Vol. 21(5), pp.198-207, May 2022
DOI: 10.5897/AJB2021.17425
Article Number: 45A319069078
ISSN: 1684-5315

http://www.academicjournals.org/AJB

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African Journal of Biotechnology

Full Length Research Paper

Preliminary verification of the adoption status of some yam (*Dioscorea rotundata* and *Dioscorea alata*) varieties in Nigeria using microsatellites markers

Nwogha J. S.[1*], J. E. Obidiegwu[1], R. N Okereke[1], R. Bhattacharjee[2] and H. O. Oselebe[3]

[1]National Root Crops Research Institute, Umudike, Umuahia, Abia State, Nigeria.
[2]International institute for Tropical Agriculture, (IITA), Ibadan, Nigeria.
[3]Department of Crop Production and Landscape Management, Faculty of Agriculture & Natural Resource Management, Ebonyi State University, Abakaliki, Nigeria.

Received 29 October, 2021; Accepted 17 December, 2021

The persistent low yield and farmers' preference of their traditional yam varieties over the improved varieties necessitated this study to verify the adoption status of the released varieties in Nigeria. A total of 48 accessions of white yam (*Dioscorea rotundata*) were sampled from six states of Ebonyi, Enugu, Benue, Kogi, Nassarawa and Oyo within Nigeria yam-belt and were genotyped for relatedness to four released varieties from the National Root Crops Research Institute (NRCRI), Umudike yam breeding programme, while 14 accessions of water yam (*D. alata*) were sampled from four states of Benue, Kogi, Nassarawa and Oyo and were also genotyped for relatedness to three released varieties from International Institute for Tropical Agriculture (IITA), Ibadan. A total of 29 alleles were found in 5 sets of primers analyzed for 52 *D. rotundata* accessions and the number of alleles ranged from 5 (Dald08, SSR 51 and YM 34) to 8 (Dab2E07) with an average of 5.8 per locus. The observed heterozygosity ranged from 0.19 (YM34) to 0.77 (YM30). A total gene diversity of 0.63 according to Nei (1978) genetic distance coefficients was observed among the 52 *D. rotundata* accessions. Similarly, a total of 37 alleles were observed when 17 *D. alata* accessions were analysed with the 7 selected sets of primers. An average of 5.29 alleles was observed per locus. The observed heterozygosity varied from 0.47 (Dab2D06) to 0.82 (YM34). A total gene diversity of 0.58 was observed among 17 *D. alata* accessions according to Nei' genetic distance coefficients. Cluster analysis showed that the *D. rotundata* accessions were classified into 8 clusters. While, 17 accessions of *D. alata* were classified into 4 clusters. There were relationships between some released varieties and farmers accessions and also among the farmers' accessions from different locations, indicating that farmers might have given a preferred local name to the released varieties.

Key words: Verification, adoption, status, yam, microsatellites-markers.

INTRODUCTION

Yam (*Dioscorea* species), a vegetatively propagated crop cultivated for its underground edible tubers, is a crucial food and income source for millions of Nigerians. Nigeria alone accounts for 65% of global yam production. About 48 million tons of yams are produced in Nigeria from 5.9 million hectares of land (FAO, 2018). Yam ranks as an important source of dietary calories. Between 2006 and 2010, 300 million people derived an average of more than 200 kilocalories per person per day from yam (Nweke et al., 2013). Hence, yam is important for food security and income generation for at least 60 million people (that is, domestic retail price of $0.49 per kg for

the 48 million tons produced in Nigeria). A typical yam farmer in Nigeria has an average of 2.38 ha of farmland, of which 1.53 ha (64%) is dedicated to yam production. Yam is also integral to the socio-cultural life of the people (Obidiegwu and Akpabio, 2017).

Yams belong to the monocotyledonous *Dioscorea* genus. This genus has about 613 species and about 10 of *Dioscorea* spp. have been domesticated (Ayensu and Coursey, 1972). *Dioscorea rotundata* (white yam) and *Dioscorea alata* (water yam) are two dominant species of economic importance in Nigeria. Studies on efficiency-equity trade-offs and poverty-based priority setting have together demonstrated the possibility of directing greater benefits to the poor through yam improvement (Alene and Hassan, 2006; Alene and Manyong, 2007). If improved varieties and sustainable technology were used by farmers, at least a 30% yield increase will be actualised within the same area of production annually (YIIFSWA Yamnomics Factsheet, 2016). While population growth is on the increase, yam productivity per hectare is declining. Since 2000, the rate of annual increase in yam production has been decelerating compared to earlier dramatic increases associated with area expansion into the savannah. It has been predicted that this decrease could be catastrophic unless expedited steps are taken. The decline in productive potential is attributed to a combination of factors mostly associated with the intensification of cultivation due to shortened fallow periods, deteriorating soil fertility, poor seed quality, and inadequate yield potential of popular yam varieties and landraces. These obstacles reduce the total food supply in Nigeria, undermine value chain stakeholder's ability to generate sustainable incomes, and disproportionately impact rural women.

In a bid to meet the aforementioned targets, yam improvement strategy has been deployed since 1980s. National Root Crops Research Institute (NRCRI) Umudike, Nigeria and International Institute for Tropical Agriculture (IITA) have been at the forefront of developing market-oriented varieties with the first release in year 2001. The *D. rotundata* is believed to have originated from West Africa (Maass et al., 2007; Scarcelli et al., 2019; Yu et al., 2020). The domestication process has led to the evolution of numerous landraces across Nigeria. These farmers preferred landraces remain the benchmark for varietal improvement. *D. alata* is believed to have originated from South East Asia (Nabeshima et al., 2020) and subsequently introduced to other parts of the world including West Africa. Some of these introduced varieties have been cultivated over years through selection process. These landraces have been inherent in them. Due to the cultural ties of the local yam farming communities, it is envisaged that most of the released yam varieties end up being converted to the locally preferred names by farmers. This has created bottlenecks in varietal tracking and identification based on the clonal attributes of yam. Till date there is no evidenced based study that tries to validate the status of yam adoption in Nigeria, Morphological markers are not reliable in identifying yam varieties, and molecular markers like SSRs have been revealed to be reliable alternative (Obidiegwu et al., 2009b, c; Siqueira et al., 2011; Silva et al., 2016). This preliminary study was conducted to verify the adoption status of seven (7) released varieties including *D. rotundata* and *D. alata* in Nigeria using Simple Sequence Repeats (SSRs).

MATERIALS AND METHODS

Plant

For this study, six (6) states were selected based on their active participation on National Coordinated Research programs and on farm verification trials prior to the release of improved varieties. These states include Ebonyi, Enugu, Benue, Nasarawa, Kogi and Oyo known for being major yam producing regions in Nigeria (Figure 1). The particular sample locations and their coordinates are presented in Table (1).

Forty-eight (48) *D. rotundata* and fourteen (14) *D. alata* leaves were sampled from sixty-two individual plants. The seven released improved varieties (4 *D. rotundata* and 3 *D. alata*) to be identified were sampled from the yam germplasm managed by the 2International institute for Tropical Agriculture (IITA) and National Root Crops Research Institute (NRCRI) yam breeding programmes (Table 2). All samples were collected into conical filter paper and store in silica gels at room temperature to dry.

DNA extraction

Silica gel dried leaf samples were transported to the Bioscience Laboratory, IITA, Ibadan, Nigeria. DNA was isolated from 100 mg of dried yam leaf samples using a modified CTAB extraction method as described by Sharma et al. (2008). The DNA extracts were eluted in 100 µl sterile TE buffer and the quality and concentration were assessed by gel electrophoresis using 1% agarose with known concentrations of undigested lambda DNA (Sigma, St Louis, MO, USA). The extracts were further quantified using a Nanodrop spectrophotometer and stored at -20°C for genotyping. Prior to PCR analysis, the samples were standardized to 25 ng/µl.

DNA quality and molecular concentration

All 52 samples of *D. rotundata* and 17 samples of *D. alata* produced high molecular weight DNA with very good quality. The average concentration of DNA extracted was 2707.4 ng/µl, ranging from 1277.8 to 4317.3 ng/µl. Purity of the DNA extracts was on the scale of A260/280 and an average of 1.88, ranging from 1.78 to 1.95.

*Corresponding author. E-mail: nwoghajerrys@gmail.com.

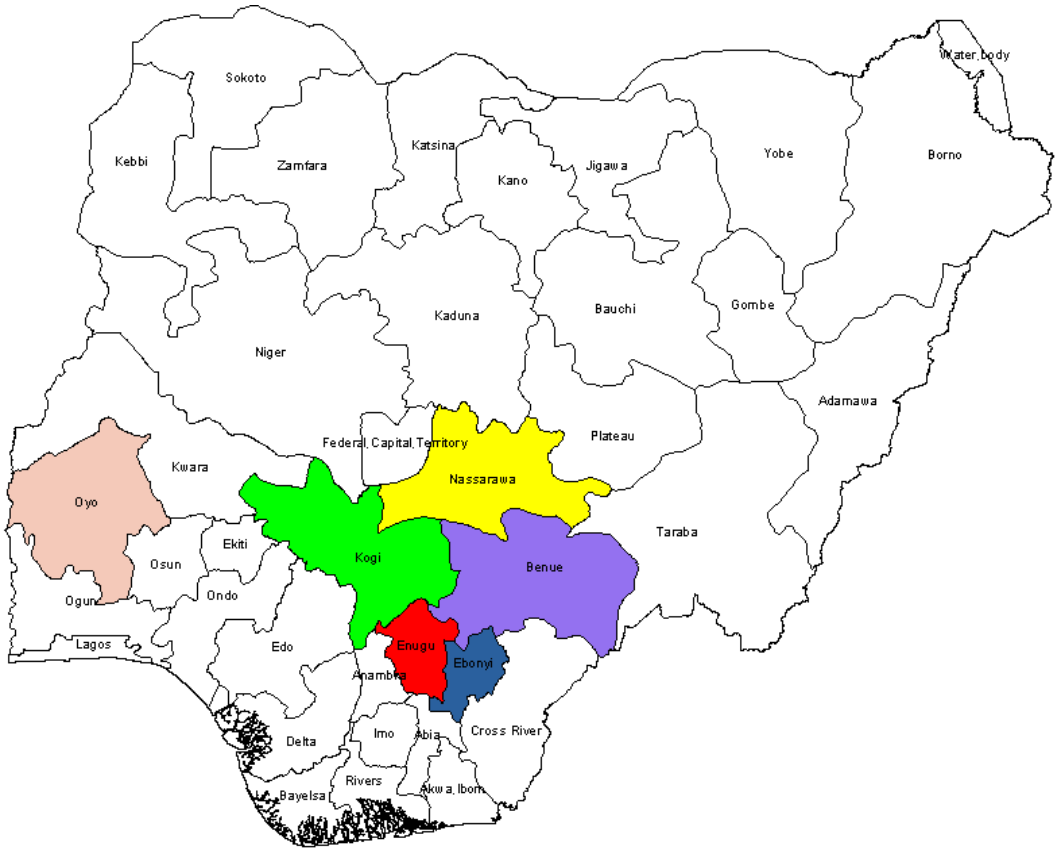

Figure 1. Nigerian administrative map showing the geographic location of the states where samples were collected.
Source: Author

PCR genotyping

Twenty-three SSR primer pairs developed from various yam species were selected and used to analyse the samples according to Tamiru et al. (2015) and Tostain et al. (2007). The primer pairs were tested on the released varieties and five (5) were chosen for *D. rotundata* and seven (7) for *D. alata* based on the capacity to reveal polymorphism and reproducibility. PCR reactions were conducted on a thermocycler (Applied Biosytems Veriti 96 well plates) in 10 µl volumes containing 1 µl of template DNA, 100 µM each of dNTP, 2.5 mM $MgCl_2$, 0.5 µM, 10X reaction buffer and 2 units of Taq DNA polymerase. Depending on the loci used, different touch down PCR cycle program was used. The PCR amplicons were electrophoresed on 2% agarose gel in 0.5 TBE buffer along with a DNA molecular size marker. Gels were photographed using a gel documentation system.

Gel scoring and fragment analysis

PCR amplicons (2 µL) were mixed with loading dye and subjected to further electrophoresis in 6% polyacrylamide gels at 100 V for 30 min. The resolved and unambiguous DNA bands generated from the separation of the PCR products were counted by starting from the top to the bottom of the lanes and were also scored as presence (1) and absence (0) of bands. The binary data generated was analysed using Gstudio (Rodney, J.D.) R package, to determine genetic diversity parameters such as allele numbers per locus (A), the effective allele numbers per locus (Ae), polymorphic information content (PIC), observed (Ho), and expected (He) heterozygosity, respectively, genetic distant, as well as cluster analysis.

RESULTS

Genetic diversity across yam accessions

A total of 29 alleles were found in 5 sets of primers analyzed for 52 *D. rotundata* accessions. The number of alleles ranged from 5 (Dald08, SSR 51 and YM 34) to 8 (Dab2E07) with an average of 5.8 per locus (Table 3). The observed heterozygosity (Ho) ranged from 0.19 (YM34) to 0.77 (YM30). Genetic distance coefficients were observed among the 52 *D. rotundata* accessions. The discriminative power of each SSR primer was assessed using the polymorphic information content (PIC). PIC values ranged from 0.58 (Ym34) to 0.73 (Ym30) with an average of 0.64. Similarly, a total of 37 alleles were observed when 17 *D. alata* accessions were analysed with the 7 selected sets of primers. An average of 5.29 alleles was observed per locus (Table 4). The observed heterozygosity varied from 0.47 (Dab2D06) to

Table 1. List of sampled accessions, sample states and sample site physical coordinates.

Sample state	Sample local name	Sample location coordinates
D. rotundata		
Ebonyi	Agric-3_EB	06°20'13.3N" 008° 11'47.3E"
Ebonyi	Agric-4_EB	06°20'13.3N" 008° 11'47.3E"
Ebonyi	Agric-5_EB	06°20'13.3N" 008° 11'47.3E"
Enugu	Agric-2_EN	06°14'50.9N" 007°25'50.0E"
Enugu	Agric-1_EN	06°14'50.9N" 007°25'50.0E"
Kogi	Unknown-1_KG	07°26'23.9N" 007°35'27.1E"
Kogi	Unknown-2 _KG	07°26'23.9N" 007°35'27.1E"
Kogi	Unknown-3 _KG	07°27'20.1N" 001°37'17.8E"
Kogi	Unknown-4 _KG	07°27'20.1N" 001°37'17.8E"
Kogi	Unknown-5 _KG	07°27'20.1N" 001°37'17.8E"
Kogi	Unknown-6 _KG	07°27'20.1N" 001°37'17.8E"
Kogi	Unknown-7 _KG	07°27'20.1N" 001°37'17.8E"
Oyo	Lasmi-2	09°05'52.3N" 003°49'38.3E"
Oyo	Lasiri-3	09°05'52.3N" 003°49'38.3E"
Oyo	Ojuiyawo	09°05'52.3N" 003°49'38.3E"
Oyo	Ajidawa	09°07'03.7N" 003°53'18.1E"
Oyo	Zaria	09°07'03.7N" 003°53'18.1E"
Oyo	Sofinni	09°07'03.7N" 003°53'18.1E"
Oyo	Lasiri-4	09°07'03.7N" 003°53'18.1E"
Oyo	Agbaowobe	09°07'03.7N" 003°53'18.1E"
Oyo	Ndu	08°47'29.0N" 003°48'47.2E"
Oyo	Ojuiyawo-3	08°47'25.5N" 003°48'43.4E"
Oyo	IITA 1	08°47'38.5N" 003°48'47.3E"
Oyo	Ketuketu	08°47'23.5N" 003°48'43.4E"
Oyo	Talaaba	08°47'38.5N" 003°48'47.3E"
Oyo	Lasiri-1	08°47'38.5N" 003°48'47.3E"
Oyo	Lasiri-2	08°47'38.5N" 003°48'47.3E"
Oyo	Yalanba	08°49'46.4N" 003°46'59.4E"
Oyo	Ofegi	08°49'46.4N" 003°46'59.4E"
Oyo	Ehuru	08°49'46.4N" 003°46'59.4E"
Oyo	Lasiri	08°49'46.4N" 003°46'59.4E"
Oyo	Ojuiyawo-1	08°49'46.4N" 003°46'59.4E"
Nasarawa	Dandiopu	08°22'55.1N" 008°36.45.0E"
Nasarawa	Pepa	08°22'55.1N" 008°36.45.0E"
Nasarawa	Okah	08°22'55.1N" 008°36.45.0E"
Nasarawa	Adaka	08°22'55.1N" 008°36.45.0E"
Nasarawa	Aloshi	08°22'55.1N" 008°36.45.0E"
Nasarawa	Hembakwesi (NAS)	08°22'55.1N" 008°36.45.0E"
Nasarawa	Aloshi	08°29'33.8N" 008°34'34.2E"
Nasarawa	Ame	08°29'33.8N" 008°34'34.2E"
Nasarawa	Pepa	08°29'33.8N" 008°34'34.2E"
Benue	Hembakwesi (BEN)	07°42'51.0N" 008°41'06.2E"
Benue	Unknown-1_BEN	07°42'51.0N" 008°41'06.2E"
Benue	Unknown-2_BEN	07°42'59.1N" 008°41'02.9E"
Benue	Tokula_BEN	07°42'59.1N" 008°41'02.9E"
Benue	Tokula_BEN-1	07°42'59.1N" 008°41'02.9E"
Benue	Unknown -3_BEN	07°42'51.0N" 008°41'06.2E"
Benue	Unknown-4 _BEN	07°42'51.0N" 008°41'06.2E"
D. alata		
Oyo	Agric-2	08°47'38.5N" 003°48'47.3E"

Table 1. Contd

Oyo	Agric-3	08°49'46.4N" 003°46'59.4E"
Oyo	Ehura	08°47'23.5N" 003°48'43.4E"
Oyo	Oharan	08°49'46.4N" 003°46'59.4E"
Oyo	Agric	09°05'52.3N" 003°49'38.3E"
Oyo	Boko	08°47'38.5N" 003°48'47.3E"
Oyo	Agric-1	08°47'58.5N" 003°48'47.3E"
Kogi	Local-1	07°27'20.1N" 007°37'17.8E"
Kogi	Local-2	07°27'20.1N" 007°37'17.8E"
Nassarawa	Shakata	08°22'55.1N" 008°36'45.0E"
Benue	Tokula-1	07°42'59.1N" 008°41'02.9E"
Benue	Tokula-2	07°42'59.1N" 008°41'02.9E"
Benue	Tokula-3	07°42'59.1N" 008°41'02.9E"
Benue	Local-3	07°42'51.0N" 008°41'06.2E"

0.82 (YM34). A total gene diversity of 0.58 was observed among 17 *D. alata* accessions according to Nei' genetic distance coefficients. All seven primer pairs produced amplicons with varying levels of polymorphism revealing an average of 69.81% polymorphism. The polymorphic information content ranged from 0.42 (Dab20C5) to 0.69 (Dab2E07) with an average of 0.66.

Genetic relatedness among accessions

The genetic distance for the microsatellite data using 52 *D. rotundata* and 17 *D. alata* accessions were constructed based on Nei (1978) and the relationships between accessions were depicted on dendogram graphs. The *D. rotundata* accessions were classified into 8 clusters (Figure 2), with released variety TDr89/02461 in cluster 5 and other released varieties TDr 95/19158, TDr 89/02665 and TDr 89/02677 in cluster 8. Cluster 5 is further classified into 2 subgroups, with TDr 89/02461 in the sub-cluster with Pepa sampled from Nasarawa and Lasri-4, sampled from Oyo. Cluster 8 is made up of 3 subgroups. In group1 TDr 95/19158 is clustered with Ajidawa from Oyo State, while TDr 89/02665 clustered with Lasiri and Lasiri-2 sampled also from Oyo State, as well as unnamed variety (Unknown-1_KG) sampled from Kogi State as seen in group 2. Group 3 showed that TDr 89/02677 is clustered with Lasmi-2 sampled from Oyo, with unnamed varieties sampled from Kogi (Unknown-4_KG) and Benue (Unknown-2_BEN) and also Tokula-1 from Benue as well. Figure 3 shows that 17 accessions of *D. alata* were classified into 4 clusters. Two of the released varieties (TDa 00/00194 and TDa 98/01176) are in cluster 3. Two accessions, local-3 and Tokula-2 sampled in Benue from two different farmers also show close relationship with each other and cluster also with released varieties (TDa00/00194 and TDa98/01176) as seen in cluster 3. Released variety TDa98/01168 as shown in cluster 4 is clustered with accessions (Agric-2 and Agric-1) from Oyo, (Tokula-1) from Benue and (Local-2) from Kogi.

DISCUSSION

The genetic diversity

D. rotundata

The present study provides a baseline for evaluating the adoption rate of some released varieties. On the average, 5.8 alleles per locus were detected for *D. rotundata*. Genetic diversity of 0.63 was observed among the *D. rotundata* accessions. These results demonstrate a sufficient genetic polymorphism in accessions of both species sampled from farmers' field and improved varieties in research institutes' managed breeding programmes. The genetic diversity among the accessions provides insight on the range of genetic base of cultivars that were used in the study. Gene diversity of 0.63 observed among D*. rotundata* accessions indicates that samples utilized in this study constitute a substantive proportion of Nigerian *D. rotundata* diversity, when compared with 0.677 gene diversity reported by Obidiegwu et al. (2009b) after sampling the whole country. This result also suggests a wide range of genetic diversity of *D. rotundata* accessions that were used in this study and equally reaffirm the inference that Nigeria is a centre of its diversity. It has been reported that the high genetic diversity among yam accessions might be due to the crop being vegetatively propagated which usually maintains high heterozygosity (Siqueira et al., 2011). Similarly, Obidiegwu et al. (2009b) stated that the high genetic diversity of *D. rotundata* accessions is due to its dioecious nature and thus, spontaneous hybridization must have contributed to the ancestry of some of the accessions. Meanwhile, the selection of somatic mutants by farmers might also be a source of genetic variability in

Table 2. Released *D. rotundata* and *D. alata* varieties, used, with year of release and improved qualities.

Released variety	Outstanding characteristics	Year of release
D. rotundata		
TDr 89/02677	Stable yield, very good cooking and pounding qualities, cream tuber parenchyma, 25% tuber dry matter content.	2001
TDr 89/02461	Stable yield, very good as cooking and pounding qualities, cream parenchyma, 26.7% tuber dry matter	2001
TDr 89/02665	Stable yield, very good cooking and pounding qualities, cream non-oxidizing parenchyma, 35.3% tuber dry matter.	2003
TDr 95/19158	High yielding, pests and diseases tolerant, good for pounded yam, frying and boiling (29.4 t/ha)	2008
D. alata		
TDa 98/01168	High yielding, pests and diseases tolerant, good for pounded yam, frying and boiling (24-28 t/ha)	2008
TDa 00/00194	High yielding, pests and diseases tolerant, very good for yam, fufu, frying and boiling (37.5 t/ha)	2009
TDa 98/01176	High yielding, pests and diseases tolerant, very good for pounded yam, frying and boiling, suitable for both rainy and dry seasons yam production (26-30 t/ha)	2008

their plant improvement practices. Toasten et al. (2007) attributed a similar genetic diversity of 0.56 among *D. rotundata* in Benin Republic to genetic mutation as result of adaptation mechanism to marginal environment such as very poor soils, flood and long periods of drought as well as farmers' strong selection.

D. alata

An average of 5.3 alleles per locus and genetic diversity of 0.58 were observed among *D. alata* accession. The relative low diversity among the accessions of *D. alata* compared to *D. rotundata* suggests a narrower genetic base of *D. alata* accessions used. This could be attributed to small number of states (four) within Nigeria's yambelt. Therefore, these accessions might not be a good representative of Nigeria's *D. alata* germplasm. This assertion is supported by the findings of Obidiegwu et al. (2009c) who reported genetic diversity of 0.669 among *D. alata* accessions in Nigeria indicative of a wide range of its genetic base in Nigeria. Although, sampling took place only in four states of the thirty-six in Nigeria, those states ((Oyo, Benue, Kogi and Nassarawa) are the hotspots of yam production in Nigeria and thus were expected to be a good representative of *D. alata* germplasm in the country.

PIC values ranged from 0.58 to 0.73, with an average of 0.64 for *D. rotundata* accessions. While PIC values ranging from 0.42 to 0.69 with an average of 0.66 were observed in *D. alata* accessions. PIC refers to the value of a marker for detecting polymorphism within a population, d**e**pending on the number of observable alleles and the distribution of their frequency. It has been proven to be a general measure of how informative a marker is (Siqueira et al., 2011). PIC values in this study demonstrate that the SSRs used on average presented a high level of information and were sufficiently discriminatory. Similarly, PIC values have been reported in previous studies by Tostain et al., 2007; Obidiegwu et al., 2009b, c; Siqueira et al., 2011).

Genetic relatedness among accessions

In this study, the adoption status of the released varieties were evaluated using the genetic distance of microsatellite data from 52 *D. rotundata* and 17 *D. alata* accessions to construct cluster dendrograms based on Nei (1978). The relationships between released and farmers' accessions are also shown on dendrogram graphs. *D. rotundata* accessions were distributed into 8 clusters (Figure 2), with released varieties: TDr 95/19158, TDr 89/02665 and TDr 89/02677 in cluster 8, indicating that these varieties might be progenies of common genetic pedigree. In addition, they also share cluster 8 with many other farmers' accessions, indicating diverse genetic relationships with farmers' accessions from various locations. For instance, TDr89/02677 is closely related to Lasiri from Oyo, Unknown-4_KG from Kogi, Tokula_BEN-2 and Unknown-2_BEN. The nature of the linkage indicates that the farmers' accessions shared genetic background with the released variety TDr89/02677 or can even be its mutants but with little genetic variations due to adaptation to different environments as earlier adduced by Tostain et al. (2007). Similarly, released variety TDr89/02665 was closely related to Lasiri-2 from Oyo or can be the same as Lasiri-2, but with farmers' name and not breeders' code. While Unknown-1_KG from

Table 3. Characteristics of SSR markers used in analysis of 52 *D. rotundata* accessions.

Locus	Sequence	A	Ae	Hobs	PIC
Dald08	AATGCTTCGTAATCCAAC – F CTATAAGGAATTGGTGC - R	5	2.61	0.71	0.62
YM 30	CCACAACTAAAAACACATGGAC - F GTGGTAGGGTGTGTAGCTTCTT - R	6	3.63	0.77	0.73
Dab2E07	TTGAACCTTGACTTTGGT – F GAGTTCCTGTCCTTGGT -R	8	2.94	0.46	0.66
SSR 51	GAATACATATGGTGCATTCGAG - F GCTGCTTACAACTGACAAAGTC - R	5	2.58	0.29	0.61
YM 34	GGTAATAGAGGGCAAAGTGGC - F AGACCTCCTACCATGCTCAAG – R	5	2.40	0.19	0.58
Average		5.8	2.83	0.48	0.64

Number of alleles per locus (A), observed heterozygosity (Ho), effective alleles (Ae) and polymorphic information content (PIC).
Source: Author's computation.

Table 4. Characteristics of SSR markers used in analysis of 17 *D. alata* accessions.

Primers	5' to 3' Primer sequence	*A*	Ae	Hobs	PIC
Dab20C5	CCCATGCTTGTAGTTGT -F TGCTCACCTCTTTACTTG -R	3	1.74	0.53	0.42
D 83	TCGGAATTCAACTGTGATGGC -F AGCACACCATTCACACATAGG -R	6	2.56	0.59	0.61
D 100	GTGTGTGGATGGAGTTTCAAT -F GAATACCCCCAACAGATGTAAT -R	5	2.32	0.77	0.57
Dab2E07	TTGAACCTTGACTTTGGT -F GAGTTCCTGTCCTTGGT -R	6	3.18	0.65	0.69
Ym 34	GGTAATAGAGGGCAAAGTGGC -F AGACCTCCTACCATGCTCAAG -R	5	2.44	0.82	0.59
Ym 51	GAATACATATGGTGCATTCGAG -F GCTGCTTACAACTGACAAAGTC -R	7	2.98	0.57	0.66
Dab2D06	TGTAAGATGCCCACATT -F TCTCAGGCTTCAGGG – R	5	2.92	0.47	0.66

Number of alleles per locus (A), observed heterozygosity (Ho), effective alleles (Ae) and polymorphic information content (PIC).
Source: Author's computation.

Kogi and Lasiri also from Oyo either shared genetic pedigree with it or are its mutants. Similarly, released variety TDr95/19158 is closely related with farmer's accession Ajidawa from Oyo. In cluster 5, TDr89/02461

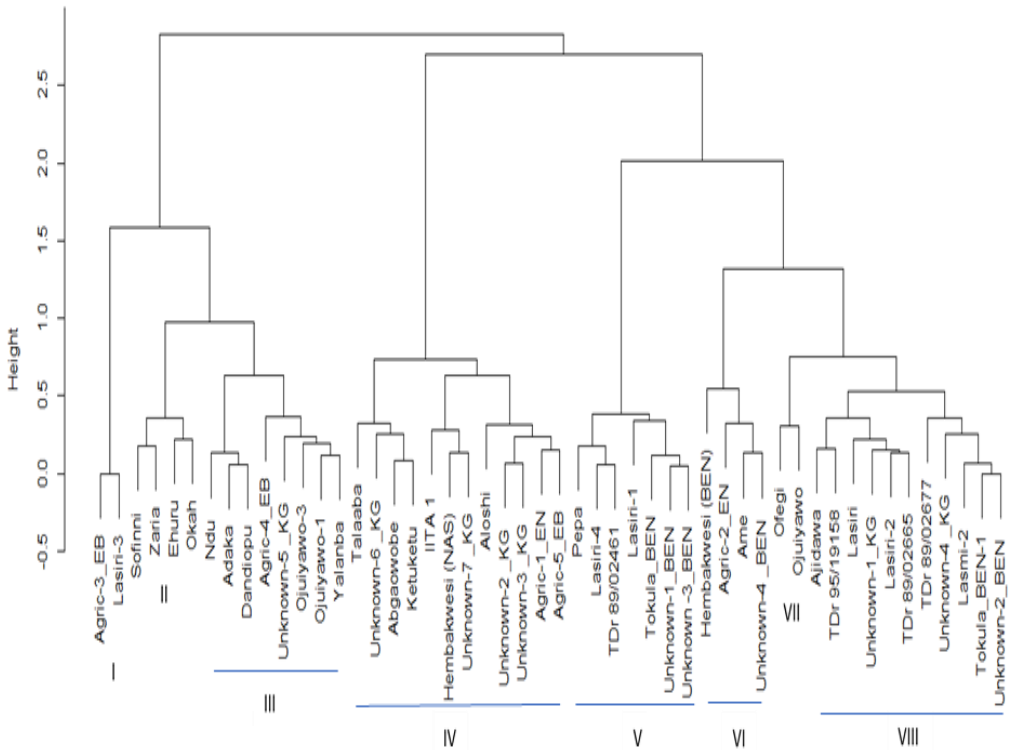

Figure 2. Dendrogram for the 52 *D. rotundata* cultivars constructed from SSRs data analysis using Unweighted Pair-group Arithmetic Average similarity matrices computed according to Nei coefficients.
Source: Author's computation.

is closely related to Lasiri-4 from Oyo and pepa form Nasarawa, indicating that both Lasiri-4 from Oyo and Pepa from Nasarawa might be the same as released variety TDr89/02461, but with different farmers' names at different locations. Also, there are strong relationships among the farmers' varieties from different locations, indicating that some of these might be the same but with different names at different locations.

In Figure 3, the 17 *D. alata* were classified into four main groups. Two of the three released varieties were in cluster 3; again, indicating that both of them might have the same genetic pedigree, while the third one was in cluster 4 indicating that it is more genetically distant from the previous two. In cluster 3, the two released varieties, TDa98/01176 and TDa00/00194 were in the same level of linkage with Tokula-2 and Local-3 all from Benue, implying that these accessions could be the same as either TDa98/0076 or TDa00/00194. Cluster 4 indicates that released variety TDa98/01168 is closely related to Agric-2 and local-1 from Oyo and Kogi, respectively. The accessions could also be thesame but named differently by farmers at different locations, similar to Agric-1 and Tokula-1 also from Oyo and Benue, respectively, which are of similar accessions but with different names at different locations; all mutants of TDa98/01168. The name "Agric" given to the accession in Oyo further buttresses the fact that it is a released variety as most improved crop accessions is commonly given such name by Nigerian farmers especially when it out-performs their local accessions.

Conclusion

The study revealed significant adoption of the released varieties in Nigeria, which have been renamed by farmers at different locations. Hence, there is a need for pragmatic paradigm shift in breeding approach, to make it more farmer-participatory. These will allow farmers, especially those who participated in the final evaluation (verification trials), to be involved in the final naming of the yet-to-be released varieties. Although this approach is already being deployed by the breeding programmes in the country with the aim that it will ease released variety identification and improve adoption efficiency. Also, the study equally revealed that adoption of these released varieties took place at Oyo, Kogi, Nasarawa and Benue axis and not in any other part of the country. This is expected as Oyo is the epicenter of yam breeding activities in Africa with the siting of IITA, while Kogi, Nasarawa and Benue are the yam production hotspots in the country where advanced breeding lines are evaluated.

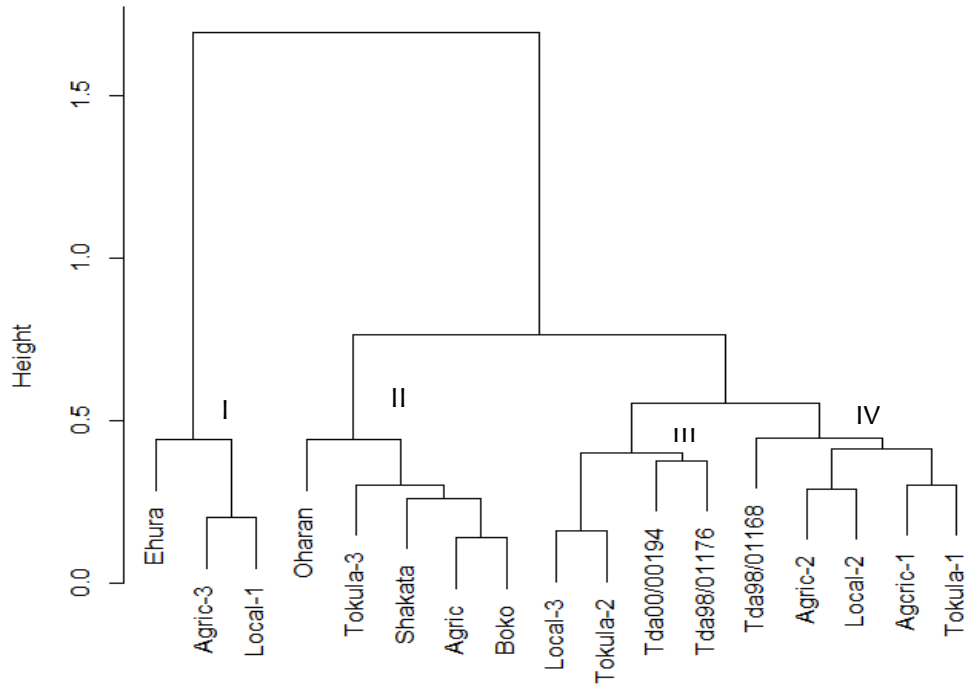

Figure 3. Dendrogram of 17 *D.alata* accessions developed from micro-satellite data using unweighted pair group of arithmetic means (UPGMA) based on Nei's (1978) genetic distance.

The implication here is that outside the farmers who participated in advanced evaluation of these released varieties, it is likely that other farmers, especially from outside the evaluation regions where yam production also takes place, have adopted the varieties so far released.

In addition, some of the farmers' accessions from different locations linked closely with each other; an indication that these accessions are similar, but differently named by farmers at different locations. Hence, this study's findings show the efficiency of SSRs used and the importance of using molecular markers in adoption studies.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Alene AD, Manyong VM (2007). The effects of Education on agricultural productivity under traditional and improved technology in northern Nigeria: an endogenous switching regression analysis. Empirical Economics 32(1):141-159.

Alene AD, Hassan RM (2006). The Efficiency of Traditional and Hybrid Maize Production in Eastern Ethiopia: An Extended Efficiency Decomposition Approach. Journal of African Economies 15(1):91-11

Ayensu ES, Coursey DG (1972) 'Guinea yams the botany, ethnobotany, use and possible future of yams in West Africa'. Economic Botany 26(4):301-318.

Food and Agricultural Organisation of the United Nations (FAO) (2018). Statistics, Division. Report. Available at: http://www.fao.org/faostat/en/#data/QC

Maass BL, Becker H, Oli MT (2007). Genetic Diversity in Yam Germplasm from Ethiopia and Their Relatedness to the Main Cultivated Species Assessed by AFLP Markers Genetic Diversity in Yam Germplasm from Ethiopia and Their Relatedness to the Main Cultivated Dioscorea Species Assessed by AFLP. Crop Science 47(4):1747-1753.

Nabeshima EH, Moro TMA, Campelo PH, Sant'Ana AS, Maria Teresa PS, Clerici MTPS (2020). Tubers and roots as a source of prebiotic fibers. Advances in Food and Nutrition Research 94:267-293. Available at: https://doi.org/10.1016/bs.afnr.2020.06.005

Nei M (1978). Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics 89(3):583-590.

Nweke FI, Robert A, Okoye B (2013). Yam consumption patterns in West Africa. Unpublished report prepared for Bill and Melinda Gates Foundation. Available at: https://doi.org/10.21955/gatesopenres.1115430.1

Obidiegwu JE, Asiedu R, Ene-Obong EE, Muonek CO, Kolesnikova-Allen M (2009b). Genetic characterization of some water yam (Dioscorea alata L) accessions in West Africa with simple sequence repeats Genetic characterization of some water yam (Dioscorea alata L) accessions in West. Journal of Food, Agriculture & Environment 7(3&4):634-638. 2009.

Obidiegwu JE, Akpabio EM (2017). The geography of yam cultivation in southern Nigeria; Exploring its meanings and cultural functions. Journal of Ethnic Foods 4(1):28-35.

Obidiegwu JE, Muoneke CO, Asiedu R. (2009c). SSR markers reveal diversity in Guinea yam (Dioscorea cayenensis / D. rotundata) core set. African Journal of Biotechnology 8(12):2730-2739.

Scarcelli N, Cubry P, Akakpo R, Anne-Celine T, Obidiegwu J, Baco MN, Otoo E, Sonke B, Dansi A, Djadatin G, Mariac C, Couderc M, Causse S, Alix K, Chair H, Francois O, Vigouroux Y (2019). Yam genomics supports West Africa as a major cradle of crop domestication. Science Advances 5(5):eaaw1947.

Sharma K, Mishra AK, Misra RS (2008). A simple and efficient method for extraction of genomic DNA from tropical tuber crops. African

Journal of Biotechnology 7(8):1018-1022.
Silva DM, Siqueira MVBM, Carrasco NF, Montello CC, Nascimnto WF, Veasey EA (2016). Genetic diversity among air yam (Dioscorea bulbifera) varieties based on single sequence repeat markers. Genetics and Molecular Research 15(2):15027929.
Siqueira MVBM, Marconi TG, Bonatelli ML, Zucchi MI, Veasey EA (2011). New microsatellite loci for water yam (Dioscorea alata, Dioscoreaceae) and cross-amplification for other Dioscorea species', American Journal of Botany 98(6):144-146.
Yu S, Darkwa K, Yaegashi H, Natsume S, Shimizu M, Abe A, Hirabuchi A, Ito K, Oikawa K, Tamiru-Oli M, Ohta A, Matsumoto R, Paterne A, De Koeyer D, Babil P, Yamanaka S, Muranaka S, Takagi H, White B, Asiedu R, Innan H, Asfaw A, Adebola P, Terauchi R (2020). Genome analyses reveal the hybrid origin of the staple crop white Guinea yam (Dioscorea rotundata). Proceedings of the National Academy of Sciences 117(50):31987-31992.
Tamiru M, Yamanaka S, Mitsuoka C, Babil P, Takagi H, Lopez-Montes A, Sartie A, Asiedu R, Terauchi R (2015). Development of genomic simple sequence repeat markers for yam', Crop Science 55(5):2191-2200.
Tostain S, Agbangla C, Scarcelli N, Mariac C, Dainou O, Berthaudi J, Pham J (2007). Genetic diversity analysis of yam cultivars (Dioscorea rotundata Poir.) in Benin using simple sequence repeat (SSR) markers. Plant Genetic Resources 5(2):71-81.