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RESEARCH ARTICLE

Potential Molds and Bacterial Species Associated with Deterioration of Sweet potatoes in Kebbi State, Northern Nigeria

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ABSTRACT

The present study aimed to assess the types of microorganisms associated with two different varieties of sweet potatoes yellow skin with white flesh and white skin with yellow flesh cultivated in Kebbi. The analysis of microorganisms was done using the pour plate method. Two L.G.A and three collection points from each L.G.A were selected and sampled. Eight bacteria and five fungal species were isolated and identified from the two varieties of sweet potatoes. Bacterial species identified were; *Staphylococcus aureus, Salmonella* spp., *E. coli, Bacillus* spp., *Pseudomonas* spp., *L. monocytogens, Klebsiella* spp., and *Erwinia* spp., while fungal species isolates are *Aspergillus* spp., *Mucor recemosus*, *Rhizopus* spp., *Fusarium oxysporium, and Penicillum* spp., in both samples. Results revealed that yellow skin with white flesh sweet potato from Gumben kure had the highest bacterial load 7.2 x 10^4 cfu/ml. The lowest bacterial load obtained from yellow skin with white-fleshed variety in Gwadangwaji 3.2 x 10^4cfu/ml. The highest fungal load spore in yellow skin with white-fleshed sweet potato 2.0 x 10^4sfu/ml was obtained from Kardi and the lowest fungal spores observed in Gulumbe white skin with yellow flesh variety 4.0 x 10^4sfu/ml. The pathogen city test results revealed that all microorganisms isolated in this research showed varying degrees of tubers rot with *Rhizopus* spp., had highest and bacterial ranged from 4.0 to 2.0 depths (cm). In conclusion, the presence of these microorganisms isolated and identified from two varieties of sweet potato showed that these species are responsible for these tubers' spoilage in the study area.

Keywords: *Ipomea batatas*; Microoganisms; Microbial load; Kebbi state

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INTRODUCTION

The sweet potato (Ipomoea batatas Lam.) is a dicotyledonous plant known as Dankali or Kudaku in Hausa. Only Ipomoea batatas types are economically important as food (Onwueme, 1982). Ipomea batatas is a vital crop in various parts of Kebbi State and the world, grown in over 100 nations. In tropical and subtropical countries, however, this tuber crop is a staple food crop for rural and urban residents alike (Ferris et al., 2002). According to Keta (2018), sweet potato tubers are used to make dishes including chips, starch, chin-chin, fatin dankali, amala, and others. Sweet potato produces the most edible energy per hectare per day of all major food crops (Horton & Fano, 1985; Singh et al., 2008). As a food security crop, it has a short growth season (90-180 days depending on variety and climate), stores well in the soil, and performs well in marginal ground (Kapinga et al., 2007; Keta, 2018).

Yellow and white skinned sweet potatoes are good sources of vitamin A, which is often inadequate in the diets of most African farmers, especially Nigerian farmers. Besides these uses, sweet potatoes are used to manufacture sustainable plant products like ethanol and starch (Woolfe, 1992). Vitamins A and B are abundant, as is vitamin C. Sweet potatoes grow swiftly in poor soil, but distorted roots develop in heavy clay or sandy soil when farmed. Spoilage is a microbial-induced metabolic process that degrades food quality features, making it unfit for human ingestion (Doyle, 2007). This type of deterioration is typically connected with sweet potatoes, resulting in postharvest losses due to mould change or activity. Mechanical damage during harvest, storage, or transportation has been linked to tuber storage rots (Snowdon, 1991). The most important element in tuber deterioration is pathogenic contamination (Degras, 1993). However, to my knowledge, there is no published data on moulds and bacteria infecting sweet potatoes in study Birnin Kebbi and Maiyam L.G.A. To alleviate food shortages, socio-economic activity, and food security in Kebbi state, it is important to examine the moulds and bacterial species responsible for the degeneration of the two most popular sweet potato varieties.

MATERIALS AND METHODS

A sampling of sweet potatoes was made using a stratified sampling design. Two local government areas of Kebbi state were selected for sampling and sample collections namely, Birnin Kebbi and Maiyama L.G.A. A total of 300 samples of white and yellow variety each of sweet potatoes were collected from the collection points in each local government area. A total of 600 samples of white and yellow sweet potatoes were collected from the study areas using poly-ethene bags and were labelled accordingly to identify the collection points. Three villages from each local government area served as collection points, and thirty samples from each village were collected. Thirty healthy tubers, each making a total of sixty tubers of healthy sweet potato, were randomly selected and collected from these communities in separates sterile and labelled polythene bags as control samples and were brought to the Department of Plant Science and Biotechnology, Laboratory, Kebbi State University of Science and Technology, Aliero for analysis.

The molds species were identified with the aid of Mycological Atlas (Robert and Ellen, 1988). The cultural characteristics, color, size, shape and elevation of the colony were noted on culture media. The spores, hyphae, and arrangement of conidia and spores were observed with a microscope's aid (Robert and Ellen, 1998).

The bacteria isolates were characterized and identified based on the colonial morphology. Biochemical test includes gram staining, Indole test, Eosine metal blue agar test, Tripple sugar Iron Test, and Catalase test as described by Cheesbrough (2003). The data generated from work was processed and subjected to descriptive statistics.

RESULTS

From the viable microbial count obtained in Birnin Kebbi, Kardi yellow skin with white flesh sweet potato had the highest bacteria 4.8 x 10^4 count and a fungal load of 2.0 x 10^4 as presented in Table 1. While lowest mean counted were observed in Gulumbe 4.0 x 10^6 Fungi, 3.2 x 10^4 in bacteria. Mayalo had the highest mean count of 7.2 x 10^4 and 1.8 x 10^4 in bacteria and fungi (Table 2). Pathogenicity test measurement of sweet potato tubers rots revealed different degree, as showed in Table 3. Microscopic and biochemical characterization of isolated bacteria on Sweet Potato and Morphological and microscope examination of fungi isolates from the sweet potato was presented in Table 4 and 5.

Table 1. Microbial viable count of Birnin Kebbi Local Government Sweet Potatoes

Collection points and Sample	No. of colonies		cfu/ml Load	
	Bacteria	Fungi	Bacteria	Fungi
Gulumbe/WF[a]	44	4	4.4 x 10^6	4.0 x 10^6
Gulumbe/YF[b]	36	8	3.6 x 10^4	8.0 x 10^4
G/Gwaji/WF[a]	44	12	4.4 x 10^4	1.2 x 10^4
G/Gwaji/YF[b]	32	16	3.2 x 10^4	1.6 x 10^4
Kardi/WF[a]	48	16	4.8 x 10^4	1.6 x 10^4
Kardi/YF[b]	56	20	5.6 x 10^4	2.0 x 10^4

WF[a], White skin with yellow flesh sweet potato
YF[b], Yellow skin with white flesh sweet potato

Table 2. Microbial viable count of Maiyama local government sweet potato

Collection points and Sample	No. of colonies		cfu/ml Load	
	Bacteria	Fungi	Bacteria	Fungi
Sambawa/ WF[a]	60	12	6.0 x 10^6	1.2 x 10^6
Sambawa/ YF[b]	58	10	5.8 x 10^4	1.0 x 10^4
Gumben K /WF[a]	70	16	7.0 x 10^4	1.6 x 10^4
Gumben K /YF[b]	60	10	6.0 x 10^4	1.0 x 10^4
Mayalo/ WF[a]	56	8	5.6 x 10^4	8.0 x 10^4
Mayalo/ YF[b]	72	18	7.2 x 10^4	1.8 x 10^4

WF[a] ,White skin with yellow flesh sweet potato
YF[b], Yellow skin with white flesh sweet potato

Table 3. Pathogenicity Test Measurement of Sweet Potato Tubers Rots

Fungal isolated	Width (cm)	Depth (cm)
*Aspergillus*spp	2.0	3.0
Mucor recemosus	1.5	2.4
Rhizopus spp	2.0	4.2
Fusarium oxysporium	1.0	2.0
Penicillum spp	1.0	1.0
Bacterial Isolated	**Width (cm)**	**Depth (cm)**
Klebsiella spp	1.0	4.0
Erwinia species	1.2	3.4
Salmonella species	1.8	2.2
Staphylococcus species	1.0	2.3
Bacillus species	1.5	3.0
L. monoytogene	1.0	2.0
Escheria coli	1.5	2.0
Pseudomonas	1.5	2.5

DISCUSSION

Sweet potato ranked the most susceptible to microorganisms due to the environmental factors and nutrients content of this crop that favor these microbes' growth and reproductions in the study areas. The results obtained in this study revealed that sweet potatoes samples contained 7 bacteria species.

Table 4. Microscopic and Biochemical Characterization Chart of Isolated Bacteria Sweet Potato

Isolated species	Gram Biochemical Characterization Chart								
	Catalase	Coagulase	Indole	Urease	Methylred	Citerete	H_2S	Sucrose	Glucose
Erwinia sp.	+	+	-	+	+	-	-	+	+
Salmonella sp.	-	-	-	-	+	-	-	+	-
Staphylococcus sp.	-	+	-	+	+	-	-	+	+
Bacillus sp.	+	+	-	+	+	-	-	+	-

L. monoytogene	-	-	+	+	+	-	-	+	+
Klebsiela sp.	+	+	-	+	+	-	-	+	AG
Escheria coli	+	+	-	+	+	-	-	+	-
Pseudomonas	+	+	-	+	+	-	-	+	-

Note: +, Positive; - , Negative

Table 5. Morphological and microscope examination of fungi isolates from the sweet potato (Oyeleke and Manga, 2008)

Colony Appearance	Microscopic Examination	Mold Species
Colonies consisting dense felt of dark green	Conidiphore intermediate with aerial hyphae bearing conidiophore, conidial head typically columner	*Aspergillus* spp
Colonies were white cottony or wooly	Porogiosphore branched, the short branched sometimes recovered with on casted wall	*Mucor racemosus*
Felty whitish or purple ting more intence near the medium surface	Chlamatosphore in hyphae or in candida hyphae	*Fusarium oxysporium*
Colonies were green and velty. The reverse side was pale yellow	Hyphae were septate with smooth walled conidiosphore bearing long chains of conidia	*Penicillium* spp
Colonies were whitish becoming grayish brown due to brownish sporongiosphore and brown black sporangia	Hyphae were non septate with erect simple branched sprangiophores bearing rhizooids and sporangia	*Rhizopus* spp

The bacteria isolated were *Erwinia* spp., *Salmonella* spp., *Bacillus* spp., *Pseudomonas, E. coli*, *S. aureus*, *Klebsiela* spp., and *L. monoytogene*. It concurs with the findings of Oladoye et al. (2013) in Kwara State, Nigeria. All the samples obtained from collection points were associated with *Erwinia* species and *S. aureus* spp, which was also related toh bacterial soft rot in potatoes (Olivleri et al., 2004; Mahmoud et al., 2008). In Nigeria, Adisa (2006) reported *Erwinia* spp. as one of the most important bacteria causing essential spoilage.

Fungal species associated with post-harvest deterioration of these two varieties of sweet potatoes in the study were; *Rhizopus stolonifer*, *Mucor recemosus*, *Fusarium oxysporium, Aspergillus niger* and *Penicillium* spp. The organisms were confirmed with several workers, including Ray *et al.* (2000), Doyle (2007) Onuegbu (2002), Oyeyipo (2012) had isolated these organisms on rotted potatoes tubers.

On the other hand (Singh et al., 2008; Tester et al., 2005) indicated that factors such as ambient temperature, light and air moisture, and mechanical damage of tubers also accelerate the degradation of the tubers.

All the isolated fungi in this study were pathogenic to healthy sweet potato tubers with differences in rots degree depth (cm) as *Aspergillus* spp (3.0), *Mucor recemosus* (2.4), *Rhizopus* spp (4.4), *Fusarium oxysporium* (2.0). Penicillium spp (1.0) (Table 3) had some correlation with the findings of Khatoon *et al.* (2017) as they reported that the percentage of rotting was found to be 74 % by *R. oryzae*, 56 % by *A.niger*, 31 % by *A. flavus*, 26 % by *F. oxysporum* and 14 % by *G. candidum*. This variation in the two works could be attributed to the difference in the number of days of incubation period in ratio (10:15 days), parameters used in measurement, and prevailing abiotic factors during the pathogenicity test.

CONCLUSION

These microorganisms isolated and identified from two varieties of sweet potato showed that these species are responsible for the spoilage of the varieties of sweet potatoes tubers in the study area. Thus, this may result in potential problems for consumer's health and economic loss to the farmers.

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DISCLOSURE STATEMENT

The author declares no competing interests

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