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RESEARCH ARTICLE

Development of a West African yam *Dioscorea* spp. core collection

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Abstract Yams (*Dioscorea* spp.) are important crops in some West African locations. The West African yam collections held at the IITA were characterized using the standard descriptor list for this crop (IPGRI/IITA. 1997. Descriptors for yam (*Dioscorea* spp.). International Institute of Tropical Agriculture, Ibadan, Nigeria/International Plant Genetic Resources Institute, Rome, Italy) to assess the extent of diversity and develop a core collection employing 77 out of 86 descriptors and the Shannon–Weaver diversity index. The core collection consists of 391 accessions (13% of entire collection). It represents all the six cultivated and two wild *Dioscorea* taxa. The appropriateness of the procedure was confirmed by comparing the mean and diversity distributions of 11 (out of 13) quantitative traits. This article explains the relevance of this core collection of yams for West Africa yam cropping and improvement.

Keywords Breeding · *Dioscorea* · *Ex situ* conservation · Genebank · Genetic resources · Sampling

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Introduction

Yams (*Dioscorea* spp.) are important tuber crops in humid and sub-humid tropics, particularly in West Africa, where four million hectares produce over 37 millions t of tuber (FAO 2004), and account for 93% of the world's production. Nigeria alone produces 70% of this total. The tubers are processed into pounded yam, boiled yam, roasted or grilled yam, fried yam slices, yam balls, mashed yams, yam chips, and yam flakes. Fresh yam tubers are also peeled, chipped, dried, and milled into flour that is used to prepare a dough called *amala* or *telibowo*.

The *Dioscorea* species shows a wide ploidy polymorphism but most important cultivars accounting for 99% of all food yams among 600 *Dioscorea* species belong to white Guinea yam (*D. rotundata* Poir.; $2n = 40, 80$), yellow Guinea yam (*D. cayenensis* Lam.; $2n = 36–140$) and trifoliate yam (*D. dumetorum* (Kunth) Pax; $2n = 36–54$)—all indigenous to West Africa, water or greater yam

(*D. alata* L.; *2n* = 20–80) and Chinese or lesser yam (*D. esculenta* (Lour.) Burkill; *2n* = 30–100)—native to Asia, aerial yam (*D. bulbifera* L.; *2n* = 30–100) from both Asia and Africa, and cush-cush-yam (*D. trifida* L. f.; *2n* = 54–81), which originated in the American continent (Hahn 1995). Among these many species of yams, white Guinea yam, was the first to be domesticated, and was the basis of the new tuber crop farming, which enabled the population to grow in the northern savanna from about 5000 BC.

Domestication appears to still occur in West Africa, thereby leading to the establishment of new genotypes in the farming systems (Dumont and Vernier 2000). White and yellow yam are the most important because of their tuber taste after cooking in West Africa, where farmers also grow water yam, the second more important as per its total produce and with the widest spread in the tropics. The farmers prefer high and stable yield of marketable tubers with acceptable quality; i.e., dry matter content, cooking texture, taste, dormancy and rate of enzymatic browning.

The International Institute for Tropical Agriculture (IITA, Ibadan, Nigeria) holds in trust in its genebank one of the largest world collections of yams, which includes eight species of West African accessions. This germplasm collection was set up to preserve the genetic diversity of crop species and their wild relatives, for further use in the genetic enhancement of the crop. The assessment of yam diversity could be more easily fulfilled by developing sub-sets of the whole collection, called core collections, The objectives of this research were therefore to characterize the West African yam accessions available in IITA's genebank using passport data and botanical descriptors (IPGRI/IITA 1997), and analyze this diversity to define a core sub-set, which may be a valuable entry point to the entire collection for further research or use by plant breeders.

Materials and methods

IITA genebank holds 3,017 accessions of eight species of West African yams (Table 1). The genebank records include passport data with information on the collecting site. Data on 99 botanical descriptors were collected in 10 plants per accession following the internationally agreed descriptor list (IPGRI/IITA 1997). Most of these descriptors are included in the basic list for characterizes the edible *Dioscorea* species. Although the characterization of the germplasm was done over years, the majority of the descriptors (86) are qualitative and considered highly heritable; i.e., the influence of environment if any is therefore expected to be a minimum.

Table 1 Distribution of *Dioscorea* species accessions from West and Central Africa held at the genebank of the International Institute of Tropical Agriculture and total number of accessions included in its West African yam core collection

Country	*D. alata*	*D. rotundata*	*D. bulbifera*	*D. cayenensis*	*D. dumetorum*	*D. esculenta*	*D. manganotiana* Miège	*D. preussii* Pax
Benin	79	138	3	10	4			
Burkina Faso		2	2					
Congo	8	4	5	3				
Côte d' Ivoire	34	119		6		2		
Equatorial Guinea	1	3	2					
Gabon	4		13		2			
Ghana	77	157	2	14	4	1		5
Guinea		29	1			1	1	
Nigeria	163	790	14	17	9	2	6	1
Sierra Leone	22	5	4					
Togo	384	808	19	7	12	13		
Unknown		5						
Entire collection	772	2060	65	57	31	19	7	6
Core collection	72	237	14	21	14	9	2	2

Following the characterization of the entire collection of West African yam accessions, this collection was stratified according to species, followed by the country of origin. Descriptor multi-variation analysis was used for clustering into groups, from which the accessions to form the core sub-set were chosen. The data were subjected to hierarchical cluster algorithm based on Euclidean distances between and among accessions using Ward's (1963) algorithm, and the number of clusters retained were those at an R^2 (squared multiple correlation) in excess of 75% (SAS 1989). Ward's algorithm is often used for agglomerative cluster hierarchy when a precise solution for a specified number of groups is not practical. Given N sets, this procedure reduces them to N–1 mutually exclusive sets by considering the union of all possible N (N–1)/2 pairs and selecting a union having a maximal value for the functional relation, or objective function, which reflects the criterion chosen. By repeating this process until only one group remains, the complete hierarchical structure and a quantitative estimate of the loss associated with each stage in the grouping can be obtained according to $\mathrm{ESS} = \sum x_i^2 - (1/\mathrm{N})(\sum x_i)^2$. For each country by biological group, the percentage of accessions to be chosen was determined according to the size of the collection and importance of yam in the country's agriculture. The number of accessions chosen in each cluster group for the core collection was determined as a proportion of the number of accessions in the cluster group relative to the total number of accessions in the entire collection. At least one accession from each cluster group was chosen to ensure all the cluster groups represented. Accessions were chosen randomly within cluster members.

The diversity for each trait in the entire and core collections were measured using the Shannon and Weaver (1949) diversity index (S-W). This index was calculated for each character over all accessions within each year of testing as follows $\mathrm{S-W} = -\sum^{n} p_1 \log_2 p_1$, where n and p_1 are the number of classes for the trait and the proportion of accessions in the ith class of a trait. Homogeneity of distribution of the entire and core collection for each trait was measured by comparing the frequency distribution of the trait using the χ^2 test.

Data for 13 quantitative descriptors were used independently to assess the sampling used in the entire collection to define the core collection. The means and standard errors of the 13 quantitative traits were calculated for each trait in both the entire and core collections, and a t-test at 5% probability level was used for assessing the sampling for each trait. Phenotypic correlations between the 13 quantitative traits in both the core and entire collections were estimated independently to assess whether any of the linked traits, which may be under genetic control, were lost in the sampling of the core collection, or putative correlations in the entire collections were the result of the sample size rather than genetic associations due to linkage or pleiotropy. Significant values of the linear correlation coefficients (r) become smaller as the population size increases (Little and Hills 1978, Table A.7, p. 310), and r can be also expected to be smaller from a selected germplasm sample viz. a viz. the corresponding r value computed from a world germplasm collection (Gomez and Gomez 1984, p. 421).

Results

The yam accessions held at IITA genebank showed a wide polymorphism range for most of the qualitative descriptors recorded. Low polymorphism was found for barky patches in young stems, non-twining habit, wax on older stems, distance between lobes in a mature leaf, early (<6 months) or late (9–10 months) tuber maturity after emergence, perennial tuber growth, sprouting at harvest, and many wrinkles in the tuber surface. Multi-variation patterns were used for clustering the accessions of the six species grown by West African farmers. This clustering assisted for grouping similar accessions within each species, and from each cluster group at least one accession was chosen to ensure all the cluster groups were included in the core-subset. The accessions were chosen randomly within cluster members. As the stratification was within a country for species, this approach would not bias the grouping strategy but would ensure maximum available information available across a large

number of accessions in a country for each of the yam species.

Core collection

The West African yam core collection includes 391 individuals. The sampling strategy for this core subset included about 10% of the two species with the largest number of accessions (water and white yams), and a proportionally higher number of accessions (viz. a viz. the entire collection) for the other species, particularly the two wild species (Table 1).

The analysis of both the Shannon–Weaver diversity index and the homogeneity of frequency distributions for the 86 qualitative descriptors recorded in young and adult plants (Table 2), leaves (Table 3), flowers (Table 4) and tubers (Table 5) suggest the appropriate sampling by the core collection of the variation available in the entire collection. The frequency distributions were not homogenous ($P > 0.05$) between entire and core collections only for presence of hair on young stems, twining direction, spine length, undulation of leaf margin, leaf shape, corm shape, spininess of root, and tendency for tuber branching; i.e., 9% of the total descriptors recorded. With the exception of the last two descriptors, the Shannon–Weaver index was larger in the core than in the entire collection. The Shannon–Weaver diversity index provides a measurement of both allelic richness and allelic evenness. A low index shows that frequency classes are unbalanced for a trait lacking genetic diversity, e.g. the core collection includes more accessions showing slightly branched tubers (46%) whereas in the entire collection 44% of the accession had highly branched tubers. Similarly, 85% of the accessions in the core collection had sparse root spininess while most accessions of the entire collection (20%) showed dense spininess in the roots.

There were 22 missing descriptor states (or 9.65% of the 230 states for the 86 qualitative descriptors) in the core subset for traits in which

Table 2 Phenotypic diversity of qualitative descriptors for young stem (20 days after emergence) and plant characteristics of core and entire collections

	Class	Core	Entire	χ^2; P
Young stem descriptors				
Young stem color	3	0.62	0.65	0.973; 0.615
Presence of wax on young stem	2	0.25	0.23	0.510; 0.475
Presence of wings on young stem	2	0.51	0.48	0.660; 0.416
Presence of hair on young stem*	2	0.13	0.07	6.640; 0.010
Presence of spine on young stem	2	0.55	0.53	0.483; 0.487
Presence of colored spot on the base of spine	2	0.38	0.38	0.959; 0.321
Presence of barky patches	2	0.00	0.02	1.039; 0.308
Plant descriptor				
Plant type	3	0.09	0.11	1.542; 0.462
Plant vigor	3	0.80	0.81	0.002; 0.999
Bearing type	3	0.69	0.71	0.847; 0.655
Layering habit	2	0.05	0.07	1.036; 0.309
Twining habit	2	0.03	0.02	0.326; 0.568
Twining direction*	2	0.30	0.17	16.242; <0.001
Stem height at 8 weeks after planting	3	1.02	0.97	5.908; 0.052
Stem color	3	0.20	0.25	1.767; 0.413
Number of internodes at first branching	4	0.45	0.43	3.292; 0.349
Presence of wax on older stems	2	0.03	0.03	0.092; 0.761
Presence of wings on old stem	2	0.54	0.54	0.010; 0.921
Presence of hair on old stem	2	0.68	0.68	0.041; 0.840
Presence of spine on old stem	2	0.51	0.46	2.192; 0.139
Spine shape	3	1.04	1.01	3.156; 0.206
Spine length*	3	1.06	1.03	6.059; 0.048
Presence of coalescent spines	2	0.69	0.69	0.239; 0.625
Presence of color spot at spine base	2	0.27	0.23	0.005; 0.945
Color of spots at spine base	4	0.29	0.24	1.813; 0.612
Types of pigmentation	5	0.48	0.44	0.950; 0.917
Hairiness of upper lower surface	4	0.46	0.55	5.150; 0.161

* Indicates that frequency distributions are not homogenous between entire and core collections at $P \leq 0.05$

Table 3 Phenotypic diversity of qualitative descriptors for leaf characteristics of core and entire collections

Descriptor	Class	Core	Entire	χ^2; P
Leaf arrangement	3	0.18	0.13	2.529; 0.282
Leaf density	4	0.89	0.87	7.048; 0.070
Leaf type (simple, compound)	2	0.05	0.04	0.091; 0.763
Leatheriness of leaf (yes , no)	2	0.60	0.60	0.060; 0.807
Onset of leafing	3	0.27	0.24	0.626; 0.429
Undulation of leaf margin (few, many)*	2	0.57	0.45	15.878; <0.001
Leaf color	4	0.83	0.80	1.827; 0.609
Leaf shape*	7	1.59	1.53	15.859; 0.014
Waxiness of upper/lower leaf surface	3	0.68	0.72	4.933; 0.085
Leaf shape apex	3	0.69	0.71	1.214; 0.545
Distance between lobes	2	0.00	0.02	0.934; 0.334
Leaf base shape*	3	1.05	0.98	8.357; 0.015
Upward folding of leaf along main vein	2	0.52	0.52	0.031; 0.859
Downward arching of leaf along main vein	2	0.69	0.69	1.246; 0.264
Downward arching of leaf lobes to form a cup	2	0.18	0.19	0.010; 0.921
Upward arching of leaf lobes	2	0.64	0.62	1.706; 0.192
Position of the widest part of leaf	3	0.46	0.46	5.106; 0.078
Leaf tip length	3	0.88	0.88	0.114; 0.944
Leaf tip color	3	0.24	0.30	1.588; 0.452
Petiole length	3	0.68	0.66	3.485; 0.175
Petiole hairness (sparse, dense)	2	0.69	0.69	0.607; 0.436
Petiole spot color	3	0.50	0.48	1.692; 0.429
Presence of stipule	2	0.30	0.28	0.435; 0.510

* indicates that frequency distributions are not homogenous between entire and core collections at $P \leq 0.05$

Table 4 Phenotypic diversity of qualitative descriptors for flower characteristics of core and entire collections

Descriptor	Class	Core	Entire	χ^2; P
Flowering (none, some years, every year)	2	0.50	0.54	1.389; 0.499
Presence of inflorescence smell	2	0.22	0.19	0.427; 0.513
Sex (male or female)	2	0.58	0.57	0.044; 0.834
Inflorescence position	2	0.32	0.30	0.108; 0.743
Number of inflorescence per plant	3	0.10	0.10	1.464; 0.481
Inflorescence type	3	0.65	0.58	3.230; 0.199
Average length of inflorescence	4	0.27	0.25	2.255; 0.521
Number of flowers per inflorescence	3	0.36	0.32	1.436; 0.488
Flower color at maturity	3	0.11	0.12	2.235; 0.313
Female flower length	3	0.74	0.58	4.416; 0.110
Male flower diameter	3	0.64	0.60	0.904; 0.635
Fruit formation	2	0.60	0.56	0.547; 0.460

such state frequency was often below 0.5% (or a maximum of 15 accessions in the entire collection), being the mode 1 accession (0.03% of the entire collection); i.e., a rare type. The core subset lacks therefore accessions with barky patches (0.27% in the entire collection), high internode number up to the first branching (0.03%), red spots at the spine base (0.07%), hairiness of lower leaf surface (0.17%), alternate at base/opposite above leaf arrangement (0.03%), purplish green leaf color (0.11%), wax in the lower leaf surface (0.54%), emarginated leaf apex shape (0.33%), intermediate distance between leaf lobes (0.25%), purple spots on petiole (0.10%), every year flowering (0.05%), large (>16 cm) inflorescence length, early (<6 months) or late (>9 months) tuber maturity at emergence (0.04% and 0.12% respectively), perennial tuber growth (0.04%), sprouting at harvest (0.05%), other tuber skin color than maroon or grey (0.10%), and many wrinkles of tuber surface (0.05%). The sampling for the core collection omitted however small tuber length (<20 cm), which was a trait shown by 52 accessions (1.75%) in the entire collection.

Table 5 Phenotypic diversity of qualitative descriptors for tuber characteristics of core and entire collections

Descriptor	Class	Core	Entire	χ^2; P
Tuber growth	3	0.00	0.00	0.134; 0.714
Tuber maturity at emergence	3	0.00	0.01	0.536; 0.765
Number of tubers per hill	3	0.81	0.77	4.396; 0.111
Relationship among tubers	3	0.93	0.96	2.401; 0.301
Presence of corms on tubers	2	0.25	0.18	3.256; 0.071
Corm size in relation to tuber size	3	0.33	0.32	1.008; 0.604
Corm ability to be separated from tuber	2	0.42	0.36	1.792; 0.181
Corm shape*	3	0.69	0.66	5.214; 0.022
Spininess of root*	2	0.42	0.50	4.984; 0.026
Sprouting at harvest	2	0.00	0.00	0.138; 0.710
Aerial tuber formation	2	0.17	0.19	0.362; 0.548
Skin color	4	0.78	0.81	0.934; 0.817
Surface texture	2	0.59	0.59	0.021; 0.885
Bumps on tuber	2	0.54	0.54	0.012; 0.913
Skin thickness	2	0.60	0.60	0.026; 0.872
Tuber shape	4	1.11	1.09	5.253; 0.262
Uniformity in tuber shape	3	0.19	0.30	4.255; 0.119
Tendency for tuber branching*	3	1.02	1.04	6.927; 0.043
Place where tuber branch	3	0.94	0.91	4.194; 0.123
Tuber length	3	0.69	0.77	5.572; 0.062
Spiny roots at tuber surface	2	0.34	0.39	0.695; 0.404
Rootlets on tuber surface	2	0.66	0.68	0.717; 0.397
Wrinkles on tuber surface	2	0.00	0.00	0.141; 0.707
Cracks on tuber surface	2	0.41	0.40	0.006; 0.941

* indicates that frequency distributions are not homogenous between entire and core collections at $P \leq 0.05$

Validating the core collection sampling

Differences between the means of the entire collection and the core subset of West African yams were found to be non-significant for most of the 13 quantitative traits recorded, except stem length and internode number (Table 6). The core collection accessions had on average more internodes and larger stems than the average of the entire collection. The Shannon–Weaver diversity index for both traits was smaller in the core subset than in the entire collection, which confirms that a larger number of core collection accessions with large stems bearing several internodes. The variances of the entire collection and core subset were homogeneous ($P < 0.05$) for all the traits except terminal leaflet width, which exhibited larger variation in the entire than in the core collection but with a slight bias towards lower size frequency class as shown by the Shannon–Weaver index for this quantitative trait.

There about 2/3 (50 out of 78) of significant phenotypic correlations between the 13 quantitative traits in the entire collection (Table 7). However, such results needs to be taken with caution because with such a large number of degrees of freedom, correlation coefficients with an absolute value greater than 0.004 are significant at $P = 0.05$. It was therefore not surprising that about 30% (15) of these weak associations ($r < 0.11$) were not significant in the smaller core subset. There were however, other 10 significant correlations with $r > 0.23$ that remain significant in the core collection, which suggest some meaningful associations arising out of co-adapted gene complexes. For example early emergence results in higher survival of late maturity yam accessions. Yam accessions with strong stems (as measured by their length and width) bear a large leaf number at 20 days after emergence. The two highest significant phenotypic correlations in both the entire and core collections were between stem length and internode number, and between this trait and terminal leaflet length; i.e., yams with a large stem with many internodes bears big leaftlets. There was one significant correlation ($r = 0.2$) in the core subset that was not significant associations in the entire collection: between stem length and tuber width. As indicated before, the core subset sampling omitted small size tubers,

Table 6 Phenotypic diversity of quantitative traits of core and entire collection and Shannon–Weaver (S–W) diversity index

Quantitative traits	Core		Entire		S-W diversity index		
	Mean	S.E.	Mean	S.E.	Class	Core	Entire
Days to emergence	26.2	0.81	25.2	0.17	6	1.20	1.22
Number of surviving plants at 4 weeks after planting	4.6	0.07	4.6	0.02	5	0.94	0.92
Leaf number at 20 days after emergence	35.7	1.35	33.5	0.47	6	0.89	0.93
Number of veins per leaf	7.6	0.06	7.7	0.02	13	1.43	1.47
Stem diameter at 15 cm from the base (cm)	4.5	0.09	4.5	0.03	6	1.35	1.33
Terminal leaflet length (cm)	12.1	0.20	11.8	0.08	6	1.32	1.26
Terminal leaflet width (cm)	9.3	1.39	7.7	0.19	6	1.23	1.26
Stem length (cm)*	102.4	2.73	92.6	0.64	6	1.34	1.55
Internode length (cm)	10.8	0.16	10.7	0.06	6	1.46	1.45
Internode number*	11.1	0.22	10.3	0.08	6	1.31	1.43
Days to flowering from emergence	70.4	1.56	68.0	0.57	6	1.42	1.42
Number of branch with pigmentation	6.0	0.12	5.8	0.04	11	0.72	0.75
Tuber width (cm)	29.4	0.86	28.5	0.25	6	1.37	1.41

* indicates that the means of the entire and core collection are significantly different at $P \leq 0.05$

S.E. = standard error

and this significant correlation in the core subset may arise from the sampling rather than a true phenotypic correlation in yams.

Discussion

The standard yam descriptor list (IPGRI/IITA 1997) was a useful tool for assessing the available variation among West African accessions held in one of the largest germplasm collections for this crop. The polymorphism showed for 86 qualitative descriptors and 13 quantitative traits confirm that both the selected descriptors and the states for each included in this standard descriptor list are appropriate for appraising yam germplasm diversity.

The core subset of West African yams was defined after the assessment of multi-variate patterns of variation in the entire collection. The 391 core collection accessions miss about 9% of the states for qualitative descriptors with low frequency in the entire collection (i.e., <0.0054) or due to sampling large tuber size (1.75% of the entire collection accessions showed this trait). Such a sampling result for defining a core collection of West Africa yams was not surprising because a good core collection avoids redundancy but it is large enough and of manageable size to yield reliable results. The core collection sampling procedure is based on the theory of neutral marker alleles and considers the incorporation of rare widespread alleles in the core collection. The accessions included in the core subset may therefore miss rare localized alleles, which are shown by a few accessions of the entire collection, as was the case with most of the 22-descriptor states missing in the West African core collection.

This core collection should simplify management and enhance the utilization of West African yam genetic resources. Of course, the commitment for preserving by other means in the genebank the entire collection remains but priority for long-term conservation through cryo-preservation should be given to the 391 accessions of this core collection, and to the accessions in the entire collection showing the missing descriptor states in the core subset. In this way, the whole known diversity of West African yams can be maintained for further use by next generations or farmers, researchers and other end-users.

This core collection will be also an important point of entry to further research and the proper exploitation of the genetic resources available in West African yams. For example, genetic diversity and relationships among West African yams can be more accurately assessed in the core subset with isozyme or DNA markers previously used in random samples of this germplasm (Mignouna et al. 1998, 2002a, c, and references therein). Such

Table 7 Phenotypic correlations between quantitative traits in entire (above diagonal) and core collection (below diagonal)

Trait	DTE	SP4	LNE	NVL	SDB	TLL	TLW	SLN	ILN	INR	DTF	NBP	**TBW**
DTE	–	–0.272*	–.0153*	0.063*	–0.006	–0.117*	–0.037	–0.120*	–0.044*	–0.052*	–0.225*	0.023	–0.003
SP4	–0.253*	–	–0.103*	–0.073*	–0.086*	0.085*	0.034	0.012	–0.062*	0.031	0.167*	0.182*	0.096*
LNE	–0.102*	–0.143*	–	–0.003	0.248*	0.095*	–0.030	0.232*	0.048*	–0.032	–0.061*	–0.303*	–0.162*
NVL	0.196*	–0.040*	0.013	–	0.198*	0.216*	0.026	–0.110*	0.214*	–0.152*	–0.078*	–0.177*	0.132*
SDB	0.014	–0.124*	0.290*	0.263*	–	0.307*	0.004	0.020	0.197*	–0.116*	–0.151*	–0.192*	0.098
TLL	–0.127*	0.166*	0.056	0.210*	0.292*	–	0.119*	0.087*	0.272*	–0.017	0.006	–0.059*	0.194*
TLW	–0.016	–0.028	–0.062	–0.012	–0.071	0.027	–	0.030	0.013	0.018	0.042	0.031	0.042
SLN	–0.098	0.049	0.174*	–0.055	0.018	0.242*	0.023	–	0.127*	0.555*	0.009	0.036	0.027
ILN	0.027	0.066	0.025	0.170*	0.232*	0.300*	–0.075	0.104*	–	0.038*	–0.005	–0.164*	0.072*
INR	–0.068	0.085	–0.069	–0.160*	–0.137*	0.095	–0009	0.575*	0.079	–	0.077*	0.111*	0.115*
DTF	–0.248*	0.313*	–0.106	–0.117	0.183*	–0.187*	0.014	0.113		0.173*	–	0.138*	0.007
NBP	–0.103	0.204*	–0.277*	–0.058	–0.221*	–0.066	0.047	0.044	–0.067	0.182*	0.068	–	0.126*
TBW	–0.016	0.050	–0.147*	0.027	0.047	0.283*	–0.030	0.202*	0.077	0.350*	–0.007	0.174*	–

* indicates significant at $P \leq 0.05$

DTE = days to emergence, SP4 = number of surviving plants at 4 weeks after planting, LNE = leaf number at 20 days after emergence; NVL = number of veins per leaf; SDB = stem diameter at 15 cm from the base (cm), TLL = terminal leaflet length (cm), TLW = terminal leaflet width (cm), SLN = stem length (cm), ILN = internode length (cm), INR = internode number; DTF = days to flowering from emergence, NBP = number of branch with pigmentation; TBW = tuber width (cm)

diversity assessment of the core collection with DNA markers could provide a means for identifying potential gaps in the entire collection and further guiding target collecting missions, rather than the conventional approach of searching for new genebank accessions in farmers' fields and markets.

The white yam sub-set (237 accessions) of the West African core collection could be also a valuable germplasm resource for genetic research, e.g. association mapping with DNA markers available in maps for this crop (Mignouna et al. 2002c, e). Likewise, this core collection provides a means for comparative genetics by utilizing the white and water yam core subsets along with DNA markers available for both groups (Mignouna et al. 2001a, 2002b, c, d, e). The yam core collection provides a proper working collection for the extensive searching of desired alleles and a point of entry to the entire germplasm collection for further use of other accessions sharing same trait and other important characters for end-users. After this desired characteristic or allele(s) is found, yam breeders may go back to the remaining accessions of the core collection to screen accessions of similar clusters or geographical area to incorporate more diversity into their genetic improvement program. Molecular aided-breeding coupled with appropriate yam germplasm sources can further accelerate the genetic enhancement of this research-neglected crop that feed West African and other people in the tropics worldwide.

High levels of host plant resistance bred into the cultivars against the two most important diseases of the crop, i.e., yam anthracnose disease caused by *Colletotrichum gloeosporioides* and yam mosaic virus (YMV), contribute significantly to the high level and stability of field performance (Ortiz et al. 2006). This bred yam germplasm and the West African yam core collection could now be assessed at multiple sites in the yam producing locations of West Africa for suitability to local farming and food systems in comparison with popular indigenous cultivars and with active participation of potential farmers. Such distinct local selections of new cultivars ensuing from client-oriented breeding coupled with on-farm management of yam genetic resources will allow

the preservation of yam meta-diversity in West Africa.

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