

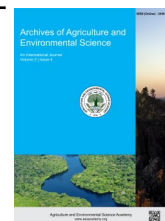


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ORIGINAL RESEARCH ARTICLE



Screening of some sweet potato (*Ipomoea batatas* (L.) Lam) genotypes for yield and damage by *Cylas puncticollis* under rainfed conditions in Umudike, Southeastern Nigeria

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ABSTRACT

A field experiment was conducted at the National Root Crops Research Institute, Umudike, Southeastern Nigeria during the 2015 and 2016 cropping seasons to evaluate diversity among F₁ population of sweet potato, namely: Sauti × 442162 (6), Ligri × Faara (17), Sauti × Bohye (17), including two checks (Umuspo 3 and TIS 87/0087). This experiment was laid out in a randomized complete block design with three replicates under rainfed condition. Data on fresh storage root yield were recorded at 120 days after planting. Analysis of variance, correlation and principal component analysis were utilized for data analysis. The study revealed that yield of fresh storage root showed significant differences ($P \leq 0.05$) among the sweet potato genotypes. Sauti X Bohye produced the highest storage root yield (19.33 t/ha) in 2015 and performed better than the national check TIS 87/0087 that recorded a storage root yield of 10.84 t/ha. The result from the study showed that out of the forty genotypes evaluated, twenty-six (26) genotypes recorded attack of *C. puncticollis*. The extent of the damage recorded among the genotypes attacked by *C. puncticollis* ranged from severe damage to little damage among the genotypes that recorded fresh storage root damage. SautiXBohye/11, SautiXBohye/13, SautiXBohye/17 recorded severe damage caused by *C. puncticollis* while LigriXFara/15 recorded moderate damaged caused by *C. puncticollis*. Fifteen (15) genotypes did not record any infestation by *Cylas puncticollis*. All characters except unmarketable storage root weight at harvest exhibited positive and significant ($P \leq 0.01$) correlation with total roots weight (yield). Principal component analysis had three main principal components explaining 84.25% of the total variation with number of marketable roots, weight of marketable roots, storage root yield and *Cylas* incidence contributing the most to the first PCA. These genotypes could possess resistance genes to *Cylas puncticollis* and these genotypes could be incorporated in breeding programs for further trail.

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INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is a principal crop consumed as food across the globe and utilized as an importance raw material for industrial purposes (Korada *et al.*, 2010). Sweet potato is cultivated across different continents of the world on

approximately 8.21 million hectare (ha) with an estimated annual yield of 104.02 million tonnes (FAOSTAT, 2014). The world's annual average yield of sweet potato is 15.9 tha^{-1} , average yield in Africa (9.6 tha^{-1}), China (22.0 tha^{-1}) and Nigeria (3.0 tha^{-1}) (FAO, 2015; Nwankwo and Basse, 2021). Sweet potato production in Nigeria is challenged with numerous constraints

including biotic, abiotic, unavailability of improved varieties, which have contributed to the existing low yields of 3t/ha compared to the potential productivity of the crop varying from 15 to 23 t ha⁻¹ (Sebastiani et al., 2007). Among these constraints, sweet potato weevil (*Cylas puncticollis*) has caused considerable damage and losses in the production of sweet potato in Sub Saharan Africa (Devi et al., 2016). Sweet potato weevil (*Cylas* spp.) is known as the most destructive pest of the crop in sweet potatoes (*Ipomoea batatas* L. (Lam)) because its infestation directly contributes to high storage root damage intensity, making high storage root yield loss inevitable (Smith and Beuzelin 2015; Chen 2017). High storage root yield is threatened by *Cylas* species infestation. *Cylas* spp is considered the most destructive biotic problem that undermines sustainable sweet potato production, with a record of up to 97% storage root losses (Yan et al., 2020). *Cylas* spp. attacks sweet potato tuber in the field as well as in storage. Infested tubers are dotted with several small holes and cracks, often dark in colour and squishy in appearance. Consequent upon the damaging activities caused by this pest, entry of soil-borne pathogens intensifies (Devi, 2016). Even minimal incidence of sweet potato weevil reduces the storage root quality and produces an unpleasant taste, drastically reducing its nutritive and market values as well as its shelf life (Mbua et al., 2016).

The most common strategy for controlling the sweet potato weevil (SPW) is chemical control (Smith and Beuzelin 2015; Chen, 2017), but this approach is not thought to be environmentally friendly. Therefore, it is strongly advised to decrease the use of synthetic pesticides and to support more environmentally friendly management methods. More so, considering that weevils live underground and spend the majority of their development cycles inside the roots, the usage of chemical control methods does not always prove to be effective (Anyanga, 2015). A promising solution to this prevailing problem is to develop sweet potato cultivars with high yields and significant resistance to SPW. This can be achieved by identifying at the onset of varietal development using the existing and newly introduced sweet potato genotypes. The earlier generation selected clones can incorporate the desired traits. Screening of newly developed genotypes under rainfed conditions would allow for the identification and selection of genotypes that demonstrates superior agronomic traits and resistance to *Cylas* spp. The objective of this study is therefore to screen newly developed sweet potato genotypes for fresh storage root yield and damage by *Cylas puncticollis*

MATERIALS AND METHODS

Experimental site

The experiments were carried out during the early cropping seasons in 2016 and 2017 at the National Root Crops Research Institute, (NRCRI) Umudike, Southeastern Nigeria, on latitude 05° 29' N, longitude 07° 33' E of the equator and on an elevation of 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).

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 Southeastern, 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.

Experimental designs

The land for the trial site was cleared, plowed, harrowed and skinned. The prepared land was demarcated in plots of 1.5 m² (1 m x 1.5 m). The field was laid out in an extended three replicate design and two control varieties were planted at intervals. The planting distance was 1m x 0.3m. This resulted in five stands of sweet potatoes per parcel, equivalent to 33,333 stands per hectare. Therefore, the land area for this investigation was 240 m². Planting was done on July 21, 2016 and April 18, 2016 with five vines on each plot. The crops were fed with rain. 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.

Planting materials

Forty seeds (40) of sweet potato from three (3) different families, sourced from International Potato Center, Kumasi, Ghana, including two varieties (Umuspo 3 and TIS 87/0087) which served as checks, were used for the experiment. The dormancy of the seeds was broken by soaking in cold water for twenty-four hours before planting.

Harvesting and data collection

Harvesting was done 120 DAP. Plots were harvested by uprooting the five stands from the center of each row. Vines were first cut with cutlasses and the storage roots were uprooted with fork. Data were taken on the following characters. Harvest data were collected at 16 WAP (Ezulike et al., 2001) which included the number of roots per plot, marketable root size (> 100 g) and unmarketable root size (<100 g) (Levett, 1993). Severity of damage by *Cylas puncticollis* (Stathers et al., 2003) was scored. The number of tubers infected by *C. puncticollis* were counted and their percentages determined as:

Then, the severity of damage was indicated for each accession using a five point (1-5), where:

1 = 0%: no observable damage of sweet potato tubers by weevils (*C. puncticollis*)

2 = 1%-25% sweet potato root tubers attacked by *C. puncticollis* indicating very little damage.

3 = 26%-50% sweet potato root tubers attacked by *C. puncticollis* indicating moderate damage.

Table 1. Sweet potato genotypes and their sources.

S.No.	Genotypes	Source
1	LigriXFaara/1	Centre International des Potato (CIP), Platform Kumasa, Ghana
2	LigriXFaara/2	Centre International des Potato (CIP), Platform Kumasa, Ghana
3	LigriXFaara/3	Centre International des Potato (CIP), Platform Kumasa, Ghana
4	LigriXFaara/4	Centre International des Potato (CIP), Platform Kumasa, Ghana
5	LigriXFaara/5	Centre International des Potato (CIP), Platform Kumasa, Ghana
6	LigriXFaara/6	Centre International des Potato (CIP), Platform Kumasa, Ghana
7	LigriXFaara/7	Centre International des Potato (CIP), Platform Kumasa, Ghana
8	LigriXFaara/8	Centre International des Potato (CIP), Platform Kumasa, Ghana
9	LigriXFaara/9	Centre International des Potato (CIP), Platform Kumasa, Ghana
10	LigriXFaara/10	Centre International des Potato (CIP), Platform Kumasa, Ghana
11	LigriXFaara/11	Centre International des Potato (CIP), Platform Kumasa, Ghana
12	LigriXFaara/12	Centre International des Potato (CIP), Platform Kumasa, Ghana
13	LigriXFaara/13	Centre International des Potato (CIP), Platform Kumasa, Ghana
14	LigriXFaara/14	Centre International des Potato (CIP), Platform Kumasa, Ghana
15	LigriXFaara/15	Centre International des Potato (CIP), Platform Kumasa, Ghana
16	LigriXFaara/16	Centre International des Potato (CIP), Platform Kumasa, Ghana
17	LigriXFaara/17	Centre International des Potato (CIP), Platform Kumasa, Ghana
18	SautiXBohye/1	Centre International des Potato (CIP), Platform Kumasa, Ghana
19	SautiXBohye/2	Centre International des Potato (CIP), Platform Kumasa, Ghana
20	SautiXBohye/3	Centre International des Potato (CIP), Platform Kumasa, Ghana
21	SautiXBohye/4	Centre International des Potato (CIP), Platform Kumasa, Ghana
22	SautiXBohye/5	Centre International des Potato (CIP), Platform Kumasa, Ghana
23	SautiXBohye/6	Centre International des Potato (CIP), Platform Kumasa, Ghana
24	SautiXBohye/7	Centre International des Potato (CIP), Platform Kumasa, Ghana
25	SautiXBohye/8	Centre International des Potato (CIP), Platform Kumasa, Ghana
26	SautiXBohye/9	Centre International des Potato (CIP), Platform Kumasa, Ghana
27	SautiXBohye/10	Centre International des Potato (CIP), Platform Kumasa, Ghana
28	SautiXBohye/11	Centre International des Potato (CIP), Platform Kumasa, Ghana
29	SautiXBohye/12	Centre International des Potato (CIP), Platform Kumasa, Ghana
30	SautiXBohye/13	Centre International des Potato (CIP), Platform Kumasa, Ghana
31	SautiXBohye/14	Centre International des Potato (CIP), Platform Kumasa, Ghana
32	SautiXBohye/15	Centre International des Potato (CIP), Platform Kumasa, Ghana
33	SautiXBohye/16	Centre International des Potato (CIP), Platform Kumasa, Ghana
34	SautiXBohye/17	Centre International des Potato (CIP), Platform Kumasa, Ghana
35	SautiX442162/1	Centre International des Potato (CIP), Platform Kumasa, Ghana
36	SautiX442162/2	Centre International des Potato (CIP), Platform Kumasa, Ghana
37	SautiX442162/3	Centre International des Potato (CIP), Platform Kumasa, Ghana
38	SautiX442162/4	Centre International des Potato (CIP), Platform Kumasa, Ghana
39	SautiX442162/5	Centre International des Potato (CIP), Platform Kumasa, Ghana
40	SautiX442162/6	Centre International des Potato (CIP), Platform Kumasa, Ghana
41	Umuspo 3	NRCRI, Umudike, Nigeria
42	TIS 87/0087	NRCRI, Umudike, Nigeria

4 = 51%-75% sweet potato root tubers attacked by *C. puncticollis* indicating extensive damage.

5 = 76%-100% sweet potato root tubers attacked by *C. puncticollis* indicating severe damage.

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 using Statistical Package for Social Scientists (SPSS), Version 22. Pearson's correlation analysis was done to show association among yield and yield related components of sweet potato genotypes. Principal component analysis was done for the yield related traits.

RESULTS AND DISCUSSION

To achieve a successful breeding program for any given crop, it is necessary to ascertain the occurrence of phenotypic and genetic diversity. The results presented in Table 2 showed that in 2015 cropping season, the analysis of variance revealed there were significant ($P < 0.05$) differences among genotypes for unmarketable root number, marketable root number, marketable root weight, yield 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 ($P < 0.05$) differences among genotypes for unmarketable root number, marketable root number, and unmarketable root weight yield but there was no signifi-

Table 2. Means of 40 sweet potato 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	Cylas Incidence	Cylas Severity
LigriXFaara/1	4.00	3.00	1.80	0.25	13.66	3.00	3.00	0.90	0.09	6.57	3.00	2.00
LigriXFaara/2	4.00	2.00	2.05	0.15	14.67	3.50	1.50	0.85	0.05	5.97	0.50	1.50
LigriXFaara/3	5.00	0.50	2.40	0.01	16.02	2.00	0.50	0.53	0.04	3.76	0.50	1.50
LigriXFaara/4	3.00	1.00	1.00	0.05	7.00	4.00	2.00	1.25	0.10	9.00	0.00	0.00
LigriXFaara/5	3.50	2.50	1.10	0.20	8.66	4.50	3.00	0.55	0.09	4.23	2.00	2.50
LigriXFaara/6	4.50	1.50	1.45	0.10	10.33	2.50	5.00	0.65	0.20	5.63	1.50	1.50
LigriXFaara/7	5.00	0.00	1.15	0.00	7.67	2.00	3.00	0.50	0.08	3.83	0.00	0.00
LigriXFaara/8	2.50	1.50	0.45	0.10	3.66	3.00	1.50	0.75	0.10	5.36	0.00	0.00
LigriXFaara/9	3.50	1.50	0.75	0.10	5.66	3.00	2.00	0.75	0.05	5.33	1.50	1.50
LigriXFaara/10	4.00	2.00	0.95	0.15	7.33	2.00	2.50	0.30	0.10	2.67	1.50	1.50
LigriXFaara/11	4.00	1.00	0.85	0.05	6.00	2.50	3.50	0.75	0.10	5.65	0.50	1.50
LigriXFaara/12	2.50	0.50	0.70	0.05	5.00	2.50	1.50	0.83	0.05	5.80	0.50	1.00
LigriXFaara/13	3.50	0.00	0.85	0.00	5.66	3.50	0.00	0.85	0.00	5.66	1.00	0.50
LigriXFaara/14	3.00	1.00	0.40	0.10	3.33	3.00	1.00	0.40	0.10	3.33	0.00	0.00
LigriXFaara/15	3.00	2.00	1.10	0.10	8.00	3.00	2.00	1.10	0.10	8.00	1.00	3.00
LigriXFaara/16	4.00	2.00	0.95	0.15	7.33	3.00	3.00	0.55	0.09	4.23	1.50	1.50
LigriXFaara/17	4.00	1.00	0.85	0.05	6.00	3.00	2.50	0.95	0.10	6.97	0.50	1.50
SautiXBohye/1	5.50	0.00	2.30	0.00	15.30	3.00	1.00	1.10	0.10	8.00	0.00	0.00
SautiXBohye/2	4.50	2.00	2.75	0.15	19.33	4.00	0.00	0.90	0.00	6.00	2.50	1.00
SautiXBohye/3	4.00	2.00	2.25	0.15	16.00	2.00	1.00	0.50	0.08	3.86	0.50	1.50
SautiXBohye/4	4.00	1.50	1.95	0.11	13.65	2.50	2.00	0.48	0.10	3.80	0.50	1.50
SautiXBohye/5	3.00	0.50	1.35	0.05	9.32	3.00	1.00	0.75	0.05	5.33	0.00	0.00
SautiXBohye/6	4.50	1.00	2.30	0.10	15.98	2.00	1.00	0.50	0.15	4.33	0.50	1.00
SautiXBohye/7	3.00	1.50	1.28	0.00	8.47	1.00	2.00	0.40	0.05	3.00	0.00	0.00
SautiXBohye/8	2.00	4.00	0.50	0.20	4.66	4.00	2.00	1.20	0.10	8.06	0.00	0.00
SautiXBohye/9	2.00	0.00	0.80	0.00	5.33	3.00	4.00	1.10	0.10	8.00	0.00	0.00
SautiXBohye/10	2.00	0.00	0.55	0.00	3.66	1.00	4.00	0.20	0.10	2.00	0.00	0.00
SautiXBohye/11	3.00	2.00	0.50	0.10	4.00	2.00	5.00	0.40	0.10	3.30	2.00	5.00
SautiXBohye/12	6.00	1.00	0.40	0.10	3.33	2.00	3.00	0.55	0.09	4.26	0.00	0.00
SautiXBohye/13	2.00	7.00	0.50	0.30	5.33	3.00	0.00	0.40	0.00	2.66	3.00	5.00
SautiXBohye/14	3.00	4.00	0.60	0.10	4.66	3.00	1.00	0.40	0.10	3.33	0.00	0.00
SautiXBohye/15	1.00	0.00	0.20	0.00	1.33	3.00	2.00	1.10	0.10	8.00	0.00	0.00
SautiXBohye/16	2.00	0.00	0.55	0.00	3.66	2.00	0.00	0.55	0.00	3.66	0.00	0.00
SautiXBohye/17	3.00	2.00	0.50	0.10	4.00	3.00	2.00	0.50	0.10	4.00	2.00	5.00
SautiX442162/1	4.50	3.50	3.35	2.55	8.20	2.00	4.50	0.45	0.08	3.45	1.00	1.00
SautiX442162/2	3.50	4.50	1.60	0.20	11.40	2.50	4.00	0.63	0.08	4.70	1.50	1.50
SautiX442162/3	2.50	1.50	0.60	0.13	4.83	3.00	4.00	0.75	0.08	5.53	1.50	1.50
SautiX442162/4	2.00	1.00	0.50	0.03	3.50	2.00	2.50	0.60	0.07	4.47	0.00	0.00
SautiX442162/5	6.00	1.00	1.80	0.05	12.03	3.00	3.00	0.85	0.08	5.83	2.00	2.50
SautiX442162/6	2.00	2.50	0.15	0.06	1.37	2.00	2.50	0.15	0.06	1.37	0.50	1.00
Umuspo 3	3.00	0.00	1.10	0.00	7.33	3.00	2.50	0.65	0.05	8.06	1.50	2.00
TIS 87/0087	4.00	0.00	1.30	0.00	8.66	3.50	3.50	0.60	0.05	8.33	1.00	0.50
Grand mean	3.45	1.56	1.15	0.14	7.89	2.73	2.26	0.67	0.08	5.13	0.85	1.21
LSD _{0.05}	1.31	1.82	1.1	NS	6.69	1.08	1.94	NS	0.05	2.74	NS	1.78

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

cant difference among the genotypes for marketable root weight (Table 2). In 2015 cropping season, SautiX442162/1 recorded the highest mean of marketable root weight (3.50 kg/ha) while SautiXBohye/2 produced the highest fresh storage root yield in 2015 cropping season (19.33 t/ha). The fresh storage root yield of both check varieties Umuspo 3 and TIS 87/0087 were 8.66 t/ha and 7.86 t/ha, respectively (Table 2). In 2016 cropping season, LigriXFaara/4 recorded the highest mean of marketable root weight (1.25 kg/ha) and highest fresh storage root yield (9.00 t/ha). The fresh storage root yield of both check varieties Umuspo 3 and TIS 87/0087 were 8.06 t/

ha and 8.33 t/ha, respectively. 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 LigriXFaara/4 produced higher fresh storage root yield than the national check. According to Jindal et al. (2010) widespread variability among characters immensely contributes to crop improvement through selection. The current result of this study is with the findings of Andrade et al. (2009), who reported that the total storage root yields of five sweet potato varieties from Sub-Saharan Africa ranged between 0.5 and 65 t/ha. Consistent with the results of this

study, Wassu et al. (2015) noted significant variations between 116 sweet potato genotypes 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. Also, results of this study are supported by the findings of Mcharo and Ndolo (2013) and Nedunchezhiyan et al. (2007), who reported large differences between sweet potato clones in terms of root yield due to genetic variation. The results of the storage root yield of both years indicated that higher yield was recorded among the sweet potato populations compared to the yield obtained in 2016 cropping season. The difference in storage root yield in both cropping seasons could be attributed to the variation in environmental and weather conditions of the experimental site in both cropping seasons. Vagaries in environmental factors as well as climatic conditions could result to variation in storage root yield (Osiru et al., 2009; Mwololo et al., 2012).

As shown in Table 2, the root damage intensity was scored from 1 to 5 (Stathers et al., 2003) and utilized to categorize the resistance degree of the evaluated sweet potato genotypes. The result as presented in Table 2 indicated that out of the forty genotypes evaluated, twenty-six (26) genotypes recorded attack of *C. puncticollis*. The extent of the damage recorded among the genotypes attacked by *C. puncticollis* ranged from severe damage to little damage among the genotypes that recorded fresh storage root damage. Severity of damage scored according to the percentages determined by (Stathers et al., 2003) indicated that three genotypes; SautiXBohye/11, SautiXBohye/13, SautiXBohye/17 recorded severe damage caused by *C. puncticollis* while LigriXFaaara/15 recorded moderate damaged caused by *C. puncticollis*. Out of the twenty-six genotypes that recorded root damage caused by *C. puncticollis*, twenty-one genotypes recorded moderate to little damage. This result indicates varying degrees of *C. puncticollis* resistance among the evaluated sweet potato genotypes. The two varieties used as checks in this study; Umuspo 3 and TIS87/0087 recorded moderate and very little damage caused by *C. puncticollis*, respectively. Fifteen (15) accessions (LigriXFaaara/4, LigriXFaaara/7, LigriXFaaara/8, LigriXFaaara/14, SautiXBohye/1, SautiXBohye/5, SautiXBohye/7, SautiXBohye/8, SautiXBohye/9, SautiXBohye/10, SautiXBohye/12, SautiXBohye/14, SautiXBohye/15, SautiXBohye/16 and SautiX442162/4) recorded no attack of *Cylas puncticollis*, which affect sweet potato production in southeastern Nigeria, and could be included in breeding programs to further trails.

The results of this study are in line with those of Rais et al. (2004), who found that 10 SPW out of the 70 accessions evaluated were resistant sweet potato genotypes. Out of 55 sweet potato PI accessions, Jackson et al. (2012) found numerous SPW resistant genotypes. All of these findings suggest that the genetic background of the germplasm evaluated and, to a lesser extent, the impact of planting environments that affect the nutritional quality of sweet potato storage root that affect the preference of SPW are key factors in the success of finding sweet potato genotypes with good SPW resistance (Parr et al. 2016). However, the results of this investigation are at odds with those of other studies (Zuraida et al. 2005; Mau et al. 2019), in which SPW resistant genotypes were scarcely ever found. One SPW-resistant clone was found by Zuraida et al. (2005) out of 50 genotypes tested, while one was discovered by Mau et al. (2019) out of 10 tested clones. In addition, Adom et al. (2018) found that one out of four sweet potato genotypes evaluated was less vulnerable to *C. puncticollis*.

The differences *Cylas* spp. incidence and severity among this sweet potato population could be attributed to the disparity in the chemical elements in the storage roots (Stevenson et al., 2009; Anyanga et al., 2013). In similar studies conducted in Uganda, it was discovered that there are significant levels of esters of hydroxycinnamic acid in root latex of sweet potato which could be associated with weevil resistant in sweet potato (Stevenson et al., 2009) and esters of caffeic and coumaric acid in epidermal and root surface (Anyanga et al., 2013). Diversity in the genetic constitution, environmental conditions and storage root morphology could contribute to the variability in response to sweet potato weevil infestation and damage (Stathers et al., 2003; Muyinza et al., 2012). Ezulike et al. (2001) noted that the resistance of crops significantly influences pest damage and suggested the use of resistant genotypes in areas with reoccurring incidence of *Cylas* spp. Table 3 showed the Pearson correlation co-efficients (γ) for the storage root parameters for forty genotypes. Total storage root yield had significant and positive ($P < 0.01$) correlation coefficient with number of marketable roots and marketable weight/ha but negative correlation coefficient with number of unmarketable roots.

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 ($P < 0.01$) correlation with total roots weight (yield). Some of the traits

Table 3. Pearson Correlation Co-efficients (γ) for the storage root parameters for the 40 sweet potato genotypes.

	MRN	URN	MRW	URW	Yield	<i>Cylas</i> incidence	<i>Cylas</i> severity
MRTN							
UMRTN	-0.087						
MRTW	0.603**	0.108					
UMRTW	0.122	0.363**	0.458**				
Yield	0.591**	0.083	0.857**	-0.028			
<i>Cylas</i> Incidence	0.207	0.495**	0.189	0.025	0.317**		
<i>Cylas</i> Severity	0.039	0.497**	0.092	0.005	0.205	0.759**	

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

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

Table 4. Principal component analysis of the 40 sweet potato genotypes.

	Component		
	PCA 1	PCA 2	PCA 3
MRN	.627	-.519	-.165
URN	.468	.640	.380
MRW	.809	-.499	.190
URW	.344	-.035	.901
Yield	.795	-.408	-.278
Cylas incidence	.673	.568	-.266
Cylas severity	.563	.680	-.243
Total	2.788	1.882	1.227
% of Variance	39.834	26.883	17.533
Cumulative %	39.834	66.717	84.250

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

also exhibited significant and positive association among themselves as well as significant and negative association. Yield at harvest had a positive association with number of unmarketable fresh storage root ($r = 0.08$). Yield at harvest, however, had a negative association with the weight of unmarketable fresh storage root ($r = -0.02$). Yield at harvest had a positive and significant association with root *Cylas* spp incidence ($r = 0.31$) and a positive association with root *Cylas* spp. Severity ($r = 0.20$). Marketable root number had a positive association with storage root *Cylas* spp incidence ($r = -0.20$) and root *Cylas* spp. severity ($r = -0.03$). According to Yohannes et al. (2010), total storage root yield had significant and positive association with marketable storage root yield and average storage root weight. The result of this study indicated a positive correlation established between the fresh storage root yield and *Cylas* incidence and severity. According to Smit (1997), these could correlation between fresh storage root yield and *Cylas* incidence and severity attributed to that fact that during root formation stage, the storage roots cause cracks in the soil or may the exposed above the soil surface, which increases the chance of accessibility to the weevil.

Principal component analysis

Only the first three principal component axes (PC1, PC2 and PC3) in the PCA analysis had eigen values up to 1.0, presenting cumulative variance of 84.250% (Table 4). Principal component one (PC1), with eigen value of 2.78, contributed 39.83% of the total variability, while PC2, with eigen value of 1.88, accounted for 26.88% of total variability observed among the 40 sweet potato genotypes. PC3 had eigen value of 1.22 and contributed with 17.53% to the total observed variability. In PC1, the traits that accounted for most of the 39.83% observed variability among the 40 genotypes included number of marketable roots, with vector loading of 0.627, unmarketable storage root number (0.468), weight of marketable roots (0.809), weight of unmarketable roots (0.344), yield (0.795), roots incidence and severity of *Cylas* spp. (0.673 and 0.563, respectively).

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) reported a total variance of 76.00% for the first three axes in the evaluation 21 sweet potato genotypes. There were

found to be four primary components (PC), which accounted for 67.22% of the overall variation between accessions (Koussao et al., 2014). Placide et al. (2015) utilized PCA to analyze the variation between 54 sweet potato genotypes and discovered that the first seven major component axes had a cumulative variance of 77.83%. Given that there was sufficient variation to allow for the selection of genotypes, the findings of this study concur with those of these authors.

Conclusion

The present study revealed a widespread variability in terms of fresh storage root yield and damage caused by sweet potato weevil, *Cylas puncticollis*, among the tested sweet potato genotypes. SautiXBohye/2 produced the highest fresh storage root yield in 2015 cropping season (19.33t/ha) while LigriXFaara/4 recorded the highest fresh storage root yield (9.00 t/ha.) in 2016 cropping season. Variation in yield could be attributed to environmental factors as well as genetic factors. Thirteen genotypes produced higher fresh storage root yield than the national check (TIS 87/0087). Fifteen (15) genotypes recorded no incidence of resistant to *Cylas puncticollis*. The sweet potato genotypes have shown a rich diversity yield and dissimilarity in reaction to attack of *Cylas puncticollis*, which can serve as a good yardstick for selection in relation to genetic advancement. Three genotypes; SautiXBohye/11, SautiXBohye/13, SautiXBohye/17 recorded severe damage caused by *C. puncticollis* while LigriXFaara/15 recorded moderate damaged caused by *C. puncticollis*. This study showed that nine genotypes LigriXFaara/2, LigriXFaara/3, LigriXFaara/11, LigriXFaara/12, LigriXFaara/17, SautiXBohye/3, SautiXBohye/4, SautiXBohye/6 and SautiX442162/6 that were damage free and were among the high yielding genotypes which could be incorporated into breeding programs for hybridization purposes.

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