

MOLD AND BACTERIA SPECIES ASSOCIATED WITH SPOILAGE OF TUBERS OF SWEET POTATO (*Ipomoea batatas*) IN TWO LOCAL GOVERNMENT AREAS OF KEBBI STATE, NIGERIA

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Abstract

A comparative investigation of the microbial susceptibility of two varieties of sweet potato (*Ipomoea batatas*) tubers was conducted across two local government areas (LGAs), Birnin Kebbi and Maiyama, in Kebbi State, Nigeria. The objective was to identify the mold and bacterial species responsible for postharvest spoilage and to determine the variety and locality associated with optimal production and storage potential. Microbial populations were enumerated on Nutrient Agar and Potato Dextrose Agar, and isolates were identified through standard morphological, microscopic, and biochemical procedures. Eight bacterial species, namely *Staphylococcus aureus*, *Salmonella* spp., *Escherichia coli*, *Bacillus* spp., *Pseudomonas* spp., *Listeria monocytogenes*, *Klebsiella* spp., and *Erwinia* spp., together with five fungal species, *Aspergillus* spp., *Mucor racemosus*, *Rhizopus* spp., *Fusarium oxysporum*, and *Penicillium* spp., were isolated and identified from the two varieties. The yellow skin with white flesh variety collected from Gumben Kure recorded the highest bacterial load (7.2×10^4 cfu/mL), while the lowest bacterial count (3.2×10^4 cfu/mL) was obtained from Gwadangwaji. The highest fungal load (8.0×10^4 cfu/mL) was recorded in the yellow skin with white flesh variety from Gulumbe, and the lowest fungal count (0.8×10^4 cfu/mL) was recorded in the white skin with yellow flesh variety from Mayalo. Pathogenicity tests revealed that all isolated fungi produced varying degrees of tuber rot, with *Rhizopus* spp. causing the deepest rot (4.2 cm), while *Klebsiella* spp. produced the deepest bacterial rot (4.0 cm). These findings confirm the microbial basis of sweet potato spoilage in the study areas and underscore the need for improved postharvest handling to safeguard consumer health and reduce economic losses.

Keywords: *Ipomoea batatas*; Bacteria; Fungi; Microbial load; Postharvest spoilage; Kebbi State; Pathogenicity

1. Introduction

Sweet potato (*Ipomoea batatas* (L.) Lam.) is a root tuber crop of considerable nutritional and economic importance in tropical and subtropical regions of the world. It ranks among the seven most important food crops globally and is cultivated in over 100 countries (Woolfe, 1992). In Nigeria, and particularly in Kebbi State, sweet potato occupies a prominent place in local food systems, serving as a versatile staple that can be consumed boiled, fried, mashed, or processed into secondary products such as chips, starch, and flour (Keta, 2018). The tuber also finds application in the industrial production of ethanol and starch, further broadening its utility beyond the food sector (Woolfe, 1992).

From a nutritional standpoint, sweet potato delivers one of the highest amounts of edible energy per hectare per day among the world's major food crops (Harton and Fano, 1985; Singh *et al.*, 2008). The yellow and white fleshed varieties are valued sources of provitamin A carotenoids and ascorbic acid (vitamin C), nutrients that are frequently deficient in the diets of rural and periurban communities across Sub Saharan Africa (Jakahata *et al.*, 1993; Kapinga *et al.*, 2007). The short growing period of 90 to 170 days, combined with the crop's tolerance of marginal soils and its capacity for in ground storage, has earned sweet potato the designation of a food security crop in many developing nations (Kapinga *et al.*, 2007; Keta, 2018).

Despite these attributes, sweet potato tubers are highly perishable and susceptible to postharvest deterioration. Spoilage is a metabolic process brought about by microbial action that renders food undesirable or unacceptable for human consumption through the deterioration of quality characteristics (Doyle, 2007). Postharvest rots of sweet potato have been attributed to physical, physiological, and microbiological factors. Mechanical damage sustained during harvesting, transportation, and storage predisposes tubers to infection by opportunistic microorganisms (Snowdon, 1991). The entry of pathogenic agents through natural openings or wounds is considered the most critical factor in tuber decay (Degras, 1993). Fungal pathogens such as *Rhizopus stolonifer*, *Aspergillus niger*, and *Fusarium oxysporum*, together with bacterial agents including *Erwinia* spp. and *Staphylococcus aureus*, have been widely implicated in the spoilage of root and tuber crops across West Africa (Oladoye *et al.*, 2013; Onuegbu, 2002).

Postharvest losses in sweet potato can reach alarming proportions in the absence of adequate storage infrastructure and handling practices. In addition to the direct economic consequences for smallholder farmers, microbial spoilage carries public health implications, since several of the organisms associated with tuber rot, notably *Salmonella* spp., *E. coli*, and

Staphylococcus aureus, are recognized foodborne pathogens (Doyle, 2007; Oyeyipo, 2012). Environmental conditions prevailing in Kebbi State, including high ambient temperatures, elevated relative humidity, and pronounced rainfall, create a microclimate that is particularly conducive to the proliferation of spoilage organisms in stored tubers (Keta, 2018).

Although previous investigations have examined fungal and bacterial diseases of various tuber crops in other parts of Nigeria, there exists, to the best of the authors' knowledge, no documented report on the identity and pathogenicity of mold and bacterial species colonizing sweet potato tubers specifically within Birnin Kebbi and Maiyama Local Government Areas of Kebbi State. The present study was therefore undertaken to isolate, identify, and evaluate the pathogenicity of fungal and bacterial species associated with the postharvest spoilage of two common varieties of sweet potato cultivated in these areas, with the ultimate aim of informing better storage and disease management strategies that could reduce food losses and improve food security in the region.

2. Materials and Methods

2.1 Study Area and Sample Collection

The study was conducted in two local government areas (LGAs) of Kebbi State, northwestern Nigeria: Birnin Kebbi and Maiyama. Three villages were selected within each LGA as collection points. In Birnin Kebbi LGA, samples were collected from Gulumbe, Gwadangwaji, and Kardi, while in Maiyama LGA, the collection points were Sambawa, Gumben Kure, and Mayalo. A stratified sampling approach was employed. A total of 300 tubers of each of the two sweet potato varieties, the white skin with yellow flesh (WF) and the yellow skin with white flesh (YF), were collected from each LGA, giving a cumulative total of 600 tuber samples. Twenty five samples were obtained from each village collection point. All samples were collected in sterile polythene bags, labelled according to variety and location, and transported to the Department of Plant Science and Biotechnology Laboratory, Kebbi State University of Science and Technology, Aliero, for analysis. In addition, 30 healthy tubers of each variety (60 total) were randomly selected from the study communities to serve as controls.

2.2 Culture Media Preparation and Inoculation

Nutrient Agar (NA) and Potato Dextrose Agar (PDA) were prepared in accordance with the manufacturers' instructions. To achieve selective growth, 50 mg/L of Nystatin was incorporated into the NA to suppress fungal contamination, while 0.1% streptomycin was added to the PDA after sterilization to inhibit bacterial growth (Sabarifard, 2014). Inoculated plates were incubated at room temperature ($28 \pm 2^\circ\text{C}$) for 5 to 7 days and

examined daily for colony development (Balaili *et al.*, 1995; Oyeyipo, 2012). Colonies that appeared were promptly subcultured, and slant preparations were made for subsequent analysis.

2.3 Identification of Mold Species

Fungal isolates were identified with the aid of a standard mycological atlas (Robert and Ellen, 1988). Cultural characteristics, including colony colour, size, shape, and elevation on the culture medium, were recorded. Microscopic examination was performed to determine the type of spores, the nature of the hyphae (septate or non septate), and the arrangement of conidia and sporangia.

2.4 Isolation and Identification of Bacterial Species

Bacterial isolates were obtained following the method described by Ahmed *et al.* (2000). Inoculated plates were incubated at 27 ± 1 °C for 48 to 72 hours, after which colonies in deep cavities were subcultured onto NA and stored on slant bottles until further analysis. Identification was carried out on the basis of colonial morphology and a battery of biochemical tests, including Gram staining, Indole test, Eosin Methylene Blue (EMB) agar test, Triple Sugar Iron (TSI) test, and catalase test, following the protocols of Cheesbrough (2003).

2.5 Pathogenicity Test

Fresh, healthy sweet potato tubers were washed with tap water and surface sterilized with 70% ethanol for 2 minutes. Cylindrical cores were removed from the tubers using a 5 mm cork borer. Discs of PDA medium (4 mm diameter) bearing 7 day old cultures of each fungal and bacterial isolate were inserted into the resulting cavities and sealed with sterile Vaseline. Control tubers were prepared identically, except that uninoculated PDA discs were used. All treated tubers were placed individually in sterile polythene bags and incubated at 28 ± 2 °C for 10 days. At the end of the incubation period, the tubers were sectioned longitudinally and the extent of rotting was assessed by measuring the width and depth of the discoloured zone with a calibrated ruler (Khatoon *et al.*, 2017).

2.6 Data Analysis

Data generated from the study were processed and subjected to descriptive statistical analysis. Microbial colony counts were expressed as colony forming units per millilitre (cfu/mL), and pathogenicity measurements were recorded in centimetres.

3. Results

3.1 Viable Microbial Counts in Birnin Kebbi LGA

Viable microbial counts of bacteria and fungi in the two sweet potato varieties varied appreciably across the three collection points in Birnin Kebbi LGA, as presented in Table 1 and Figure 1. The highest bacterial count (5.6×10^4 cfu/mL) was recorded in the yellow flesh variety from Kardi, followed by the white flesh variety from the same location (4.8×10^4 cfu/mL). The overall average bacterial count across the LGA was 4.3×10^4 cfu/mL. With respect to fungal populations, the Gulumbe collection point recorded the highest viable fungal count (8.0×10^4 cfu/mL) in the yellow flesh variety, which was notably higher than all other collection points. The white flesh variety from Gulumbe also exhibited a comparatively elevated fungal count of 4.0×10^4 cfu/mL. The average fungal colony count in the Birnin Kebbi LGA was 2.9×10^4 cfu/mL.

Table 1. Viable microbial counts of bacteria and fungi associated with sweet potato tubers in Birnin Kebbi LGA.

Collection Point / Variety	Bacteria (cfu/mL $\times 10^4$)	Fungi (cfu/mL $\times 10^4$)
Gulumbe / WF	4.4	4.0
Gulumbe / YF	3.6	8.0
Gwadangwaji / WF	4.4	1.2
Gwadangwaji / YF	3.2	1.6
Kardi / WF	4.8	1.6
Kardi / YF	5.6	2.0
Average	4.3	2.9

WF = White skin with yellow flesh; YF = Yellow skin with white flesh.

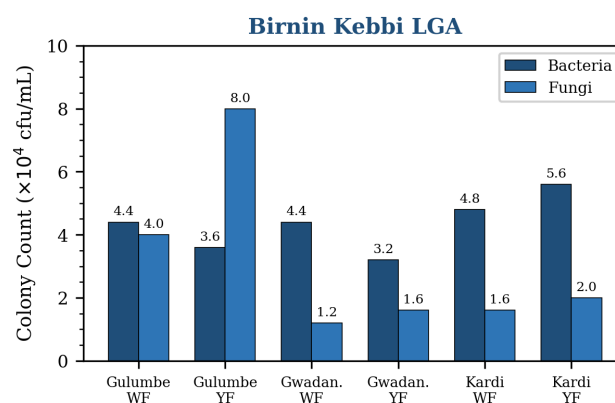


Figure 1: Bacterial and fungal colony counts across collection points in Birnin Kebbi LGA.

3.2 Viable Microbial Counts in Maiyama LGA

The microbial load distribution in Maiyama LGA is presented in Table 2 and Figure 2. The yellow flesh variety from Mayalo recorded the highest bacterial count (7.2×10^4 cfu/mL), closely followed by the white flesh variety from Gumben Kure (7.0×10^4 cfu/mL). The average bacterial count across the Maiyama

LGA was 6.3×10^4 cfu/mL, which was appreciably higher than the average recorded in Birnin Kebbi LGA (4.3×10^4 cfu/mL). Conversely, fungal populations in Maiyama LGA were lower overall, with an average count of 1.2×10^4 cfu/mL compared to 2.9×10^4 cfu/mL in Birnin Kebbi LGA. The highest fungal count in Maiyama was 1.8×10^4 cfu/mL, recorded in the yellow flesh variety from Mayalo.

Table 2. Viable microbial counts of bacteria and fungi associated with sweet potato tubers in Maiyama LGA.

Collection Point / Variety	Bacteria (cfu/mL $\times 10^4$)	Fungi (cfu/mL $\times 10^4$)
Sambawa / WF	6.0	1.2
Sambawa / YF	5.8	1.0
Gumben Kure / WF	7.0	1.6
Gumben Kure / YF	6.0	1.0
Mayalo / WF	5.6	0.8
Mayalo / YF	7.2	1.8
Average	6.3	1.2

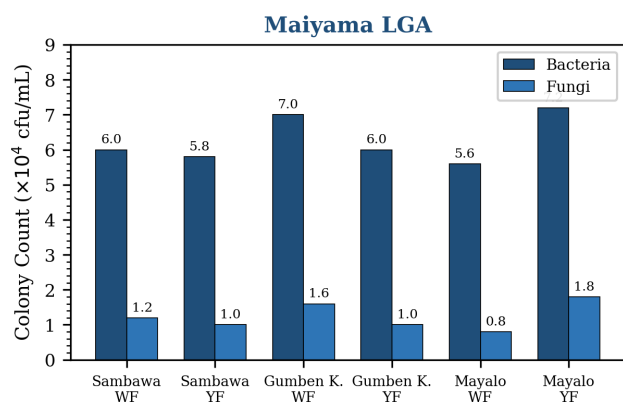


Figure 2: Bacterial and fungal colony counts across collection points in Maiyama LGA.

3.3 Comparative Microbial Load between LGAs

A comparative analysis of the average microbial loads between the two LGAs is depicted in Figure 3. Maiyama LGA exhibited a markedly higher mean bacterial count (6.3×10^4 cfu/mL) relative to Birnin Kebbi LGA (4.3×10^4 cfu/mL), representing a 47% increase. In contrast, the mean fungal count was higher in Birnin Kebbi LGA (2.9×10^4 cfu/mL) than in Maiyama LGA (1.2×10^4 cfu/mL). This inverse relationship between bacterial and fungal prevalence across the two localities may reflect differences in local soil microflora, ambient humidity, or agronomic practices that selectively favour one group of microorganisms over the other.

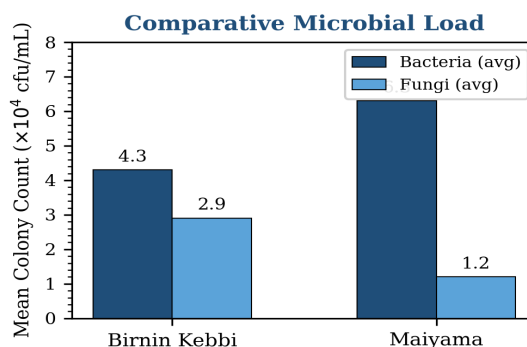


Figure 3: Comparative mean bacterial and fungal colony counts between Birnin Kebbi and Maiyama LGAs.

3.4 Pathogenicity Test

The results of the pathogenicity test are presented in Table 3, and the associated measurements are illustrated graphically in Figures 4 and 5. Among the fungal isolates, *Rhizopus* spp. produced the most extensive tuber rot, with a width of 2.0 cm and a depth of 4.2 cm, indicating its aggressive tissue degradation capacity. *Aspergillus* spp. also caused substantial rot (2.0 cm width, 3.0 cm depth), while *Penicillium* spp. produced the least rot (1.0 cm width, 1.0 cm depth). Among the bacteria, *Klebsiella* spp. induced the deepest rot (4.0 cm), followed by *Erwinia* spp. (3.4 cm depth). *Salmonella* spp. produced the widest bacterial lesion (1.8 cm), while *Listeria monocytogenes* caused the shallowest bacterial rot (2.0 cm depth).

Table 3. Pathogenicity test measurements of sweet potato tuber rots caused by fungal and bacterial isolates.

Organism	Width (cm)	Depth (cm)
Fungal Isolates		
<i>Aspergillus</i> spp.	2.0	3.0
<i>Mucor racemosus</i>	1.5	2.4
<i>Rhizopus</i> spp.	2.0	4.2
<i>Fusarium oxysporum</i>	1.0	2.0
<i>Penicillium</i> spp.	1.0	1.0
Bacterial Isolates		
<i>Klebsiella</i> spp.	1.0	4.0
<i>Erwinia</i> spp.	1.2	3.4
<i>Salmonella</i> spp.	1.8	2.2
<i>Staphylococcus</i> spp.	1.0	2.3
<i>Bacillus</i> spp.	1.5	3.0
<i>L. monocytogenes</i>	1.0	2.0
<i>Escherichia coli</i>	1.5	2.0
<i>Pseudomonas</i> spp.	1.5	2.5

Fungal Pathogenicity

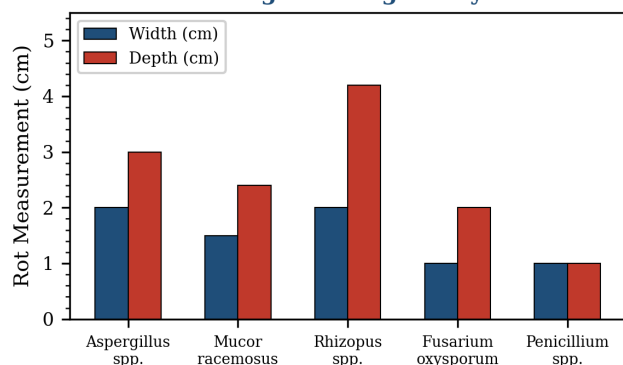


Figure 4: Width and depth of tuber rot caused by fungal isolates in pathogenicity tests.

Bacterial Pathogenicity

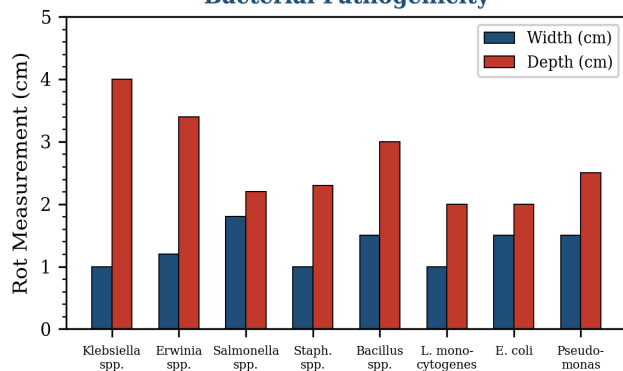


Figure 5: Width and depth of tuber rot caused by bacterial isolates in pathogenicity tests.

3.5 Identification of Microbial Isolates

The bacterial isolates were characterized through Gram staining and a battery of biochemical tests (Table 4). Eight distinct bacterial species were identified: *Klebsiella* spp., *Erwinia* spp., *Salmonella* spp., *Staphylococcus aureus*, *Bacillus* spp., *Listeria monocytogenes*, *Escherichia coli*, and *Pseudomonas* spp. The five fungal species identified through colony morphology and microscopic examination (Table 5) were *Aspergillus* spp., *Mucor racemosus*, *Rhizopus* spp., *Fusarium oxysporum*, and *Penicillium* spp. The relative distribution of these isolates is illustrated in Figure 6.

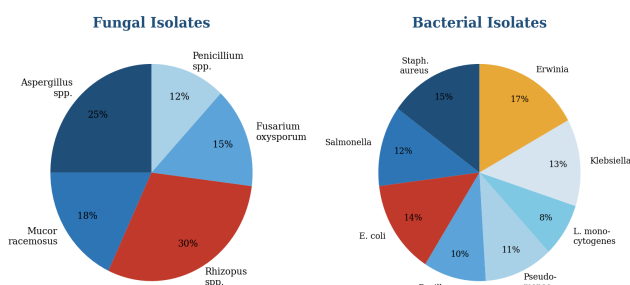


Figure 6: Relative distribution of fungal (left) and bacterial (right) species isolated from sweet potato tubers across the study areas.

4. Discussion

The findings of this study confirm that sweet potato tubers cultivated in Birnin Kebbi and Maiyama LGAs of Kebbi State are colonized by a diverse consortium of bacterial and fungal organisms capable of causing postharvest rot. The spectrum of organisms isolated in the present investigation is broadly consistent with reports from other sweet potato producing regions of Nigeria. Oladoye *et al.* (2013), working in Kwara State, isolated an almost identical suite of bacterial species from spoiled sweet potato tubers. The ubiquitous presence of *Erwinia* spp. and *Staphylococcus aureus* across all collection points in the present study is particularly significant, as both organisms have been identified as principal agents of bacterial soft rot in potatoes and sweet potatoes by several investigators (Olivieri *et al.*, 2004; Mahmoud *et al.*, 2008; Adisa, 2006).

The isolation of *Pseudomonas* spp. from sweet potato tubers is noteworthy. Although *Pseudomonas* has not traditionally been regarded as a primary agent of potato spoilage, its recovery from samples in this study is consistent with its well established ecology as a soil dwelling organism and opportunistic plant pathogen (Collins *et al.*, 2004). The presence of *Pseudomonas* in the tubers may be attributed to contamination from surrounding soil during harvesting or from contact with unclean surfaces during transportation and storage. Its ability to produce pectinolytic enzymes enables it to contribute to tissue maceration when the host defences are compromised by mechanical injury or concurrent infection by other pathogens.

The fungal species recovered in this study, namely *Rhizopus stolonifer*, *Mucor racemosus*, *Fusarium oxysporum*, *Aspergillus niger*, and *Penicillium* spp., are well documented agents of postharvest deterioration in root and tuber crops (Ray *et al.*, 2000; Doyle, 2007; Onuegbu, 2002; Oyeyipo, 2012). Snowden (1991) observed that these fungi produce localized discolouration and disrupt the surrounding tissues of infected tubers, leading to alterations in appearance, texture, and, in many cases, flavour. Clark and Moyer (1988) further noted that postharvest fungal rots are a major determinant of market value reduction and economic hardship for smallholder farmers in tropical regions.

The pathogenicity results demonstrated that *Rhizopus* spp. was the most aggressive fungal pathogen, producing the deepest rot (4.2 cm) among all fungal isolates tested. This finding is consistent with the known enzymatic capacity of *Rhizopus*, which secretes a potent battery of pectinases and cellulases that rapidly degrade plant cell wall polysaccharides (Arinze, 1985; Clerk and Hoy, 1994). Among the bacteria, *Klebsiella* spp. and

Erwinia spp. were the most destructive, producing rot depths of 4.0 cm and 3.4 cm, respectively. The aggressive tissue degradation by *Erwinia* is attributed to its production of pectic enzymes that cause the characteristic soft rot observed in tuber crops. The pathogenicity pattern observed in this study correlates with the findings of Khatoon *et al.* (2017), who reported varying percentages of tuber rotting caused by different fungal species, although the absolute values differ, probably as a result of differences in incubation duration, measurement parameters, and prevailing environmental conditions.

The elevated bacterial counts in Maiyama LGA relative to Birnin Kebbi LGA may be attributable to differences in local soil composition, water availability, and handling practices during and after harvest. The higher fungal load observed in the Gulumbe collection point of Birnin Kebbi LGA, particularly in the yellow flesh variety, may reflect the greater moisture retention capacity of the soils in that locality, as elevated soil moisture is a well established predisposing factor for fungal colonization of root crops (Singh *et al.*, 2008; Tester *et al.*, 2005). The high rainfall pattern, high humidity, and temperatures ranging from 19 °C to 31 °C in Kebbi State collectively create an environment that strongly favours the development of fungal species both in the field and in storage (Mandal, 1981). The onset of *Aspergillus niger* infection, characterised by softening of internal tissue and the development of a black spore mass over the infected area, typically begins around a wound as a small water soaked area with white mycelial growth, followed by profuse black sporulation (Mandal, 1981).

The public health significance of the findings should not be overlooked. The recovery of recognized foodborne pathogens, including *Salmonella* spp., *E. coli*, *S. aureus*, and *L. monocytogenes*, from spoiled tubers underscores the potential for these commodities to serve as vehicles for the transmission of gastrointestinal and systemic infections if consumed without adequate processing or if cross contamination occurs during food preparation (Doyle, 2007). Furthermore, certain fungal species, particularly *Aspergillus* spp., are capable of producing mycotoxins that pose chronic health risks to consumers (Onifade *et al.*, 2014). These considerations reinforce the imperative for improved postharvest management strategies, including proper curing of harvested tubers, avoidance of mechanical injury, use of well ventilated storage facilities, and the application of biological or chemical control agents where appropriate.

5. Conclusion

This study has demonstrated that a diverse community of fungi and bacteria is responsible for the postharvest spoilage of sweet potato tubers in Birnin Kebbi and Maiyama LGAs of Kebbi

State, Nigeria. Five fungal species (*Aspergillus* spp., *Mucor racemosus*, *Rhizopus* spp., *Fusarium oxysporum*, and *Penicillium* spp.) and eight bacterial species (*S. aureus*, *Salmonella* spp., *E. coli*, *Bacillus* spp., *Pseudomonas* spp., *L. monocytogenes*, *Klebsiella* spp., and *Erwinia* spp.) were isolated and confirmed through morphological and biochemical characterization.

No substantial distinction was observed between the two LGAs in terms of the range of microbial species recovered, although the relative abundance of bacteria and fungi differed between localities. Maiyama LGA exhibited higher average bacterial counts, while Birnin Kebbi LGA recorded higher average fungal counts. Pathogenicity testing confirmed that all isolated organisms are capable of causing tuber rot, with *Rhizopus* spp. and *Klebsiella* spp. being the most aggressive fungal and bacterial pathogens, respectively. The presence of known foodborne pathogens among the isolates highlights the public health risks associated with the consumption of poorly stored sweet potato tubers.

The identification of these spoilage organisms provides a foundation for the development of targeted disease management and postharvest handling protocols. Future research should investigate the efficacy of biological control agents, essential oil based fumigants, and improved storage technologies in reducing microbial contamination and extending the shelf life of sweet potato tubers in the study areas. Such interventions would benefit both the economic livelihoods of smallholder farmers and the food security of consumers in Kebbi State and beyond.

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