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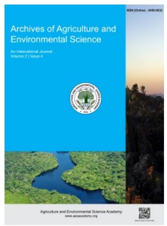

ORIGINAL RESEARCH ARTICLE

CrossMark

High yield and pest resistant genotypes of sweet potato (*Ipomoea batatas* (L.) Lam.) for cultivation in Umudike, Southeastern, Nigeria

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ABSTRACT

Newly developed progenies of sweet potato were evaluated to identify promising genotypes with high storage root yield, dry matter, starch content and susceptibility to *Cylas* spp. at the National Root Crops Research Institute, Umudike, Southeastern Nigeria during the 2015 and 2016 cropping seasons to evaluate variation among crosses of different sweet potato families, namely: LigriXFaara (17), LigriXApomoen (9) and LigrixSauti (8), including two check varieties (Umuspo 3 and TIS 87/0087). Analysis of variance, correlation and principal component analysis were employed for data analysis. In this study, four genotypes; LigriXFaara/3 (16.02t/ha), LigriXFaara/2 (14.67t/ha), LigriXFaara/1 (13.66t/ha) and LigriXFaara/6 (10.33t/ha) produced higher fresh storage root yield than the national check (TIS 87/0087). Four genotypes recorded starch content above 50mg100-1; LigriXApomoden/1 (69.71mg100-1), LigriXApomoden/3 (62.98mg100-1), LigriXApomoden/2 (60.89mg100-1), LigriXApomoden/4 (57.53 mg100-1). Among the thirty-four genotypes evaluated, twenty-nine genotypes were susceptible to the attack of *C. puncticollis*. LigriXFaara/1 recorded the highest attack of *C. puncticollis*, followed by LigriXApomoden/5, LigriXFaara/4, LigriXApomoden/3, LigriXSauti/3, LigriXFarra/5 while five genotypes; LigriXFaara/4, LigriXFaara/5, LigriXSauti/5, LigriXFaara/8, LigriXFaara/7 and LigriXFaara/14 did not show any sign of vulnerability of *C. puncticollis*. Promising genotypes that recorded high yield, dry matter and resistance to *Cylas* spp. could be subjected to advanced yield trail and incorporated into further breeding program.

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INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is a dicotyledonous crop from the *Convolvulaceae* family and it is an important stable crop that is consumed in many developing countries in the tropics (Thottappilly and Loebenstein, 2009). China ranks highest in terms of sweet potato production across the globe while Nigeria accounts for the highest production of sweet potato in the African continent. (FAOSTAT, 2014). In the tropics, the average yield potential of sweet potato ranges from 20 – 50 t/ha and the annual world production is 131 million tons, on approximately 9 million hectares with mean estimated yields of 13.7 t/ha while an average yield of 3 t/ha has been recorded in Nigeria has been adjudged as one of the poorest sweet potato yields across the globe (FAO, 2015).

Majority of sweet potato farmers in Nigeria are small holder farmers, whose preference for the crop is largely due to its short gestation period of about four to five months, depending on the variety and it ability to survive on different ecology types (Antiaonong and Bassey, 2008). Sweet potato production in

Nigeria is faced with numerous constraints 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 (Sebastiani *et al*., 2007). Amongst these constraints, sweet potato weevil infestation caused by *Cylas puncticollis* constitutes a serious factor limiting sweet potato production in Nigeria. Predominately, sweet potato weevils (*Cylas puncticollis*) are reported to be a main insect pest damaging the fresh storage roots of sweet potato in the field. Sweet potato weevil species were reported to have inflicted severe damage every harvestable part of the plant with yield losses up to 80% (Smit *et al*., 2001; Rees *et al*., 2003). Infestation by sweet potato weevil to sweet potato storage causes both severe injury to the storage roots as well as quantitative loss. It is also capable of causing depreciation in terms of quality and loss of market value because of the unpalatable terpenoids produced by the plant in response to infestation caused by the weevil (Stathers *et al*., 2003). To minimize the infestation of sweet potato weevils, good agronomic practices such as proper field sanitation, early planting and early harvesting, as well as application of agro-chemical have been implemented by farmers (Lebot and Bradshaw, 2010). There are however, environmental and health hazards associated with the use of agro-chemical constitute a limiting factor coupled with the fact that it has minimal effects on the juvenile weevils that develop in roots and vines (Lebot and Bradshaw, 2010). Therefore, the aim of this study was to evaluate different genotypes obtained from controlled cross to identify promising genotypes with high root yields, dry matter and susceptibility to *Cylas puncticollis*.

MATERIALS AND METHODS

Experimental site

The experiment was carried out during the 2015 and 2016 planting seasons at the National Root Crops Research Institute, Umudike, Southeastern 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 Utisol (NRCRI, 2012).

Nursery management and agronomic practices

The nursery was prepared in the greenhouse of the National Root Crops Research Institute, Umudike, Southeastern, Nigeria using polyethylene bags containing 1 kg of soil mixture of a top-soil, organic material and river sand in a ratio of 3: 2: 1. 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. The land for the trial site was cleared, plowed, harrowed and skinned. The prepared land was partitioned into plots of 1.5 m^2 (1.0m × 1.5 m). The field was laid out in an augmented design with three replicates and two check varieties were planted within each plot. The planting distance was 1m x 0.3m, which resulted in five stands of sweet potatoes per plot, equivalent to 33,333 stands per hectare. The field size for this investigation was 240m^2. Planting was done on July 21, 2015 and April 18, 2016. Weeding was done 4, 8 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) about the number of roots per plot, marketable (> 100 g) and unmarketable roots (<100 g), severity of damage by *Cylas puncticollis* (Stathers *et al*., 2003) (Table 1).

Table 1. List of planting materials and their sources.

S.N.	Progenies	Source
1.	LigriXFaara/1	CIP, Kumasa, Ghana
2.	LigriXFaara/2	CIP, Kumasa, Ghana
3.	LigriXFaara/3	CIP, Kumasa, Ghana
4.	LigriXFaara/4	CIP, Kumasa, Ghana
5.	LigriXFaara/5	CIP, Kumasa, Ghana
6.	LigriXFaara/6	CIP, Kumasa, Ghana
7.	LigriXFaara/7	CIP, Kumasa, Ghana
8.	LigriXFaara/8	CIP, Kumasa, Ghana
9.	LigriXFaara/9	CIP, Kumasa, Ghana
10.	LigriXFaara/10	CIP, Kumasa, Ghana
11.	LigriXFaara/11	CIP, Kumasa, Ghana
12.	LigriXFaara/12	CIP, Kumasa, Ghana
13.	LigriXFaara/13	CIP, Kumasa, Ghana
14.	LigriXFaara/14	CIP, Kumasa, Ghana
15.	LigriXFaara/15	CIP, Kumasa, Ghana
16.	LigriXFaara/16	CIP, Kumasa, Ghana
17.	LigriXFaara/17	CIP, Kumasa, Ghana
18.	LigriXApomoden/1	CIP, Kumasa, Ghana
19.	LigriXApomoden/2	CIP, Kumasa, Ghana
20.	LigriXApomoden/3	CIP, Kumasa, Ghana
21.	LigriXApomoden/4	CIP, Kumasa, Ghana
22.	LigriXApomoden/5	CIP, Kumasa, Ghana
23.	LigriXApomoden/6	CIP, Kumasa, Ghana
24.	LigriXApomoden/7	CIP, Kumasa, Ghana
25.	LigriXApomoden/8	CIP, Kumasa, Ghana
26.	LigriXApomoden/9	CIP, Kumasa, Ghana
27.	LigriXSauti/1	CIP, Kumasa, Ghana
28.	LigriXSauti/2	CIP, Kumasa, Ghana
29.	LigriXSauti/3	CIP, Kumasa, Ghana
30.	LigriXSauti/4	CIP, Kumasa, Ghana
31.	LigriXSauti/5	CIP, Kumasa, Ghana
32.	LigriXSauti/6	CIP, Kumasa, Ghana
33.	LigriXSauti/7	CIP, Kumasa, Ghana
34.	LigriXSauti/8	CIP, Kumasa, Ghana
35.	Umuspo3 (Local check)	NRCRI, Umudike
36.	TIS 87/0087 (National check)	NRCRI, Umudike

The sweet potato storage root tubers in each plot were harvested and 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.

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.

Dry matter determination

Dry matter content was determined within twenty four (24) hour of harvesting, 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 × 100

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 sweet potato described by Wang *et al.* (1989) was followed, i.e., y = 0.86945x - 6.34587, in which y is the starch content and x are the dry matter content.

Data 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. 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

The results presented in Table 2 showed the analysis of variance of thirty four genotypes of sweet potato. In 2015 cropping season, there was significant ($P \leq 0.05$) differences among genotypes for unmarketable root number, marketable root number, marketable root weight, unmarketable root weight and yield (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, marketable root weight and unmarketable root weight yield but there was no significant difference among the genotypes for yield (Table 2). In 2015 cropping season, LigriXFaara/3 recorded the highest mean of marketable root weight (2.40kg/ha) and produced the highest storage root yield in 2015 cropping season (16.02t//ha). LigriXFaara/2 and LigriXFaara/1 produced storage root yield (14.67t/ha and 13.66t/ha) higher than the national checks, respectively. In 2015 cropping season, the fresh storage root yield of both check varieties Umuspo 3 and TIS 87/0087 were 12.60t/ha and 10.00t/ha, respectively (Table 2). LigriXSauti/2 recorded the lowest yield (2.00t/ha). This result in this present study agrees 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. Similarly, the results of this study follow the same trend as observed by 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 range of values for the fresh storage root yield among the genotypes in this study is consistent with earlier studies carried out at different regions across the globe (Kabi *et al.*, 2001; Stathers *et al.*, 2003; Tigabu and Tilahun, 2013; Amare *et al.*, 2015; Mansaray *et al.*, 2015). Fresh storage root yields obtained from this investigation performed below their yield potential (ranging from 18 to 30 t/ ha) reported by CSIR-Crops Research Institute (MoFA, 2014). Ragassa *et al.* (2015) suggested that one of the ways of improving sweet potato genotypes is by crossing promising genotypes with superior ones in a given environment. Hence, genotypes with tuber yields below 13t/ha could be crossed with the top yielders.

In 2016 cropping season, Ligri X Sauti/8 recorded the highest mean of marketable root weight (1.45 /ha) and highest fresh storage root yield (9.60t//ha.) In 2016, cropping season, the fresh storage root yield of both check varieties Umuspo 3 and TIS 87/0087 were 4.26t/ha and 5.13t/ha, respectively (Table 2).

Table 2 showed that in 2015 cropping season, three genotypes; LigriXFaara/3 (16.02t/ha), LigriXFaara/2 (14.67t/ha) and LigriXFaara/1 (13.66t/ha) produced higher fresh storage root yield than the national check (Umuspo3) while four genotypes; LigriXFaara/3 (16.02t/ha), LigriXFaara/2 (14.67t/ha), LigriXFaara/1 (13.66t/ha) and LigriXFaara/6 (10.33t/ha) produced higher fresh storage root yield than the national check (TIS 87/0087). In 2016 cropping season, nineteen genotypes produced higher fresh storage root yield than the national check variety; TIS87/0087 (5/13t/ha) while twenty-two genotypes produced higher fresh storage root yield than the check variety; Umuspo 3 (4.26 t/ha). The storage root yield of both years showed that the genotypes produced higher yield in 2015 cropping season than in 2016 cropping season. This could be attributed to the effect of early planting and decline in rainfall during the vegetative stage of the crop in 2016 cropping. Early planting in month of April when the soil and atmospheric temperature was higher could affect the growth of sweet potato. This finding was confirmed by Alloli *et al.* (2011) who studied the effect of planting date on sweet potato. The variation in the

Table 2. Means of thirty four genotypes for total storage root yield and yield components for 2015 and 2016 planting seasons.

Genotype	MRTN 2015	UMRTN 2015	MRTW 2015	UMRTW 2015	Yield 2015	MRTN 2016	UMRTN 2016	MRTW 2016	UMRTW 2016	Yield 2016	Cylas incidence	Cylas severity	Dry matter	Starch
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	45.84	32.83
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	44.80	31.45
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	47.84	33.08
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	48.11	32.65
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	47.11	30.77
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	49.24	33.14
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	45.97	29.45
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	51.50	32.14
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	50.31	30.45
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	39.73	27.13
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	49.07	26.30
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	48.87	31.27
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	49.44	27.51
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	50.10	23.31
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	48.39	31.74
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	48.24	31.93
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	47.60	31.33
LigriXApomoden/1	2.50	2.50	0.80	0.10	5.70	2.50	2.50	0.78	0.10	5.80	1.50	1.50	30.29	69.71
LigriXApomoden/2	1.00	2.50	0.28	0.10	2.46	2.50	4.00	0.63	0.08	4.70	0.50	1.50	39.12	60.89
LigriXApomoden/3	2.50	2.50	0.95	0.20	6.77	2.00	3.00	0.70	0.10	5.33	2.00	1.50	37.03	62.98
LigriXApomoden/4	2.00	1.00	0.50	0.05	3.67	4.00	1.00	1.00	0.08	7.20	2.00	3.00	42.47	57.53
LigriXApomoden/5	3.50	0.00	1.10	0.00	7.43	4.00	0.00	1.30	0.00	8.86	2.00	2.50	43.72	24.65
LigriXApomoden/6	3.00	0.00	0.90	0.00	5.97	3.00	0.00	1.10	0.00	7.33	1.50	2.00	22.97	25.19
LigriXApomoden/7	2.50	1.00	0.95	0.05	6.67	2.00	3.00	0.55	0.09	4.26	1.50	2.50	37.40	21.41
LigriXApomoden/8	3.00	2.00	1.00	0.15	7.67	3.00	5.00	0.70	0.07	5.13	1.50	1.50	46.11	23.94
LigriXApomoden/9	2.50	1.00	1.05	0.10	7.67	3.00	3.00	0.80	0.09	5.93	1.50	2.00	45.16	24.24
LigriXSauti/1	3.00	4.00	1.10	0.10	8.00	1.00	4.00	0.20	0.10	2.00	1.00	2.00	43.99	22.45
LigriXSauti/2	1.00	4.00	0.20	0.10	2.00	2.00	5.00	0.40	0.10	3.30	1.00	2.00	42.61	21.42
LigriXSauti/3	2.00	5.00	0.40	0.10	3.30	2.00	3.00	0.55	0.09	4.26	2.00	3.00	44.68	24.81
LigriXSauti/4	2.00	3.00	0.55	0.09	4.26	3.00	5.00	0.70	0.07	5.13	1.00	3.00	48.37	26.10
LigriXSauti/5	3.00	5.00	0.70	0.07	5.13	3.00	3.00	0.80	0.09	5.93	0.00	0.00	43.23	19.63
LigriXSauti/6	3.00	3.00	0.80	0.09	5.93	2.00	4.00	0.50	0.05	3.60	1.00	2.00	43.19	20.85
LigriXSauti/7	2.00	4.00	0.50	0.05	3.60	2.00	4.00	0.50	0.05	3.60	1.00	2.00	42.98	27.22
LigriXSauti/8	4.00	0.00	1.45	0.00	9.60	4.00	0.00	1.45	0.00	9.60	1.00	1.00	38.82	23.70
Umuspo3	4.00	3.00	1.90	0.00	12.60	2.00	3.00	0.55	0.09	4.26	0.00	0.00	42.98	27.22
TIS87/0087	4.00	3.00	1.50	0.00	10.00	3.00	5.00	0.70	0.07	5.13	0.00	0.00	39.24	23.73
Grand Mean	3.15	1.93	0.98	0.08	7.07	2.78	2.64	0.73	0.08	5.37	1.04	1.50	44.07	31.23
$LSD_{0.05}$	1.20	1.44	0.65	0.09	4.61	0.95	1.91	0.41	0.04	NS	NS	NS	1.34	0.82

MRTN = Marketable Root Number, UMRTN = Unmarketable Root Number, MRTW = Marketable weight, UMRTW = Unmarketable weight

fresh storage root yield between both cropping seasons could be attributed to environmental factors and partly be as a result of climatic conditions (Osiru *et al.*, 2009; Mwololo *et al.*, 2012).
The result as presented in Table 2 indicated the analysis of variance revealed that there were no significant (P≤0.05) differences among genotypes for Cylas incidence and Cylas severity. Among the thirty four genotypes evaluated, twenty nine genotypes were susceptible to the attack of *C. puncticollis*. Twelve (12) genotypes; five genotypes; LigriXFaara/4, LigriXFaara/5, LigriXSauti/5, LigriXFaara/8, LigriXFaara/7 and LigriXFaara/14 which did not record any attack of *Cylas* Spp could possess resistence gene. The different reaction of these sweet potato genotypes to *Cylas* spp. could be as a result of the variation in the chemical elements in the storage roots (Stevenson *et al.*, 2009; Anyanga *et al.*, 2013). In studies conducted in Uganda, a remarkable level of esters of hydroxylcinnamic acid in root latex were recorded in some weevil resistant sweet potato (Stevenson *et al.*, 2009) and esters of caffeic and coumaric acid in epidermal and root surface (Anyanga *et al.*, 2013). These genotypes could be incorporated in breeding programs to produce hybrid varieties that are high yielding and resistance to *Cylas puncticollis.* Diversity in the genetic constitution, environmental conditions and storage root morphology could be responsible for the dissimilarity in response to sweet potato weevil infestation and damage (Stathers *et al.*, 2003; Muyinza *et al.*, 2012).
The result presented in Table 2 showed that dry matter and starch content differ significantly (P≤0.05). The starch content ranged from 69.71mg100g^{-1} to 19.63mg100^{-1}. LigriXApomoden/1 had the highest starch content, 69.71mg100g^{-1} while LigriXSauti/5 recorded the lowest starch content, 19.63mg100^{-1}. The mean of the genotypes for dry matter ranged from 51.50 % to 22.79%. LigriXFaara/8 had the highest dry matter (51.50%) while LigriXApomoden/6 recorded the lowest dry matter (22.97%). Among the thirty four genotypes evaluated, twenty four genotypes had dry matter content above 43%. Four genotypes recorded starch content above 50mg100^{-1}; LigriXApomoden/1 (69.71mg100^{-1}), LigriXApomoden/3 (62.98mg100^{-1}), LigriXApomoden/2 (60.89mg100^{-1}), LigriXApomoden/4 (57.53 mg100^{-1}). In this study, the results on dry matter content among the sweet potato genotypes of this study differs from the findings obtained by Laurie *et al.* (2013) who reported dry matter content of some OFSPs as 19.4- 22.6%, but similar to the value reported by Sanouss *et al.* (2016) in Benin of 25.09 to 46.12 %. High dry matter content is one of the primary objectives in sweet potato breeding programs. Dry matter content varies due to factors such as variety, location, climate, incidence of pests and diseases, cultural practices and soil types (Manrique and Hermann, 2000; Shumbusha *et al.*, 2010; Vimala and Hariprakash, 2011). Most genetic studies and the existence of several enzymes involved in starch biosynthesis indicated that dry matter content shows quantitative inheritance (Cervantes-Flores *et al.*, 2008). Eleazu and Ironua (2015), high dry matter content contributes to better storability, good texture, product yield, and therefore it has the potentials of been used for industrial purposes and for flour production in confectioneries. Dry matter content is influenced by several factors such as the age of the plant, crop season, location, variety and efficiency of the crop to trap sunlight.
Table 3 showed the Pearson correlation co-efficient (γ) for the storage root parameters for thirty-four 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 nine traits of the thirty-four sweet potato genotypes are presented in Table 3. All traits exhibited positive and significant (*P<0.05* and *P<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 and significant (*P≤0.01*) association with marketable root number (r=0.678) as well as marketable root weight (r=0.99) (Table 3). Yield at harvest had a positive and significant (*P≤0.05*) association unmarketable root weight (r=0.248). Unmarketable root number a had positive and significant (*P≤0.01*) association unmarketable root weight (r=0.618). Yield at harvest, however, had a positive association with unmarketable fresh storage root weight (r = -0.248). Yield at harvest had a positive and significant (*P≤0.05*) association with dry matter (r = -0.027) but had a negative association with starch (r = -0.154) (Table 3). *Cylas* incidence had a positive and significant (*P≤0.01*) association with fresh storage root yield (r=0.325) and *Cylas* severity had a positive and significant (*P≤0.01*) association

Table 3. Pearson correlation co-efficient (γ) for the storage root parameters for the thirty four genotypes of sweet potato.

—>	MRN	URN	MRW	URW	Yield	*Cylas* Incidence	*Cylas* Severity	Dry matter	Starch
MRN	1								
URN	-0.192	1							
MRW	0.691**	0.020	1						
URW	0.003	0.618**	0.127	1					
Yield	0.678**	0.102	0.991**	0.248*	1				
Cylas incidence	0.172	0.341**	0.260*	0.453**	0.325**	1			
Cylas Severity	-0.002	0.382**	0.195	0.386**	0.254*	0.802**	1		
Dry matter	0.150	-0.028	0.009	0.035	0.027	-0.176	-0.114	1	
Starch	-0.318**	0.076	-0.162	0.195	-0.154	0.112	0.073	-0.292*	1

**. Correlation is significant at the 0.01 level (2-tailed).
*. Correlation is significant at the 0.05 level (2-tailed).

Table 4. Principal component analysis of thirty three sweet potato genotypes.

—>	Component		
	PCA 1	PCA 2	PCA 3
MRN	0.587	-0.653	-0.039
URN	0.386	0.609	0.400
MRW	0.802	-0.489	-0.168
URW	0.534	0.535	0.322
Yield	0.858	-0.410	-0.107
Cylas incidence	0.708	0.456	-0.119
Cylas Severity	0.626	0.515	-0.030
Dry matter	-0.021	-0.304	0.796
Starch	-0.089	0.514	-0.496
Total	3.059	2.320	1.200
% of variance	33.993	25.776	13.332
Cumulative %	33.993	59.769	73.101

with *Cylas* incidence (r=0.802) (Table 3). Correlation studies enable the breeder to understand the mutual component characters in which selection can be based for genetic improvement. Adebisi *et al.* (2001) studied the relationships among different traits in different crops such as soybean, cassava, sweet potato amongst other crops and can be used by plant breeders to enhance their quest for new and economically potential varieties that will meet the needs of ever increasing world population. Yohhanes *et al.* (2010) reported that total storage root yield had significant and positive association with marketable storage root yield and average storage root weight. Tesfaye (2006) obtained positive association between total storage root yield and marketable storage root yield. Islam *et al.* (2002) indicated that traits that had negative correlation coefficient could not be improved with total storage root yield in positive direction. In contrast to this Yohannes *et al.* (2010), reported unmarketable number of roots and yield as well as total marketable number of roots had positive correlation with total storage root yield.

Three main principal component axes (PC1 PC2 and PC3) were obtained in the principal component analysis (PC analysis had eigen values up to 1.0, presenting cumulative variance of 73.10% (Table 4). Principal component one (PC1), with eigen value of 3.05, contributed 33.99% of the total variability. PC2, with eigen value of 2.32, accounted for 25.77% of total variability while PC3, with eigen value of 1.20, accounted for 13.33% of total variability observed among the twenty one sweet potato genotypes, In PC1, the traits that accounted for most of the 33.99% observed variability among the thirty three genotypes included number of marketable roots, with vector loading of 0.587, weight of marketable roots (0.802), yield (0.858), *Cylas* incidence and *Cylas* severity (0.708 and 0.626, respectively) (Table 4). 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 sweet potato genotypes, found important traits to be the genotypes they worked with. Four main 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 sweet potato 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.

Conclusion

Storage root yield in 2015 cropping season ranged from 16.02 to 2.00 t/ha with an average 7.07t/ha and starch content ranged from 69.71mg100g^{-1}to 19.63mg100^{-1}. LigriXFaara/3 (16.02t/ha), LigriXFaara/2 (14.67t/ha) and LigriXFaara/1 (13.66t/ha) produced higher fresh storage root yield than the check variety (Umuspo3) while four genotypes; LigriXFaara/3 (16.02t/ha), LigriXFaara/2 (14.67t/ha), LigriXFaara/1 (13.66t/ha) and LigriXFaara/6 (10.33t/ha) produced higher fresh storage root yield than the national check (TIS 87/0087). LigriXApomoden/1 had the highest starch content, 69.71mg100g^{-1} while LigriXFaara/8 had the highest dry matter (51.50%). Four genotypes recorded starch content above 50mg100^{-1}; LigriXApomoden/1 (69.71mg100^{-1}), LigriXApomoden/3 (62.98mg100^{-1}), LigriXApomoden/2 (60.89mg100^{-1}), LigriXApomoden/4 (57.53 mg100^{-1}). Among the thirty four genotypes evaluated, five genotypes; LigriXFaara/4, LigriXFaara/5, LigriXSauti/5, LigriXFaara/8, LigriXFaara/7 and LigriXFaara/14 did not record attack of *C. puncticollis*. Eleven promising genotypes that recorded high yield and starch could be subjected to advanced yield trail and incorporated into further breeding program, while genotypes that recorded infestation of *Cylas* Spp. be expunged from the list of potential sweet potato genotypes of the environment. However, genotypes with tolerance to *Cylas* Spp. among the high yielding genotypes could be incorporated into hybridization with already known resistant genotypes for the purpose of breeding for horizontal resistance.

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Conflict of interest

Authors have declared that no competing interests exist.

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