

**EVALUATION OF STORAGE ROOT YIELD, DRY MATTER AND STARCH CONTENT IN F<sub>1</sub> PROGENIES OF SWEETPOTATO (*Ipomoea batatas* (L.) Lam) OBTAINED FROM CONTROLLED CROSS SYSTEM**

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<https://doi.org/10.35410/IJAEB.2021.5682>

**ABSTRACT**

High yield and dry matter are important characteristics of sweetpotato varieties in addition to starch content which has industrial applications. The objective of this study was to evaluate the performance of progenies sweetpotato obtained from controlled cross system for higher root yield, dry matter and starch content. Field experiment was conducted at the National Root Crops Research Institute, Umudike, Southeast Nigeria during the 2015 and 2016 cropping seasons to evaluate diversity across progenies of three (3) sweetpotato families; SautiX442162 (6), LigriXFaaara (17), SautiXBohye (17), including two check varieties (Umuspo3 and TIS 87/0087). This experiment was laid out in a randomized complete block design with three replicates. The variables observed included: number of root per plot, the weight of root per plot, dry matter content, root yield and starch content. The analysis of variance showed a significant difference among the tested genotypes in most of traits observed. Root yield ranged from 2.2– 19.33t/ha and starch content ranged from 80.11mg100g<sup>-1</sup> to 20.76mg100<sup>-1</sup>. SautiX442162/1 had the highest starch content, 80.11mg100g<sup>-1</sup> while SautiXBohye/9 had the lowest starch content, 20.76mg100<sup>-1</sup>. Five promising genotypes; LigriXFaaara/2 (14.67t/ha), LigriXFaaara/3 (16.02t/ha), SautiXBohye/1 (15.03t/ha), SautiXBohye/2 (19.33t/ha), SautiXBohye/3 (16.00t/ha) recorded high yield above the world's estimated annual average yield of 13.7t/ha. Six promising genotypes recorded starch content above 50mg100<sup>-1</sup>; SautiX442162/1 (80.11mg100<sup>-1</sup>), SautiX442162/3 (77.51mg100<sup>-1</sup>), SautiX442162/2 (66.14mg100<sup>-1</sup>), SautiX442162/6 (57.36 mg100<sup>-1</sup>), SautiX442162/4 (57.19 mg100<sup>-1</sup>), SautiX442162/5 (55.99 mg100<sup>-1</sup>). Eleven promising genotypes that recorded high yield and starch could be subjected to multi-location trail and incorporated into further breeding program.

**Keywords:** Dry matter, *Ipomoea batatas*, Progenies, Storage root, Starch, Sweetpotato.

**1. INTRODUCTION**

Sweetpotato (*Ipomoea batatas* (L.) Lam) is a dicotyledonous tuber from the Convolvulaceae family and it is an important staple crop that is consumed in many developing countries in the tropics (Thottappilly and Loebenstein, 2009). Sweetpotato is a low-cost crop that is commonly utilized as a food, feed and a good source of starch (Odebode, 2004). Across the globe, the

annual sweetpotato production is estimated at 110.7t over an area of 8.2 million ha with a productivity of 13.5t/ha. China is the world's largest producer of around 79 ton around 3.5 million ha (FAO, 2013). The crop is predominately grown in developing nations of the world where over 95% of the global production is recorded (Loebenstein, 2009). Africa accounts for about 15% of the sweetpotato production across the globe (Loebenstein, 2009). Worldwide, the average annual production of sweetpotato is around 131 million tonnes, grown on an estimated 9 million hectares with an estimated yield of 13.7 t/ha (FAOSTAT, 2009). In Nigeria, annual yields of common local varieties of sweetpotato in the south-eastern zone is approximated while in the northern part of the country, it is 3.5t/ha, except for Plateau and Bauchi States with an annual average yield of 7 to 8t/ha (Tewe, *et al.*, 2003). Fresh storage root of sweetpotato has low glycaemic index, considering the slow rate of digestion of its complex carbohydrate and its lower rate of absorption of sugars into the blood stream. It is therefore, a suitable source of food for the diabetics (Willcox *et al.*, 2009). Sweetpotato has numerous industrial uses (Lin *et al.*, 2007). It is a common source of industrial raw materials such as starch and alcohol, yielding 30 – 50% higher starch compared to rice, corn and wheat sources under same environmental conditions (Rahman *et al.*, 2003). 70 percent of the dry weight of sweetpotato is constituted by the starch content and high dry matter content serves as a significant characteristic of a good sweetpotato variety (Mwanga *et al.*, 2007). Starch contributes to the textural properties of foods products and it is widely used for food and industrial applications as thickener, colloidal stabilizer, and gelling, bulking and water retention agent (Singh *et al.*, 2008).

Evaluation of newly developed progeny in yield trial could reveal some promising genotypes with high root yields and other desirable agronomic traits. The aim of this study was to evaluate forty sweetpotato progenies obtained from controlled cross system for storage root yield, dry matter and starch content.

## **2. MATERIALS AND METHOD**

**Study Site:** The experiment was carried out during the 2015 and 2016 planting seasons at the National Root Crops Research Institute, Umudike, Southeast Nigeria. Umudike is located at latitude 05° 29' N, longitude 07° 33' E, altitude 122m above sea level. Umudike is located in the humid tropics and has a total rainfall of around 2,177 mm per year, an average annual temperature of around 26 °C and its soil is classified as sandy-loamy Uutisol (NRCRI, 2012).

**2.1 Nursery Management:** The nursery soil consisted of a mixture of topsoil, organic material and river sand in a ratio of 3: 2: 1. The nursery was prepared in the greenhouse of the National Root Crops Research Institute, Umudike and Southeast, Nigeria using polyethylene bags containing 1 kg of soil. After the seeds were soaked in cold water for about twenty-four hours to break the dormancy, some of the seeds that germinated and were carefully isolated from the container with cold water and sown separately in the well-watered soil in polyethylene bags.

**2.2 Agronomic practices:** The land for the trial site was cleared, ploughed, harrowed and skinned. The prepared land was demarcated in plots of 1.5 m<sup>2</sup> (1 mx1.5m). The field was laid out in an extended three replicate design and two control varieties were planted at intervals. The planting distance was 1mx0.3m. This resulted in five stands of sweetpotato per parcel, equivalent to 33,333 stands per hectare. Therefore, the land area for this study was 240m<sup>2</sup>. Planting was done on July 21, 2015 and April 18, 2016 with five vines on each plot. The crops were rainfed.

Weeding was done 6 and 12 weeks after planting (WAP). Compound fertilizer (NPK 15:15:15) was applied at a rate of 400 kg/ha 4 WAP with side placement. Data were collected at 16 WAP (Ezulike *et al.*, 2001) on the number of roots per plot, marketable (less than 100g) and unmarketable roots (greater than 100 g) (Levett, 1993).

**Table 1: Progenies of Sweetpotato and their sources.**

No.	Genotypes	Sources
1.	LigriXFaaara/1	CIP, Kumasa, Ghana
2.	LigriXFaaara/2	CIP, Kumasa, Ghana
3.	LigriXFaaara/3	CIP, Kumasa, Ghana
4.	LigriXFaaara/4	CIP, Kumasa, Ghana
5.	LigriXFaaara/5	CIP, Kumasa, Ghana
6.	LigriXFaaara/6	CIP, Kumasa, Ghana
7.	LigriXFaaara/7	CIP, Kumasa, Ghana
8.	LigriXFaaara/8	CIP, Kumasa, Ghana
9.	LigriXFaaara/9	CIP, Kumasa, Ghana
10.	LigriXFaaara/10	CIP, Kumasa, Ghana
11.	LigriXFaaara/11	CIP, Kumasa, Ghana
12.	LigriXFaaara/12	CIP, Kumasa, Ghana
13.	LigriXFaaara/13	CIP, Kumasa, Ghana
14.	LigriXFaaara/14	CIP, Kumasa, Ghana
15.	LigriXFaaara/15	CIP, Kumasa, Ghana
16.	LigriXFaaara/16	CIP, Kumasa, Ghana
17.	LigriXFaaara/17	CIP, Kumasa, Ghana
18.	SautiXBohye/1	CIP, Kumasa, Ghana
19.	SautiXBohye/2	CIP, Kumasa, Ghana
20.	SautiXBohye/3	CIP, Kumasa, Ghana
21.	SautiXBohye/4	CIP, Kumasa, Ghana
No.	Genotypes	Sources
22.	SautiXBohye/5	CIP, Kumasa, Ghana
23.	SautiXBohye/6	CIP, Kumasa, Ghana
24.	SautiXBohye/7	CIP, Kumasa, Ghana
25.	SautiXBohye/8	CIP, Kumasa, Ghana
26.	SautiXBohye/9	CIP, Kumasa, Ghana
27.	SautiXBohye/10	CIP, Kumasa, Ghana
28.	SautiXBohye/11	CIP, Kumasa, Ghana
29.	SautiXBohye/12	CIP, Kumasa, Ghana
30.	SautiXBohye/13	CIP, Kumasa, Ghana
31.	SautiXBohye/14	CIP, Kumasa, Ghana
32.	SautiXBohye/15	CIP, Kumasa, Ghana
33.	SautiXBohye/16	CIP, Kumasa, Ghana
34.	SautiXBohye/17	CIP, Kumasa, Ghana

35.	SautiX442162/1	CIP, Kumasa, Ghana
36.	SautiX442162/2	CIP, Kumasa, Ghana
37.	SautiX442162/3	CIP, Kumasa, Ghana
38.	SautiX442162/4	CIP, Kumasa, Ghana
39.	SautiX442162/5	CIP, Kumasa, Ghana
40.	SautiX442162/6	CIP, Kumasa, Ghana
41.	Umuspo 3	Check Variety, Nigeria
42.	TIS 87/0087	Check Variety, Nigeria

### 2.3 Dry Matter Determination

Dry matter content was determined within twenty four (24) hour after harvest, two medium sized fresh storage roots per genotypes was sliced into small pieces and 100g of each tuber samples was dried in hot air oven at 80°C for 24 hours until a constant mass was attained. Dry matter content was determined by weighing the initial and final weight, and calculating the percentage of dried weight. The same procedures were followed for all the replications.

Dry matter (%) = Dry weight of the tuber/ Fresh weight of the tuber x 100

### 2.4 Determination of Starch Content

Starch content was determined based on dry matter content of storage roots. Using a dry weight conversion method, dry matter was measured by the percentage of dry weight to the fresh weight of the storage roots. The conversion formula of the starch content in sweetpotato described by Wang, *et al.* (1989) was followed, i.e.,  $y = 0.86945x - 6.34587$ , in which y is the starch content and x is the dry matter content.

### Statistical Analysis

Harvest data were subjected to Analysis of variance (ANOVA) and mean separation was carried out using the Least Significant Difference (LSD) test at 5% level of significance. Data for dry matter and starch content were subjected to an Analysis of Variance (ANOVA). Pearson's correlation analysis was done to show association among yield and yield related components of sweetpotato genotypes. Principal component analysis was done for the yield related traits.

## 3. RESULTS

The results presented in Table 2 showed that in 2015 cropping season, the analysis of variance revealed there were significant ( $P \leq 0.05$ ) differences among genotypes for unmarketable root number, marketable root number, marketable root weight, yield, dry matter and starch contents but there was no significant difference among the genotypes for unmarketable root weight (Table 2). In 2016 cropping season, analysis of variance showed that there were significant ( $P \leq 0.05$ ) differences among genotypes for unmarketable root number, marketable root number, unmarketable root weight yield, dry matter and starch contents but there was no significant difference among the genotypes for marketable root weight (Table 2). In 2015 cropping season, SautiXBohye/2 produced the highest fresh storage root yield in 2015 cropping season (19.33t/ha). The fresh storage root yield of both check varieties Umuspo 3 and TIS 87/0087

were 8.66t/ha and 7.86t/ha, respectively (Table 2). In 2016 cropping season, LigriXFaaara/4 recorded the highest mean of marketable root weight (1.25kg/ha) and highest fresh storage root yield (9.00t/ha.) The fresh storage root yield of both check varieties Umuspo 3 and TIS 87/0087 were 8.06t/ha and 8.33t/ha, respectively.

SautiXBohye/1, SautiXBohye/2, SautiXBohye/4, SautiXBohye/6, LigriXFaaara/1, LigriXFaaara/2, LigriXFaaara/3 had high yield and dry matter content. Table 2 showed that in 2015 cropping season, thirteen genotypes produced higher fresh storage root yield than the national check (TIS 87/0087) while in 2016 cropping season, only LigriXFaaara/4 produced higher fresh storage root yield than the national check.

The result presented in Table 2 showed that dry matter and starch contents differ significantly ( $P \leq 0.05$ ). The starch content ranged from 80.11mg100g<sup>-1</sup> to 20.76mg100<sup>-1</sup>. SautiX442162/1 had the highest starch content, 80.11mg100g<sup>-1</sup> while SautiXBohye/9 had the lowest starch content, 20.76mg100<sup>-1</sup>. The mean of the genotypes for dry matter ranged from 51.50 % to 19.45%. LigriXFaaara/8 had the highest dry matter (51.50%) while SautiX442162/1 had the lowest dry matter (19.45%). Among the forty genotypes evaluated, thirty five (35) had dry matter content above 40%. Six genotypes recorded starch content above 50mg100<sup>-1</sup>; SautiX442162/1 (80.11mg100<sup>-1</sup>), SautiX442162/3 (77.51mg100<sup>-1</sup>), SautiX442162/2 (66.14mg100<sup>-1</sup>), SautiX442162/6 (57.36 mg100<sup>-1</sup>), SautiX442162/4 (57.19 mg100<sup>-1</sup>), SautiX442162/5 (55.99 mg100<sup>-1</sup>).

**Table 2: Means of 40 genotypes for total storage root yield for 2015 and 2016 planting seasons**

Genotypes	MRN 2015	URN 2015	MRW 2015	URW 2015	Yield 2015	MRN 2016	URN 2016	MRW 2016	URW 2016	Yield 2016	Dry Matter	Starch
LigriXFaaara/1	4.00	3.00	1.80	0.25	13.66	3.00	3.00	0.90	0.09	6.57	45.84	32.83
LigriXFaaara/2	4.00	2.00	2.05	0.15	14.67	3.50	1.50	0.85	0.05	5.97	44.80	31.45
LigriXFaaara/3	5.00	0.50	2.40	0.01	16.02	2.00	0.50	0.53	0.04	3.76	47.84	33.08
LigriXFaaara/4	3.00	1.00	1.00	0.05	7.00	4.00	2.00	1.25	0.10	9.00	48.11	32.65
LigriXFaaara/5	3.50	2.50	1.10	0.20	8.66	4.50	3.00	0.55	0.09	4.23	47.11	30.77
LigriXFaaara/6	4.50	1.50	1.45	0.10	10.33	2.50	5.00	0.65	0.20	5.63	49.24	33.14
LigriXFaaara/7	5.00	0.00	1.15	0.00	7.67	2.00	3.00	0.50	0.08	3.83	45.97	29.45
LigriXFaaara/8	2.50	1.50	0.45	0.10	3.66	3.00	1.50	0.75	0.10	5.36	51.50	32.14
LigriXFaaara/9	3.50	1.50	0.75	0.10	5.66	3.00	2.00	0.75	0.05	5.33	50.31	30.45
LigriXFaaara/10	4.00	2.00	0.95	0.15	7.33	2.00	2.50	0.30	0.10	2.67	39.73	27.13
LigriXFaaara/11	4.00	1.00	0.85	0.05	6.00	2.50	3.50	0.75	0.10	5.65	49.00	26.30
LigriXFaaara/12	2.50	0.50	0.70	0.05	5.00	2.50	1.50	0.83	0.05	5.80	48.87	31.27
LigriXFaaara/13	3.50	0.00	0.85	0.00	5.66	3.50	0.00	0.85	0.00	5.66	49.44	27.51
LigriXFaaara/14	3.00	1.00	0.40	0.10	3.33	3.00	1.00	0.40	0.10	3.33	49.69	23.31
LigriXFaaara/15	3.00	2.00	1.10	0.10	8.00	3.00	2.00	1.10	0.10	8.00	47.43	30.33
LigriXFaaara/16	4.00	2.00	0.95	0.15	7.33	3.00	3.00	0.55	0.09	4.23	50.21	29.85
LigriXFaaara/17	4.00	1.00	0.85	0.05	6.00	3.00	2.50	0.95	0.10	6.97	50.12	26.91
SautiXBohye/1	5.50	0.00	2.30	0.00	15.30	3.00	1.00	1.10	0.10	8.00	45.35	21.76

SautiXBohye/2	4.50	2.00	2.75	0.15	19.33	4.00	0.00	0.90	0.00	6.00	44.72	25.34
SautiXBohye/3	4.00	2.00	2.25	0.15	16.00	2.00	1.00	0.50	0.08	3.86	37.37	25.78
SautiXBohye/4	4.00	1.50	1.95	0.11	13.65	2.50	2.00	0.48	0.10	3.80	45.67	22.32
SautiXBohye/5	3.00	0.50	1.35	0.05	9.32	3.00	1.00	0.75	0.05	5.33	43.51	21.58
SautiXBohye/6	4.50	1.00	2.30	0.10	15.98	2.00	1.00	0.50	0.15	4.33	44.18	26.76
SautiXBohye/7	3.00	1.50	1.28	0.00	8.47	1.00	2.00	0.40	0.05	3.00	43.97	24.10
SautiXBohye/8	2.00	4.00	0.50	0.20	4.66	4.00	2.00	1.20	0.10	8.06	45.87	24.23
SautiXBohye/9	2.00	0.00	0.80	0.00	5.33	3.00	4.00	1.10	0.10	8.00	44.00	20.76
SautiXBohye/10	2.00	0.00	0.55	0.00	3.66	1.00	4.00	0.20	0.10	2.00	44.56	25.40
SautiXBohye/11	3.00	2.00	0.50	0.10	4.00	2.00	5.00	0.40	0.10	3.30	46.50	25.82
SautiXBohye/12	6.00	1.00	0.40	0.10	3.33	2.00	3.00	0.55	0.09	4.26	43.29	22.42
SautiXBohye/13	2.00	7.00	0.50	0.30	5.33	3.00	0.00	0.40	0.00	2.66	44.44	21.61
SautiXBohye/14	3.00	4.00	0.60	0.10	4.66	3.00	1.00	0.40	0.10	3.33	44.74	26.74
SautiXBohye/15	1.00	0.00	0.20	0.00	1.33	3.00	2.00	1.10	0.10	8.00	40.53	24.23
SautiXBohye/16	2.00	0.00	0.55	0.00	3.66	2.00	0.00	0.55	0.00	3.66	45.62	24.10
SautiXBohye/17	3.00	2.00	0.50	0.10	4.00	3.00	2.00	0.50	0.10	4.00	43.66	20.89
SautiX442162/1	4.50	3.50	3.35	2.55	8.20	2.00	4.50	0.45	0.08	3.45	19.45	80.11
SautiX442162/2	3.50	4.50	1.60	0.20	11.40	2.50	4.00	0.63	0.08	4.70	33.43	66.14
SautiX442162/3	2.50	1.50	0.60	0.13	4.83	3.00	4.00	0.75	0.08	5.53	22.49	77.51
SautiX442162/4	2.00	1.00	0.50	0.03	3.50	2.00	2.50	0.60	0.07	4.47	42.41	57.19
SautiX442162/5	6.00	1.00	1.80	0.05	12.03	3.00	3.00	0.85	0.08	5.83	44.01	55.99
SautiX442162/6	2.00	2.50	0.15	0.06	1.37	2.00	2.50	0.15	0.06	1.37	42.32	57.36
Umuspo 3	3.00	0.00	1.10	0.00	7.33	3.00	2.50	0.65	0.05	8.06	42.98	27.22
TIS 87/0087	4.00	0.00	1.30	0.00	8.66	3.50	3.50	0.60	0.05	8.33	39.24	23.73
<b>Grand mean</b>	<b>3.45</b>	<b>1.56</b>	<b>1.15</b>	<b>0.14</b>	<b>7.89</b>	<b>2.73</b>	<b>2.26</b>	<b>0.67</b>	<b>0.08</b>	<b>5.13</b>	<b>44.03</b>	<b>32.32</b>
<b>LSD<sub>0.05</sub></b>	<b>1.31</b>	<b>1.82</b>	<b>1.1</b>	<b>NS</b>	<b>6.69</b>	<b>1.08</b>	<b>1.94</b>	<b>NS</b>	<b>0.05</b>	<b>2.74</b>	<b>2.17</b>	<b>3.14</b>

MRN = Marketable root number, URN = Unmarketable root number, MRW = Marketable root weight, URW = Unmarketable root weight

Table 3 showed the Pearson correlation co-efficients ( $\gamma$ ) for the storage root parameters for forty genotypes. Total storage root yield had significant and positive correlation coefficient with number of marketable roots and marketable weight/ha but negative correlation coefficient with number of unmarketable roots (Table 3). Correlation coefficients for the 7 traits are presented in Table 3. Generally, all the traits except unmarketable storage root weight at harvest exhibited positive and significant ( $P \leq 0.05$  and  $P \leq 0.01$ ) correlation with total roots weight (yield). Some of the traits also exhibited significant and positive association among themselves as well as significant and negative association. Yield at harvest had a positive association with unmarketable fresh storage root number ( $r = 0.08$ ) (Table 3). Yield at harvest, however, had a negative association with unmarketable fresh storage root weight ( $r = -0.02$ ). Yield at harvest had a negative association with dry matter ( $r = -0.036$ ) and starch ( $r = -0.034$ ) (Table 3)

**Table 3: Pearson correlation co-efficients ( $\gamma$ ) for the storage root parameters for the 40 genotypes of sweetpotato**

	MRN	URN	MRW	URW	Yield	Dry matter	Starch
<b>MRTN</b>							
<b>UMRTN</b>	-0.087						
<b>MRTW</b>	0.603**	0.108					
<b>UMRTW</b>	0.122	0.363**	0.458**				
<b>Yield</b>	0.591**	0.083	0.857**	-0.028			
<b>Dry matter</b>	0.015	-0.191	-0.245*	-0.427**	-0.036		
<b>Starch</b>	0.035	0.201	0.154	0.365**	-0.034	-0.675**	
**. Correlation is significant at the 0.01 level (2-tailed). *. Correlation is significant at the 0.05 level (2-tailed).							

\*\* . Correlation is significant at the 0.01 level (2-tailed).

\*. Correlation is significant at the 0.05 level (2-tailed).

MRN = Marketable root number, URN = Unmarketable root number, MRW = Marketable root weight, URW = Unmarketable root weight

### 3.1 Principal component analyses

Two principal component axes (PC1 and PC2) in the principal component analysis (PC analysis) had eigen values up to 1.0, presenting cumulative variance of 65.89% (Table 4). Principal component one (PC1), with eigen value of 2.64, contributed 37.57% of the total variability, while PC2, with eigen value of 1.96, accounted for 28.13% of total variability observed among the 40 sweetpotato genotypes. In PC1, the traits that accounted for most of the 37.57% observed variability among the 40 genotypes included number of marketable roots, with vector loading of 0.616, unmarketable storage root number (0.314), weight of marketable roots (0.902), weight of unmarketable roots (0.598), yield (0.700), dry matter and starch contents (-0.530 and 0.472, respectively) (Table 4).

**Table 4: Principal component analysis of the 141 sweetpotato genotypes**

	PCA 1	PCA 2
MRN	0.616	0.536
URN	0.314	-0.396

MRW	0.902	0.333
URW	0.598	-0.468
Yield	0.700	0.600
Dry matter	-0.530	0.640
Starch	0.472	-0.652
Total	2.643	1.969
% of Variance	37.757	28.136
Cumulative %	37.757	65.892

RN = Marketable root number, URN = Unmarketable root number,  
MRW = Marketable root weight, URW = Unmarketable root weight

The current result agrees with the findings of Andrade *et al.* (2009), who reported that the total storage root yields of five sweetpotato varieties from Sub-Saharan Africa ranged between 0.5 and 65t/ha. Consistent with the results of this study, Mcharo and Ndolo (2013) and Nedunchezhiyan *et al.* (2007) reported large differences between sweetpotato clones in terms of root yield due to genetic variation. Similarly, Yanggen and Nagujja, (2006) reported that population averages across varieties, locations and replications for storage root yield were low at 8.6 t/ha, but above the national average of 4.2 t/ha in Uganda. Consistent with the results of this study, Wassu *et al.* (2015) reported significant variations between 116 sweetpotato genotypes that included the genotypes tested in this experiment, with a mean total fresh root yield from storage of 10.74 (t/ha) and a range of 2.26 to 28.46 t/ha. The high yielding genotypes could be incorporated into sweetpotato breeding programs to improve the yield of other accessions. According to Afuape *et al.* (2011), within the group of genotypes, PCA is a technique to identify which plant traits is the most contributing to the observed variation. Afuape *et al.* (2011), who reported a cumulative variance of 76.00% for the first three axes in the evaluation of twenty-one sweetpotato genotypes, found important traits to be the genotypes they worked with. Four main principal components (PC) were identified, accounting for 67.22% of the total variation between accessions (Koussao *et al.*, 2014). Placide *et al.*, (2015) also used PCA to study the variability between 54 sweetpotato genotypes and found the cumulative variance of 77.83% from the first seven major component axes. The results of this study are in agreement with the results of these authors as there was enough variability to support the choice between genotypes.

#### 4. CONCLUSION

Analysis of variance showed the significant difference among the forty tested genotypes in all traits observed. The descriptive analysis showed that root yield ranged from 2.2– 19.33t/ha with an average 7.86t/ha and starch content ranged from 80.11mg100g<sup>-1</sup> to 20.76mg100<sup>-1</sup>. SautiX442162/1 had the highest starch content, 80.11mg100g<sup>-1</sup> while SautiXBohye/9 had the



lowest starch content,  $20.76\text{mg}100^{-1}$ . The mean of the genotypes for dry matter ranged from 51.50 % to 19.45% with an average 44.03%. The study showed that thirteen genotypes produced higher fresh storage root yield than the national check (TIS 87/0087). Five promising genotypes; LigriXFaara/2 ( $14.67\text{t}/\text{ha}$ ), LigriXFaara/3 ( $16.02\text{t}/\text{ha}$ ), SautiXBohye/1 ( $15.03\text{t}/\text{ha}$ ), SautiXBohye/2 ( $19.33\text{t}/\text{ha}$ ), SautiXBohye/3 ( $16.00\text{t}/\text{ha}$ ) recorded high yield above the world's estimated annual average yield of  $13.7\text{t}/\text{ha}$ . Six promising genotypes recorded starch content above  $50.00\text{mg}100^{-1}$ ; SautiX442162/1 ( $80.11\text{mg}100^{-1}$ ), SautiX442162/3 ( $77.51\text{mg}100^{-1}$ ), SautiX442162/2 ( $66.14\text{mg}100^{-1}$ ), SautiX442162/6 ( $57.36\text{mg}100^{-1}$ ), SautiX442162/4 ( $57.19\text{mg}100^{-1}$ ), SautiX442162/5 ( $55.99\text{mg}100^{-1}$ ). The low yield recorded in 2016 planting season could be attributed to early planting in the month of April. Eleven promising genotypes that recorded high yield and starch could be subjected to multi-location trail and incorporated into further breeding program.

## 5. ACKNOWLEDGMENT

The first author thanks Prof. Peter I. O. for providing thorough supervision through this study. The first author also thanks Dr Afuape S. O. (the second author) for sourcing the plant materials and support during this research. Mr. Ulasi Eugene and Mrs. Ulasi Patricia are thanked immensely for their financial support during this research.

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