to pre-Columbian times (Ayensu and Cursey, 1972). However, some of the yams originated from Africa were spread to tropical part of the world while those emanated from Asia, have been spread to Africa (Hahn *et al*., 1987). Today, they are widely cultivated throughout the tropics.

2.2 Classification and Botany of Yams

Yams are dioecious monocotyledonous plants in the genus *Dioscorea* under Dioscoreaceae. The family consists of 8-9 genera and 850 species (Mabberly, 2005). The crop belongs to the order Dioscoreales under division Magnoliophyta (Kumar *et al*., 2017). The wild species of yams are either annual, semi perennial or perennials while the domesticated species are annuals. The leaves of most of the cultivars are large, net veined, cordate, simple or acuminate having short or long petiole and some species have palmate or lobed having pointed tips. The leaves are bright green colour which may measure 26 cm wide and at times purple hues due to their anthocyanin content. Yams (*Dioscorea* species) are climber and climbs by twinning the stem. The direction of the stem twinning is anticlockwise or clockwise direction (that is right to left or left to right). This forms peculiar characteristics for identification of the species within the genus. Some right

twinning wild *Dioscorea* species includes *D. oppositifolia* L., *D. hamilllonic* Hook F., *D. pubera, D. wallichi* Hook. F and *D. glabra* which have simple leaves. Those species with compound leaves are *D. hispida* Dennst and *D. pentaphylla* which are left twiner species (Behera *et al*., 2009). Most of the commercially cultivated *Dioscorea* species such as *D. alata, D. rotundata, D. opposita*, *D. cayennensis* and *D. japonica* are recorded under *Enantiophyllum* section (Peter, 2007). Other domesticated species such as *D. esculenta* is placed under *combilium* section. *D. trifida* L.F. in *macrogynodium, D. dumetorum* (Kunth) Pax belongs to *Lasiophyton* (Peter, 2007).

The flowers of the *Dioscorea* species are dioecious in nature, having male and female flowers on separate plants. The male or female flower grows on the axillary spikes of the leaf axils. The male flowers are glabrous, sessile and spherical which are borne axially or terminally. The fruits are mostly small capsules with wings and the shape varies in different species (Behera *et al*., 2009). The seeds are light and flat in shape; the wings help for seed dispersion. Some *Dioscorea* species such as *D. bulbifera, D. alata, D. pentaphylla,* and *D. pubera* have bulbils grown on the axils. These bulbils are used as planting materials. The tuber of *Dioscorea* species varies in skin colour, ranging from dark brown to light pink and consist of soft substances (meat) with white, yellow, pink or purple colour. Tubers are usually shallow, fibrous and mostly in some cases branched. Most of the tubers are placed on the top of the soil and some are deeply buried up to 1m depth (Behera *et al*., 2009 and Kumar *et al*., 2017). The tubers are storage organ for carbohydrates, the new tuber formation and shrives of the old one occurs simultaneously when the re-growth is initiated.

2.3. Importance of Yam

2.3.1 Economic importance

Economically, yam plays a vital role in Local Commerce in West Africa and income generation to individual, group and the Nation at Large (Ariyo *et al*., 2020). It was estimated that 50,000 tubers of yam could generate two hundred and fifty million (₦250, 000,000) in a year. The production, processing and marketing of yams has provided wide opportunities ranging from exportation of the crop which serves as a source of income. It was reported that yam exportation in Ghana has contributed significantly to foreign exchange earning to Ghanaian economy (Aidoo, 2009). In Nigeria, the production, harvesting, transportation and processing of yam tubers has provided employment opportunities and income generation to the individual and group (Asiedu and Sartie, 2010). The crop is one of the popular staple foods in most part of African countries and beyond (IITA, 2009). The tubers are often processed into pounded yam, fried yam, boiled or roasted, porridge and paste (Tortoe *et al.*, 2012). Cultivation, processing, and selling of yam tubers in business area across North-Central Nigeria, have contributed to the financial status in the yam cultivated areas. Research studies equally showed that decline in the production of the crop in some of African and Subtropical regions of the world could lead to food insecurity and decline in financial status of people engaged in yam business (Agwu and Alu, 2005).

2.3.2 Socio-cultural importance

The multi-species crop is important in socio-cultural practices in some part of Africa and Nigeria. The crop form part of religious heritage of some tribes and plays essential role in religious ceremony (Sinusi and Olimonu, 2006). It have been reported that yam festival is held every year to mark the harvest of the crop. Besides, some village Chiefs and traditional title holders in Nigeria make it a religious practice by not consuming the new tuber yam until it is offered to gods. At the course of the festival, villagers offer praise and prayers, thanking their

ancestral gods for land blessing and woman fertility (Izekor and Olumese, 2011). It was also observed that many important cultural values are associated to yam, most especially when it comes to social ceremonies (marriage) and festival in Nigeria and some West Africa sub-regions (Nortey, 2012). Similarly, the size of yam enterprises an individual hasreflects his social status in the community most especially the Gbaris, Tiv, Bassa-ge and other ethnic groups in yam belt of Nigeria.

2.3.3 Medicinal importance

Medically, the major composition of yam tubers is diocin, dioscorin and saponin; these phytochemicals have been reported to have medicinal value (Blessing, 2018). In pharmacological studies, *Dioscorea* species have been reported to contain anti-microbial, anti-fungal, anti-mutagenic, hypoglycaemic and immunomodulary effects (Kumar *et al*., 2017). Extraction from *Dioscorea bulbifera* and *Dioscorea alata* showed antifungal activities on *Botryodiploidia theobromae* (Eleazu *et al*., 2013). Literatures also revealed traditional knowledge by reporting the antimicrobial and antifungal activities of wild yam, *D. pentaphylla* against both gram-positive and gram-negative bacteria such as *Staphylococcus aureus, Psudomonas aeruginosa, Streptococcus mutans, Streptococcus pyogenas, Vibro cholera, Salmonella enteric typhi, Shigella flexneri* and *Klebsiella pneumoniae* and antifungal activity against pathogenic fungi (Pravash and Hosetti, 2010; Kumar *et al*., 2013).

Alkaloid derivatives from tuber yam have been reported to have various pharmacological properties (Polycarp *et al*., 2012). In addition, flavonoid was reported as potent water soluble antioxidants and responsible for anti-microbial, anti-inflammatory properties and anti-carcinogenic activities (Bhandari and Kawabata, 2004). It was reported that cytotoxicity effect of *D. alata* extract on human cancer cell lines has proven the presence of anti-cancerous components in water yam (Das *et al*., 2014). Tannin is reported to be responsible for the

astringent taste of foods and drinks. Consequently, plants rich in tannins content have been identified for the treatment of diseases like leucorrhoea, rhinnorhoea, healing of wounds, and diarrhoea (Eleazu *et al*., 2013). Subsequently, the bitterness taste of tuber yams is due to the presence of tannins (Padhan and panda, 2020).

Saponins are naturally occurring compounds that are made up of sugar molecules in combination with triterpene or steroid glycone (Eleazu *et al*., 2013). This compound is reported to possess pharmacological potentials such as cholesterol lowering and anti-cancerous activities (Okigbo *et al*., 2009). Saponin from yam species have been used in industries for making steroid drugs (Kumar *et al.,* 2017). Similarly, anti-diabetic activities of *D. alata* (Maithili *et al.*, 2011) and *D. bulbifera* (Ghosh *et al*., 2012; Okon and Ofeni, 2013) have been verified for the management of type II diabetes. Literatures have also shown that analgesic and anti-inflammatory properties of the bulbils of *D. bulbifera* are used against paw oedema (Mbiantcha *et al.*, 2011). In addition, it was equally reported that bulbis exhibits anthelmintic activity against *Fasiola gigantica* and *Pheritima posthuma* (Adeniran and Sonibare, 2013).

Ethno-botanical studies of *Dioscorea* showed a remarkable role in traditional medicines for various diseases treatment (Kumar *et al.,* 2017). For instance, in South Asia, the tuber syrup is used to reduce labour pain and treat various diseases such as cohi pain, asthma, cough, rheumatism, and gastric problem (Foster and Duke, 2000). Extraction from the tubers of *D. deltoidea* wall is used for the treatment of urino-genital disorders, helminthes infections and constipation (Gangwar and Joshi, 2008). Furthermore, the native people of southern Thailand use tuber yams to treat warts (Maneenoon *et al.*, 2008). Also the tuber of *D. prazeri* is used to kill hair lice (Maneenoon *et al.*, 2008). Moreover, *D. hamiltonii* tuber is used as cooling agent during summer and used to cure diarrhoea (Dutta, 2015).

Ethno-botanical studies also revealed that the juice from *D. wallichii* is used to treat stomach pain and Jaudica (Rout and Panda, 2010). Powder of *D. bulbifera* is applied in hernia and affected wound of scorpion bite (Nayak *et al.*, 2004). Furthermore, *D. hamiltonii* is used to cure pile (Mishra *et al.*, 2008). Research report from Bangladesh, showed that tubers of *D. bulbifera* are used for the treatment of leprosy and Tumour and in Chinese medicine these tubers are used against throat sore (Mbiantcha *et al.*, 2011) whereas in Zimbabwe, the tubers of *D. bulbifera* are used to cure wounds and sores. Bulbils pastes are externally applied to boils in Cameroon and Madagascar (Mbiantcha *et al.*, 2011). Similarly, the tribal communities of Enugu in Nigeria used *D. alata* against fever and the tubers of *D. cayennensis* are used to treat diarrhoea (Aiyeloja and Bello, 2006).

2.4 Assessment of Genetic Diversity and Variability Studies in African Yam (*Dioscorea* spp) using Morphological and Biochemical Markers

The genus *Dioscorea* which is commonly known as yam is the largest genus in the family Dioscoreaceae, including about 602 species (Cursey, 1967) distributed mainly in tropical and subtropical regions of the world. Apart from its large morphological diversity few species are often identified for cultivation worldwide. In an attempt to recognise yam species, researchers employed various techniques such as evolutionary and morphological approaches to characterise crop species. Evolutionary approaches are used because they help to identify species at risk of extinction (Purvis *et al.*, 2005; Faith and Baker, 2006; Lee and Mishler, 2014).

Research study was carried out by Ngo Ngwe *et al.* (2015) on evolution and phylogenetic diversity of yam species in Cameroon. The study elucidated support for the placement of section *lasiophyllum* as sister to *D. esculanta* (seed *Combillum*). This however, contradicted the previous study that placed *D. dumetorum* as a sister to *D. bulbifera* of the section *opsophyton* (Wilkin *et al.*, 2005; Tostain and Pham, 2006), thus, further studies may berequired to clarify

phylogenetic relationship of *D. dumetorium*. In contrast with previous phylogenetic studies on *Dioscorea*, eleven accessions of *D. alata*, five of *D. caye*nensis, nine of *D. esculenta*, eleven of *D. dumentorum*, fifteen of *D. rotundata*, three of *D. bulbifera* and seven of *D. praechersillis* were included in the study to enable the testing of species monophyly. These highlighted the non-monophyly of most species (*D. dumetorum*, *D. alata*, *D. cayenensis*, *D. rotundata* and *D. praehensillis*). Phylogenetic estimates also provided important information on the genetic diversity of wild and cultivated species of yams. Ngo Ngwe *et al.* (2015) also reported that wild species. *D. praehensillis* has the largest phylogenetic diversity (PD) among the species studied and has been involved in domestication processes in Cameroon (Dumont *et al.*, 1994). The result also revealed large genetic pool that could be utilised for crop improvement. Studies on *Dioscorea* in Benin have shown that domestication increases the variability within population (Dumont *et al.*, 2005 and Scarcelli *et al.*, 2005). This was reported to be likely due to the farming practices in West Africa. Indeed, the farmers often collect wild species (*D. praehensillis*) in bushes (forest) and cultivate them on the fields. This practice was reported to favour the introgression of characters from wild species into cultivated ones. According to Mignouna and Dansi (2003), species collected by farmers in bushes can be of different nature (related wild species, interspecific hybrids between wild relatives or between wild species and cultivars) but they are susceptible to influence the genetic variation in a population. The practices likely explain the high phylogenetic diversity observed in some cultivated species of *D. cayenensis* and *D. dumetorum*.

Efisue (2013) studied genetic diversity of the genus *Dioscorea* using morphological traits and isozyme markers, the genotypes were observed to show individualistic morphological characteristic. *D. dumetorum* had a coefficient of similarity of 0.30 with other species; this was reported to show a high genetic distance. A group was made up of 12 cultivars of three relative species, *D. dumetorum*, *D. abyssica* and *D. schimperena* with *D. alata* (water yam), thus

indicating genetic similarities. Another cluster was made up of *D. alata* and *D. rotundata* and a high genetic similarity between *D. rotundata* and *D. cayenesis*. In addition, sub-groups were found which showed no significant differences among the cultivars within the sub-groups. Morphological data analysis revealed closer genetic relationship between the relative species of *Dioscorea* used in the study and *D. alata*. This created a broad base genetic variability of yam, the related species (*D.dumetorum*, *D. abyssica*, *D. schimperana* and *D. alata* could be genetically improved through hybridisation, tissue culture technique and molecular methods.

In addition, the morphological data analysis showed that the aforementioned yam species were distantly related to *D. rotundata* and *D. cayenesis*. Whereas, *D. rotundata* and *D. cayenesis* were closely related, and hybrid species of *D. cayenesis, D. rotundata* and *D. cayenesis* complexes identified by Zoudjihekpon *et al.* (1994); Dansi *et al.* (1999) and Dansi *et al*.(2000). The study by Efisue (2013) also revealed high correlation between the morphological and molecular data analysis. This agreed with the reports of some tuber crops (Efisue, 2013 and Maquia *et al.*, 2013) but disagreed with the reports of Tairo *et al*. (2008) who observed non-significant correlation between the isozyme and morphological traits in sweet potato cultivars examined. The studies of Sheikh and Kumar (2017) on morphological characterisation of 50 accessions of Meghalayan *Dioscorea* spp. (Yam), in North East India using 48 traits, revealed high degree of morphological polymorphism within the accessions of *Dioscorea* species. This was reported to be attributed to cross-pollination and sexual recombination and isolated human communities in diverse environment (Martin and Ruberte, 1976). The phenotypic variation observed among the Meghalayan yam accessions have been reported to be the character that can be used as makers for identifying and classifying the species. The most discriminating characteristics reported between the yam accessions were stem colour, leaf colour, leaf shape, inner petal shape, staminode absence or presence, length and width of matured leaf various research have been conducted using those markers for identifying and characterising different yam species. Bourret

(1973) studied morphological variation of *D. alata* in New Caledonia and attempted to classify more than 100 cultivars into four (4) major groups based on size and vigour of the plant size and shape of the leaves, stem and wing characteristics, presence and absence of bulbils, shape and colour of tubers. Velayudhan *et al.* (1989) conducted similar study on 140 local cultivars from India using 22 morphological agronomic characters descriptors and identified 15 groups. Similarly, Hasan *et al.* (2008) used 47 morphological characters to evaluate 70 genotypes of *D. alata*collected throughout Malaysia. The authors reported that the most contributed traits for morphological variability were shape, size, and flesh colour of the aerial tuber, position, shape, size and veins colour of the leaves and petiole colour.

Mwirigi and Kahang (2009) observed morphological variability between 43 Kenyan species using 17 morphological variables and reported that most prominent traits recorded were twining directions, stem colour, spine shape, leaf types and presence or absence of glowering above-ground, plant parts, and tuber flesh colour, skin colour, shape of the tuber, hardness of the tuber when cooked, and presence or absence of roots on the tubers surface for the parts below the ground. Bressan *et al*. (2011) equally studied morphological variation and Isozyme diversity in *D. alata* landraces from Valedo Ribeira, Brazil and reported that out of the 24 morphological characters, used the most contributed traits to variability were related to shape, size and flesh colour of underground tuber, shape and colour of aerial tuber, position, shape, size and vein colour of leaves, petiole colour, shoot growth rate, and number of days for shoot to germinates. Islam *et al.* (2011) also carried out similar study on morphological characterisation of 60 yam germplasm accessions of Bangladesh, and reported that out of 60 genotypes 51 were *D. alata* and only 1 accession was *D. bulbifera* based on observed stem twining direction, presence of winged, ridges or spines on the stem, leaf shape, shape and size of aerial tubers. In addition, Anokye *et al.* (2014) used 107 morphological traits to evaluate 49 accessions of *D. alata* from Ghana. Characters that contributed most toward differentiation of the genotypes were tuber skin

and flesh colour, leaf margin colour, leaf shape, petiole wing colour, spine shape on the stem and branching of stem above the ground, morphological traits such as leaf colour, stem colour, and leaf shape were the common variables reported by various researchers, and also in the present day study. Thus, those variables could be introduced as useful morphological markers or tools for identifying and characterising yam species. Morphological characterisation is an affordable means of quick assessment of plant species. As such it should be considered as the first step for evaluating species instead of going into depth molecular or biochemical characterisation (Anokye *et al.*, 2014).

2.5 Biochemical Composition of Yams

Chemical composition of yam genotypes on dry weight basis was reported to showgenetic diversity among and within genotypes. Yams contain good quantities of organic matter, total nitrogen, protein, fat, carbohydrates, total phosphorus, total energy, and saponin contents (Mulualem *et al.*, 2018). Review of range and mean performance of biochemical traits showed great differences among landraces. The flour moisture and dry matter contents ranged from 17.78 to 27.47 % and 15.80 to 27.28 % with a mean of 22.03 % and 21.76 %. The main dry matter content of 21.76 % was reported among Ethiopia yams, 23.1 % and 19.9 % reported by Megh *et al*. (2003) from *Dioscorea triphylla* and *Dioscorea versicolor* were different from the value obtained (Abera *et al.*, 2011). The range of organic matter and ash contents were reported to be 21.38 to 31.13 and 2.61 %. The result obtained from south west Ethiopia yams agreed with Abera *et al.* (2011) results but lower than the value (3.41 %) reported (Princewill and Ibeji, 2015).

The range of total nitrogen content recorded among southwest Ethiopia yam range from 1.00 to 1.32 % and the mean of 1.25 %. This was higher than reported value of 0.48 % (Udensi *et al.*, 2008). Crude protein of the tuber yam landraces ranged from 6.25 to 8.28 % with the mean of

7.82 %. This value was similar with the value 8.31 % reported (Udensi *et al.*, 2008) on water yam and protein content of tuber yams 10.16 % for srilankan *Dioscorea alata* (Senanayake *et al.*, 2013); and 15.75 % for some Indian varieties of *D. bulbifera* (Shanthakumari *et al*., 2008). In the same vein, protein contents higher than 4. 03 – 6.52 % was reported for Ghanaian yams (Polycarp *et al.*, 2012) and 5.30 % for Indonesian yams (Aprianta *et al*., 2014).

Similarly, crude protein content recorded differences in wet of 1.68 to 3.00 g/100g and dry wet 2.89 to 6.36 g/100g (Abera *et al.*, 2011). Crude fat content ranged from 0.09 to 0.65 % with a mean value of 0.30 %. This reported value was higher than (0.20) of Cameroonian yam species (Egbe and Treche, 1995) and wild yams tuber from central region of Nepal (Megh *et al.*, 2003). This record was consistent with Food and Agricultural Organisation (FAO, 1972; Wanasundera and Ravindran, 1994). On a contrary, mean fat content recorded from Ethiopia was lower than reported value (2.24 %) on three cultivars of *Dioscorea bulbifera* (Princewill and Ibeje, 2015). Subsequently, carbohydrate content was reported to range from 92.66 to 173.30 kcal/100 g with mean value of 21.84 % and 130.19 kcal/100 g, this report agreed with those of Megh *et al.* (2003) and Abera *et al.* (2011). But lower than the reported value of 82.50 % and 359.81 kcal/100 g of (Udensi *et al.*, 2008).The phosphorus content varied between 23.7 mg/100 g and 53.0 mg/100 g with a mean of 39.0 mg/100 g. this result was in agreement with the report of Megh *et al.* (2003) on yam species (61.61 mg/100 g for *Dioscorea bulbifera;* 33.1 mg/100 g for *Dioscorea* deltoida; 40.8 mg/100 g for *Dioscorea versicolor* and 56.6 mg/100 g for *Dioscorea triphylla*). On contrary note, the report from Mulualem *et al*. (2018) was lower than the reported value range of 120-340 mg/100 g from *Dioscorea alata* (Udensi *et al.*, 2008).

Reported result obtained from anti-nutritional factors such as Tannin and Saponin contents from southwest Ethiopia ranged from 19.80 to 181.0 mg/100 g with mean value of 64.67 mg/100 g was higher than reported value of *Dioscorea rotundata* (20 mg/100 g). The tannin reported

lethal dose in plants is 7.6-9.0 g/kg (Aleto, 1993). However, since yam tubers are consumed in cooked form, the tannin contents would have been reduced during food processing before consumption as a result of thermal degradation, denaturation and formation of insoluble complex (Akin-Idowu *et al.*, 2008). The report showed consistency with the report of Udensi *et al.* (2010) who reported a tannin content range of 46.5 to 180.25 mg/100 g in *Dioscorea alata*. In the same vein, saponin contents of yams ranged from 2.31 to 13.94 mg/100 g with a mean of 5.91 mg/100 g was quite similar with the reported saponin value (8.49-14.03 mg/100 g) of other yam species (Princewill and Ibeji, 2015).

2.6 Antioxidant Composition of *Dioscorea* Species

Research studies in yams revealed low to high contents of polyphenol and antioxidant activities (Anoma and Thamilini, 2016). The antioxidant activity of phenolic compound is mainly due to their redox mechanisms like single oxygen quenching ability, radical scaveging activity, and metal chelating activity (Ekrem and Lihami, 2008). Yams were equally reported to contain other antioxidant substances such as vitamin C and carotenoids which exerts useful physiological effects (Champagne *et al.*, 2010; Ferede *et al.*, 2010; Narkheda *et al.*, 2013). According to Sakthidevi and Mohan (2013) that the methanol extract of *D. alata* had the potential to scavenge hydroxyl, superoxide, ABTs' radicals whereas ethanol extract of the tubers showed strong DPPH radical scavenging activity. Lubag *et al.* (2008) studied the antioxidant analysis of Nine cultivars of greater yam (*D. alata)* from Philippines and reported that cultivars were greater with colour ranging from white to intense purple, had higher antioxidant activities similar or higher than the control BHA (butylhydroxy anisole) and - tocorphenol.

Different type of antioxidant activity assays has been used by many researchers to determine the antioxidant activities of yam species (Lin *et al.,* 2005; Cornago *et al.*, 2011; Ghosh *et al.*, 2013; Nakheda *et al.*, 2013; Ukom *et al.*, 2014). Bhandari and Kawabata (2004) equally reported antioxidant activity in wild yam tubers from Nepal using DPPH assay and revealed the

relationship with the total polyphenol and flavonoid to the antioxidant activity of the yam (Cornago *et al.,* 2011; Ukom *et al.,* 2014). According to the study of Ghosh *et al*. (2013), the bulbils of *D. bulbifera* showed high scavenging activities against pulse radiolysis generated OH^- (Hydroxyl) radicals and ABTs + radicals and they stated that the species could be used as a potential source for herbal therapeutic agents against various diseases caused by oxidative stress.

2.7 Assessment of Genetic Diversity using Molecular Makers

Molecular analysis comprises a large variety of DNA molecular markers, which can be used in analysis of variation. The markers have different genetic qualities (they can be dominant or co-dominant, can amplify anonymous or characterised loci; they can contain expressed or non-expressed sequences).The concept of genetic markers is not a new one, in nineteenth century, Gregor Mendel the pioneer of genetics who used phenotype-based genetic marker in his experiment. Later, phenotype-based genetic marker for *Drosophilia mehanogaster* led to the founding of the theory of genetic Loci or alleles for genes are inherited jointly. The limitations of phenotype-based genetic markers led to the development of DNA-based makers, (that is molecular markers). A molecular marker can be defined as a genomic locus, detected through probe or specific starters (primer) which by the virtue of its presence, distinguishes unequivocally the chromosomic traits which it represents as well as the flanking regions at the 3' and 5' extremity (Brarcaccia *et al.,* 2000).

Molecular markers may or may not correlate with phenotypic expression of a genomic trait. They offer numerous advantages over the conventional phenotype-based alternatives; they are stable and detectable in all tissues regardless of growth, differentiation, development or defence status of the cell. In addition, they are not controlled by environmental, pleiotropic and epistemic effects (Linda *et al.,* 2009). The methods of molecular assessment vary from each other due to important features: such as genomic abundance, level of polymorphism detected, locus

specificity, reproducibility, technical requirement and most implication.Genetic DNA based markers such as; Restriction Fragment Length, Polymorphism (RFLP), Simple Sequence Repeats (SSRs) and Amplified Fragment Length Polymorphism (AFLP) are currently in use for ecological, evolutional, taxonomical, phylogenic and genetic studies of plant sciences. These methods are well established and their advantages and limitation have been documented (Agarwal *et al.*, 2008; Primmer, 2009).

Evaluation of genetic diversity in crop has become obvious since environmental factors often affect the dynamics of crop plant species and even those with high potential for gene flow (Sork *et al.*, 2010). Research studies have equally shown that character variation among and within species are affected by environmental gradient (Hulshof *et al.*, 2013).

2.7.1 Assessing yam (*Dioscorea* spp) genetic diversity using simple sequence repeat (SSR) markers

Genetic diversity analysis of yam cultivars in Benin using simple sequence repeat (SSR) markers reported that 146 accessions of yam from Benin were analysed using 10 markers. An average of 8.4 alleles per locus was detected. The mean heterozygosity was 0.57 and the mean polymorphism information content (PIC) for polymorphic markers was 0.51-some cultivars (23 %) were identified to have an identical genotype for the 10 markers. The study also revealed that the structure of genetic diversity in Benin is as a result of the farmers' crop management practices and their technical knowhow. In addition, the cultivars diversity had a geographical component. The outcome of the study was reported useful for defining strategy for the conservation of genetic diversity in yams.

Muluneth (2015) has developed genomic simple sequence repeatmarkers for yam. In the study, 90 simple sequence repeat (SSR) markers were developed from an enriched genomic library of yellow Guinea yam (*D. cayenensis*). Cross-amplification showed that 85 (94.40 %) and 51 (56.7

%) of these SSRs could be successfully transferred to the two major cultivated species of *D. rotundata* Poir and *D. alata* L., respectively. Polymorphisms in 30 markers selected on the basis of reliability and reproducibility of DNA strands were assessed using a panel of 12 *D. cayenensis,* 480 *D. rotundata* and 48 *D. alata* accessions. Accordingly; number of alleles per locus ranged from 2 to 8 in *D. cayenensis* (mean =3.9) 3 to 30 in *D. rotundata* (mean=13.9), and 2 to 22 in *D. alata* (mean=12.1). The average observed and expected heterozygosities were 0.156 and 0.634 (*D. cayenensis*; 0.326 and 0.853 (*D. rotundata*), and 0.247 and 0.836 (*D. alata*), respectively. The clustering based on six SSRs that were polymorphic in at least four (4) of the five cultivated *Dioscorea* species studies, including *D. cayenensis, D. bulbifera, D. alata*, *D. dumetorum* (Kunth) Pax and *D. bulbifera* L., detected groups consistent with the phylogenetic relationships of the species except for *D. dumetorum*. These new SSR markers are invaluable resources for application; such as genetic diversity analysis and markers assisted breeding.

Zhag *et al*. (2014) also studied identification of candidate genes responsible for Flavonoid Biosynthesis Pathway (FBP) that facilitated understanding the molecular mechanism of controlling pigment formation in yam tubers using SSRs. The result revealed a total of 125, 123 uniqueness from the purple-flesh (DP) and white flesh (DW) cDNA libraries of which about 49.5 % (60,020 unigenes) were annotated by BLASTX analysis using the publicly available protein data base. These unigenes were further annotated functionally and subject to biochemical pathway analysis. A total of 511 genes were identified to be more than 2-fold (FDR < 0.05) differently expressed between the two yam cultivars of which 288 genes were up-regulated and 223 genes were down-regulated in the DP tubers. Transcriptome analysis detected 61 unigenes encoding multiple well-known enzymes in the FBP. Furthermore, the unigenes encoding chalcone isomerase (CHS), flavonol 4 reductase (DFR), leucoan thocyanidin dioxygenase (LDOX), and flavond 3-0 glucosyl transferase (LIF 3GT) were found to be significantly up-regulated in DP, implying that these genes where potentially associated with tuber colour

formation in this elite cultivars. The expression of these genes was potentially associated with tuber colour. Further confirmed by qRT-PCR. Finally, 11,793 SSRs were successfully identified with these unigenes and 6,082 SSRs markers were developed using primer 3.

Obidiegwu *et al*. (2009) characterised 89 accessions of water yam (*Dioscorea alata*) from Benin, Congo, Cote d'Ivoire, Equatorial Guinea, Ghana, Nigeria, Sierra Lone and Togo using thirteen (13) microsatellite loci. A total of 97 alleles were detected with an average allelelic number of 7.46 per locus. Polymorphism information content (PIC) mean value of 0.65 showed existence of variability among the accessions. Accessions from Nigeria revealed the highest gene diversity of 0.678 while those from Cote d'Ivoire had lowest diversity with 0.506. The observed mean heterozygosity value of 0.469 was identified while cluster and principal coordinate analysis showed 8 major cluster groups. There was no relationship between relatedness of the accessions and their geographical area of collection. SSR markers proved to be effective to characterise the studied *D. alata* germplasm.

2.8 Importance of Genetic Diversity

Genetic diversity has been reported to be the sum total of genetic characteristics within any species or genus (Rauf *et al.*, 2010). Genetic variability on the other hand, elucidates the variation within genetic characteristics. Plant genetic resources however, includes wild relatives of cultivated species, varieties, hybrids as well as breeding materials horticultural, medicinal, aromatic and other plants that can be utilised for breeding to provides food, medicinal and nutritional security. According to food and Agricultural organisation (FAO, 2002), the loss of biodiversity is considered as one of the major environmental threat that affected plant diversity which may have great influence on the world future population estimated to rise to nine (9) billion by 2050. Consequently, the overall genetic diversity in crop species has been reported

reduced by range of factor such as urbanization and replacement of traditional agricultural system by the modern farming method (Rauf *et al.*, 2010).

Based on the aforementioned, genetic diversity in plants has been reported as the fundamental basis for crop improvement in nature. Hence it provides the rudiment for plant breeders to create new and improved cultivars with desirable characteristic for farmers preferred trait (yield) and breeders preferred traits (Pests and diseases resistance and photosensitive). The existence of genetic diversity represented in the form of wild species, related species, breeding stocks and mutant lines may assist plant breeders in breeding climatic resilient varieties, require novel traits like tolerance towards potential new insect pests and diseases, extreme heat, extreme cold and towards various air and soil pollutants for over-changing breeding goals, different genes need to be reserved in cultivated and cultivable crops species in the form of germplasm. The presence of genetic diversity within and between crop plants species enables the plant breeders to selects superior genotype either to be directly used as new variety or to be used as parent in hybridization programme. Genetic diversity between two parents is essential to realize heterosis and obtain transgressive segregants (Bhandari *et al.*, 2017). According to the United Nations Food and Agricultural Organization reported that 75 % lost in genetic diversity can be robust using diversity to facilitate breeders to develop varieties for specific traits like quality improvement and tolerance to biotic and abiotic stresses. It also facilitates development of new lines for non-conventional uses in some crops.

2.9 Germplasm of African Yam

The concept of germplasm is used to describe any genetic material of a plant used for reproduction. The term was coined from August Weismann's theory which states that "Inheritable information is transmitted only by germ cells. Plant germplasm have been reported to be total gene pool of a species consisting Landraces, advanced breeding lines, popular

cultivars, wild and weedy relatives (Upadhyaya *et al.*, 2010). The word forms a genetic base of a particular relative that may contribute genetically to the breeding and crop improvement programme.The germ cells formed the genetic basis for recombination and selection in crop development programmes required for polygenic traits such as yield, responseto a changing pathogen pressure, such as new races or introduction of new pathogens and provision of the basis for genetic buffering within and among cultivars that can reduce losses to unexpected environmental changes.

African yam (*Dioscorea* spp) germplasm collection and characterisation have been reported to play significance role for identification of desirable genotype trait for insertion in breeding programmes (Chimiray and Vernooy, 2017). Similarly, Hasan *et al.* (2008) used 47 morphological traits to evaluate 70 accessions of *Dioscorea alata* collected in Malaysia. The report showed that *D. alata* exhibits morphological variability in the shape, size and flesh colours of underground tubers, shape and colours of aerial tuber, leaves and petiole colour. This variability is an indication that yam germ cells contain promising gene pool that can be used to supplement yam developmental programmes in Nigeria. Similarly, Etchiha *et al.* (2019) studied present day cultivars diversity in yam and farmer perception on their tolerance to tuber Dry Rot caused by the nematode *Scutellonema bradys*. The report showed significance morphological variability within the 10 yam cultivars perceived by the farmers as tolerant or resistance to *S. bradys*. This variant germ cell discovered resistance to nematode infection can be utilized to build a hybrid that will be nematode resistance. Therefore, germplasm collection of the indigenous landraces will help to understand biodiversity existing within African yam where promising agro-morphological traits will be selected for the creation of hybrid crop or improvement of the existing ones.

2.10 Yam Germplasm from Nigeria

Yam germplasms collection conserved in field and in Vitro genebanks constitute a huge genepool for yam development activities in order to actualize its optimum potentials for food security and income generation for farmers. According to the international institute of tropical agriculture and consultative group on international agricultural research (IITA, 2020) report, on the basis of geographical origin, Nigeria has contributed the highest number of germplasm accessions (5,839) to the gene bank of Africa. This total assemblage comprised of ten cultivated species of *D. rotundata* (68%), *D. alata* (21.88), *D. Burkilian* (6.29), *D. abbyssica* (1. 06%), *D. cayenesis* (1.50 %) *D. dimentorum* (1.30 %), *D. bulbefera* (1.20 %), *D. esculenta* (0.40 %), *D. preusii* (0.17 %) and mangenotiana (0.14 %). However, 75 % (391) of the total collections was achieved using morphologicaldescriptorsand country of origin Gezahegn *et al*. (2018).

2.11 Plant Genetic Resources (PGR)

The history of genetic variations was recognized and captured based on the visual appraisal of phenotypic variation perceived in plant species. These variations have myriad of resources that play integral role in the life of man, his domesticated animals and those of their wild counterpart. This is practicable in the provision of food, cloth, house and medicinal services. It was reported that plant genetic resources (PGR) account for 80 percent of human diet (FAO, 2013). Plant genetic resources are gene pools through which desirable traits are derived for improvement of new varieties. Indeed, genetic materials have significantly contributed in actualization of global food security, poverty alleviation and sustainable development (Upadhyaya and Crowda, 2006). Consequently, some of these resources are band to loss due to introduction of new varieties and human attempt of exploring the nature to improve living standard socially and economically (Upadhyaya *et al.*, 2008). To protect these valuable resources, conservation may be necessary since more economic, medicinal and social plants are threatened and endangered of extinction (John, 2010). Similarly, exploding world population,

climatic change, biotic and abiotic factors militating against the flora have led human to search new resilient and nutritional crops that can withstand some of these threatening factors to crop production.

Plant genetic resources were considered as any materials of plant origin that contain healthy and functional hereditary base for use. These resources include reproductive or propagating materials such as cultivated cultivars currently in use and newly developed varieties, obsolete species, primitive varieties or landraces, wild and weed species, near relatives of cultivated varieties and special genetic stocks including elite and current breeders' lines and mutants (FAO, 2013). Plant genetic resources are required by farmers and plant breeders to develop quality and productivity of crop plant.

2.12 Cluster Analysis of Yam

Cluster analysis was reportedly used to assess yam genotypes based on their area of origin. Analysis of clusters reported from yams showed that the genetic distances between landraces in different clusters were generally not wide (Mulualem and Mohammed, 2013). The low divergence among the landraces indicated the possibility that the landraces originated from different genetic backgrounds. Padulosi (1993), reported high level of resemblance among yam landraces which could be attributed to their cross pollinating nature.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Collection of Yam Germplasm

Germplasm collection and exploration of fifty (50) accessions of African yam (*Dioscorea* spp.) was carried out in collaboration with the Agricultural Development Project (ADP) extension officer in the Six (6) selected major yam producing states and local government areas across North Central States in Nigeria, within the month of December, 2018 to March, 2019. The states visited included Benue, Kogi, Kwara, Niger, Nasarawa and Federal Capital Territory (FCT) Abuja. These states were geo-referenced and represented in a simple map using map tools and map plots software packages (Bivand and Lawin-koh, 2015) (Figure 3.1). Furthermore, collection of data from the peasant farmers was carried out using one hundred questionnaires administered to the respondents accompanied with verbal interview. The questionnaires were structured into sections (A and B). Section 'A' was based on demographic information of the farmers and 'B' was on agricultural practices by the farmers, purpose of yam production, species cultivated and cultural practice (Appendix I).

3.2 Phenotypic Characterisation of Yam Germplasm

Yam tubers accessions collected were characterised according to indigenous knowledge (Ikechi, 2014; Efisue, 2015). The characterisation was carried out based on the tuber skin colour, tuber shape, hairiness of the tuber and sprouted young stem colour.

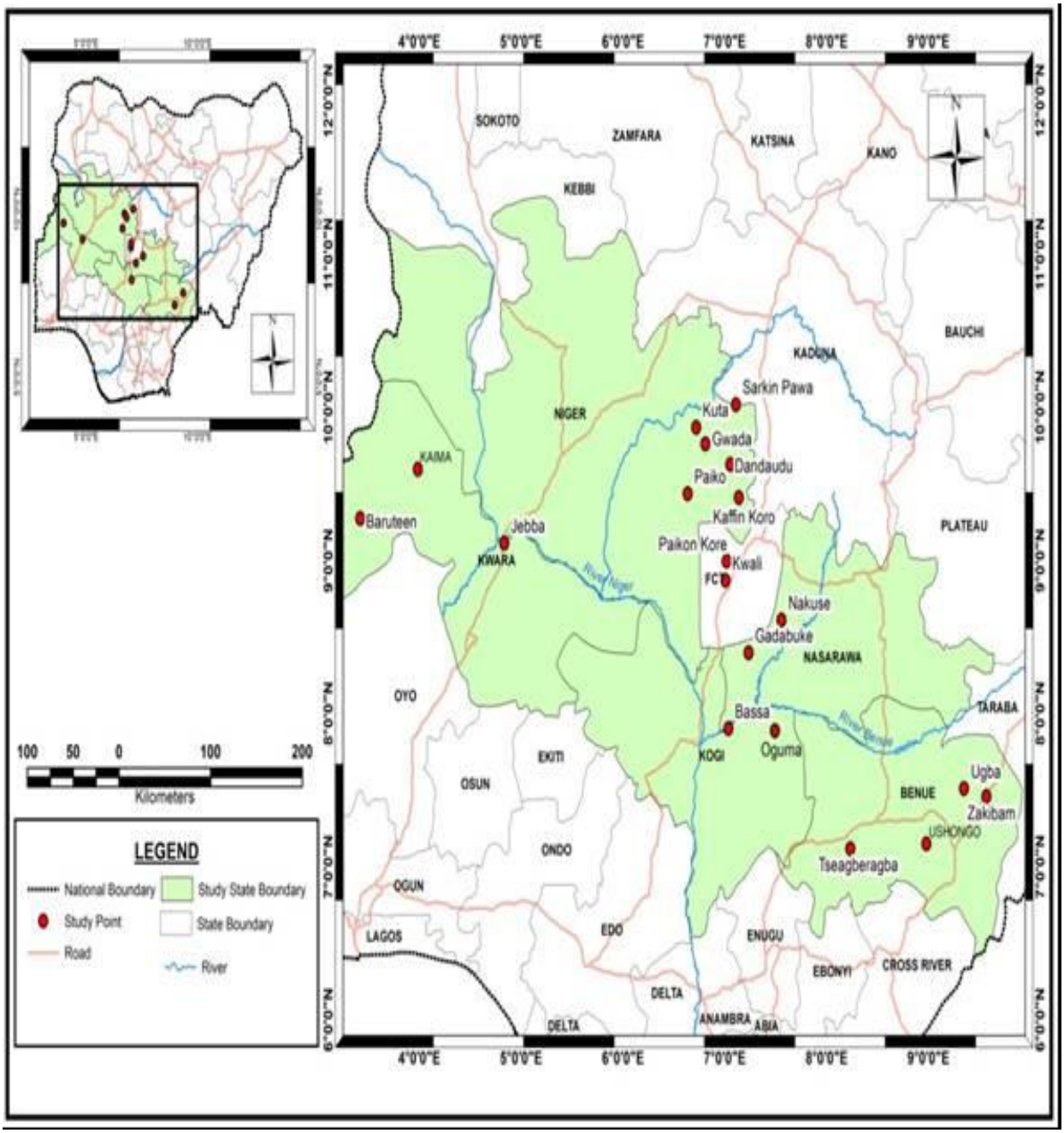

Figure 3.1: African Yam Germplasm Collection in North Central Nigeria

Source: Field Survey

3.3 Experimental Site

The study was conducted at Tungan Mallam in Paikoro Local Government Area of Niger State, Nigeria. Geographically, the village is located in North-Central geo-political zone. The region is a Guinea Savannah with annual average rainfall of 1,000 mm to 1,300 mm and the mean temperature of 37 ^{o}C during the dry season (Figure 3.2).

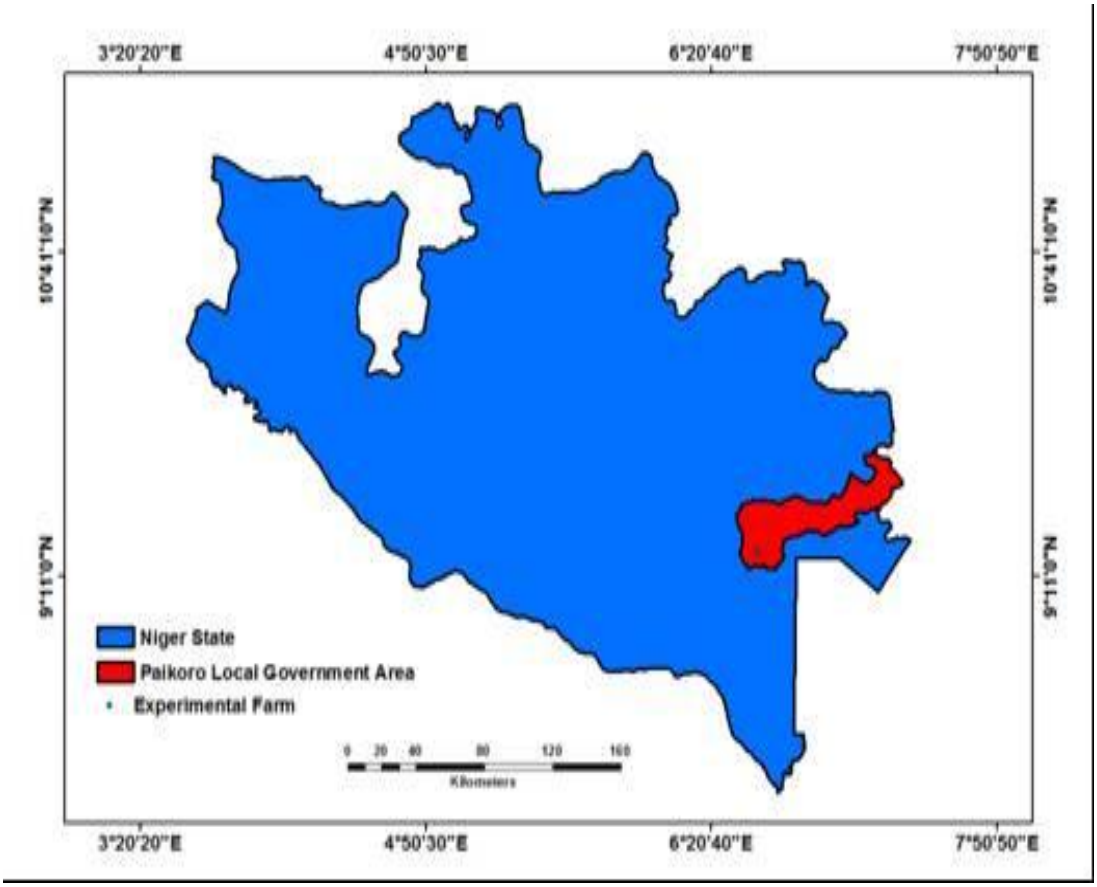

Figure 3.2: Geographical Location of the Experimental site.

Source: Field Sourse

3.4 Experimental Design

The experiment was designed in a Randomised Complete Block Design (RCBD) with five (5) replicates (Appendix II). One sample was planted in a heap with inter and intra-raw spacing of one meter on lines. The heaps were covered with mulching materials (Vincent, 2016), to avoid excessive heat and to enhance vigorous sprouting of the yam. Weeding was observed manually using hoe until the crop was due for harvest.

3.5 Viability Test of the Accession

After the collection and characterisation, the accessions were assembled in the yam barn at the experimental farm. Viability of the tuber was determined after four (4) months of harvest when the tubers rejuvenated into a whole plant growth under natural condition (FAO, 2013).

3.6 Measurement of Agro-Morphological Parameters

Morphological parameters were investigated using standard procedures of International Plant Genetic Resources Institution (IPGRI) descriptors for yam (IPGRI, 1997). Both qualitative and quantitative parameters were considered, qualitative traits observed and selected as presented in Table 3.1. Quantitative parameters measured include, number of tuber per plant (NTP), petiole length (PL), tuber length (TL), tuber breath (TB), and stem length per plant (SLPP) were measured using meter rule. The weight of each tuber was equally taken using weighing balance (spring weighing balance).

Table 3.1 Description and Score of Qualitative Traits of Africa Yam

Code	Traits	Score and traits
	Qualitative characters Stem	
1.	Young stem colour	1 - Green;2 - Purplish green 3 - Brownish green; 4 –Dark-brown, 5 - Purple 99. Other: maroon; purplish green spotted
2.	Twining habit	0 - No 1; Yes
3.	Twining direction	1 - Clockwise; 2 – Anticlockwise
4.	Matured stem colour	1 - Green; 2 - Purplish green 3 - Brownish green; 4 – Dark-brown; 5 – Purple
5.	Absence/Presence of ridges	0 - Absent; 1 - Present
6.	Stem glabrous/pubescent	0 - Absent; 1 – Present
7	Absence/presence of wings	3 - Few; 7 – Many
8	Spines on stem base	3 - Few; 7 – Many
9	Spines on stem above base	1 - Alternate; 2 – Opposite
10	Position of leaves	3 - Alternate at base/opposite above 99. Others
11	Leaf type	1 – Simple; 2 – Compound
12	Number of leaflets	1 - Mainly; 3- (Trifoliate) 2 – Mainly; 5 - (Quinate) 3 - More than five
13	Leaf colour	1 - Yellow; 2 - Pale green; 3 – Dark-green; 4 - Purplish green 5 - Purple 99. Purplish Pale.
14	Hairiness of upper leaf	3 - Sparse; 7 – Dense
15	Leaf shape	1 - Ovate; 2 - Cordate; 3 - Cordate long; 4 – cordate-broad; 5 – Sagittate-broad; 6 - Sagihate long; 7 - Hastate 99-others;
16	Leaf Apex shape	1 - Obtuse; 2 – Acute; 3 - Emarginate 99. other
17	Position of widest part of the leaf	1 - Third upper; 2 – Middle; 3 - Third lower; 4 - Other entire;
18	Petiole colour	1 - All greenish with purple base; 2 - All greenish with purple leaf junction; 3 - All green with purple at both ends; 4 - All purplish green with purple base; 5 - All purplish green with leaf junction; 6 - All purplish green with purple at both ends; 7 - Green; 8 - Purple; 9 - Brownish green; 10 - Brown 11 – Dark-brown 99. Others
19	Flowering	0 - No flowering; 1 - Flowering in some year; 2 - Every year;
20	Inflorescence position	1 - Pointing upwards; 2 - Pointing downwards
21	Inflorescence smell	0 - Absent; 1 - Present;
22	Fruit formation	0 - No; 1 - Yes
23	Fruit position	1 - Pointing upward; 2. Pointing downward
24	Fruit shape	1 - Equal in length and width; 2. Elongated 3 - Trilobated capsule;

25	Absence/presence of seed	0 – Absent, 1. Present
26	Absence/presence of aerial tuber	0 – Absent; 1. Present
27	Aerial tuber shape	1 – Round; 2. Oval; 3 – Irregular; 4. Elongated
28	Aerial tuber skin colour	1 – Greyish; 2. Light brown; 2 - Dark brown 99.other
29	Absence/presence of bumps	0 - Absent; 1. Present
30	Flesh colour	1 – White; 2. Yellowish white; 3 – Yellow; 4. Orange 5 - Light purple; 6 - Purple; 7 - Purplish with white 8 - White with purple; 9. Outer purple/inner yellow 99.other
31.	Absence/presence of underground tuber	0 - Absent; 1. Present
32	Maturity after emergence	0 - 5 months 1 - Up to 6 month 2 - 7-8 months; 3-9-10 months
33	Number of tuber per hill	1 - One 2 - Few; 3. Several
34	Relationship of tubers	1 - Completed separated and distant; 2-Completely separated but closed; 3 - Fused at neck
35	Tuber shape	1 - Round; 2 – Oval; 3 - Oval oblong; 4 - Cylindrical 5 - Flattened
36	Tendency of tuber to branch	3 - Slightly branched; 5 – Branched; 7 - Highly branched
37	Place where tuber branches	1 - Upper third; 2 – Middle; 3 – Lower
38	Roots on tuber surface	3 – Few; 7 – Many
39	Place of roofs on tuber	1 - Lower; 2 – Middle; 3 – Upper; 4. Entire
40	Absence/presence of cracks on tuber	0 - Absent; 1 - Present
41	Tuber skin colour beneath the bark	1 - Light maroon; 2 – Dark-maroon; 3 - Greyish 99 others
42	Texture of flesh	1 - Smooth; 2 - Grainy; 3- Very grainy
43	Flesh oxidation colour	1 - Grey; 2- Purple; 3 - Orange 99. Others.
44	Petiole length	1 - < 5cm; 2 – 6-9cm; 3 - ≥10cm
45	Stem length per plant	1 - < 2m; 2 – 2-10m; 3 - >10m
46	Tuber number per hill at harvest	1 – one; 2 – few (2-5); 3 – several (>5).
47	Tubers length	1 - < 20cm; 2 – 21-40cm; 3 - ≥ 41cm
48	Tuber breath	Measured in centimetre (cm) using ruler in widest part

Source: IPGRI (1997)

3.7 Determination of Biochemical Composition of Selected African yam (*Dioscorea* spp.) Landraces in North-Central Nigeria

Thirty-two (32) distinct genotypes of yam tubers obtained from morphological evaluation of the fifty (50) genotypes were selected for biochemical composition and molecular analyses. One healthy tuber from each unique genotype was randomly selected from the bulk of freshly harvested tubers washed with clean water, peeled manually and sliced into rectangular sizes using stainless knife. The sliced tubers were introduced into hot air dryer according to the method described by Omari *et al*. (2018) with slight modification. The dried chips were milled into fine flour (0.5 mm) and stored in well labelled sample polythene bags at 20 ^{o}C for biochemical analysis (Association of Official Analytical Chemists, 2012)..

3.7.1 Determination of proximate analysis

The analysis was conducted using standard methods of the Association of Official Analytical Chemists (AOAC, 2012). The proximate composition determined includes the crude proteins, crude fibre and crude fat analysis. The parameters determined include; total ash content, crude fat, crude fibre and moisture, while the nitrogen free extract (NFE) of the samples was determined by subtracting the percentage of the crude fibre from total carbohydrate (Ndidi *et al*., 2014). The Gross Energy (GE) was analysed using a bomb calorimeter. Crude protein (Percentage total nitrogen x 6.25) was determined after Kjeldahl method. Ash was determined by the incineration of the samples in a muffle furnace and maintained at 550 ^{o}C for 5 hrs. Crude fibre was obtained by digesting 2 g of the sample with H_2SO_4 and NaOH, and incinerating residue in muffle furnace maintained at 550 ^{o}C for 5hrs. Moisture content was determined by heating 2 g of each sample to a constant weight in a crucible placed in oven maintained at 105 ^{o}C.

3.7.2 Mineral analysis

For mineral analysis, the samples were dried to a constant weight, and underwent a microwave assisted digestion. A weighted amount of each sample (200 mg) was mixed with 5 ml of 65 % HNO_3 in a Teflon reaction vessel and heated in a speed wave TM MWS – 3 + (Berghot, Germany) microwave system. Digestion procedure was conducted at different stages of 130 ^{o}C/10 min, 160 ^{o}C/15 min, 170 ^{o}C/12 min, 100 ^{o}C/7 min and 100 ^{o}C/3 min. The resulting clear solutions after the digestion were transferred into 50 mL test tubes containing 20 mL of deionised water. The element composition was determined by the use of inductively coupled plasma (ICP) optical emission spectrometer model optima TM 7000 DV ICP – OES (Dual view, Perkin Elmer life and Analytical Sciences, Shelton, CT USA) with radial plasma configuration. Standard plasma conditions were used such as 1300 W for radio-frequency power; 1.5 ml/min pump rate, and 15.0, 0.2 and 0.8 ml/min for plasma auxiliary and nebulizer gas flow, respectively.

3.8 Molecular Characterisation

3.8.1 Sample collection

Samples of fresh young leaves from the experimental field were randomly collected from each accession into a nylon bag inserted into an envelope labelled with the accession number and placed in an ice packed cooler which was transported to Bioscience Laboratory, International Institute of Tropical Agriculture, Ibadan for analysis.

3.8.2 DNA extraction

Evolutionary analyses were conducted in MEGA X (Kumar *et al*., 2018). Approximately 100 mg of leaf was grinded with Dellaporta extraction buffer (100 mMTrls pH 8, 51) ml EDTApH 8, 500 mMNaCI, 10 mMmcrcaptoethanol) and DNA extracted as described briefly. Each sample was grinded in 1000 µl of the buffer in a sterilized sample bags. Mix was collected in sterile

Eppendorf tube and 40 µl of 20 % SDS was then added, this was followed by brief vortexing and incubated at 65 ^{o}C for 10 minutes. At room temperature, 160 µl of 5 M potassium acetate was then added vortexed and centrifuged at 10000 rmp for 10 minutes. Supernatant where collected in another Eppendorf tube and 400 µl of cold is propanol was added mixed gently and kept at -20 ^{o}C for 60 minutes. Centrifugation was at 13000rmp for 10 minutes to precipitate the DNA after which supernatant was gently decanted and ensured that the pellet was not disturbed. DNA was then washed with 500 µl of 70 % ethanol by centrifuging at 10000rmp for 10 minutes. Ethanol was decanted and DNA air-dried at room temperature until no trace of ethanol was seen in the tube. Pellet was then re-suspended in 50 µl of Tris EDTA buffer to preserve and suspend the DNA.

Simple Sequece Repeat PCR Protocol and Bands Separation

Polymorphic six (6) SSR markers were used for genotyping the entire 32 genotypes. Total PCR reaction was optimized to be 15 µl and this included 2 µl of about 100 ng DNA template, 7.0 µl Dream Taq PCR master mix, 1 µl of each primer (forward and reverse primer), and 4.0µl nuclease free water. PCR protocol used for all primer pair was as follow: an initial denaturation at 94 ˚C for 5 mins followed by 35 cycles of denaturation of 94 ˚C for 15 sec. Annealing of 44-58 ˚C(check table) for 30 sec and extension of 72 ^{o}C 30 sec then a final extension of 72 ˚C for 7 mins and chill at 4 ^{o}C

Table 3.2: Properties of SSR Primers used for the Genotyping

Primer Name	Forward Primer	Reverse Primer	Annealing temperature
Dpr3B12	CATCAATCTTTCTCTGCTT	CCATCACACAATCCATC	44
Da1F08	AATGCTTCGTAATCCAAC	CTATAAGGAATTGGTGCC	54
DAB01	TATAATCGGCCAGAGG	TGTTGGAAGCATAGAGAA	54
Dab2C05	CCCATGCTTGTAGTTGT	TGCTCACCTCTTTACTTG	46
Dpr3F12	TCCCCATAGAAACAAA	TCAAGCAAGAGAAGGTG	44
ym 28	CCATTCCTATTTAAGTTCCCCT	GATGAAGAAGAAGGTGATGATG	58

3.8.3 DNA amplification

The separation of bands as produced by each primer was done in a 1.5 % Agarose gel. The buffer (1XTAE buffer) was prepared and subsequently used to prepare 1.5 % agarose gel. The suspension was boiled in a microwave for 5 minutes. The molten agarose was allowed to cool to 60 °C and stained with 3 µl of 0.5 g/ml ethidium bromide (which absorbs invisible UV light and transmits the energy as visible orange light). A comb was inserted into the slots of the casting tray and the molten agarose was poured into the tray. The gel was allowed to solidify for 20 minutes to form the wells. The 1XTAE buffer was poured into the gel tank to barely submerge the gel. Seven µl of each PCR product and loaded into the wells after the 100 bp DNA ladder was loaded into well 1. The gel was electrophoresed at 120 V for 45 minutes visualized by ultraviolet trans-illumination and photographed. The sizes of the PCR products were estimated by comparison with the mobility of a 100 bp molecular weight ladder that was ran alongside experimental samples in the gel (Kumar *et al*., 2018).

3.8.4 Evolutionary relationships of taxa

The evolutionary history was inferred using the Minimum Evolution method (Rzhetsky and Nei, 1992). The optimal tree is shown. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. The ME tree was searched using the Close-Neighbor-Interchange (CNI) algorithm (Nei and Kumar, 2000) at a search level of 1. The Neighbour-joining algorithm (Saitou and Nei, 1987) was used to generate the initial tree. This analysis involved 32 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 18 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar *et al*., 2017)

3.9 Data Analysis

The data collected from agro-morphological parameters, proximate, and mineral composition were subjected to analysis of variance (ANOVA) to determine the significant of variations that existed among the accessions. The post hoc test was done using Duncan's Multiple Range Test (DMRT) to separate the means where necessary utilizing SPSS software version 18. Pearson's Linear Correlation analysis was computed to examine the degree of association among the morphological traits. Values were considered significant at 5 % P-value.

The data generated were subjected to Principal Component Analysis (PCA) to determine patterns of variation and major traits contributing to the delineation. Principal Component Analysis (PCA) with Eigen-value above one (1) was considered significant. Agro-morphological loading greater than $\pm$ 0.30 were considered meaningful (Hair *et al*., 2014). A clustered analysis was observed based on Euclidean distance matrix in hierarchical order to determine the diversity and similarity of the accessions from diverse region of the state using PAST software.

For the DNA fingerprinting using SSR molecular technique, binary data was generated for each primer sets using 1 (presence of positive amplification at a particular band size) and 0 (absence of positive amplification at a particular band size). The generated binary data was the used to create a data matrix which was analysed using the Power marker V2.35 software. Genetic diversity parameters such as major allele frequency, gene diversity and polymorphic information content were then generated using the power marker software. The genetic relationship among treated samples were also estimated by constructing a dendrogram through un-weighed pair group method with arithmetic means [UPGMA] using the mega 6 softwareand genetic distance were computed also using the mega 6 software.

3.9.1 Genetic parameters estimate

The analysis of variance, the phenotypic, environmental and genotypic components of variance were estimated using the formula adopted by Medagam *et al*. (2015).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{mg - me}{r} \qquad 3.3$$

Where:

Mg = mean sum of squares of Genotypes (treatment)

Me = mean sum of squares of error

r = number of replications (blocks)

phenotypic variance ($\sigma^2 p$)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e \qquad 3.4$$

Where:

$\sigma^2 e$ = environmental variance

$$\text{Phenotypic Coefficient of Variation PCV (\%)} = \frac{\sqrt{\text{Phenotypic Variance}}}{\text{Grand Mean}} \text{ X } 100 \qquad 3.5$$

$$\text{Genotypic Coefficient of Variation GCV (\%)} = \frac{\sqrt{\text{Genotypic Variance}}}{\text{Grand Mean}} \text{ X } 100 \qquad 3.6$$

Broad sense heritability ($h^2 bs$) was also estimated for all the characters as the ration of genotypic variance total or phenotypic variance (Lush, 1940). The heritability values were considered as low (<30%), moderate (30-60%) and high (>60%) as adopted by Daudu *et al*. (2016).

Broad sense heritability $h^2 bs$.

$$h^2 bs = \frac{\text{genotypic variance } (\sigma^2 g)}{\text{phenotypic variance } (\sigma^2 p)} \text{ x } 100 \qquad 3.7$$

Genetic Advance (GA) at 5% selection intensity was calculated in accordance with procedure of Allard (1999). The genetic advance with the value (<10%) was considered as low, moderate (10-20%) and high (>20%), as adopted by Daudu *et al*. (2016).

$GA = h^2bs \times a^2p\ vk$

Where:

σ^2p = phenotypic standard deviation of the traits.

K = standard selection differential which is 2.06 at 5 percent selection intensity.

CHAPTER FOUR

4.0 RESULTS AND DISCUSSION

4.1 Results

4.1.1 Germplasm Collection of African Yam in North Central Nigeria

One hundred local yam growers (farmers) were visited in five (5) villages each across the 6 states. Fifteen percent (15 %) of these were female while eighty - five percent (85 %) were male. Sixty percent (60 %) practice subsistence agriculture, while fourty percent (40 %) were producing yam tubers for commercial purpose and only two percent (2 %) were cultivating yams for medicinal purpose. In addition, 70 % were cultivating the yam for food, 28 % were cultivating the yam for sale; white yam (*D. rotundata*) was the major accessions cultivated throughout the growing areas. Meanwhile, the cultural practice was rain-fed with 96 % of the yam cultivation and production depending on rain.

The yam accession was identified and classified into four (4) species according to farmer description. The most abundant accession recorded were *Discorea rotundata* (white yam or Guinea yam) with 44 accessions; followed by *Dioscorea alata* (water yam or greater yam); then *Dioscorea dumetorum* and the least was *Dioscorea bulbifera* (Table 4.3). Various local names were used for the *D. rotundata* landraces by farmers and consumers in different languages in area of production as*:* 'Arima', (Gbari), 'Dan'anacha', (Gbari), 'Amula', (Bassange), 'Army', (Bassange), 'Ajan', (Tiv), 'Bazjenbyi', (Gbari), 'Didiya', (Gbari), 'Danbala/Jeep', (Bassange), 'Faketsa', (Tiv), 'Giga', (Gbari), 'Ogoja/Gbari', (Tiv/Gbari), 'Gbongu', (Tiv), 'Hembakwatse', (Tiv), 'Ishipun', (Tiv), 'Iko', (Gbari), 'Ihyara/Kongo', (Tiv), 'Koch', (Tiv), 'Kpako', (Gbari), 'Loshi', (Gbari), 'Mana', (Gbari), 'Mumuye', (Gbari), 'Naira/Pasabunga', (Gbari), 'Noryo', (Tiv), 'Suba', (Gbari), 'Punch', (Tiv), 'Shindo', (Gbari), 'Tameyo', (Tiv), 'Taribe', (Gbari), 'Yangbeje', (Gbari), 'Zagi', (Gbari), 'Antura', (Tiv), 'Alakpa', (Tiv), 'Gyu'ua', (Tiv), 'Azungul', (Tiv), 'Anyisha', (Tiv), 'Pepa', (Gbari), 'Ipua', (Tiv), 'Annasuwe', (Tiv), 'Shamura',

(Gbari), ‘Bazje’, (Gbari), ‘Sofini’, (Nupe/Yoruba) and ‘Ehura’ (Yoruba). Similarly, *Dioscorea dumetorum* were equally known and called ‘Surukokoi’; (Gbari), ‘Suruwowoi’ (Gbari), and *Dioscorea bulbifera* (aerial yam) was also called ‘Kandu’ (Nupe/Gbari).

Phenotypically, the results revealed great variability in the African yam species. The skin colour showed variations as light brown, Brown, dark brown, dark and ash-brown. Furthermore, diversity in tuber shapes were observed as cylindrical, oval, irregular and snake shaped. Germplasm collected showed that Niger State had the highest number of accessions (twenty-one), followed by Benue with Nineteen (19) genotypes. (Table 4.1)

Table 4.1: Gender Representation and Agricultural Practices among Yam Farmers in North-Central Nigeria

Gender	Number of farmers	Percentage
Male	85	85%
Female	15	15%
Agricultural Practices		
Subsistence	60	60%
Commercial	40	40%

Source: Field work.

Table 4.2: Purpose of Yam Production and Cultural Practices

Purpose of production	Number of farmers	Percentage
Food	70	70%
Sell	28	28%
Medicine	2	2%
Total	**100**	**100%**
Cultural practices		
Rainfed	96	96%
Irrigation	4	4%
Total	**100**	**100%**

Source: Field work.

Table 4.3: Sources and Basic Information about the Yam Accessions Collected from North-Central Nigeria

Accession Number	*Local Name*	*D. alata*	*D. bulbifere*	*D. dumetorum*	*D. rotundata*	*Local Government*	*State*	*Status*	*Rare Species*
NGr.001	Arima				1	Paikoro	Niger	Landraces	Rear
NGr.002	Dan'anacha				1	Paikoro	Niger	Landraces	Rear
NGr.006	Bazhenbyi				1	Paikoro	Niger	Landraces	Rear
NGr.008	Didiya				1	Shiroro	Niger	Landraces	Abundant
NGr.012	Giga/Biwara				1	Shiroro	Niger	Landraces	Abundant
NGr.020	Koch				1	Bosso	Niger	Landraces	Abundant
NGr.021	Kpako				1	Paikoro	Niger	Landraces	Rear
NGr.022	Loshi				1	Paikoro	Niger	Landraces	Abundant
NGr.023	Mana				1	Paikoro	Niger	Landraces	Rear
NGr.028	Suba				1	Paikoro	Niger	Landraces	Rear
NGr.029	Shindo				1	Paikoro	Niger	Landraces	Rear
NGr.036	Taribe				1	Paikoro	Niger	Landraces	Rear
NGr.038	Zagi				1	Paikoro	Niger	Landraces	Rear
NGr.037	yangbeje				1	Paikoro	Niger	Landraces	Abundant
NGr.007	Bazje				1	Paikoro	Niger	Landraces	Rear
NGd.031	Suruwowwoi			1		Gurara	Niger	Landraces	Abundant
NGa.033	Shamma-khadna	1				Paikoro	Niger	Landraces	Rear
NGr.024	Maragbagi				1	Katch	Niger	Landraces	Rear
NGb.019	Kandu		1			Katch	Niger	Landraces	Rear
NGr.017	Jeep/sarki debo				1	Muya	Niger	Landraces	Abundant
NGr.015	Iko				1	Paikoro	Niger	Landraces	Rear
BNr.044	Ajan				1	Zakibiam	Benue	Landraces	Abundant
BNr.038	Faketsa				1	Zakibiam	Benue	Landraces	Abundant
BNr.077	Ugoja/gbari				1	Zakibiam	Benue	Landraces	Rear
BNr.059	Gbongu				1	Ushongo	Benue	Landraces	Rear
BNr.063	Hembakwatse				1	Zakibiam	Benue	Landraces	Abundant
BNr.066	Ishipua				1	Ushongo	Benue	Landraces	Rear
BNr.067	Ihyara/kongo				1	Ushongo	Benue	Landraces	Abundant
BNr.071	Noryo				1	Ushongo	Benue	Landraces	Abundant
BNr.083	Punch				1	Katsinala	Benue	Landraces	Abundant
BNr.075	Tameyo				1	Ushongo	Benue	Landraces	Abundant
BNr.050	Alakpa				1	Ushongo	Benue	Landraces	Abundant
BNr.061	Gyu'ua/Akpoki				1	Ushongo	Benue	Landraces	Abundant
BNr.055	Anzungul				1	Ushongo	Benue	Landraces	Abundant
BNr.051	Ayisha				1	Konshisha	Benue	Landraces	Abundant
BNr.065	Ipua				1	Konshisha	Benue	Landraces	Abundant
BNr.048	Annasuwe				1	Konshisha	Benue	Landraces	Abundant
BNd.030	Suru kokoi			1		Konshisha	Benue	Landraces	Abundant
BNa.054	Anenga beer	1				Konshisha	Benue	Landraces	Abundant
BNr.056	Agboyo/Akura				1	Konshisha	Benue	Landraces	Abundant
FCr.073	Mumuye				1	Gwagwalada	FCT/Abuja	Landraces	Rear
FCr.095	Naira/Pasabunga				1	Kwali	FCT/Abuja	Landraces	Rear
FCr.079	Akanji				1	Kuje	FCT/Abuja	Landraces	Abundant
KGr.043	Amula				1	Bassa	Kogi	Landraces	Abundant
KGr.003	Army				1	Dekina Ida	Kogi	Landraces	Abundant
KGr.121	Dambala				1	Ijumu	Kogi	Landraces	Abundant
NSr.027	Pepa				1	Toto	Nasarawa	Landraces	Rear
NSr.097	Shamura				1	Karu	Nasarawa	Landraces	Abundant
Kwr.133	Sofini				1	Buruti	Kwara	Landraces	Abundant
Kwr.134	Ehura	1				Kaima	Kwara	Landraces	Abundant
G total	**50**	**3**	**1**	**2**	**44**	**21**	**6**	**50**	**20**

Source: Field work.

4.1.2 Morphological characterisation of African yam germplasm in North – central Nigeria

Morphological characterisation of African yam germplasm genotypes showed variation in different traits within and among the genotypes. The highest number of stem per plant (NSPP) was recorded in NGr.024 (3.90). This value was significantly different at ($p<0.05$) from the values of all other genotypes (Table 4.4), while the least number of stem per plant (1.30) was obtained in BNr.059 and NGr.001. This value differ significantly from the value of all other genotypes. Significant highest and least number of internode per plant was recorded in BNr.063 and FCr.079, respectively with average value of 15.80 and 7.30 internodes, respetively. Similary, significant highest internode lenght 25.47cm was recorded BNr.063, while the least 8.07cm was obtained in NGr.024. This highest value obtained in BNr.063 was not significant to the value of 22.09cm and 22.64cm recorded in KWr.134 and NGr.037, respectively.

The highest petiole length (PL) was obtained from genotype BNd.030 (12.77 cm). This value was significantly different at ($p<0.05$)with petiol length of all other genotypes. The least petiol length value 4.05cm was recorded from BNr.056, which was not significantly different from the values of BNr.054 (5.17 cm), BNr.051 (5.57 cm), BNr.059 (6.21 cm), BNr.063 (5.43 cm), BNr.067 (4.51 cm), KGr.006 (5.90 cm), NGr.008 (5.97 cm), NGr.038 (5.79 cm) and NSr.097 (5.14 cm). The highest number of leaf per plant (NLPP) was recorded from genotype BNr.063 (655.30). This value was significantly different from all other values, while the least number of leaf per plant (NLPP) was recorded from NGb.019 (34.10). This was significantly different from all other values recorded. The highest number of branch per plant (NBPP) (70.40) was recorded from KGr.006. This value was significantly different from all other values recorded, while the least value recorded (11.10) obtained from NGa.033 was significantly different from other values. Furthermore, genotype BNr.063 have the highest stem length (551.43 cm), this stem length was significantly the same with those of KGr.043, NGr.001 and NGr.022 (339.82 cm,

367.90 cm, and 340.73 cm), respectively. In addition, the maximum auxiliary number of branch per plant (ANBPP) was recorded from genotype KGr.043 (24.50).This value was significantly different from all other genotypes, while the least value (0.00) recorded from NGb.019 was different significantly from other values. Similarly, the least number of roots per plant was obtained from NGr.020 (5.60). This was different significantly from values of other genotypes, while the highest number of roots per plant was recorded from genotype KWr.134 (19.60). This value was the same significantly with those of BNr.071 and NGr.022 (18.80, and 19.40), respectively.

Table 4.4: Morphological Parameters of 32 Selected Cultivated Yam Landraces in North Central Nigeria

Parameters	NSPP	NIPP	IL	PL	NLPP	NBPP	SLPP	ANBPP	NRPP
BNa.054	1.80±0.25^{cde}	9.70±0.50^{bc}	13.98±1.09^{c}	5.17±0.24^{a}	161.20±4.07^{bc}	27.60±4.23^{de}	229.28±29.31^{g}	1.20±0.36^{ab}	10.60±0.34^{de}
BNd.030	1.40±0.16^{ab}	8.10±0.75^{ab}	15.17±1.03^{cd}	12.77±1.02^{h}	63.60±5.66^{b}	14.30±1.47^{abc}	188.21±25.14^{e}	7.00±1.32^{cd}	13.00±1.44^{fg}
BNr.051	1.60±0.22^{abc}	10.80±0.61^{c}	17.55±0.99^{d}	5.57±0.20^{a}	269.10±46.56^{e}	51.60±7.42^{ij}	120.17±16.62^{ab}	13.20±1.29^{hij}	9.60±0.34^{cd}
BNr.056	1.60±0.22^{abc}	9.80±0.89^{bc}	11.61±0.64^{c}	4.05±0.34^{a}	208.90±25.75^{d}	37.20±3.58^{efg}	167.37±24.84^{d}	8.80±1.01^{de}	10.20±1.40^{de}
BNr.059	1.30±0.15^{a}	10.10±1.13^{bc}	16.09±1.55^{cd}	6.21±0.36^{a}	188.50±29.09^{cd}	39.40±4.36^{fgh}	118.41±21.19^{ab}	11.20±1.26^{efg}	8.20±0.39^{bc}
BNr.063	1.70±0.21^{cd}	15.80±1.13^{g}	25.47±1.70^{j}	5.43±0.27^{a}	655.30±176.42^{i}	58.60±7.67^{j}	551.43±103.64^{j}	23.00±3.20^{mn}	18.30±2.15^{jk}
BNr.065	2.70±0.30^{ef}	9.40±0.69^{bc}	13.95±1.50^{cd}	4.91±0.23^{bc}	112.00±10.59^{b}	17.70±2.41^{bcd}	144.28±20.06^{bcd}	12.80±1.16^{fg}	13.80±1.16gh
BNr.067	1.70±0.21^{cd}	9.80±0.57^{bc}	18.39±1.66^{e}	4.51±0.23^{a}	241.90±26.95^{de}	37.70±3.74^{efg}	212.66±10.69^{ef}	13.60±1.35^{hijk}	14.20±0.95^{ghi}
BNr.071	1.50±0.17^{ab}	11.70±0.86^{cd}	20.13±0.34^{h}	6.21±0.37^{ab}	153.20±10.13^{bc}	18.20±1.06^{bcd}	177.18±3.53^{de}	15.20±1.44^{ijk}	18.80±0.77^{k}
BNr.083	2.10±0.28^{ef}	12.70±0.97^{d}	22.58±1.22^{i}	7.00±0.47^{ab}	160.60±28.06^{bc}	18.70±2.20^{bcd}	232.69±15.56^{gh}	12.50±0.76^{ghi}	12.20±0.25^{efg}
FCr.079	2.70±0.21^{ef}	7.30±0.75^{a}	11.25±0.56^{ab}	4.13±0.24^{ab}	173.10±15.75^{cd}	50.30±5.46^{hij}	158.50±15.74^{bc}	16.80±1.24^{jkl}	12.00±0.56^{ef}
KGr.003	1.80±0.20^{cde}	8.50±0.85^{ab}	19.61±1.07^{f}	8.66±0.54^{b}	342.30±27.53^{fg}	59.00±4.46^{j}	252.70±22.14^{h}	17.20±1.45^{jkl}	13.40±0.45^{g}
KGr.006	2.60±0.31^{ef}	11.20±0.55^{cd}	21.96±1.28^{g}	5.90±0.29^{a}	436.20±41.10^{gh}	70.40±3.97^{k}	244.84±13.43^{g}	15.50±1.26^{ijk}	7.40±0.50^{ab}
KGr.043	2.60±0.34^{ef}	12.40±0.45^{d}	13.21±0.94^{a}	7.10±0.60^{ab}	337.60±34.53^{f}	50.40±4.92^{hij}	339.82±20.34^{i}	24.50±1.82^{n}	9.60±0.91^{cd}
KGr.121	1.90±0.28^{cde}	9.30±0.68^{b}	18.74±1.23^{e}	4.59±0.58^{ab}	110.00±11.22^{b}	22.00±1.55^{bcd}	94.10±9.04^{ab}	12.60±1.15^{ghi}	11.50±0.81^{def}
KWr.134	1.80±0.25^{cde}	10.80±0.77^{c}	22.09±2.66^{i}	9.09±3.93^{efg}	154.80±12.14^{bc}	23.10±2.01^{bcd}	146.83±22.61^{bcd}	16.50±1.82^{jk}	19.60±1.54^{k}
Nga.033	2.20±0.29^{ef}	9.40±0.76^{b}	12.57±1.35^{c}	9.55±0.68^{g}	51.70±6.69^{ab}	11.10±1.89^{ab}	79.60±7.05^{a}	1.10±0.35^{ab}	13.80±1.31^{gh}
NGb.019	1.50±0.17^{ab}	10.10±0.97^{c}	14.09±1.24^{b}	6.97±0.29^{d}	34.10±8.43^{a}	3.60±0.40^{a}	133.13±6.36^{abc}	0.00±0.00^{a}	8.20±0.39^{bc}
NGd.031	1.40±0.16^{ab}	9.70±0.79^{bc}	18.46±1.10^{d}	9.29±0.53^{fg}	70.40±7.01^{b}	12.40±1.48^{bc}	134.59±9.53^{abc}	5.60±0.90^{cd}	14.50±1.59^{ghi}
NGr.001	1.30±0.15^{a}	9.90±0.62^{bc}	19.53±1.38^{f}	7.81±0.50^{ab}	184.30±16.62^{cd}	28.90±1.70^{def}	367.90i±46.89^{i}	11.70±0.63^{efg}	15.10±1.22^{hi}
NGr.008	2.10±0.23^{ef}	12.50±0.97^{d}	19.54±0.67^{f}	5.97±0.37^{a}	192.60±18.63^{d}	23.20±1.60^{cd}	220.98±27.91^{f}	9.60±0.54^{def}	17.80±0.68^{j}
NGr.017	1.60±0.22^{abc}	13.20±1.20^{e}	18.98±2.47^{e}	4.67±0.32^{ab}	272.40±12.30^{e}	28.50±2.01^{def}	151.50±13.51^{bcd}	14.20±1.25^{ijk}	16.20±1.58^{i}
NGr.020	2.60±0.43^{ef}	14.80±1.06^{f}	20.84±0.90^{h}	8.39±3.74^{b}	171.10±25.00^{c}	22.90±3.01^{bcd}	185.90±13.57^{e}	17.80±1.37^{kl}	5.60±0.34^{a}
NGr.021	1.80±0.29^{cde}	9.10±0.64^{bc}	18.40±2.09^{e}	6.02±0.37^{ab}	98.10±18.05^{b}	19.60±3.21^{bcd}	143.83±27.65^{bcd}	11.80±1.18^{efg}	18.40±0.62^{jk}
NGr.022	1.40±0.16^{ab}	11.90±0.99^{cd}	20.30±0.68^{h}	7.27±0.57^{ab}	478.70±62.27^{h}	27.20±2.24^{de}	340.73±40.57^{i}	20.20±1.24^{lm}	19.40±0.81^{k}

NGr.023	1.60±0.22^{abc}	9.70±0.50^{bc}	17.15±1.21^{d}	6.28±0.31^{ab}	160.50±12.25^{cd}	12.60±1.29^{abc}	125.19±16.87^{ab}	12.80±1.14^{hij}	15.00±1.61^{hi}
NGr.024	3.90±0.38^{g}	8.30±0.73^{ab}	8.07±0.66^{ab}	4.16±0.23^{ab}	51.20±8.41^{ab}	11.40±1.66^{ab}	51.71±9.85^{a}	4.20±0.49^{bc}	12.20±1.55^{efg}
NGr.028	2.80±0.49^{ef}	11.40±1.03^{cd}	17.29±1.18^{d}	7.29±0.60^{ab}	337.10±45.62^{f}	46.20±5.01^{ghi}	172.93±23.00^{de}	18.00±1.35^{l}	16.40±1.67^{i}
NGr.037	1.50±0.22^{ab}	10.70±1.13^{bc}	22.64±2.15^{i}	8.64±0.75^{e}	211.40±26.80^{d}	41.30±6.20^{ghi}	204.50±23.01^{ef}	12.00±1.14^{efg}	18.60±0.97^{jk}
NGr.038	2.30±0.30^{ef}	10.30±0.70^{c}	20.09±1.89^{h}	5.79±0.30^{a}	239.00±83.72^{e}	23.70±3.13^{cd}	127.93±8.22^{ab}	15.40±2.24^{ijk}	18.40±0.91^{jk}
NSr.027	1.60±0.22^{abc}	12.20±1.22^{d}	14.02±1.45^{b}	4.48±0.20^{ab}	155.90±21.36^{bc}	23.00±1.83^{bcd}	145.95±18.79^{bcd}	12.30±1.32^{fgh}	11.20±1.23^{def}
NSr.097	2.50±0.40^{ef}	10.80±0.80^{c}	18.38±1.68^{d}	5.14±0.63^{a}	205.20±23.66^{d}	22.90±1.77^{bcd}	162.27±13.34^{cd}	14.50±1.18^{ijk}	13.40±1.19^{g}

Values are Mean ± Standard Error of mean. Value with the same superscript letter(s) along the column are not significantly different at $P < 0.05$.

Note:

NSPP – Stem number per plant, NIPP- number of Internode per plant, IL-Internode length, PL-Petiole length, NLPP-Leaf number per plant, NBPP-Number of Branch per plant, SLPP- Stem length per plant, ANBPP-Auxillary number of branch per plant, NRPP- Number of Root per plant.

4.1.3 Yield parameters of 32 selected African yam landraces in North Central Nigeria

A wide range of variation in yield traits was recorded among the genotypes. The number of tuber per plant recorded ranges from 1.00 to 13.60 (Table 4.5). The highest number of plant tuber was 13.60 recorded in genotypes NGb.019 was significantly different ($P < 0.05$) from the values of all other genotypes. The least value was 1.00 obtainedin NGa.033; this was significantly different ($P < 0.05$) from the values of all other genotypes. Similarly, the tuber length (TL) varied significantly ($P<0.05$); the highest tuber length recorded was accessions NGa.033 (68.98 cm); this value was significantly different from the values of all other genotypes. However, KGr.003 (55.10cm), BNr.063 (51.52 cm), and NGr.022 (51.25 cm), were not significantly different from one another. Meanwhile, the least TL (3.40 cm) obtained in NGb.019 was significantly different ($P<0.05$) from the values of other genotypes (Table 4.5).

The highest tuber breath (TB) (24.60 cm) was recorded from genotype BNr.063, this value was significantly different ($P<0.05$) from the values of all other genotypes.The least value (6.34 cm) obtained from FCr.079, which was significantly different from the value of other genotypes. Furthermore, the highest tuber weight (TW) was recorded in genotype NGr.017 with the value of (34.68 kg); this value was different significantly ($P<0.05$) from the weight of all other genotypes.The least tuber weight value (0.85 kg) recorded from NGb.019, was significantly different from the values of other genotypes, except for those of NGr.021 and NGr.020 with the value of 20.80 kg and 21.30 kg, respectively. Subsequently, the highest leaf index measured (182.90 cm) obtained from NGa.033 this was followed by genotype KGr.043 with (170.31 cm). These values were significantly different from one another and from the values of all other genotypes.

Similarly, the least leaf index (39.87 cm) was recorded from FCr.079. This value was significantly different from the values of all other genotypes.

Table 4.5: Yield Parametersof 32 selected African Yam Landraces in North Central Nigeria

Genotypes	Tuber number per heap	Tuber length(cm)	Tuber breath(cm)	Tuber weight(kg)	Leaf length (cm)
NGr.001	2.00±0.26^{c}	35.06±2.00^{ef}	12.36±0.74^{bc}	17.84±0.59^{d}	91.25±4.31^{bc}
KGr.043	3.40±0.27^{e}	42.86±1.81^{f}	19.72±1.02^{de}	17.30±0.74^{d}	170.31±7.44^{g}
KGr.003	2.20±0.25^{c}	53.10±1.36^{gh}	20.20±0.55^{de}	22.68±1.09^{f}	72.29±6.01^{bc}
KGr.006	2.60±0.27^{cd}	40.40±3.18^{ef}	16.40±0.34^{cd}	30.34±1.74^{h}	44.10±5.76^{ab}
NGr.008	2.40±0.16^{bcd}	32.12±1.44^{e}	16.66±1.67^{cd}	17.98±0.51^{d}	83.20±0.99^{bc}
BNr.059	3.20±0.25^{e}	39.86±1.76^{ef}	20.62±0.96^{de}	18.20±0.69^{de}	71.99±10.46^{bc}
BNr.063	1.80±0.25^{bc}	51.52±3.58^{gh}	24.60±1.61^{e}	33.66±0.65^{i}	64.18±7.68^{abc}
BNr.067	3.60±0.34^{e}	32.70±1.85^{e}	13.96±0.98^{bc}	13.92±0.47^{b}	52.24±7.12^{ab}
NGr.020	2.00±0.21^{c}	44.24±1.87^{fg}	19.40±0.99^{de}	21.30±1.22^{a}	64.77±6.92^{abc}
NGr.021	2.00±0.21^{c}	41.46±2.08^{f}	20.94±0.46^{de}	20.80±0.46^{a}	113.01±13.37^{cd}
NGr.022	2.20±0.25^{c}	51.25±3.80^{gh}	20.04±1.06^{de}	29.10±1.84^{h}	93.77±7.81^{bcd}
NGr.023	1.60±0.16^{b}	32.16±1.05^{e}	16.72±1.18^{c}	17.82±0.68^{d}	105.43±16.02^{bcd}
BNr.071	3.00±0.30^{e}	31.20±1.57e	17.06±0.78^{cd}	11.80±15.81^{j}	88.54±9.77^{bc}
NGr.028	2.20±0.25^{c}	43.02±2.75^{f}	17.48±0.81^{cd}	19.14±0.90^{e}	99.33±12.74^{bcd}
BNr.083	2.00±0.21^{c}	44.92±2.69^{fg}	18.06±0.38^{d}	27.22±1.09^{g}	81.92±14.81^{bcd}
NGr.038	3.00±0.21^{e}	28.18±0.79^{d}	16.34±1.87^{cd}	17.18±0.84^{d}	73.13±9.32^{bc}
NGr.037	2.60±0.34^{bcd}	38.94±2.49^{ef}	20.22±0.54^{de}	23.04±1.12^{f}	75.91±13.54^{bc}
BNr.051	3.80±0.25^{ef}	27.20±1.17^{d}	16.70±1.11^{cd}	18.38±0.94^{de}	119.58±8.41^{cd}
NSr.027	2.20±0.25^{c}	38.00±2.05^{ef}	19.78±0.67^{d}	26.54±0.67^{g}	72.38±10.08^{bc}
BNr.065	3.60±0.45^{e}	25.58±1.06^{d}	13.84±1.04^{bc}	20.54±0.74^{ef}	78.16±10.27^{bc}
NSr.097	1.60±0.16^{b}	29.96±1.36^{de}	18.50±0.86^{d}	21.72±1.09^{f}	92.32±10.26^{bcd}
KWr.134	2.20±0.13^{c}	41.24±1.23^{f}	18.20±0.89^{d}	26.16±1.62^{g}	109.64±7.46^{bcd}
BNd.030	2.90±0.23^{d}	10.66±0.63^{b}	10.90±0.66^{b}	16.80±0.62^{c}	123.59±14.97^{fg}
NGd.031	2.40±0.16^{bcd}	10.60±0.63^{b}	11.30±1.35^{b}	17.40±0.74^{d}	86.08±8.10^{bcd}
NGa.033	1.00±0.00^{a}	68.98±8.51^{i}	11.24±0.67^{b}	17.38±0.58^{d}	182.90±29.20^{h}
BNa.054	5.00±0.21^{g}	44.56±2.04^{fg}	13.90±1.23^{bc}	18.24±0.99^{de}	148.55±20.39^{efg}
NGr.024	4.00±0.30^{f}	13.12±1.22^{bc}	10.52±1.02^{b}	12.18±0.46^{b}	51.80±1.96^{ab}
BNr.056	4.20±0.44^{f}	32.66±1.77^{e}	14.84±2.19^{bc}	15.84±1.24^{c}	113.83±15.07^{cd}
NGb.019	13.60±1.20^{h}	3.40±0.38^{a}	12.46±1.14^{b}	0.85±0.06^{a}	153.17±28.10^{fgh}
NGr.017	1.50±0.17^{b}	41.90±2.65^{f}	21.16±2.32	34.68±2.07^{i}	94.34±5.49^{bcd}
KGr.121	2.60±0.31^{bcd}	19.20±0.57^{c}	17.16±1.43^{cd}	21.50±1.26^{f}	72.51±5.89^{bc}
FCr.079	2.60±0.22^{bcd}	10.58±0.81^{b}	6.34±0.68^{a}	11.48±0.62^{b}	39.87±3.54^{a}

Values are Mean ± Standard Error of mean. Values with the same superscript along the column are not significantly different at $P < 0.05$.

4.1.4 Principal component analysis (PCA)

The principal components analysis of the morphological traits was grouped into fourteen (14) components to give 100 % variability among the accessions studied (Table 4.6). The significant Eigen value were recorded for the first thirteen (13) components with the values of 22946.10, 2724.92, 1144.87, 214.82, 98.05, 87.37, 29.59, 15.76, 10.53 6.08, 2.60, 1.97, and 1.55 for PC 1 to 13 respectively. The first four (4) principal components contributed to 99.07 % of variability. One hundred percent (100 %) variability was also recorded in the first thirteen (13) components for the evaluated traits in the yam accessions. The variability in PCI (84.10 %) and PC2 (9.99 %) were due to the leaf petiole length per plant (LPP) and stem length per plant (SLPP), with component value of 0.86 cm and 0.50 cm respectively for PC1 and 0.45 and 0.84 respectively for PC2. In addition, auxiliary branch per plant (ABPP) and Roots number per plant (RPP) were the major traits attributed to PC7, PC8, and PC10. In the same vein, tuber breath (TB) was the main trait that contributed to the higher percentage variance in PC7, PC8, PC9 and PC10. Internode length per plant (IPP) was the trait that contributed to PC11, PC12 and PC13 with percentage (1%) variance of 99.98% and 100% respectively.

Similarly, leaf index and length measurement and tuber weight were the major contributed traits to PC3 and PC4 with component values of 0.97 cm and 0.94 cm respectively. Furthermore, tuber length and branch number per plant contributed to PC5 and PC6 trait with the component value of 0.94 and 0.93 respectively. In addition, in PC7, the contributed traits were due to auxiliary branch per plant with the value of 0.80; in the same vein, Roots number per plant and tuber breath with the component value of 0.39 and 0.84 were the major in trait in PC7 and PC8 respectively. Furthermore, tuber breath was the major trait with the value of 0.39 and 0.44 that contributed to PC7 and PC8 respectively. The contributed traits in PC9 and PC10 were due to internode length with the value of 0.87 and 0.30 respectively; meanwhile, tuber length per plant and petiole length are the contributed trait in PC11 and PC12 with the component value of 0.94 and 0.93 respectively.

Table 4.6: Principal Component Analysis of 32 Selected Genotypes of African Yam in North-central Nigeria

Parameters	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10	PC 11	PC 12	PC 13	PC 14
SPP	0.00	0.00	0.00	-0.01	0.01	0.01	0.03	0.01	-0.09	-0.04	0.10	-0.04	-0.05	0.99
IPP	0.01	0.00	0.00	0.03	0.01	-0.04	0.03	-0.04	0.10	0.01	0.26	-0.20	0.93	0.02
IL	0.01	0.00	-0.02	0.07	0.02	-0.06	0.11	0.21	0.87	-0.30	0.08	-0.22	-0.16	0.04
PL	0.00	0.01	0.01	0.01	0.02	0.00	-0.01	0.11	0.19	-0.16	-0.08	0.93	0.21	0.07
LPP	0.86	-0.48	0.11	0.01	-0.06	-0.12	-0.02	0.00	-0.02	-0.01	-0.01	0.01	0.00	0.00
BPP	0.09	-0.10	0.03	-0.19	0.17	0.93	-0.10	0.05	0.13	0.14	-0.03	-0.02	0.03	0.01
SLPP	0.50	0.84	-0.19	-0.04	0.00	0.04	-0.01	0.00	0.00	0.01	0.00	-0.01	0.00	0.00
ABPP	0.03	-0.02	0.00	0.03	0.05	0.19	0.80	-0.21	-0.21	-0.45	0.13	0.02	-0.04	-0.08
RPP	0.01	0.00	-0.01	0.08	0.03	-0.02	0.39	0.84	-0.13	0.35	-0.02	-0.01	0.03	-0.01
TPP	0.00	0.00	0.01	-0.04	-0.09	0.02	-0.09	0.03	-0.02	0.14	0.94	0.16	-0.22	-0.09
TL	0.04	0.01	0.09	0.24	0.94	-0.12	-0.10	0.00	-0.06	-0.05	0.08	0.00	-0.04	-0.02
TB	0.01	-0.01	0.00	0.08	0.07	-0.08	0.39	-0.44	0.32	0.72	-0.06	0.11	-0.04	0.06
TW	0.01	0.01	-0.05	0.94	-0.22	0.24	-0.10	-0.03	-0.04	-0.01	0.01	0.01	-0.02	0.01
LFM	-0.01	0.23	0.97	0.02	-0.10	0.02	0.02	0.00	0.01	0.00	-0.01	-0.02	0.00	0.00
Eigenvalue	22946.10	2724.92	1144.87	214.82	98.05	87.37	29.59	15.76	10.53	6.08	2.60	1.97	1.55	0.26
% variance	84.10	9.99	4.20	0.79	0.36	0.32	0.11	0.06	0.04	0.02	0.01	0.01	0.01	0.00
CV	84.10	94.09	98.28	99.07	99.43	99.75	99.86	99.92	99.95	99.98	99.99	99.99	100.00	100.00

Note: Stem number per plant (SPP), Internode number per plant (IPP), Internode length (IL), Petiole length (PL), leaf number per plant (LPP), branch number per plant (BPP), stem length per plant (SLPP), Auxiliary Branch number per plant (ABPP), root number per plant (RPP), tuber number per plant (TPP), tuber length (TL) tuber breath (TB) leaf index (LFM).

4.1.5 Cluster analysis

The dendrogram summarises the similarity and dissimilarity of the fifty (50) genotypes of Africa yam across North- central state of Nigeria based on agro-morphological traits (Figure 4.1). The genotypes were clustered into Nine (9) major groups with the highest number of genotypesin cluster eight (8) containing nineteen (19) genotypes of the total collectedacross the states. Four of these were from Niger, Nine (9) in Benue, Federal Capital territory (FCT) Abuja two (2) and two (2)each from Kwara and Nasarawa, respectively. Thus, all genotypes grouped under this cluster were of the same species *(D. rotundata)* except one *(D. alata)* recorded from Benue (BNa.054). Similarly, cluster 6 forms the second larger cluster group containing 10 of the total genotypes. This group contains three different genotypes (*D. rotundata, D. dumetorum* and *D. bulbifera*). This revealed strong interrelationship among the genotypes in these groups. Similarly, cluter 4, cluter 5 and 9 had one genotype each of the same species expect genotypes in cluter 5 with different spieces. Furthermore, cluster one (1) and three (3) contain two genotypes each of the same species from Benue, Niger and Kogi, respectively. The three cultivars grouped in clusters 6 were obtained from Benue, Kogi and Niger state, respectively.

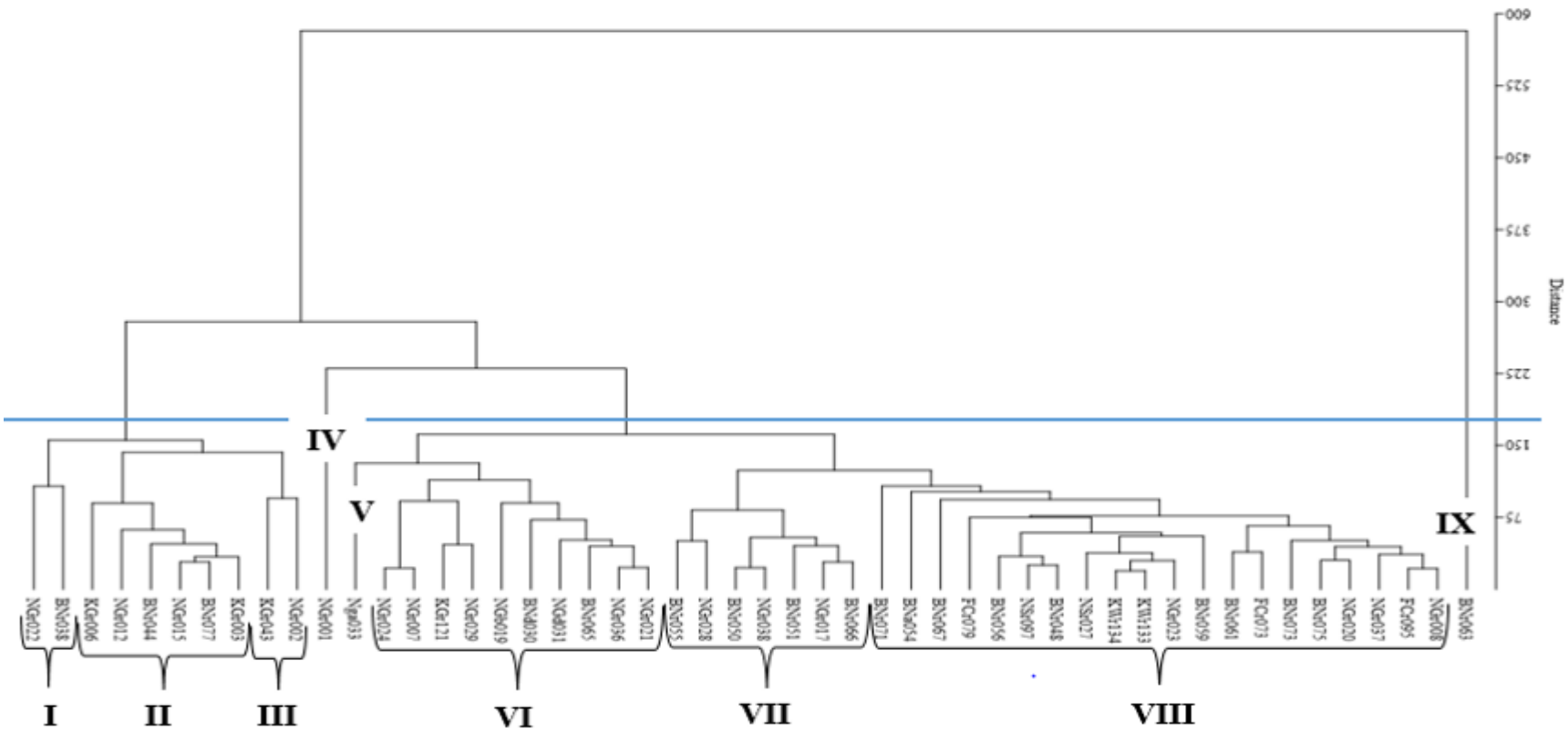

Figure 4.1: UPGMA Dendogram of Genetic Diversity of African Yam using Agro-morphological and Biochemical Traits

4.1.6 Correlation of morphological and yield parameters of cultivatedyam genotypes in north central Nigeria

The results obtained from correlation of agro-morphological parameters showed a significant and positive correlation between the parameters considered (Table 4.7), except for the number of stem per plant (NSPP) and petiole length (PL) that were not significantly.Number of tuber per plant (NTPP) was significant and negatively correlated with internode length (IL), number of leaf per plant (NLPP), number branches per plant (NBPP), axillary branch per plant (ABPP) and number roots per plant (NRPP); with the correlation value of -0.18, -0.16, -0.15, -0.34 and -0.20, respectively at $P < 0.01$ and with number of internode per plant (NIPP) ($P < 0.05$; $r= -0.11$). Similarly, with the exception of number of stem per plant and petiole length, tuber length (TL) was positive and significantly correlated, with NTPP,NIPP, IL, NLPP, NBPP, stem length per plant (SLPP), ABPP with the value of 0.45, 0.32, 0.27, 0.41, 0.27, 0.26, and 0.22, respectively at $p<0.02$ and NRPP at $p<0.05$, $r=0.16$. The result also showed that tuber weight (TW) has negative correlation with all the parameters studied except for axillary branch per plant (ABPP) and number root per plant (NRPP) which has positive significant correlation with the value of 0.17 and 0.17 respectively.

Table 4.7: Correlation of Morphological and Yield Parameters of 32 Selected Yam Landraces in North Central Nigeria

	NSPP	NIPP	IL	PL	NLPP	NBPP	SLPP	ABPP	NRPP	NTPP	TL	TB	TW	LFM
SPP	1.00													
NIPP	0.03^{ns}	1.00												
IL	-0.11^{ns}	0.23^{**}	1.00											
PL	-0.15^{**}	-0.04^{ns}	0.15^{**}	1.00										
NLPP	0.01^{ns}	0.23^{**}	0.24^{**}	-0.04^{ns}	1.00									
NBPP	0.04^{ns}	0.09^{ns}	0.12^{*}	-0.07^{ns}	0.64^{**}	1.00								
SLPP	-0.11^{ns}	0.23^{**}	0.26^{**}	0.07^{ns}	0.48^{**}	0.40^{**}	1.00							
ABPP	0.06^{ns}	0.23^{**}	0.25^{**}	-0.08^{ns}	0.41^{**}	0.40^{**}	0.36^{**}	1.00						
NRPP	-0.09^{ns}	0.08^{ns}	0.24^{**}	0.08^{ns}	0.07^{ns}	-0.10^{ns}	0.10^{ns}	0.12^{*}	1.00					
NTPP	-0.06^{ns}	-0.11^{*}	-0.18^{**}	-0.03^{ns}	-0.16^{**}	-0.15^{**}	-0.10^{ns}	-0.34^{**}	-0.20^{**}	1.00				
TL	-0.09^{ns}	0.32^{**}	0.27^{**}	0.11^{ns}	0.41^{**}	0.27^{**}	0.26^{**}	0.22^{**}	0.16^{*}	0.45^{**}	1.00			
TB	-0.08^{ns}	0.39^{**}	0.33^{**}	0.04^{ns}	0.35^{**}	0.22^{**}	0.30^{**}	0.43^{**}	0.22^{**}	-0.24^{**}	0.47^{**}	1.00		
TW	-0.09^{ns}	0.02^{ns}	0.12^{ns}	-0.00^{ns}	0.10^{ns}	-0.00^{ns}	0.07^{ns}	0.17^{*}	0.17^{*}	-0.15^{ns}	0.13^{ns}	0.16^{*}	1.00	
LFM	-0.06^{ns}	-0.04^{ns}	-0.10^{ns}	0.13^{ns}	-0.15^{ns}	-0.20^{**}	-0.03^{ns}	-0.13^{ns}	0.00^{ns}	0.24^{**}	0.14^{ns}	-0.08^{ns}	0.01	1.00

** = significant at P<0.01

* = significant at P<0.05,

ns = not significant

Note: Stem number per plant (NSPP), number of internode per plant (NIPP), Internode length (IL), Petiole length (PL), number of leaf per plant (NLPP), number of branch per plant (NBPP), stem length per plant (SLPP), Auxiliary Branch number per plant (ABPP), number of root per plant (NRPP), number of tuber per plant (NTPP), tuber length (TL), tuber breath (TB), Tuber length (TW,) leaf measurement (LFM).

4.1.7 Genetic parameter estimate of selected Africa yam in North central Nigeria

Genetic parameters estimated for agro morphological traits are presented in table (4.9). The result revealed high phenotypic coefficient of variance for all the characters measured. The highest genotypic variance (GV) and phenotypic variance (PV) was recorded in number of leaf per plant (NLPP) with the value of 53574.34 and 72161.09, respectively. This was followed by stem length per plant (NSPP) with the GV and PV value of29354.94 and 36931.77 each and the least was obtained from number of stem per plant (NSPP) with the GV and PV value of 0.91 and 1.62 each. Besides, the petiole length (PL), tuber weight (TW), and leaf index measurement (LFM) with environmental variance (EV) valueof 11.23, 521.47 and 2017.34, respectively, were higher than the GV (9.33, 326.75 and 1307.51) estimated.The GV for most of the traits observed were higher than their correspondent EV. High coefficient variability (value > 30) was obtained for both genotypic and phenotypic variances in all the parameters measured except for tuber breadth (TB) with genotypic coefficient variance (GCV) of 29.70 %. Thus, phenotypic coefficient variance (PCV) of these characters were comparatively higher than those of GVC for all the traits studied. Broad sense heritability obtained was moderate (30 – 60 %) for NSPP (56 %), internode number per plant (NIPP) (56 %), (TW) (39 %) and LFM (39 %).High-broad sense heritability percentage was obtained (>60), with the highest value in number of tuber per plant (NTPP) (93 %) followed by tuber length (TL) with the percentage value of 92 %. In the same vein, Genetic Advance (GA) was high (> 60) for internode length with the value of 64.65 % and petiole length of 64.88 %; while all other traits were moderate with the (GA) within 30 to 60 % (Table 4.8).

Table 4.8: Estimate of the Genetic Variability and Components of Related Genetic Parameters of the Selected African Yam Genotypes in North-central Nigeria

Traits	Means	Genotype variance	Phenotypic variance	Environmental variance	Broad Sense Heritability (h^2)	Genotypic Coefficient of Variability	Phenotypic coefficient of variation	GA
SSP	1.97	0.91	1.62	0.71	0.56	48.44	64.66	74.76
NIPP	10.67	9.17	16.37	7.20	0.56	28.38	37.92	43.76
IL	17.57	44.03	63.77	19.74	0.69	37.77	45.46	64.65
PL	6.53	9.33	20.55	11.23	0.45	46.75	69.40	64.88
NLPP	208.81	53574.34	72161.09	18586.75	0.74	110.85	128.65	196.75
NBPP	29.83	852.22	980.91	128.69	0.87	97.85	104.98	187.89
SLPP	191.47	29354.94	36931.77	7576.83	0.79	89.48	100.37	164.34
ABPP	12.59	106.79	124.34	17.54	0.86	82.09	88.58	156.73
NRPP	13.64	45.17	57.36	12.19	0.79	49.26	55.51	90.05
NTPP	2.97	14.75	15.83	1.09	0.93	129.34	134.01	257.15
TL	34.29	330.81	359.56	28.75	0.92	53.04	55.30	104.81
TB	16.49	23.98	30.49	6.52	0.79	29.70	33.49	54.25
TW	23.06	326.75	848.22	521.47	0.39	78.38	126.28	100.21
LFM	93.25	1307.51	3324.85	2017.34	0.39	38.78	61.83	50.09

Note: Stem number per plant (SPP), number of internode per plant (NIPP), Internode length (IL), Petiole length (PL), number of leaf per plant (NLPP), number of branch per plant (NBPP), stem length per plant (SLPP), Auxiliary Branch number per plant (ABPP), number of root per plant (NRPP), number of tuber per plant (NTPP), tuber length (TL), tuber breath (TB), Tuber length (TW), leaf measurement (LFM)

4.1.8 Variability in stem traits of the 32 selected yam genotypes in north-central Nigeria

The genotypes exhibited high level of variability (Table 4.9). The young stem colour was heterogeneous in nature across the cultivated genotypes. The young stem colour varied from green, purplish green, brownish green, dark brown, maroon, dark green and orange green (plate I). The most abundant of these colours was green (65.65 %), with 18 recorded in *D.rotundata.* This was followed by dark brown and maroon with (9.37 %) each. The least was recorded in purplish green, brownish and orange green with 3.25 % respectively (Table 4.9). Subsequently, twinning habit was observed in all the cultivated genotypes. Predominant of twinning habit was anticlockwise twinning direction (100 %) recorded in all the genotypes (Plate II). The major matured stem colour was green, this was followed by brownish green with (34.38 %) and the least (3.15 %) recorded in publish green. Furthermore, most of the stem observed was without ridges (90.65 %). However, few others were with ridges. The absence and presence of wings was observed across the genotypes, the minimum of these (12.5 %) do not produce wings; meanwhile, maximum number (87.5 %) bear wings. Besides, spines were also examined on the stem of the genotypes; this varied from few to many. However, predominate of the genotypes (81.25 %) had few spines on their stems above base and the least (9.38 %) was recorded from stems having many spines on stem base (Plate III). Futhermore, stem branch was observed to vary from monopodia, dipodia, tyripodia and tetrapodia across the genotypes (Plate IV).

Table 4.9: Variability in Young Stem Colour of 32 selected African Yam Genotypes in North-Central Nigeria.

S/No	Traits	*D.rotundata*	*D.dumetorum*	*D.bulbifera*	*D.alata*	*Total*	*Percentage %*
1	Young stem colour.						
	Green	18	1	1	1	21	65.5
	Purplish green	-	-	-	1	1	3.15
	Brownish green	1		-	-	1	3.15
	Dark brown	3	-	-	-	3	9.38
	Maroon	3	-			3	9.38
	Dark green	2	-	-	-	2	6.25
	Orange green	-	1	-	-	1	3.15
		84.38	**6.25**	**3.15**	**6.25**	**32**	**100**
2	Twining habit and direction						
	Habit. 1. yes	27	2	1	2	32	100
	Direction 2. anticlockwise	27	2	1	2	32	100
		84.38	**6.25**	**3.15**	**6.25**	**100**	
3	Matured stem colour.						
	1 Green	10	1	1	1	13	40.65
	2 Purplish green	-	-	-	1	1	3.15
	3 Brownish green	10	1	-	-	11	34.35
	4 Dark brown	7	-	-	-	7	21.88
		84.38	**6.25**	**3.15**	**6.25**	**100**	
4	Absence/presence of ridges						
	0 absence	27	2	-	-	31	96.88
	1 presence	-	-	1	-	1	9.375
		84.38	**6.25**	**3.15**	**6.25**	**100**	
5	Absence/presence of wings						
	0 Absence	-	2	-	2	4	12.59
	1 Presence	27		1		28	87.57
		84.38	**6.25**	**-**	**6.25**	**3.15**	**100**
6	Spines on stem base						
	0 No	-	-	1	2	3	9.37
	1 Yes	27	2			29	90.65
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
7	Spines on stem above						
	3 Few	26	2	-	-	28	87.5
	7 Many	2	2	-	-	4	3.15
		84.38	**6.25**	**3.15**	**6.25**	**100**	

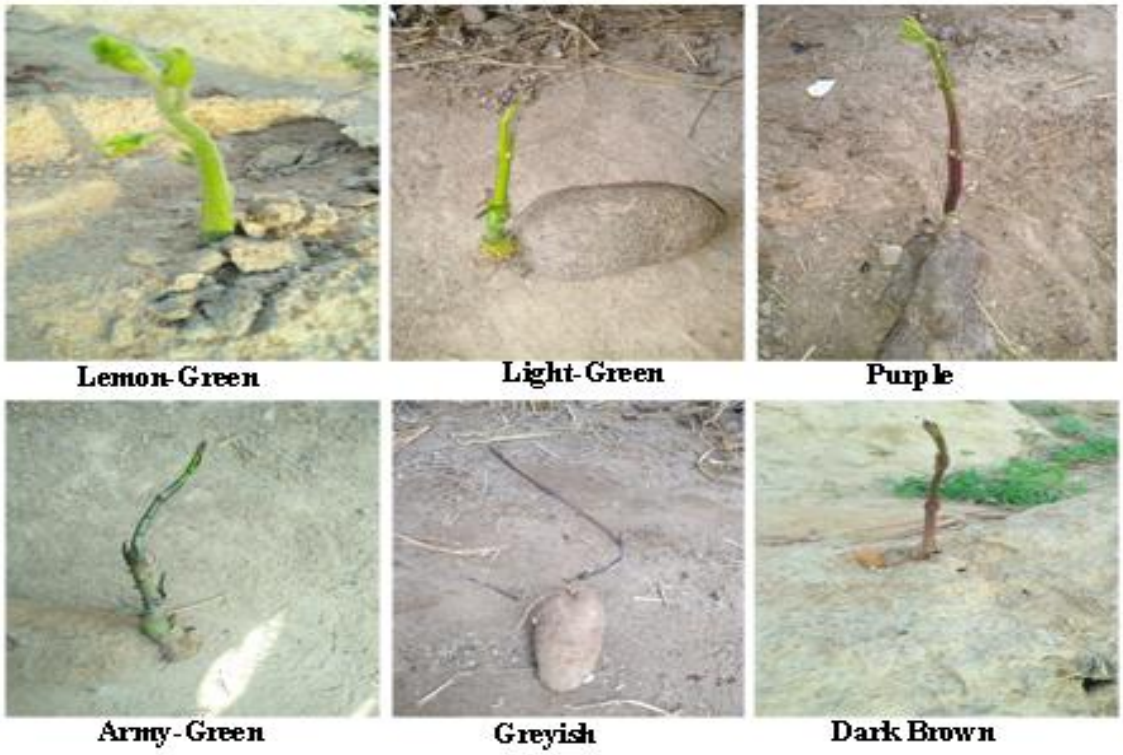

Plate 1: Variability in Young Stem Colour from Selected Yam Genotype in North Central Nigeria

Young **Matured**

Plate II: Twinning Direction in Young and Matured Stem of Selected African Yam Genotype in North-Central Nigeria.

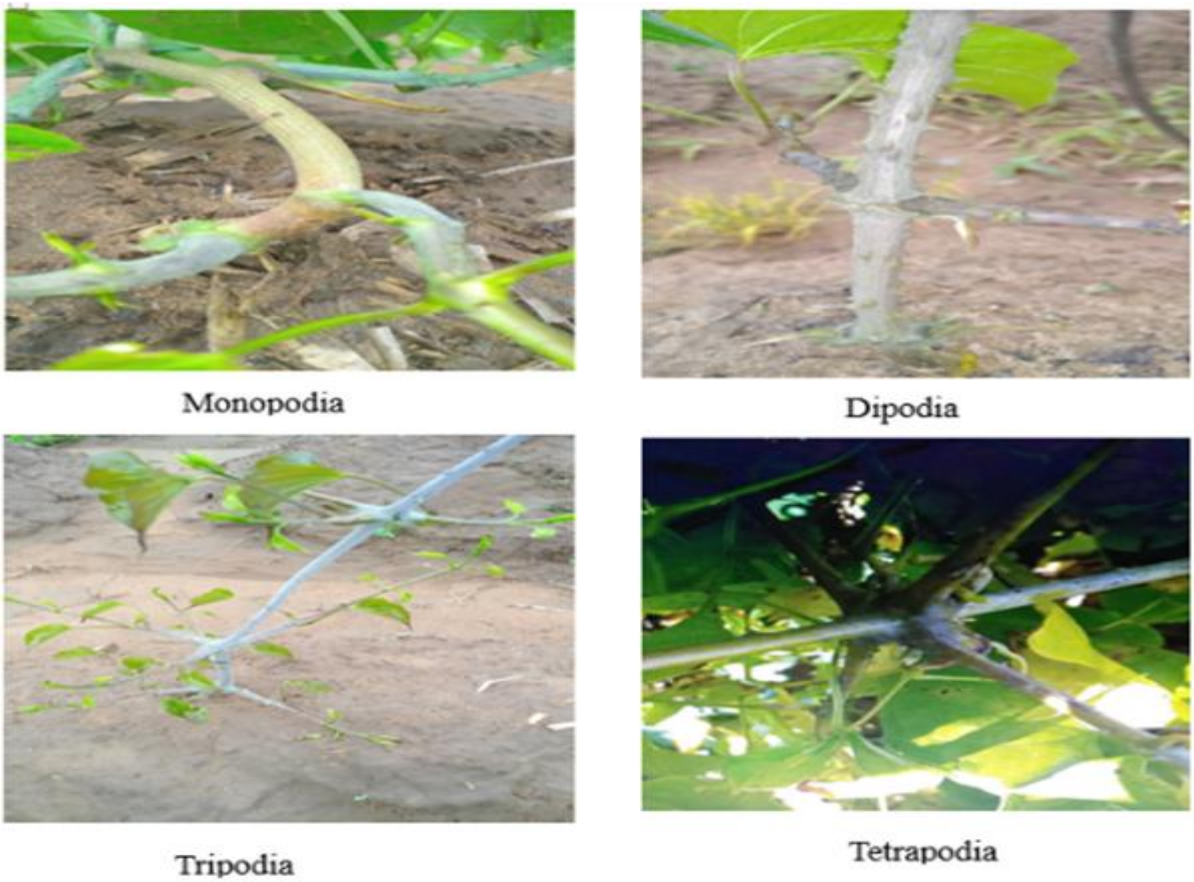

Plate III: Variability in Stem Branch in Selected African Yam Genotype in North-Central Nigeria

4.1.9 Variability in leaf types and leaf traits of 32 selected African yam in north central Nigeria.

The arrangement of leaves on the stem was examined (Table 4.10), the dominant matured leaf position on the stem recorded was opposite arrangement (100 %). Similarly, leaf type varied from simple to compound (Plate IV). The commonest type of leaves obtained was simple leaf with (93.75 %); followed by compound leaf (6.25 %). Furthermore, four leaf colours (maron, light green, dark green and pale grey) were observed (Plate V), the most abundant of these was light green colour with (87.5 %), and the least was dark green colour (12.5 %). The shape of the leaves also varied from cordate, cordate long, cordate broad and sagitted long (Plate VI). The most widespread leaf shape obtained was the cordate shape (68.72 %), this was followed by

cordate long and cordate broad shape with (12.5 %) each; and the least was sagitted long. In the same vein, two leaf apex shape was observed, predominant of these were acute shape recorded in twenty-five (25) *D. rotundata* genotype; and the least was the obtuse shape with (6.25 %) (Table 4.10). Furthermore, the most abundant petiole colour recorded was greenish (93.75 %) and the least was all green with purple colour at both end.

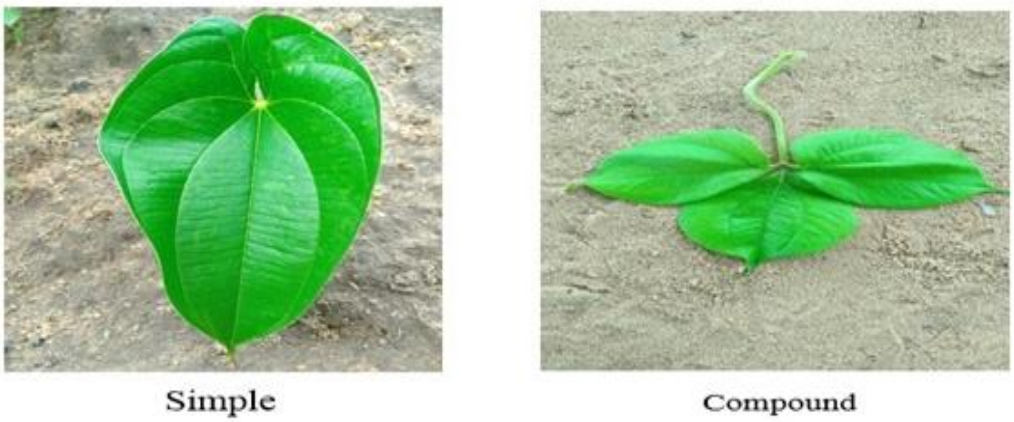

Plate IV: Variability in Leaf Types of the Yam Genotypes in North Central Nigeria

Plate V: Variability in Leaf Colour of the Yam Genotypes in North Central Nigeria

Table 4.10 Variability in Leaf Type and Leaf Traits of 32 Selected African Yam in North Central Nigeria.

S/No	Traits	*D.rotundata*	*D.dumetorum*	*D.bulbifera*	*D.alata*	*Total*	*Percentage %*
1	Matured leaves position						
	2 opposite	27	2	1	2	32	100
		84.38	**6.25**	**3.15**	**6.25**	**100**	
2	Type of leaf						
	1 simple	27	-	1	2	30	93.75
	2 compound		2	-	-	2	6.25
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
3	Leaf colour						
	1 light green	23	2	1	2	28	87.5
	2 dark green	4	-	-	-	4	12.5
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
4	Leaf shape						
	1 cord ate	22	0	-	-	22	68.72
	2 cord ate long	-		1	2	3	9.38
	3 cord ate broad	3					
	4 sagittated long	2	-	-	-	2	6.25
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
5	Leaf Apex shape						
	1 obtuse	2	-	-	-	2	6.25
	2 Acute	25	2	1	2	30	93.75
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
6	Petiole colour						
	1 All green with purple at end	-	-	-	2	2	6.25
	2 Green	27	2	1	-	30	93.75
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
7	Matured leaves position						
	2 opposite	27	2	1	2	32	100
		84.38	**6.25**	**3.15**	**6.25**	**100**	
8	Type of leaf						
	1 simple	27	-	1	2	30	93.75
	2 compound		2	-	-	2	6.25
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
9	Leaf colour						
	1 light green	23	2	1	2	28	87.5
	2 dark green	4	-	-	-	4	12.5
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
10	Leaf shape						
	1 cord ate	22	0	-	-	22	68.72
	2 cord ate long	-		1	2	3	9.38
	3 cord ate broad	3					
	4 sagittated long	2	-	-	-	2	6.25
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
11	Leaf Apex shape						
	1 obtuse	2	-	-	-	2	6.25
	2 Acute	25	2	1	2	30	93.75
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
12	Petiole colour						
	1 All green with purple at end	-	-	-	2	2	6.25
	2 Green	27	2	1	-	30	93.75
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**

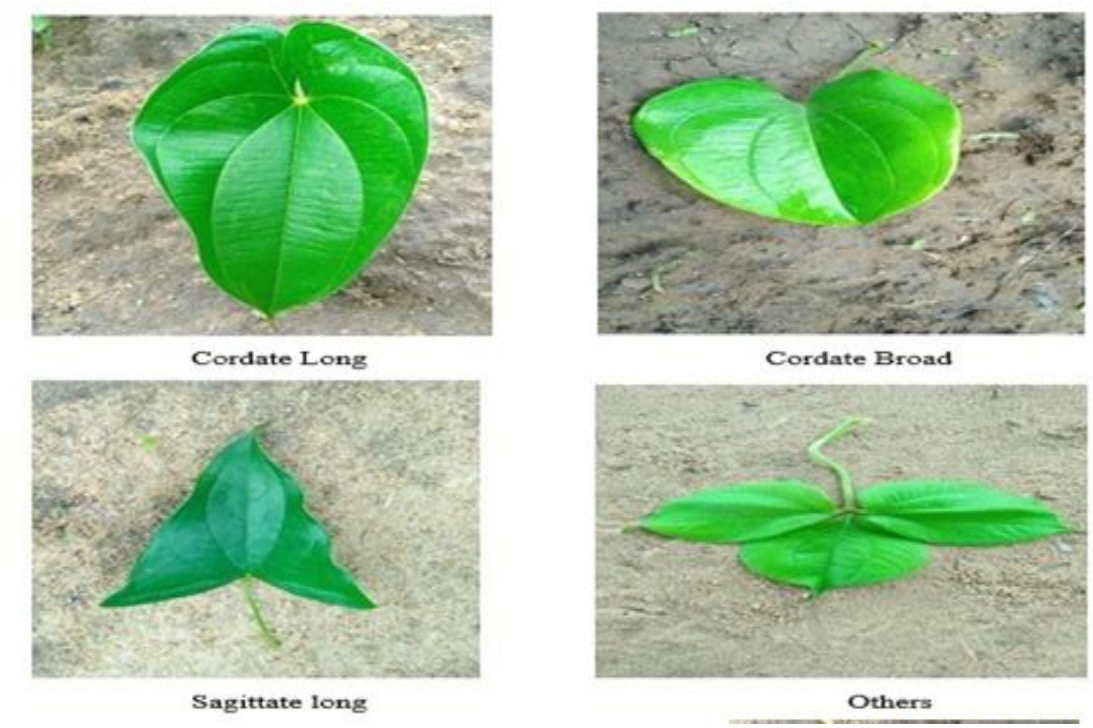

Plate VI: Variability in Leaf Shape of Yam Genotypes in North-central Nigeria

4.1.10: Variability in flower and fruit traits of 32 selected Africa yam in north central Nigeria.

The rate of flowering among the genotypes varied (No flowering, flowered in some years and flower every year) (plate VII). The most abundant of these was obtained in landraces that produced flowers every year (56.25 %) (Table 4.11). This was followed by those that do not produced flowers (37.5 %) and the least (6.25 %) was recorded from genotypes that produced flowers in some years. In addition, the major inflorescence position noted across the genotypes weredownward positioned (100 %). However, most of the inflorescence did not produce scent (100 %). Furthermore, fruit formation, fruit position and absent or present of seed was examined. It was observed that (56.85 %) was obtained in landraces that produced fruit, while (56.25 %) was recorded from genotypes that their fruit pointed downward. Thus, majority of the landraces produced seed or fruits (59.38 %) each. While the least (40.65 %) was recorded in those that do not produce fruit or seed.

Plate VII: Veriability in Flowers of the 32 African Yams in North Central Nigeria

Table 4.11: Variblility in Flower and Fruit Traits of 32 Selected African Yam North-Central Nigeria.

S/No	Traits	*D.rotundata*	*D.dumetorum*	*D.bulbifera*	*D.alata*	*Total*	*Percentage %*
1	Flowers						
	0 No flowering	11	-	-	2	13	43.75
	1 flower in some years	-	-	1	-	1	3.15
	2 Every year	16	2	-	-	18	56.25
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
2	Infloresence position						
	1 position upward	-	-	-	-	-	
	2 position downward	27	2	1	2	32	100
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
3	Inflorescence scent						
	0 Absence	27	2	1	2	32	100
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
4	Fruit formation						
	0 No	11	2	-	2	15	46.87
	1 Yes	16	-	1	-	17	53.125
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
5	Fruit position						
	1 pointing upward	-	-	-	-	-	
	2 pointing downward	30	-	2	-	32	56.25
		50	**-**	**6.25**	**-**	**56.25**	
6	Absence/presence of seed (fruit)						
	0 Absence	11	-	-	2	13	40.65
	1 presence	16	2	1	-	19	59.38
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**

4.1.11: Variability in aerial tubers traits of 32 African yam in north central Nigeria.

The absence and presence of aerial tuber was observed among the genotypes, the most abundant of this was the absence of aerial tuber with (62.5 %) and the least (37.5 %) was recorded from the stems having aerial tubers. The presence and absence of bumps was also observed across the landraces and the most abundant aerial tuber obtained were those without bumps on their skin surface. A wide range of variability was observed in flesh colour of the lower tuber part (white, yellowish white, yellow, orange and white with purple colour). The most abundant of these lower flesh colours was white with (62.5 %) and the least (3.15 %) recorded in orange and green colour each (Table 4.12).

Plate VIII: Variability in Aerial Tuber Shape on the Stem of Yam Genotypes in North-Central Nigeria

4.1.12 Variability in underground tuber traits of the 32 selected African yam.

The tuber maturity after emergence ranged (5 months, 6 month and 7 to 8 months) (Table 4.12). The widespread of these (46.88 %) was recorded in 6 months, followed by 5 months (31.25 %) and the least (21.88 %) obtained in 7 to 8 months. Similarly, the number of tubers per hill per stem varied from one, few and several. The most prevalent (43.75 %) was recorded in few tubers per hill per stem. This was followed by one tuber per hill per stem (40.65 %) Five (5) types of variability in aerial and underground tuber shape was observed among the genotypes (oval-oblong, cylindrical, flattered and irregular) (Plate VIII and IX); and the most predominate of these among underground tubers (62.5 %) was cylindrical shape, followed by flattered shape (21.88 %) and the least (6.25 %) was recorded in Elliptical shape (Plate IX). In addition, tuber branch (fork) tendency was noticed among the genotypes. The highest (31.25 %) was obtained in branched tubers, this was followed by slightly branched tubers with (21.88 %) and the least (3.25 %) was obtained in those that do not produced branch. Beside, the place where tuber branched was examined this also varied from (upper, middle and lower) (Plate X); and the most predominant (78.15 %) was recorded in genotypes that branched at the lower portion, followed by (12.5 %) obtained from landraces that branched at the upper end. While the least (6.25 %) was recorded in those that branched at the middle part of the tuber.

The presence of roots was observed on the surface of the tubers; this varied from few to many with the highest (62.5 %) obtained in genotypes with few roots on tuber surface. This was followed by (34.38 %) and the least (3.25 %) obtained from tubers without roots on their skin surface. Moreover, greater number of the landraces (100 %) were with roots on the entire tuber surface. In the same vein, the presence of cracks on tuber skin surface was observed among the genotypes with the leading (81.25 %) recorded from tuber without cracks on the skin surface. The skin colour of the tubers beneath the bark also varied from (light green, yellowish, white purple spotted, grayish milk spotted and milk) (Plate XI).

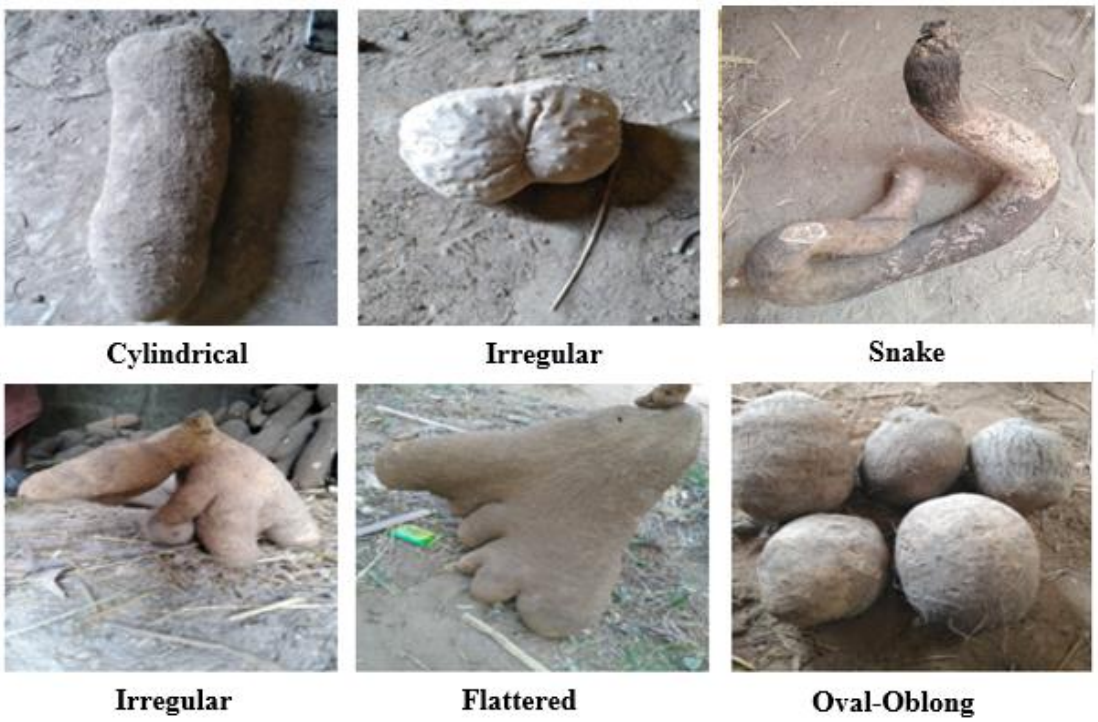

Plate IX: Variability in Tuber Shape of the Yam Genotypes in North-Central Nigeria

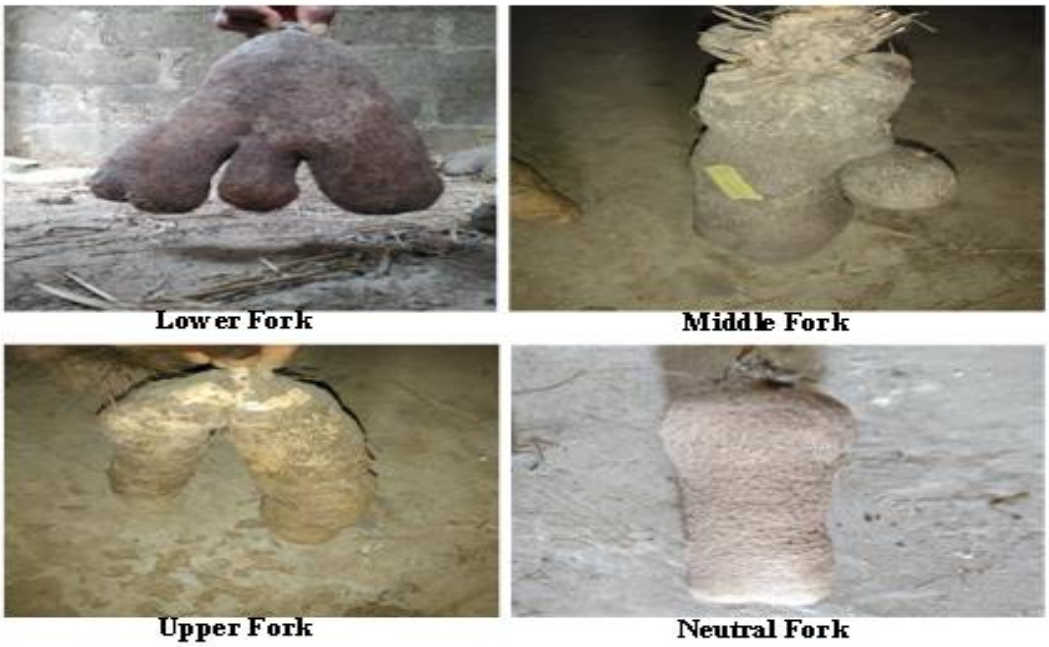

Plate X: Variability in Forking Point of the Yams in North-Central Nigeria

Table 4.12 Variability in Aerial and Underground Tubers Traits of 32 Selected African Yam in North-Central Nigeria.

S/No	Traits	*D.rotundata*	*D.dumetorum*	*D.bulbifera*	*D.alata*	*Total*	*Percentage %*
1	Absence/presence of aerial tuber(bulbis)						
	0 Absence	18	2	-	-	20	62.5
	1 presence	9	-	1	2	12	37.5
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
2	Absence/presence of bumps						
	0 Absence	27	2	-	2	31	96.875
	1 presence	-	-	1	-	1	3.15
		84.38	**6.25**	**3.15**	**-**	**100**	**100**
3	Flesh colour of flower part of tuber						
	1 white	19	-	-	1	20	62.5
	2 yellowish white	7	-	-	-	7	21.88
	3 yellow	-	2	-	-	2	6.25
	4 orange	1	-	-	-	1	3.15
	5 white with purple	-	-	-	1	1	3.15
	Green	-	-	1	-	1	3.15
		84.38	**6.25**	**3.15**	**3.15**	**100**	
4	Maturity after emergence						
	0 5months	10	-	-	-	10	31.25
	1 6months	12	2	1	0	15	46.88
	2 7-8 months	5	-	-	2	7	21.88
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
5	Number of tubers/hill						
	1 one	12	-	-	1	13	40.65
	2 few	12	1	-	1	14	43.75
	3 several	3	1	1	-	5	15.65
		84.38	**6.25**	**3.15**	**6.25**	**100**	**100**
6	Tuber shape						
	1 Elliptical	-	1	-	1	2	6.25
	2 cylindrical	19	1	-	-	20	6.25
	3 flattered	6	-	-	1	7	21.88
	4 irregular	2	-	1	-	3	9.38
		84.38	**6.25**	**3.15**	**6.25**	**100**	
7	Tendency of tuber to branch						
	1 slightly branched	18	1	-	1	20	21.88
	2 branched	8	-	-	1	10	31.25
	3 highly branched	1	-	-	-	1	3.15
	4 Absence	-	-	1	-	1	3.15
		84.38	**6.25**	**3.15**	**6.25**	**100**	

8	Place where tuber branched						
	1 upper	2	1	-	1	4	12.5
	2 middle	2	-	-	-	2	6.25
	3 lower	23	1	-	1	25	78.15
	4 Absence	-	-	1	-	1	3.15
		84.38	**6.25**	**3.15**	**6.25**	**100**	
9	Root on tuber surface						
	1 few	17	2	-	1	20	62.5
	2 many	10	-	-	1	11	34.38
	3 Absence	-	-	1	-	1	3.15
		84.38	**6.25**	**3.15**	**6.25**	**100**	
10	Place of roots on tuber						
	1 Entire	27	2	-	2	31	96.88
	2 Absence	-	-	1	-	-	3.15
		84.38	**6.25**	**3.15**	**6.25**	**100**	
11	Absence/presence of cracks on surface						
	0 Absence	22	2	0	2	26	81.25
	1 presence	5	-	1	-	6	18.75
		84.38	**6.25**	**3.15**	**6.25**	**100**	
12	Tuber skin colour beneath the bark						
	1 light green	-	-	1	-	1	3.15
	2 yellowish	5	2	-	-	7	21.88
	3 white purple spotted	-	-	-	2	2	6.25
	4 yellow purple spotted	5	-	-	-	5	15.65
	5 Greyish milky spotted	3	-	-	-	3	9.35
	6 milky	14	-	-	-	14	43.75
		84.38	**6.25**	**3.15**	**6.25**	**100**	

4.1.13: Variability in tuber skin colour beneath the back, flesh texture and oxidation colour in 32 selected African yam in north central Nigeria

The results from tuber skin colour beneath the back, flesh texture and flesh oxidation colour observed showed heterogeneity in colour across the genotypes (Plate IX). The skin colour beneath varied from yellow, greyish, green and purple. The results also revealed variation in flesh texture from 3.15 % to 68.75 % (Table 4.13) with the highest diversity (68.75 %) recorded in smooth texture, and the least (28.15 %) obtained from very grainy texture. Subsequently, flesh oxidation colour varied from light green, yellow, white purple spotted, yellow purple spotted, greyish, milk spotted and milky colours (Plate XII). The highest of these flesh oxidation colour was obtained from yellowish colour (32.38 %), this was followed by milky colour with (28.12 %) and the least (3.15 %) recorded in orange and light green colours respectively (Table 4.13).

Table 4.13 Variability in tuber skin colour beneath the back and oxidation colour in 32 selected African Yam in north-central Nigeria.

S/No	Traits	*D.rotundata*	*D.dumetorum*	*D.bulbifera*	*D.alata*	*Total*	*Percentage %*
1	Texture of the flesh						
	1 smooth	18	2	1	1	22	68.75
	2 Grainy	8	-	-	1	9	28.13
	3 very grainy	1	-	-	-	1	3.13
		84.38	6.25	3.15	6.25	100	
2	Flesh oxidation colour						
	1 orange	-	1	-	-	1	3.13
	2 yellowish	10	1	-	-	11	34.38
	3 light green	-	-	1	-	1	3.13
	4 greyish with milky spot	4	-	-	-	4	12.5
	5 milky	8	-	-	1	9	28.13
	6 white with purple spot	3	-	-	1	4	12.5
	7 yellow with purple spot	2	-	-	-	2	6.25
		84.38	**6.25**	**3.15**	**6.25**	**100**	

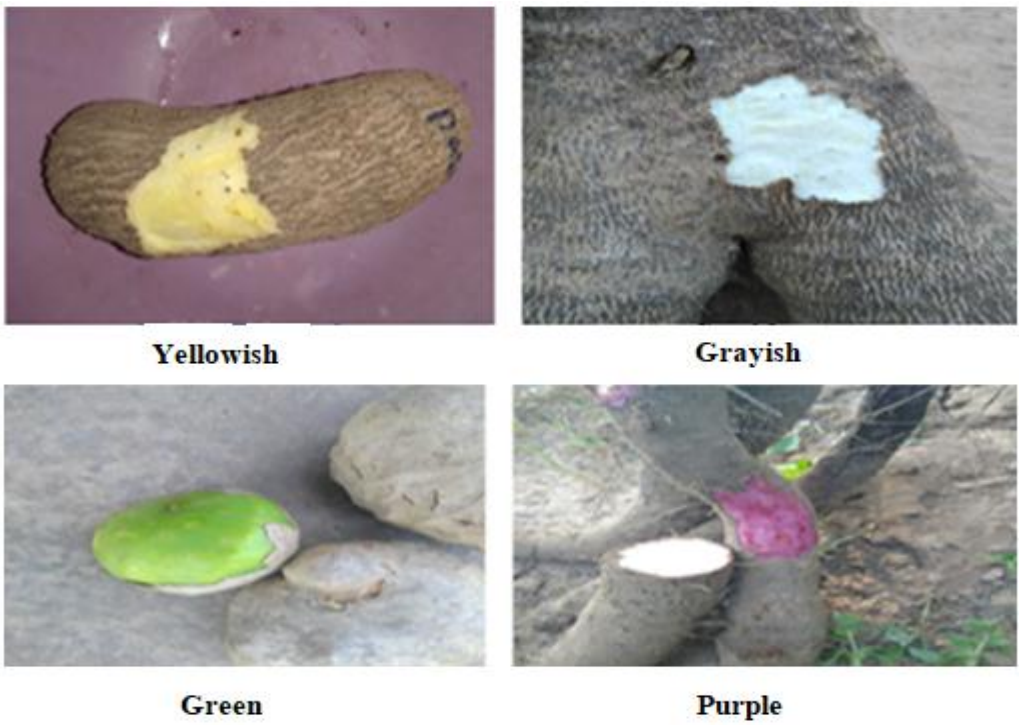

Plate XI: Variability in Flesh Colour Beneath the Skin of African Yam in North-Central Nigeria

Plate XII: Variability in Flesh Oxidation Colour of African Yam in North-Central Nigeria.

4.1.14 Nutritional composition of selected genotypes of African yam in North central Nigeria

The result of the statistical analysis revealed significant differences in nutritional contents among the genotypes (Table 4.14). Moisture contents ranged from 10.87 % - 16.23 %; with the highest content (16.23 %) recorded from NGr.022. This value was significantly different ($P<0.05$) from the values of all other genotypes. While the least moisture content (10.87 %) obtained from BNr.065 was not different significantly from the value of genotype NGd.031 (11.23 %). Crude protein content also varied significantly ($P<0.05$) with the highest content (5.36 %) taken from genotype NSr.027. Thus, this value was not significantly different from 5.12 %, 5.33 % and 5.11 % recorded from BNr.067, NGr.023 and NSr.097 respectively; and differs significantly ($P<0.05$) from the values of all other genotypes. Similarly, genotype FCr.079 has the least crude fibre content of 1.20 %. This value was different significantly ($P<0.05$) from all other values, except for those of NGr.037 (1.25 %) and NGr.020 (1.24 %). While the highest crude fibre (5.13 %) recorded from BNr.051 was significantly the same with those of NGd.031 (4.29 %) and BNr.065 (4.96 %); and different significantly from the values of all other genotypes.

The highest ash contents (4.29 %) obtained from BNr.063, this value was significantly different from the values of all other genotypes; and the least ash contents (1.11 %) taken from KGr.006 was significantly different ($P<0.05$) from other genotypes except for NGr.001 (1.22 %), NGr.020 (1.19 %), BNr.065 (1.20 %), KGr.121 (1.27 %) and FCr.079 (1.23 %). Subsequently, the highest fat content was obtained from genotype KGr.003 with the value of 2.45 %. This value was significantly different from the values of other genotypes; and the same with those of NGr.021, BNr.083 and NGb.019 (2.44 %, 2.43 % and 2.41 %) respectively. Consequently, the least value (1.18 %) was recorded from genotype BNr.065; was significantly the same with the values recorded from kGr.006 (1.98 %), KWr.134 (1.60 %), and NGr.017 (1.94 %). Similarly,

genotype BNr.065 has the highest NFE/CHO contents (80.77 %) this value was significantly the same with that of NGr.023 (80.25 %) and significantly different from the values of all other genotypes.

Table 4.14: Nutritional Composition of 32 Selected Genotypes of African Yam from North - Centre, Nigeria.

Parameter	Moisture (%)	Crude protein (%)	Crude Fibre (%)	Ash (%)	Fat (%)	NFE/CHO (%)
NGr. 001	15.21±0.13^{fg}	4.10±0.06^{e}	2.14±0.09^{b}	1.22±0.11^{a}	2.07±0.07^{bcd}	76.83±0.40^{c}
KGr.043	13.03±0.15^{de}	3.49±0.17^{bc}	2.43±0.13^{bc}	1.77±0.15^{be}	2.32±0.10^{ef}	78.66±0.36^{d}
KGr.003	14.73±0.15^{fg}	3.92±0.17^{d}	2.10±0.15^{b}	2.22±0.12^{cd}	2.45±0.23^{f}	76.77±0.53^{c}
KGr.006	13.11±0.17^{de}	4.87±0.21^{f}	3.84±0.11^{def}	1.11±0.08^{a}	1.98±0.09^{a}	76.80±0.30^{c}
NGr.008	13.07±0.30^{de}	4.13±0.21^{e}	2.41±0.22^{bc}	2.58±0.30^{d}	2.24±0.15^{def}	78.40±0.38^{d}
BNr.089	13.39±0.20^{e}	4.49±0.07^{ef}	2.77±0.10^{c}	2.74±0.08^{e}	1.89±0.29^{bcd}	78.14±0.44^{d}
BNr.063	15.48±0.26^{g}	4.55±0.32^{ef}	3.54±0.13^{d}	4.29±0.15^{i}	2.27±0.11^{bcd}	72.38±0.42^{b}
BNr.067	13.09±0.07^{de}	5.12±0.13^{g}	1.93±0.05^{b}	2.04±0.15^{c}	2.07±0.04^{bcd}	75.33±0.34^{bc}
NGr.020	15.44±0.23^{fg}	4.97±0.30^{fg}	1.24±0.17^{a}	1.19±0.10^{a}	1.75±0.05^{bcd}	74.47±0.30^{bc}
NGr.021	15.41±0.21^{fg}	3.40±0.05^{bc}	4.22±0.15^{f}	1.79±0.15^{bc}	2.44±0.22^{f}	74.69±0.25^{bc}
NGr.022	16.23±0.13^{h}	4.92±0.13^{f}	2.45±0.07^{bc}	1.17±0.09^{ab}	2.24±0.13^{def}	74.41±0.39^{bc}
NGr.023	11.22±0.12^{b}	5.33±0.39^{g}	2.24±0.39^{bc}	2.00±0.33^{c}	2.24±0.13^{def}	80.25±0.40^{e}
BNr.071	13.29±0.16^{e}	4.37±0.32^{e}	2.16±0.09^{b}	2.07±0.04^{c}	2.17±0.09^{cde}	78.78±0.20^{d}
NGr.028	15.83±0.24^{gh}	3.53±0.11^{c}	3.65±0.25^{de}	2.66±0.09^{d}	1.18±0.06^{bcd}	73.94±0.22^{b}
BNr.083	12.50±0.29^{bcd}	3.99±0.08d	3.56±0.30^{d}	3.78±0.11^{e}	2.43±0.21^{f}	78.09±0.44^{d}
NGr.038	14.37±0.24^{f}	3.70±0.13^{cd}	2.79±0.15^{c}	2.71±0.13^{de}	1.64±0.12^{abc}	75.44±0.41^{bc}
NGr.037	15.22±0.36^{f}	4.29±0.07e	1.25±0.16^{a}	1.40±0.26^{b}	1.79±0.10^{bcd}	77.04±0.30^{cd}
BNr.051	12.87±0.19^{de}	1.77±0.17a	5.13±0.10^{g}	2.23±0.12^{cd}	2.11±0.08^{bcde}	78.11±0.55^{d}
NSr.027	15.52±0.40^{g}	5.36±0.23g	4.14±0.34^{ef}	4.22±0.37^{hi}	2.35±0.37^{ef}	72.50±0.43^{b}
BNr.065	10.87±0.19^{a}	2.49±0.08^{ab}	4.96±0.14^{g}	1.20±0.12^{a}	1.18±0.06a	80.77±0.21^{e}
NSr.097	12.53±0.29^{bcd}	5.11±0.16g	2.34±0.13^{b}	2.30±0.11^{cd}	2.04±0.07^{bcd}	76.92±0.26^{c}
KWr.134	13.12±0.07^{de}	3.69±0.09^{cd}	3.67±0.13^{de}	3.68±0.16^{fg}	1.60±0.14^{a}	77.26±0.39^{cd}
BNd.030	14.10±0.06^{f}	3.87±0.08^{cd}	2.14±0.09^{b}	4.14±0.08^{ghi}	2.20±0.08^{def}	75.19±0.62^{bc}
NGd.031	11.23±0.15^{a}	3.60±0.20c	4.29±0.17^{g}	1.36±0.13^{ab}	2.27±0.14^{def}	78.88±0.59^{d}
NGa.033	12.73±0.15^{cde}	4.90±0.07^{f}	2.42±0.17^{b}	1.84±0.16^{bc}	2.16±0.10^{cdef}	77.13±0.30^{cd}
BNa.054	15.65±0.09^{gh}	3.61±0.05^{c}	4.14±0.10^{ef}	4.12±0.06^{h}	2.05±0.06^{bcd}	71.35±0.33^{b}
NGr.024	11.95±0.27^{b}	4.23±0.21^{e}	2.74±0.21^{c}	2.69±0.12^{de}	2.18±0.14^{bcd}	75.02±1.41^{bc}
BNr.056	15.28±0.40^{fg}	3.93±1.72^{d}	2.28±0.15^{b}	2.18±0.10^{c}	2.30±0.12^{ef}	60.70±7.05^{a}
NGb.019	15.27±0.15^{f}	3.99±0.13^{d}	3.66±0.14^{de}	3.34±0.17^{f}	2.41±0.44^{f}	73.35±0.35^{b}
NGr.017	15.40±0.11^{fg}	2.51±0.10^{ab}	3.50±0.24^{d}	3.72±0.13^{fgh}	1.94±0.05^{a}	74.59±0.40^{bc}
KGr.121	14.53±0.29^{f}	3.82±0.10^{cd}	3.43±0.11^{d}	1.27±0.14^{a}	2.25±0.06^{def}	76.63±0.31^{c}
FCr.079	12.33±0.17^{bc}	4.40±0.14^{ef}	1.20±0.11^{a}	1.23±0.19^{a}	2.22±0.08^{def}	78.92±0.16^{d}

Values are Mean ± Standard Error of mean. Value with the same superscript along the column are not significantly different at $P < 0.05$.

4.1.15 Mineral composition of 32 selected genotypes of African yam in north-central Nigeria

Mineral composition of the genotypes showed a wide range of difference among and within the genotypes (Table 4.15). Manganese (Mn) contents varied from 0.26 mg/100g to 0.56 mg/100g with the highest contents (0.56 mg/100g) recorded in genotype BNr.071. This value is significantly different ($P<0.05$) from the values of all other genotypes; except (0.55 mg/100g) recorded in BNr.059. the least value (0.26 mg/100g) recorded in NGr.024 is not significantly different ($P<0.05$) from the values of NGr.006 (0.27 mg/100g) and NGd.031 (0.27 mg/100g); sodium (Na) content also range from (6.85 mg/100g), with the least value recorded in genotypes KGr.043 (6.85 mg/100g). This value is significantly different from the values of other genotypes. The highest sodium (Na) content was recorded in BNr.071 with the values of 26.22 mg/100g. This is significantly different from value of all other genotypes. Similarly, the least phosphorus (P) content obtained in NSr.097 (0.32 mg/100g). This value is not significantly different from 0.33 mg/100g, 0.33 mg/100mg and 0.34 mg/100mg recorded in BNr.063, NGd.031 and NGr.024, respectively.

The highest phosphorus content (0.55 mg/100g) was recorded in genotype KGr.003, this value was not difference significantly ($P<0.05$) from the values recorded fron NGr.059, BNr.065, BNr.071 and NGb.019. Genotype BNr.083 has the least content of potassium (K) with the value of (4.44 mg/100g). This value is not significantly different from the values of all other genotypes except KGr.043 (5.33 mg/100g), NGr.023 (5.50 mg/100g), BNr.065 (5.50 mg/100g) and FCr.079 (5.35 mg/100g). The highest potassium (K) content (16.90 mg/100g), was difference significantly from the values of all other genotypes except 13.05 mg/100g, 12.30 mg/100g, 12.35 mg/100g, 13.21 mg/100g and 12.05 mg/100g recorded from BNr.063, BNr, 0.71, KGr.003, NSr.027 and NGa.030, respectively. Iron (Fe) highest content was recorded in BNr.063 (5.24 mg/100g). This value is significantly different fron the value of all other

genotypes. The least value (0.24 mg/100g) is significantly different from all other values except 2.50 mg/100g obtained in NGr.008; 2.20 mg/100g (BNr. and 2.40 mg/100g recorderd in (NGr. 024). Magnesium (Mg) content veried significantly from 8.35 mg/100g to 12.35 mg/100g with least value 8.35 mg/100g recorded in BNr.059. This value is significantly different from the values of all other genotypes except, BNr.065 (8.38 mg/100g). The highest value (12.35 mg/100g) also differed significantly from the value of all other genotypes. Likewise, Copper (Cu) highest value (0.40 mg/100g) recorded from KGr.043 is significantly different from the values of all other genotypes. The least (0.12 mg/100g) recoreded from BNr.063 differs significantly from all other genotype values except 0.13 mg/100g obtained in NGr.037. Genotype BNd.030 has the highest content of Zinc (Zn) with the value of (0.65 mg/100g). This value is significantly different from the values of all other genotype, while the least (0.33 mg/100g) was obtained inNGr.001, BNr.059, NGr.022, BNr. 071, NGr.038, BNr.051, BNr.065, KWr.134, NGr.017 and FCr.079.

Table 4.15: Mineral Composition of 32 Selected Genotypes of African Yam in North-Centeral Nigeria

Parameter	Mn (mg/100g)	Na (mg/100g)	P (mg/100g)	K (mg/100g)	Fe (mg/100g)	Mg (mg/100g)	Cu (mg/100g)	Zn (mg/100g)
BNr059	0.46±0.03fg	19.29±0.17f	0.50±0.01gh	6.03±0.01a	0.80±0.00a	8.35±0.01a	0.35±0.02h	0.34±0.01a
BNr063	0.32±0.03bc	11.35±0.01d	0.33±0.01a	13.05±0.02b	5.24±1.91c	8.40±0.01ab	0.12±0.01a	0.45±0.01c
BNr067	0.48±0.04g	8.50±0.03b	0.45±0.02f	9.81±2.63ab	2.20±0.00b	9.25±0.01e	0.25±0.01ef	0.50±0.01d
BNr059	0.55±0.04h	20.45±0.34g	0.52±0.01h	6.73±0.01a	0.37±0.01a	10.05±0.01f	0.22±0.01dc	0.50±0.01d
BNd030	0.32±0.03bc	9.99±0.07c	0.48±0.01g	11.85±0.03ab	0.33±0.01a	9.50±0.01e	0.35±0.01i	0.65±0.01f
BNr051	0.34±0.03cd	8.00±0.01b	0.35±0.01abc	8.40±0.00a	2.20±0.00b	9.25±0.01e	0.14±0.01ab	0.33±0.01a
BNr056	0.33±0.03c	12.28±0.52e	0.44±0.01ef	4.94±0.02a	0.38±0.01a	12.25±0.01i	0.20±0.01cd	0.40±0.01b
BNr065	0.28±0.03ab	11.73±0.34d	0.53±0.02h	5.50±0.03a	0.38±0.00a	8.38±0.01a	0.14±0.01ab	0.33±0.01a
BNr071	0.56±0.03h	26.22±1.01j	0.53±0.02h	12.30±0.01b	0.40±0.00a	9.50±0.01e	0.20±0.01c	0.33±0.01a
BNr083	0.43±0.01f	9.85±0.01cd	0.36±0.02bc	4.44±0.01a	0.45±0.01a	10.15±0.01f	0.14±0.01ab	0.45±0.01c
FCr079	0.40±0.03e	12.45±0.02e	0.44±0.01ef	5.35±0.00a	0.38±0.01a	8.75±0.01c	0.14±0.01ab	0.33±0.01a
KGr003	0.44±0.03f	10.72±0.01cd	0.55±0.03h	12.35±0.02b	0.30±0.00a	8.80±0.01d	0.35±0.01h	0.33±0.01a
KGr006	0.27±0.03a	9.65±0.01c	0.39±0.01c	8.03±0.01a	0.48±0.00a	8.85±0.01d	0.14±0.01ab	0.50±0.01d
KGr043	0.30±0.03b	6.85±0.03a	0.45±0.01f	5.33±0.01a	0.45±0.01a	9.30±0.01e	0.40±0.01j	0.45±0.01c
KGr121	0.33±0.06c	8.50±0.03b	0.45±0.02f	4.84±0.01a	0.28±0.01a	10.15±0.01f	0.20±0.01cd	0.45±0.01c
KWr134	0.44±0.03f	23.38±0.34i	0.44±0.01ef	6.23±0.02a	2.08±0.00b	8.40±0.01ab	0.14±0.01ab	0.33±0.01a
NGb019	0.38±0.02d	21.40±0.49gh	0.52±0.01h	4.57±0.03a	0.55±0.01a	8.65±0.01c	0.35±0.01i	0.45±0.01c
NGd031	0.27±0.02a	12.35±0.00a	0.33±0.01a	4.65±0.03a	0.34±0.00a	8.84±0.01d	0.30±0.01g	0.60±0.01e
NGr001	0.38±0.34d	8.75±0.21bc	0.36±0.01bc	16.90±1.05b	0.36±0.00a	8.84±0.01d	0.14±0.01ab	0.33±0.01a
NGr008	0.47±0.02g	20.54±0.02g	0.44±0.02ef	10.50±0.02ab	2.50±0.03b	9.45±0.02e	0.14±0.01ab	0.45±0.02c
NGr017	0.41±0.02f	21.77±0.87h	0.34±0.01ab	9.08±0.01a	0.30±0.01a	9.27±0.06e	0.25±0.01ef	0.33±0.01a
NGr020	0.37±0.04d	12.15±0.01de	0.51±0.01gh	12.51±0.02b	0.35±0.01a	10.25±0.01f	0.34±0.01h	0.60±0.01e
NGr021	0.35±0.02cd	9.95±0.01c	0.40±0.01d	4.85±0.02a	2.15±0.01b	8.84±0.01d	0.28±0.01fg	0.45±0.01c
NGr022	0.49±0.03g	8.50±0.03b	0.35±0.01abc	6.05±0.01a	0.25±0.00a	8.55±0.01b	0.17±0.04bc	0.33±0.01a
NGr023	0.46±0.04fg	22.35±0.01hi	0.44±0.01ef	5.50±0.03a	0.35±0.02a	8.82±0.01d	0.14±0.01ab	0.45±0.01c
NGr024	0.26±0.04fa	21.50±0.33h	0.34±0.01a	7.06±0.00a	2.40±0.01b	8.85±0.01d	0.14±0.01ab	0.33±0.01a
NSr027	0.39±0.03e	21.70±0.33h	0.42±0.01de	13.21±0.01b	3.10±0.01b	8.40±0.01ab	0.24±0.01e	0.50±0.01d
NGr028	0.32±0.01bc	21.82±0.33h	0.40±0.05d	7.81±0.01a	2.15±0.00b	8.43±0.02ab	0.25±0.01ef	0.50±0.01d
NGa033	0.45±0.03fg	9.52±0.34c	0.44±0.02ef	12.05±0.02b	0.24±0.02a	8.50±0.01b	0.25±0.01ef	0.55±0.01e
NGr037	0.53±0.03gh	10.77±0.33cd	0.45±0.01f	9.15±0.03ab	0.55±0.02a	11.20±0.00g	0.13±0.00a	0.46±0.00c
NGr038	0.46±0.04fg	8.45±0.01b	0.46±0.02f	10.25±0.01ab	0.38±0.01a	12.35±0.02h	0.35±0.01i	0.33±0.01a
NSr097	0.43±0.04f	21.14±0.54gh	0.32±0.01a	4.84±0.01a	0.45±0.01a	10.50±0.01fg	0.25±0.01ef	0.40±0.01b

Values are Mean ± Standard Error of mean. Value with by the same superscript along the column are not significantly different at $P < 0.05$.

4.1.16 Anti-nutritional composition of 32 selected genotypes of African yam in North central Nigeria

A range of variation in anti-nutritional content was recorded among the genotypes (Table 4.16). Tannin content varied from 0.88 mg/100g to 2.19 mg/100g. The highest Tannin (2.19 mg/100g) recorded in BNr.056 is significantly different from the value of all other genotypes; except for the value obtained from NSr.097 (2.00 mg/100g), KWr.134 (2.00 mg/100g) and BNd.030 (2.14 mg/100g).The least value (0.88 mg/100g) recorded in BNr.083 was significantly different from all other values of genotypes. Similarly, saponnin value varied significantly with highest value recorded in NGr.037 (17.86 mg/100g). This value is not significantly different from the values recorded in NGr.021 (17.82 mg/100g), NGr.023 (17.55 mg/100g) and NGr.028 (17.84 mg/100g).The least saponnin was obtained from NGr.027 (7.08 mg/100g); this value is significantly different from other values recorded across the genotypes. The least alkaloid value (0.02 mg/100g) was recorded from genotypes (BNr.063, BNr.083, NGr.024, NGr.027, NGr.028, NGr.037, NSr.097, NGr.001, BNr.023, FCr.079, KGr.003, KGr.043, KGr.121, NGr.008, NGr.020, NGr.022, NGr.023). These valueswere significantly different from the values recorded in other genotypes, and highest alkaloid value obtained in BNd.030 (0.08 mg/100g),is alsosignificantly different from all other genotypes, except in NGd.031 (0.07 mg/100g). Furthermore, the highest flavonoid value 4.30 mg/100g recorded in BNd.030 is significantly different from any other value except that of NGd.031 (4.20 mg/100g); while the least value (3.14 mg/100g) taken from BNr.059, BNr.056, BNr.071, BNr.083, KGr.003, NGr.017, NGr.020 and NSr.097, is significantly the same with that of NGr.001 (3.15 mg/100g); and different from the values of other genotypes. In the same vein, the least oxalate value was recorded in KGr.043 (8.85 mg/100g) followed by 8.90 mg/100g obtained from BNr.067. These values were significantly different from one another and from the values of all other genotypes, while the

highest value (10.15 mg/100g) of oxalatewas obtained in BNd.030, this value is significantly different ($P < 0.05$) from the values of all other genotypes except (Table 4.16).

Table 4.16: Anti-nutritional Composition of 32 Selected African Yam in North-Central Nigeria

Parameter	Tannin (mg/100g)	Saponnin (mg/100g)	Alkaloid (mg/100g)	Flavonoid (mg/100g)	Oxalate (mg/100g)
BNr059	1.16±0.20^{abcde}	10.68±0.19^{cdef}	0.04±0.01^{cd}	3.14±0.01^{a}	9.02±0.01^{d}
BNr063	1.23±0.12^{abcde}	10.52±0.19^{cdef}	0.02±0.01^{a}	3.32±0.01^{c}	9.05±0.01^{efg}
BNr067	1.30±0.15^{abcde}	11.35±0.19^{ef}	0.03±0.01^{b}	3.34±0.01^{c}	8.90±0.01^{b}
BNa054	1.44±0.17^{cdef}	11.26±0.23^{cdef}	0.04±0.01^{cd}	3.55±0.03^{cd}	9.06±0.01^{fg}
BNd030	2.14±0.08g	9.04±0.20^{ab}	0.08±0.01^{f}	4.30±0.01^{e}	10.15±0.01^{k}
BNr051	1.01±0.17^{abc}	13.88±0.31^{hi}	0.03±0.01^{b}	3.25±0.01^{bc}	9.20±0.01^{j}
BNr056	2.19±0.11^{g}	15.79±0.4^{jk}	0.03±0.01^{b}	3.14±0.01^{a}	9.04±0.01^{ef}
BNr065	1.49±0.14^{def}	14.71±0.20^{ij}	0.04±0.01^{cd}	3.35±0.01^{bc}	9.02±0.01^{d}
BNr071	1.19±0.14^{abcde}	9.55±0.24^{bcd}	0.03±0.01^{b}	3.14±0.08^{a}	9.02±0.01^{de}
BNr083	0.88±0.10^{a}	9.49±0.18^{bcd}	0.02±0.01^{a}	3.14±0.01^{a}	9.15±0.01^{i}
FCr079	1.07±0.08^{abcd}	13.59±0.09^{hi}	0.02±0.01^{a}	3.15±0.01^{ab}	9.03±0.01^{d}
KGr003	1.19±0.09^{abcde}	10.93±0.36^{bcdef}	0.02±0.01^{a}	3.14±0.01^{a}	9.05±0.01^{efg}
KGr006	1.16±0.11^{abcde}	13.47±0.09^{gh}	0.04±0.01^{cd}	3.45±0.02^{cd}	9.10±0.01^{gh}
KGr043	1.34±0.08^{bcde}	9.47±0.29^{bcd}	0.02±0.01^{a}	3.30±0.01^{c}	8.85±0.01^{a}
KGr121	1.17±0.07^{abcde}	8.69±0.26^{bcd}	0.02±0.01^{a}	3.20±0.01^{b}	9.02±0.01^{d}
KWr134	2.00±0.12^{g}	10.15±0.16^{bcdef}	0.05±0.01^{de}	3.16±0.01^{ab}	9.02±0.01^{d}
NGb019	2.09±0.10^{g}	9.49±0.16^{w}	0.06±0.00^{ef}	4.02±0.01^{d}	9.05±0.02^{efg}
NGd031	1.78±0.09^{fg}	16.93±0.16^{kl}	0.07±0.01^{f}	4.20±0.01^{e}	10.05±0.01^{j}
NGr001	1.50±0.13^{def}	16.65±0.19^{kl}	0.02±0.01^{a}	3.15±0.01^{a}	9.02±0.01^{d}
NGr008	1.47±0.09^{def}	16.68±0.19^{kl}	0.02±0.01^{a}	3.20±0.01^{b}	9.01±0.03^{d}
NGr017	1.49±0.22^{def}	10.52±0.12^{cdef}	0.03±0.01^{b}	3.14±0.01^{a}	9.03±0.01^{d}
NGr020	1.10±0.11^{abcde}	16.45±0.13^{kl}	0.02±0.01^{a}	3.14±0.01^{a}	9.02±0.01^{d}
NGr021	1.32±0.17^{abcde}	17.82±0.40^{l}	0.03±0.01^{b}	3.15±0.01^{ab}	9.05±0.01^{def}
NGr022	1.10±0.08^{abcde}	9.95±0.16^{bcde}	0.02±0.01^{a}	3.17±0.01^{ab}	9.02±0.01^{de}
NGr023	1.82±0.23^{fg}	17.55±0.19^{l}	0.02±0.01^{a}	3.15±0.01^{ab}	9.03±0.01^{def}
NGr024	1.11±0.06^{abcde}	10.31±0.09^{bcdef}	0.02±0.01^{a}	3.15±0.02^{ab}	9.02±0.01^{de}
NGr027	1.54±0.14^{def}	7.08±2.57a	0.02±0.01^{a}	3.20±0.01^{b}	9.05±0.01^{efg}
NGr028	1.19±0.10^{abcde}	17.84±0.24l	0.02±0.01^{a}	3.15±0.02^{ab}	8.93±0.03^{c}
NGa033	0.98±0.08^{ab}	10.39±0.11^{bcdef}	0.03±0.01^{b}	3.85±0.03^{d}	9.08±0.01^{g}
NGr037	1.18±0.15^{abcde}	17.86±0.23^{l}	0.02±0.01^{a}	4.02±0.01^{d}	9.06±0.01^{fg}
NGr038	0.92±0.11^{ab}	12.96±0.18^{fg}	0.03±0.01^{b}	3.20±0.01^{b}	9.02±0.01^{d}
NSr097	2.00±0.11^{g}	11.67±0.14^{cdef}	0.02±0.01^{a}	3.14±0.01^{a}	9.08±0.01^{g}

Values are Mean ± Standard Error of mean. Values with by the same superscript along the column are not significantly different at $P < 0.05$.

4.1.17: DNA Fingerprinting of 32 selected African yam genotypes using SSR molecular marker

Simple Sequence Repeat (SSR) markers performances and genetic diversity pattern for the selected yam genotypes are presented in Table 4.17. Five (5) simple sequences repeat(SSR) markers (DPr3B12, DalF08, DABOI, Dab2CO5, and Dpr 3F12). Used generated eighty-four (84) reproducible fragment bands, and all (100 %) were polymorphic (Plate X).Ym20 marker has the highest reproducible amplified bands of 20 and Dpr3F12 had the least of 8 bands. Subsequently, DalF08, Dab2C05, DprF12 and Ym28 produced 15, 13, 8 and 20, respectively (Table 4.17); and 100 % polymorphism were recorded in all the makers with the number of alleles per marker ranging from 3 to 7 at an average of 4.67 (Table 4.18). The gene diversity also ranged from 0.398 in Dpr.3F12 to 0.592 in DalF08 with mean value of 0.505.

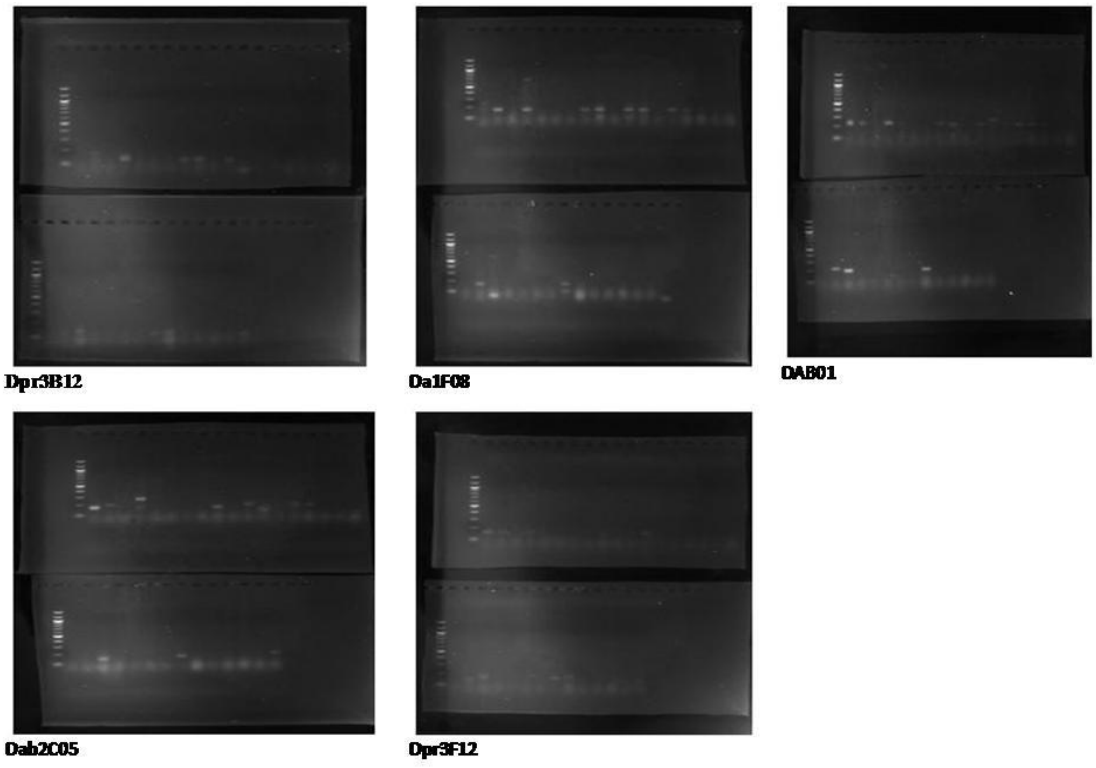

Plate XIII: Gel Electrophoresis pictures from some of the markers used

All the markers produced high PIC which ranged from 0.35 to 0.55 and an average of 0.45. In addition, DalF08 had the highest gentic diversity (GD) and polymorphic information content (PIC) with the values of 0.559 and 0.505, respectively (Table 4.18).

Table 4.17: Polymorphic Bands Produced by the SSRs Primers in the Selected Yam Genotypes

Markers	Monomorphic Band	Polymorphic Band	Total	% Polymorphism
Dpr3B12	0	11	11	100
DaIF08	0	17	17	100
DAB01	0	15	15	100
Dab2C05	0	13	13	100
Dpr3F12	0	8	8	100
Ym28	0	20	20	100
Mean	0	84	84	100

Table 4.18: Major Allelic Frequency, Allele Number, Gene Diversity and Polymorphic Information Content Detected by each of the DNA Markers

Marker	Major Allele Frequency	Sample Size	No. of Observation	Allele No.	Availability	Gene Diversity	PIC
Dpr3B12	0.69	32.00	32.00	3.00	1.00	0.457	0.371
DalF08	0.59	32.00	32.00	7.00	1.00	0.592	0.551
DAB01	0.56	32.00	32.00	4.00	1.00	0.541	0.450
Dab2C05	0..63	32.00	32.00	4.00	1.00	0.545	0.493
Dpr3F12	0.75	32.00	32.00	3.00	1.00	0.398	0.354
Ym28	0.69	32.00	32.00	7.00	1.00	0.506	0.485
Mean	0.65	32.00	32.00	4.67	1.00	0.505	3.451

4.1.18: Dissimilarity indices due to molecular analysis of 32 selected African yam genotype in north-central Nigeria

The similarity matrix was obtained after multi-variant analysis as shown in Table 14 and Figure 4.2; this was used to prepare un-weighted pair group method of arithmetic mean (UPGMA) dendrogram and has been presented in figure 4.2. The dissimilarity index ranged from 0.00 to 3.96 on a scale of 5.00, which revealed a wide ranged of genetic identity. Dissimilarity coefficient of genotype BNr.067 and BNr.056 was the highest (3.93); the genotype BNr.067 was highly different and is genetically distance from one another and most of the other genotypes. However, FCr.079, KWr.134, KGr.121, BNr.051, BNr.065, BNr.059, KGr.043 and NGr.022 have genetic dissimilarity of 0.00. In addition, NGr-001, BNr.056 and NGr.002 in another cluster also have dissimilarity of 0.00. These implied that such genotypes are the same molecularly despite certain genotypic variation in them. It also implies that the similarity observed in the genotypes were species dependent and not geographical location.

Furthermore, at a genetic distance of 0.50 from the dendrogram, the 32 genotype were divided into 8 distinct groups. Groups 1, 2, 3 and 4 contain a single distinct genotype each; (NGd.031, BNr.056, NGb.019 and BNa.054) respectively. Groups 5, 6, and 7 contain 2 genotype i.e. NGr.024 and NGa.033; cluster 5, NGr.023 and BNr.071 for cluster 6 and BNd. 030 and NGr.020 for cluster 7. Group 8 contain 69 % genotypes and it further sub-grouped into 2 broad clusters, a single distinct species (NSr.097) in the group, while the other group contain2 sub-groups; one group contain NGr.008, BNr-083 and NGr.021. The other sub-group was further sub-divided into 2 containing KGr.121and NGr.024 in one group and BNr.056 and BNr.067 in the other. Meanwhile, NGr.001, KGr.006 and NGr.022 were grouped together with dissimilarity of 0.00, implying they are genotypically the same.

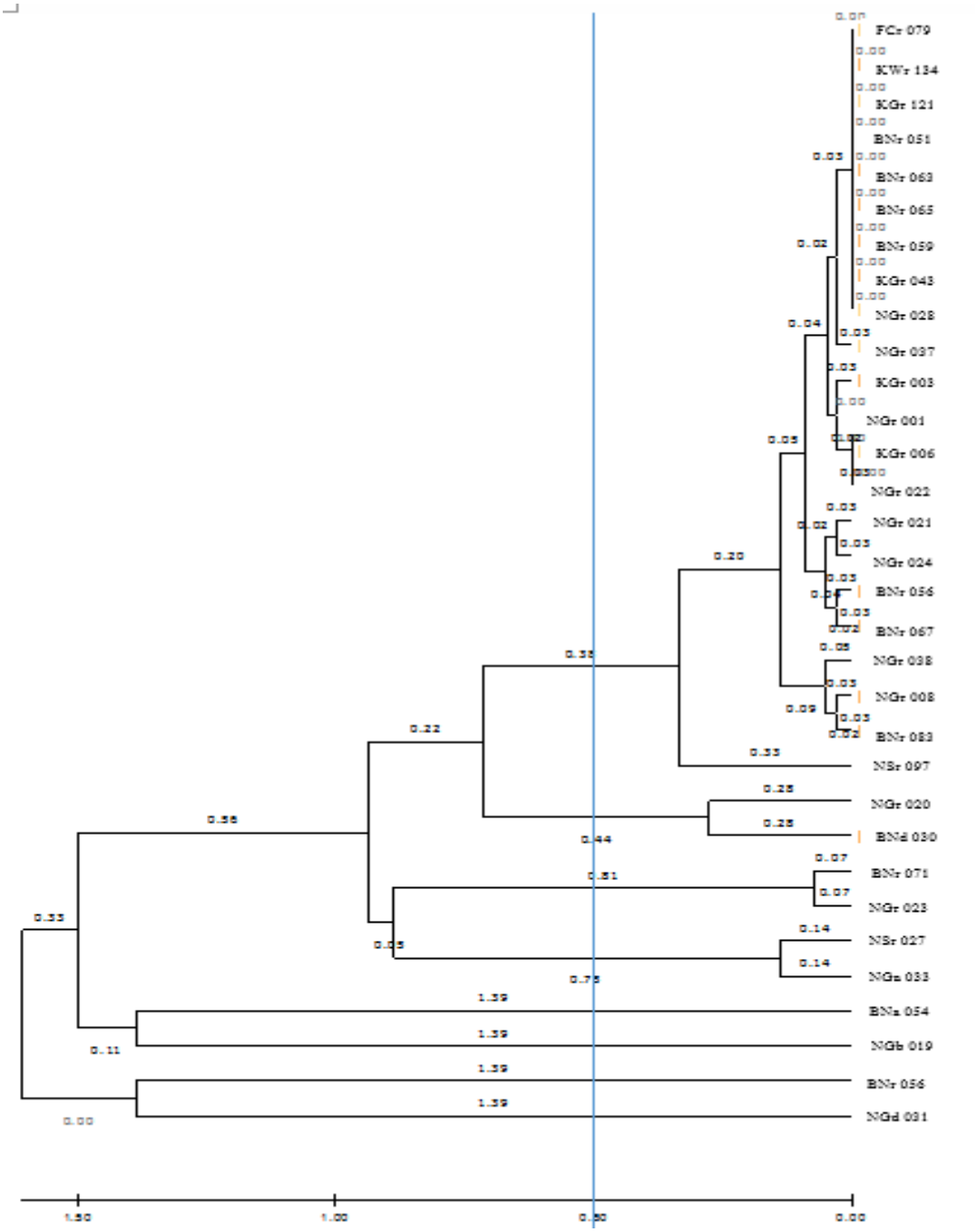

Figure 4.2: Dendrogram Based on UPGMA Analysis of Genetic Dissimilarity ofSelected Genotypes of African Yam

4.2 Discussion

4.2.1 Demographic and socio-cultural practices

Distinguished variations were observed in accessions collected, demographic presentation and cultural practices adopted by the farmers across the states. The highest number of genotypes recorded in Niger state in this study could be an indication of the state beign one of the secondary centre of the African yam. The dorminant of the yam cultivation by the male sex could be attributed to the tedious nature of the cultivaton processes, traditional and religious belief of the people in northern Nigeria. The percengtage of farmers recorded in this study is in close agreement with the earlier report of Ekunwe *et al*. (2008). Subsistence agriculture practice by most of the yam farmers, with small area of yam under cultivation of family sustainance could be the reflectioin of poor financial capacity of the farmer and land fragmentation due to inheritance. This is inconformity with the finding of Nahanga (2015), who reported that farm size has positive influence on yam production in Nigeria, and suggested that subsiding of farm input and provision of affordable loan to small holder yam growers for sustainable production. Similar to the result of this study, Seun (2016), also observed that predorminant of the farmers produce yam tuber for consumption through rain-fed cultural practices. This could be attributed to lack of reservoir for conservation of enough water to embark of irrigation and seasonal drying of the surrounding rivers. This could lead to insufficiency of the yam products most especially at the peak of dry season when the production is inadequate to meet up with the demand of the consumers.

4.2.2 Germplasm collection of the 32 selected yam from north-central Nigeria.

On the basis of the indigenous knowledge, the classification of the collected germplasm into four (4) different species dominated by *D. rotundata.*is inconformity with the earlier work of Clarke *et al*. (1986), that reported six species from 23 accessions. Contrary to their report that *D. alata* was the most common accession; *D. rotundata* was found to be the most abundantand

widely distributed genotype in North-Central Nigeria. In line with this finding, Sartie *et al*. (2012) reported that *D. rotundata* is the most preferred yam in West Africa, and this great diversity could be attributed to selection process through domestication by local farmers and breeding by research institutes. The high precense of most species in Niger state and Benue state confirmed the assertions that these states were the major yam cultivating state in the country. This is an indication that the state could be secondary centre of yam diversity. In agreement with this statement, World Data Atlas Nigeria Ranking Agriculture. (2020), reported that the top region of yam production in Nigeria are; Benue, Niger, Enugu and Kaduna which account for 50.55% of the total production in the country. Secondary centres of diversity have been reported to be the region of high diversity, developed as a result of subsequent spread of a crop (Magwe-Tindo *et al.* (2016).

4.2.3 Morphological (Qualitative and Quantitative) Parameters

Better understanding of the patterns of variability and grouppings of available lanraces have been reported to be a prerequisite for boosting yam production and enhanceds its productivity (Mulualem *et al*., 2019). Indigenous genotypes of yam are mostly heterogeneous with a blend of different individual plant occupying a significant place in the gene pool of cultivated crops (Medagram *et al*., 2015). Characterisation of Africa yam germplasm is important for the identification and classification of genotypes for introgression into breeding programmes. The difference in qualitative characters of the plant is important tool in any characterization process. Since the traits are influence by the gene (s). Based on the aforementioned statement, (Bizuayehu *et al*., 2021) reported that plants could be classified based on variations in morphological, physiological, plant cycle and tuber quality attributes. In the same vein, these variations could be attributed to genetic and ecological components which could affect the yield and yield related quality of the crop (Cervantes *et al*., 2016). Thus, high stem number per plant per hill recorded (1.30 % and 3.90 %) falls within the range value of 1.0 – 5.0 % earlier reported

by Bandana *et al*., 2019. The variability in these resultscould be attributed to physiological or ecological factors in the areas of production.

Internode number per plant recorded in this study (7.30 – 15.80 %) is inconsistent with the earlier report of 59.03 % by Christian *et al*. (2015). The variability in internode and petiole length amoung the genotypes studies could be attributed to the differences in their genetic composition. In conformity with this result Joseph *et al*. (2016) reported that internode length is one of the characters that showed that greatly varied for the species of yams grown.Thus low NIPP and IL in this study is an indication of moderate canopy of the crop. In the same vein, the ranged number of branch per plant (3.60 – 70.40 %) recorded in this study falls within the reported value of Bandana *et al*. (2019). These values revealed high genetic heritability in plant. A minimum length of stem per plant (51.71 cm) and the maximum of (551.43 cm) were obtained in this study; these values were higher than those of Tewodros *et al*. (2021). Also, these value disagreed with low length of stem (3.1 – 4.0 cm) reported by Bandana *et al*. (2019). High length of stem recorded in this study indicated high variability of the traits for improvement programme. In addition, auxiliary branch was equally noted and recorded. The highest was obtained in KGr.043 (24.50 %). However, no auxiliary branch was recorded in cultivar NGb.019. The arrangements of number of root per plat were also recorded. The highest was recorded in KWr.134 and least in NGr.020 with the value of 19.60 and 5.60 %, respectively.

4.2.4 Yield parameters

The variation in number of tubers (bulbis) was 1.00 % in NGa.033 to 13.60 % in NGr.019 in this study, this value is not inconformity with the earlier ranged of 16.1 – 54.2 cm reported by Bandana *et al*. (2019). Similarly, the variability in tuber breath from 6.34 – 54.2 cm recorded in genotypes BNr.063 to Fcr.079, respectively is inconsistent with the earliuer work of Tewodros *et al*. (2021). Similarly, highest fresh weight of tubers (34.68 kg) obtained in this study falls

within the range of 14.4 – 63 kg reported by Tewodoros *et al*. (2021). The variations in these fresh tuber breath and weight could be attributed to differences in the genetic composition of the genotypes, farming system and ecological factors. Furthermore, the variation in leaf index measurement recorded in this study could be attributed to the differences in the genetic makeup of the genotypes.

4.2.5 Principal component and cluster analysis

Principal component analysis of this study revealed the highest variance in petiole length (PL), stem length per plant (SLPP), leaf index measurement and tuber weight. This result was in conformity with the earlier report of Oyinlasha (2004). He reported that tuber size and leaf size were the main distinguished characters between yam genotypes.The clustering patterns of the genotypes into nine (9) distinct groups with each of the clusters having a fair representation of genotypes from different state across North-Central Nigeria revealed non-disstinction between states genotypes. Thus, suggested a range of distribution of yam genotypes. In the same vein, grouping of *D. alata*, *D. rotundata*, and *D. bulbifera*in the same cluster is an indication that the genotype could have strong genetic or phenotypic association. This association could be attributed to cross pollination and sexual recombination flowed by isolated human communities in diverse environment (Martin and Ruberte, 1976). In conformity with the result of this study, the grouping together of *D. alata*, *D. rotundata*and *D. cayensis* confirms that the three species belong to the same section *Entiophyllum* which contains species that twine in a clockwise direction when viewed from the ground upwards. The result of this study also confirmed the statement; with all the genotypes exhibiting twinning habit.

Similar to the results of this study, Valentine *et al*. (2020) revealed that distinctiveness of the genotypes was not based on geographical location but genotypes relatedness. These fidings are also in agrrement with those of Obidigwe *et al*. (2009) who reported non-distinction between

African yam genotypes. Malapa *et al*. (2005) affirmed that wide distribution of genotypes is as a result of clone over many years of human migration, with possibility of a common origin amoung some genotypes. In addition, farmer's cultivers had been reported to be mixture of genotypes, with some traders branded their yam as the highly preffered cultivar for financial advantage or higher price Sartie *et al.* (2012). Consequently, the variability within the clusters with the same species clustered in different group could be attributed to mutation, ecological and climatic variability of the genotypes that might had modified effects on some of the traits over a long period of cultivation time. Obidiegwu *et al*. (2009) were of the view that such mutation could result to variability amoung genotypes producing various shapes and colours for both the arial and underground parts.

4.2.6 Correlation and Associate Characters

Significant positive correlation between agro-morphorlogical and yield related parameters is inconsistent with the fidings of Emmanuel and Ikoro (2019), and those of Solomon *et al*. (2021). They reorted that weight of tuber has positive correlation with all the yield traits. Similarly, this result conformed to the work of Aremu and Ibirinde (2012), they reported positive correlation of vine length and branching pattern to yield in African yam bean (*Sphenostylis stenocarpa*). In addition, Joseph *et al*. (2016), also reported significance correlation of number of internode length and number of branches per meter, and attributed this to variability in yam species grown.

4.2.7 Genetic parameters and estimate of genetic variability

Genotype and phenotypic coefficients estimate provide a better comparison of the traits for genetic variation. Among the characters analysed in this study, PCV was higher than GCV. Showing the influence of environment clearly in the case of tuber numbers per plant (NTPP) and number of leaf per plant. This (number of leaf per plant) confirmed the earlier report of Alam *et al.* (2014). Nwankwo and Bassey (2013); reported high phenotypic coefficient of variance in

number of tubers, mean tuber weight and yield in white yam (*D. rotundata*). Besides, the higher degree of phenotypic coefficient of variation observed in tuber numbers per plant, leaf numbers per plant and tuber weight suggested better scope for selection of these traits in yam developmental programmes.

Heritable variations in a given population for a particular trait can be obtain from heritability estimate of individual concerned. High heritability estimate examined in tuber number per plant, tuber length per plant, branch number per plant and auxiliary branch per plant (0.93, 0.92, 0.87 and 0.86) respectively; suggested effective selection for these characters as high heritability could be an indication oflow influence of environment. Consequently, the lower heritability obtained in this study from tuber weight and leaf index average measurement (0.39 and 0.39) respectively were not in conformity with the report of Rishi *et al.* (1984) they reported high estimate of heritability (over 50 %) for leaf area and tuber yield per plant in *D. deltoidea.* Similarly, Rai *et al.* (1986) obtained high heritability in tuber weight per plant.

4.2.8 Variability in phenotypic traits of 32 selected African yam in north-central Nigeria.

The variability in shape and skin colour is an indication of high level of diversity among the landraces. In line with this result Mulualem *et al.* (2019) reported that there is a wide range of variability of tubers among *Discorea*species with the tuber shape of the landraces varied from irregular to oval. However, the least and unique tuber shape obtained in this study was snake shape. The presence of fewer rare/scarce species in farm lands (fields) and market among the cultivating regions with some presently at brim of extinction could be attributed to the abandoned species due to their poor yielding ability, lack of knowledge on their importance, preservation, vulnerability of the species to insects and diseases as well as poor adaptation to the environment. Mulualem *et al.* (2019) had earlier reported that variety adaptation by farmers depends on agronomic characteristics usually pertaining to productivity, resistance to pest or

adverse cropping conditions, environmental effects as well as stability of production Penet *et al.*, (2016).

4.2.9 Nutritional composition of 32 selected African yams in north-central Nigeria

Nutritional analysis of dry matter of African yam tuber from different genotype revealed wide range of variability in moisture, crude protein, crude fibre, Ash, fat and carbohydrate contents in conformity with the findings of Mohan and Kalidass (2010); Polycarp *et al.* (2012); Ogidi *et al.* (2017). They reported that yams have nutritional attributes and potential application in human diet. The moisture contents obtained in this study (11.23 - 16.23 %) was within the range of earlier reported value (10.0 - 12.3 %) of Omohimi *et al.* (2017). This content is lower than the reported value of Daramola and Aminat (2020) and Adegboyega *et al.* (2019). Moisture contents of food acts as an index to determine its water activities. A higher moisture content in yam accounts for its short-shelf life as it deteriorates easily after harvest. Thus genotypes with low moisture content could have longer shelf life and more suitable for prolonged storage (Polycarp *et al*., 2012). This has contributed to loss of income to the producer, consumers and traders (Zhag *et al.,* 2014). Similarly, higher water contents promote susceptibility to microbial growth and enzyme activities. Consequently, lower moisture contents recorded in this study isan evidence that at good harvest and storage, African yam species in North-central Nigeria could have longer life span, good pandobility and palatability. Hence it has low moisture and cannot be easily deteriorated. Delaying moisture contents of yams depends on their harvesting time, maturation period and environmental conditions (humidity and temperature) in growing period and storage condition. Osunde and Orhevba. (2009) reported the effects of storage conditions and storage period on nutritional and other qualities of stored yam (*Dioscorea* spp).

The minimum and maximum crude protein content recorded in this study varied significantly from 1.77 - 5.36 %. These value was not in conformity with those reported by earlier authors;

0.90 - 1.50 % by Obadina *et al.* (2014), 2.50 - 2.90 % by Abioye. (2012); and 3.50 - 5.70 % by Djeri *et al.* (2015), who worked on yam (*Dioscorea* spp.). However, the maximum value obtained in this study was lower than the maximum value reported by Shajeela *et al.* (2011) and Mulualem *et al.* (2018) (8.26 %) in South West Ethiopia *D.rotundata* genotype. Similarly, higher crude protein value as against this study were also reported for white yam (*Dioscorea rotundata*) by Polycarp *et al.* (2012) (4.00 - 6.50 %), Senanayake *et al.* (2013) (6.20 – 10.20 %) in *D. alata;* and Ayodele *et al.* (2013) (4.00 - 6.50 %). Protein is an essential nutrient required for repair of body tissue, synthesis of enzymes and hormones. It also contributes to energy supply. Yam was reported to have higher dietary proteins as compared to other root and tuber crops including cassava FAO, 2020; Chandrasekara and Josetreph (2016). However, the low protein obtained in this study is an evidence that the yam derived products are limited in the provision of the recommended dietary allowance (RDA) of protein in the diet. The recommended dietary allowance (RDA) of protein for adults, adolescents and children are: (0.80, 1.00 and 1.50 g protein) 1.kg body weight per day respectively Kafatos and Hatzis (2008).

Variability in crude fibre has been reported by other authors using *Dioscorea* spp. The crude fibre recorded in this study ranged from 1.20 – 5.13 %. This falls within the range of 1.66 – 4.64 % earlier reported by (Ogidi *et al*., 2017). These is not consistent with the range of 1.82 – 6.30 % in *D. bulbifera* as reported by Adebowale *et al.* (2018) with both minimum and the maximum value higher than the value recorded in this study. In contrast, lower and higher value range of 0.41 – 2.05 % was reported by Mulualem *et al.* (2019). The differences in these results could be attributed to the difference in genetic composition of the genotypes, their geographical origin and environmental factors of the experimental area. High fibre content obtained in this study show that African yam in North-central Nigeria could be utilised as potential source of dietary fibre (roughages). Fibre is known as anti-tumorigenic and hypocholestrolaemic agents. This

suggest that yam could be recommended for people with cholesterol related challenges and constipation (Gangwar and Toshi, 2008).

The concentration of Ash content recorded in this study ranged 1.11 – 4.29 %; this was in disagreement with the earlier value reported by Omohimi *et al.* (2018) (1.30 – 3.00 %); Shajeela *et al.* (2011) (0.56 – 1.90 %); and Shanthakumari *et al.* (2008) (1.30 – 3.0 %). In the same vein, lower than the higher ranged (0.03 – 10.20 %) was reported by Mohan and Kalidass (2010). Furthermore, crude ash reported in species of yam ranged between 0.17 % and 18.20 % with the lower and higher concentrations been recorded in *D. cayenesis* and *D. bulbifera* respectively. Consequently, ash contents have been reported in yams to range from 0.1% - 8.8 % compared with other root and tuber crops such as potatoes, cassava and cocoyam (Lewu *et al.* 2010; Leoret *et al.* 2017; Somendrical *et al.* 2017; Neela and Fanta (2019). The difference obtained in Ash content could be attributed to inadequate starch purification methods, this further determines the total amount of minerals that could be present in the flour. However, high Ash content obtained in this study revealed high value of minerals in African yam species in North – central Nigeria.

The concentration of fat recorded varied from 1.18 – 2.45 % with the maximum concentration (2.45 %) recorded in *D. rotundata*. This value falls within the range earlier reported by Olajumoke *et al.* (2014) in edible *D. dometorum*.The obtained value in this study fall within the report concentration of (Mulualem *et al.* (2018) (0.09 – 0.65%); Ogidi *et al.* (2017) (0.86 – 1.86 %) and Fauziah *et al.* (2020) (0.00 – 0.29 %). However, it is important to note that fat content is highly influenced by (bound or unbound) extraction. Jayakody *et al.* (2007), Monday and Mueller (1977) elucidated the possibility of tuber lipids being of limited nutritional importance, nonetheless, it enhances the cellular integrity of the cell membrane, proffers resistance to bruising and reduces enzymatic browning of the tuber. The high concentration obtained in this

study is an indication that African yam could be utilised to proffers resistance to bruising and cellular cell membrane building in human animals.

The range of (71.35 – 8.77 %) carbohydrate obtained in this study was higher than the earlier findings of Mulualem (2008) (12.71 – 33.94 %); and the reported value of (17.10 – 28.32 %) by Fauziah *et al.* (2020). Thus, reported value (22.88 mg/100 g) by Ogidi *et al.* (2017) shows higher concentration than the one obtained in this study. The differences observed in the studies could be attributed to species, geographical location of the experimental farm and storage duration.

4.2.10 Mineral composition of 32 selected African yams in North-central Nigeria

The content of macro and micro minerals of African yam varied significantly within and across the genotypes. Manganese (Mn) mean values ranged recorded in this study varied from 0.26 – 0.56 mg/100 g. This concentration was higher than the earlier findings reported by Omohimi, (2018) (0.10 – 0.9 mg/100 g) and those obtained by Jonathan *et al.* (2011) 0.20 – 0.33 mg/100g. Highest value was reported by Mee *et al.* (2012) (11.0 mg/100g) and Mason (2008) (1.2 – 2.3 mg/100g). These differences could be attributed to variation in genetic, physiological and ecological components. High value recorded in this study could be due to Ecological and genotypic differences. Sodium (Na) contents recorded in this study varied from 6.85 – 26.22 mg/100g. This concentration is significantly lower than the quantity reported by Ogidi *et al.* 2017 (27.78 – 8.7 mg/100g), Olajumoke *et al.* (2014). (10.26 – 16.20 mg/100). The lower concentration recorded in this study was an indication that yam tuber contains little amount of sodium this could attributed to environmental or physiological variation in area of cultivation. Phosphorus (P) concentration recorded in this study ranged 0.32 – 0.53 mg/100g this was in disagreement with the reported value of Ogidi *et al.* (2017) (27.78 – 8.7 mg/100g), Olajumoke *et al.* (2014), Fauziah *et al.* (2020), and Mulualum (2018) (7.97 – 9.70 mg/100g, 329.37 – 699.00 mg/100g and 23.7 – 530 mg/100g, they reported higher value, respectively. These differences

could be due to physiological factors. Similarly, the content of Potassium (K) recorded in this study varied from 4.44 – 16.9 mg/100g. This value is lower than the earlier finding report by Olajumoke *et al.* (2014), Abubakar and Mohammed (2017) and Fauziah *et al.* (2020) 13.48 – 8.58 mg/100g, 683 – 3.6 mg/100g, and 224.54 – 483.21 mg/100g, respectively. The differences could be attributed to genetic makeup of the plant. Thus, the lower value recorded in this study is an indication that the genetic makeup of the genotype is needed for improving mineral content in breeding. Iron (Fe) a vital element in synthesis of blood had a range of 0.24 – 5.24 mg/100g in this study. These contents are within the value 0.20 – 0.33 mg/100g earlier reported by Jonathan *et al.* (2011). Furthermore, the higher level of concentration reported by Omohimi *et al.* (2018); (5.8 – 19.6 mg/100g) and Fauziah *et al*. (2020) (1.4 – 13.40 mg/100g) were not consistent with the reported value in this study. Lower iron concentration obtained in this study could be attributed to the removal of other iron – rich starch based products to the flour at the course of processing. Iron is an importance mineral for red blood cell formation and function. Mason (2008) reported the recommended dietary allowance of iron (Fe) for men and postmenopausal women as 8 mg/day, while 11, 15 and 30 mg/day were recommended for adolescences, premenopausal woman and pregnant women, respectively. Consequently, the result obtained in this study is an indication that iron contents in some North central Nigerian yams is not adequate for the supply for iron (Fe) in the daily diet recommended.

Besides, the concentration of magnesium (Mg) recorded in this study varied from 8.35 – 10.5 mg/100g. This value falls within the reported values of Ogidi *et al.* (2017). (8.84 – 13.80 mg/100g). Similarly, higher concentration of magnesium (Mg) were also reported by Omohimi *et al.*(2017), Olajumoke *et al.* (2014), and Fauziah *et al.* (2020) (29.83 - 58.60 mg/100g), 28.21 – 28 mg/100g, and 1.40 – 13.40 mg/100g, respectively. These variations in the content, could be attributed to the ecological region the crop is cultivated. Thus, recommended dietary allowance of mg for adults is 350 and 170 mg/100 g for children. The recorded value in this study shows

that the element is inadequate to meet the RDA recommendation. In the same vein, the concentration of copper (Cu) recorded in this study varied from 0.12 – 0.40 mg/100g. This value is higher than the earlier finding reported by Ogidi *et al.* (2017) (0.14 – 0.45 mg/100g), this could be due to physiological or environmental factor. This is an indication that most North Central Nigerian yams could be used for the improvement of the traits rich in copper. Notwithstanding, the recommended requirement of Cu by RDA in a serving is 3 and 2 mg per day for adult and children respectively. In contrast, lower value was reported by Jonathan *et al.* (2011). Furthermore, earlier reported values by Polycarp *et al.* (2012) was in agreement with the later report. Zinc (Zn) concentration from this study ranged 0.33 – 0.65 mg/100g. This result falls within the previously reported concentration of Ogidi *et al.* (2017) (0.33 – 0.75 mg/100g). In disagreement to the lower concentration obtained in this study, higher concentration level was obtained by Omohimi *et al.* (2018); Polycarp *et al.* (2012) and Fauziah *et al.* (2020) (18.3, 6.80 and 0.43 – 2.83 mg/100g) respectively. On a contrary, lower content of 0.008 – 0.023 mg/100 g was also reported by Jonathan *et al.* (2011). These variations could be attributed to the variety used Zn as an essential mineral for cell development and replication. According to Mason (2008) recommended 8 mg per day of zinc (Zn) for females and 11mg per day for males. However, the recorded concentration obtained in this study is below the recommended value of diet for male and female.

4.2.11 Anti-nutritional composition of 32 selected African yams in North-central Nigeria.

The trace quantities of tannin available in this study varied significantly from 0.88 – 2.19 mg/100 g. This report is inconsistent with the higher quantity earlier reported by Aleto, (1993) (7.6 – 9.0 mg/100g) and Udensi *et al*. (2010) (46.5 – 180.25 mg/100g). These differences could be attributed by genetic makeup of the crop and ecological differences in region of production. The compound act as a repellent against rot in yam (Okwu and Ndu, 2006). Saponnin are considered important due to their toxicity in yam tubers (Okwu and Ndu, 2006). This implies

that most of the North Central Nigerian Yams could not be susceptible to rot diseases and cannot be suitable for anti-rot breeding. The minimum and maximum saponnin concentration obtained in this study varied (8.69 – 17.86 mg/100g). In the same vein, lower and higher range (0.78 – 19.52 mg/100g) was reported in three *Dioscorea*species by Yi *et al.* (2014). Huai *et al.* (1989) reported that this shows that the intra species diversity with respect to significant differences in the amount of saponnin in different yam varieties may be attributed to climatic factors and environmental conditions such as saponnin storage conditions. Besides, the minimum and maximum quantities of saponnin obtained in this study highlighted the pharmacological properties of the compound due to cytotoxic and antifungal properties.

The minimum and maximum concentration of alkaloid recorded in this study ranged from 0.02 – 0.08 mg/100g). This quantity falls within the lower range reported by Adebowale *et al.* (2018) (0.02 – 0.11 mg/100g). Thus, the value obtained in this study is below the earlier report of Abdulrasaq *et al.* (2018) (0.12 – 0.55 %), and Padhan and panda (2020) (7.2 - 16 mg/100g). Similarly, Senanayake *et al.* (2013), recorded alkaloid quantities of 0.94, 1.64 and 1.89 mg/100g in *D. alata* (Rajala), *D. alata* (Hunguarala) and *D. esculenta* (Kukulala), respectively. A concentration of 0.68 mg/100g was reported in *D. belophylla* (prain) (Poornima and Ravishankar, 2009). The differences in alkaloid level according to the authors could be connected to physiological properties and environmental condition in which the genotypes were cultivated. The compound is known to be toxic and can cause a wide range of physiological changes in the body when consumed. However, simple processing such as cooking removes the compound from the yam tuber (Mrinal *et al*., 2020).

Flavonoid content obtained in this study ranged 3.14 – 4.30 mg/100g. In disagreement with this Senanayake *et al.* (2013) reported a lower flavonoid concentration of 0.94 – 1.64 and 1.89 mg/100g in *D. alata* (Rajala) *D. alata* (Hingurala) and *D. esculena* (Kukulala) respectively. In

the same vein, Padhan and Panda (2020) investigated flavonoid concentration of Nine *Dioscorea*species. Their results showed a flavonoid range from 0.62 to 0.85 mg/100g of dry weight. In addition, the authors also reported potential antioxidant activities of the yam tuber extracts to range from 1.63 to 5.59 % in *D. bulbifera* and *D. pubera* with significantly higher amount of bioactive compounds such as flavonoid exhibit higher radical scavenging activity compare to other *Dioscorea* species. Flavonoid have been quantified in *D. belophyalla* (prain) stains (8.80 mg/100g), *D. alata* (Rajala) (5.20 mg/100g), *D. alata* (Hingurala) (9.80 mg/100g) and *D. esculenta* (Kukulala) (12.40 mg/100g) by Poornima and Ravishankar (2009) and Senanayake *et al.* (2013). These later flavonoid concentrations by the two authors were higher than the value obtained in this study.This could be due to environmental influence and medium of cultivation.

Oxalate salt of oxalic acid exist as a by-product of metabolism in plant tissue. It may exist as insoluble calcium oxalate, soluble oxalate or in combination of the two forms as reported in yam tubers (Otegbayo *et al.,* 2018). Oxalate concentration obtained in this study ranged from 8.85 – 10.15 mg/100g. The higher range value recorded in this study is higher than the highest value reported by Wanasundera and Ravindra (1994) (4.83 – 7.81 mg/100g) and ranged value of (0.20 – 0.63 mg/100g) reported by Polycarp *et al.* (2012). The variation in concentration level obtained in this study could be genetically or level of metabolite secretion in most North Central Nigeria yams genotypes. One of the effects of oxalate is intense skin irritation as a result of contact with *Dioscorea* mucilage. This has been linked to the presence of calcium oxalate crystals in yam tubers.

4.2.12 Molecular analysis of 32 selected African yamsusing SSR markers

Simple sequence repeat (SSR) markers have been considered to be efficient for germplasm characterisation possibly due to their co-dominant and highly polymorphic nature (Mignouna

and Dansi, 2003; Sartie *et al*., 2012). Higher number of alleles and higher polymorphism are very important for correct estimation of genetic diversity of a germplasm and effectiveness of makers development and construction of segregating populations. The 100 percent polymorphism along with high mean gene diversity (0.51) and polymorphic information content (3.45); indicate the high level of diversity among the genotypes and efficiency of the markers. This showed that SSR markers used in this study were efficient in discriminating African yams genotypes in North central Nigeria. Moghaddan *et al*. (2009), described PIC as a measure and assessment of the distribution of the frequencies of dictated alleles. However, the values recorded in this study were higher than mean PIC of 0.65 reported by Obidiegwu *et al*. (2009), from 89 genotypes of *D. alata* using SSR markers. Also, Osuagwu and Edem (2020) reported a mean total PIC value of 0.8460 from 25 genotypes of *D. bulbifera* using 10 SSR markers and Abu *et al*. (2021) reported mean PIC value of 0.97 from 42 genotypes of *D. rotundata* using SSR markers. In confirmation of the result of agro-morphorlogical traits, clustering of *D.alata*, *D.bulbifera* and *D.rotundata* in a single clade based on molecular data indicate the relaibility of the method in characterisation and classification of African yam.

CHAPTER FIVE

5.0 CONCLUSION AND RECOMMENDATION

5.1 Conclusion

This study has confirmed the existance of high variability amoung the African yams genotypes in Nigeria for distinct trait with dissimilar genotypes beign favoured by specific characters; the investigation also validates that morphological markers are credible for characterisation and agglomeration of quantitative and qualitative triats of yam genotypes. High phenotypic coefficient of variation examined indicated clearly the influence of environment, whereas, higher heritability observed in NTPP, IL, NBPP and ANBPP suggested effective selection for these characters; hence hugh heritability could be an indication for low influence of environment.

Biochemical assessment of thegenotypes based on their nutritional and anti-nutritional composition established variability in chemical components of yam genotypes that could be selected for nutritional breeding programmes. Information gathered on high diversity in addition to cluster grouping of the genotypes based on genotype relatedness rather than geographical location validates the authenticity of SSR markers in characterisation of the crop, it further suggest that the markers can serve as a base line study and reference materials for future research for development of breeding strategies.

5.2 Recommendations

i. Multi-location trial for multiplication of seeds and effective selection should be carried out on the elite landraces to obtain the true breeding genotypes.
ii. Further research on cytomorphological characterisation on elite landraces should be encouraged to a certain gene that could be utilized for breeding programme.

iii. Hybridization of distinctive traits identified for both quantitative and qualitative traits should be encouraged to ensured maximum production of the crop.
iv. Markers assisted breeding should be carried out on elite accessions to enhance the ability and efficiency of breeding programme.

5.3 Contributions to Knowledge

The thesis established that there was higher genetic variability within and among the 32 African yam genotypes characterised. Genotype BNr.063 produced the highest number of leaves at maturity (655.30) and the highest stem length (55.14 cm), while the highest axillary branch (24.50) were recorded from KGr.043.

Similarly, the highest tuber length (68.98 cm), tuber breath (24.60 cm) and tuber weight (24.68 kg) were recorded from NGa.003, BNr.063 and NGr.017 respectively. Highest moisture content of 16.23 % was recorded from NGr.023.

Also highest content of Sodium (26.22 mg/100g), Phosphorus (0.55 mg/100g), Potassium (16.90 mg/100g) and Iron (5.24 mg/100g) were obtained from BNr.071, KGr.003, NGr.003, NGr.001 and BNr.063 respectively.

The six simple sequence repeat (SSR) markers produced 100 % polymorphism indicating high genetic variability among the African yam genotypes which could be exploited in yam breeding program.

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APPENDIX 1

Germplasm Collection Data Sheet

1. Collection No: _____
2. Accession No: _____
3. Crop Species: _____
4. Collector (s): _____
5. Date: _____
6. Contry: _____
7. State: _____
8. Local Governmnet: _____
9. Village/ Destrict: _____
10. Precise Locality: _____
11. Soil: _____
12. Precipitation: <NORMAL ☐ >NORMAL ☐
13. Sample Source: Field ☐ Floor ☐ Core ☐ Market ☐
    Institution ☐ Other ☐
14. Local Name: _____
15. Type/ Race: _____
16. Ethnic Group: _____
17. Donor's Source: Own ☐ Local ☐ Market ☐ Foreign ☐
18. Cultural Practice: Rain Fed ☐ Irrigated ☐ Flooded ☐
19. Purpose of Production: Consumption ☐ Comercial (sell) ☐
20. Planting Date: _____
21. Harvesting Date: _____
22. Preffered Type: _____
23. Agronomic Score: very poor ☐ Poor ☐ Average ☐
    Good ☐ Very Good ☐

APPENDIX 2

Randomised Block Design

BLOCK I	111	112	113	114	115	116	117	118	119	110
	BNr 063	NGd 033	NGr 022	KWr 133	BNr 056	BNr 075	BNr 066	NGr 017	NGr 038	NGr 020
	121	122	123	124	125	126	127	128	129	120
	NGr021	KWr 134	FCr079	BNr 065	BNr 083	BNa 054	NSr 097	NGd 031	BNr 059	KGr 043
	131	132	133	134	135	136	137	138	139	130
	NGr 001	NGr 037	NGr 015	BNr 067	NGb 019	GNr 036	GNr 012	FCr 073	BNr 055	NGr 002
	141	142	143	144	145	146	147	149	149	140
	BNr 063	NGd 033	NGr 022	KWr 133	BNr 056	BNr 075	BNr 066	NGr 017	NGr 038	NGr 020
	151	152	153	154	155	156	157	158	159	150
	BNr 063	NGd 033	NGr 022	KWr 133	BNr 056	BNr 075	BNr 066	NGr 017	NGr 038	NGr 020

BLOCK II	211	212	213	214	215	216	217	218	219	220
	NGr 020	NGr 038	NGr 017	BNr 066	BNr 075	BNr 056	KWr 133	NGr 022	NGd 033	BNr 063
	221	222	223	224	225	226	227	228	229	230
	NGr 020	NGr 038	FCr 073	GNr 012	GNr 036	NGb 019	BNr 067	NGr 015	NGr 037	NGr 001
	231	232	233	234	235	236	237	238	239	240
	KGr 043	BNr 059	NGr 017	BNr 066	BNr 075	BNr 056	KWr 133	NGr 022	NGd 033	BNr 063
	241	242	243	244	245	246	247	248	249	250
	NGr 002	BNr 055	NGr 017	BNr 066	BNr 075	BNr 056	KWr 133	NGr 022	NGd 033	BNr 063
	251	252	253	254	255	256	257	258	259	260
	NGr 020	NGr 038	NGd 031	NSr 097	BNa 054	BNr 083	BNr 065	FCr079	KWr 134	NGr 021

BLOCK III	311	312	313	314	315	316	317	318	319	320
	NGr 020	NGr 017	NGb 019	NGr 022	NGr 002	NGd 031	BNr 056	FCr079	NGr 001	BNr 066
	321	322	323	324	325	326	327	328	329	330
	KGr 043	GNr 012	BNr 056	NGr 037	NGr 020	BNr 066	BNr 083	NGd 031	BNr 066	NGd 033
	331	332	333	334	335	336	337	338	339	340
	NGr 038	BNr 063	BNr 067	NGd 033	BNr 055	NSr 097	KWr 133	NGd 033	NGr 017	NGr 022
	341	342	343	344	345	346	347	348	349	350
	BNr 059	GNr 036	KWr 133	BNr 075	NGr 038	BNr 075	BNr 065	BNr 063	NGr 038	KWr 133
	351	352	353	354	355	356	357	358	359	360
	FCr 073	BNr 075	NGr 015	BNr 063	NGr 017	BNa 054	NGr 022	NGr 021	NGr 020	BNr 056

BLOCK IV	411	412	413	414	415	416	417	418	419	420
	NGr 022	NGr 017	NGr 022	KWr 133	BNr 056	BNr 075	BNr 066	NGr 017	NGr 038	NGr 020
	421	422	423	424	425	426	427	428	429	430
	BNr 066	KWr 133	FCr079	BNr 065	BNr 083	BNa 054	NSr 097	NGd 031	BNr 059	KGr 043
	431	432	433	434	435	436	437	438	439	440
	NGr 015	FCr 073	NGr 015	BNr 067	NGb 019	GNr 036	GNr 012	FCr 073	BNr 055	NGr 002
	441	442	443	444	445	446	447	448	449	450
	NSr 097	NGd 033	NGr 022	KWr 133	BNr 056	BNr 075	BNr 066	NGr 017	NGr 038	NGr 020
	451	452	453	454	455	456	457	458	459	460
	NGr 022	NGd 033	NGr 022	KWr 133	BNr 056	BNr 075	BNr 066	NGr 017	NGr 038	NGr 020

BLOCK V	511	512	513	514	515	516	517	518	519	520
	NGd 033	NGd 033	NGr 037	KWr 134	NGd 033	BNr 063	BNr 063	NGr 001	NGr 021	GNr 012
	521	522	523	524	525	526	527	528	529	530

	BNr 075	GNr 036	BNr 075	BNr 083	BNr 056	KWr 133	BNr 067	KWr 133	FCr079	NGr 022
	531 BNa 054	532 BNr 075	533 BNr 056	534 NGb 019	535 BNr 056	536 BNr 065	537 KWr 133	538 NGr 022	539 NGr 015	540 NGr 022
	541 NGr 020	542 NGr 002	543 NGr 020	544 BNr 059	545 NGr 038	546 NGr 017	547 FCr 073	548 NGr 017	549 NSr 097	550 BNr 066
	551 KGr 043	552 NGr 020	553 NGr 038	554 BNr 055	555 NGr 038	556 NGd 031	557 NGr 017	558 BNr 066	559 BNr 063	560 BNr 066

Plate 2: Experiment farm of the 50 landraces of African Yam

Source: Field photograph