SAR Journal of Pathology and Microbiology

Abbreviated Key Title: *SAR J Pathol Microbiol*
Home page: https://sarpublication.com/journal/sarjpm/home
DOI: https://doi.org/10.36346/sarjpm.2026.v07i01.003

ISSN 2707-7756 (P)
ISSN 2709-6890 (O)

Original Research Article

Microbial Quality of Garri Sold in Wudil Market, Wudil Local Government Area Kano State

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Article History: | Received: 22.11.2025 | Accepted: 14.01.2026 | Published: 19.01.2026 |

Abstract: Microbiological analysis of Garri samples taken from Wudil Market, Kano State, revealed levels of bacterial, fungal, and coliform contamination. The mean bacterial load ranged from 1.25×10^4 to 8.63×10^4 CFU/g, of which P10 contained the highest. The mean fungal load ranged from 1.08×10^4 to 5.01×10^4 CFU/g, also highest in P10. Most Probable Number (MPN) total coliform counts ranged from 29 to 120 MPN/g in samples. Staphylococcus aureus, Escherichia coli, Salmonella spp., and Bacillus spp. were the bacterial isolates recovered, with *S. aureus* and *E. coli* being most prevalent (35% each). Fungal isolates were *Aspergillus niger, Aspergillus flavus, Penicillium* spp., and *Cladosporium* spp., of which *A. niger* was the most frequent (32%). These findings indicate that Garri retailed in the study area holds public health-relevant microorganisms, which means that there may be associated hazards from its intake and further highlights the need for proper amplified hygiene in processing, storage, and handling.

Keywords: Microbial Quality, Bacteria Fungi Garri.

INTRODUCTION

Nigeria is one of the leading cassava producers worldwide. Cassava is crucial in addressing Africa food crisis due to its efficient food energy production, year-round availability, resilience to extreme stress conditions, and compatibility with current African farming and food systems (Ayowale *et al*., 2021). Traditionally, cassava roots are processed into various products and used in different ways based on local customs and preferences. One popular cassava product is *Garri*, widely consumed in West and Central Africa and serving as a staple food for many people in southern Nigeria. Nigeria produces an estimated ten million tonnes of *Garri* annually (Okafor *et al*., 2018). *Garri* is a well-known processed product of cassava (Manihot esculenta Crantz) tubers.

It is one of the commonly consumed cassava products in Nigeria and other West African countries (Tonukari, 2016). Other products derived from roots of cassava plants are 'Starch', '*Lafun'*, '*Tapioca'*, '*Fufu'*, and '*Attieke'* (Awoyale *et al*., 2021). *Garri* is the most preferred cassava product because it is less expensive, less bulky, easy to cook and not readily perishable (Awoyale *et al*., 2021). Adebayo *et al*., (2012) observed that almost all the cassava roots harvested from plantations in Nigeria were processed into *Garri*. Processing of cassava roots to obtain *Garri* is done in different ways depending on the locality and usage but the general process for commercial production of *Garri* involves harvesting the matured cassava roots, peeling the roots, washing the peeled roots, grinding the washed roots, de-watering the mash, fermenting the mash, wet sieving the fermented mash, dry-frying/roasting, open air-cooling on floor or mat and packaging for sale (Okafor *et al*., 2018). Consumption of *Garri* varies with localities and transverses the low, middle and high class both in urban and rural areas (Tamang *et al*., 2016). They are generally consumed soaked in water along with dried fish or groundnut or coconut or beans cake/puddin ('Akara'/'Moimoi') or soaked in hot water to make 'eba' and taken with soup. The processing conditions, retailing containers, storage containers and conditions could serve as veritable critical point of contamination of *Garri* (Akindele *et al*., 2018). The general processing method

of *Garri*, has been found to be generally unhygienic processed, and may cause serious health/environmental hazards to the final consumers. (Obadina *et al*., 2019), observed that after fermentation of the cassava product (*Garri*) a change in odour was observed. This could be caused by the fermentation process involved, yielding unwanted organisms, therefore causing smell to the final products (Obadina *et al.,* 2019).

Therefore due to other previous rese arch and findings, *Garri* is known to have high microbial content, which may be detrimental to human health. Microorganisms of public health importance such as Staphylococcus aureus, Escherichia coli, Salmonella sp., *Shigella* sp., *Aspergillus* sp., *Cladosporium* sp. and *Fusarium* sp. have been isolated from stored, retailed and ready-to-eat *Garri* from some communities in Nigeria (Okafor *et al*., 2017). To date *Garri* is still being consumed largely in students' communities without any form of thermal treatment which may expose them to serious health risk associated with microorganisms and their toxins (Orji *et al*., 2016). To date, *Garri* is still being consumed largely in students' communities without any form of thermal treatment which may expose them to serious health risk associated with microorganisms and their toxins. Hence, the need to constantly evaluate the microbiological quality of *Garri* sold is very important to ascertain their safety (Okafor *et al*., 2017). This study was based on the fact *Garri* which is the staple food of man may cause a lot of harm to his life. This is due to the unhygienic condition of the environment during processing, storage and further exposure to the market in which *Garri* is sold. These microbes can lead to food poisoning and other intoxication (ailment) which can lead to loss of man power and the loss of life. Therefore, this work is to analyze the microbial content of the *Garri* and educate the people involved in the processing, storage and selling of *Garri* about personnel hygiene on the product and how it can be stored.

MATERIAL AND METHODS

Sampling Site

The sampling site was Wudil market located in Wudil Local Government Area, Kano State. Wudil is located within the Sudan Savannah region of Nigeria. The study site is located on the latitude 11°37 and 11°56 N and longitude 8°45 and 8°57 E at an altitude of 403m above the sea level. The relative humidity of the region is always low and ranges between 41-59% (Olofin *et al*., 2006). It is bordered with Warawa to the west and north, Gaya to the east, Garko and Albasu to the South. The area has average rainfall of about 800-900mm and annual temperature range between 26-33°c. It covers the total area of about 640km 2 with about 23,066 population from 2006 census (Olofin, 2006). The main occupation of the Wudil inhabitant is farming and trading.

Sample Collection

Exactly ten (10) cups of *Garri* samples were purchased from ten (10) various vendors in Wudil market. The samples were collected aseptically by putting them into sterile polythene bags, adopting standard procedure and transported to the laboratory of Microbiology department for immediate analysis (Oranusi, 2012).

Sample Preparation

One gram (1g) of each *Garri* samples was weighed aseptically using a weighing balance and transferred into 9ml of sterilized peptone water and vigorously shaken to obtain homogenous suspension. The serial dilution was done by transferring one ml (1ml) aseptically using a sterilized syringe into a test tube containing 9ml sterilized peptone water and five-fold serial dilution will be carried out (Oranusi, 2012).

Bacterial Load Determination

According to Compendium of Methods for the Microbiological Examination of Foods (2015). The bacterial load was determined using pour plate method. 1ml of dilution factors of 10^{-2}, 10^{-3}, 10^{4} and 10^{5} were pipetted into sterile petri dishes using the sterile syringe. Sterile molten nutrient agar was added to each dish and swirled thoroughly to allow even distribution and was allowed to solidify. It was inverted so as to obtain discrete colonies and then incubated at 37°C for 24hrs. After incubation, discrete colonies were counted manually and multiplied by the reciprocal of the dilution factor obtain the bacterial load of each samples. Colonies from 30-300 were counted, recorded as CFU/g and noted for further analysis.

Fungal Load Determination

According to Compendium of Methods for the Microbiological Examination of Foods (2015). The fungal load was determined using pour plate method. 1ml of each dilution factor was then transferred into separate corresponding petri dishes in duplicates. About 15-20ml of Potato Dextrose Agar (PDA) cooled to 45°C was poured in to each plate. The sample and the agar medium was mixed by rotating the plate on a flat surface and allowed to solidify. The plates were left at room temperature for 2-5 days. The morphologies of the colonies formed were taken. Plates containing between 30-300 colonics were selected and counted. Those plates that contain more than 300 colonies were considered as too numerous to count (TNTC). The number obtained was multiplied by the reciprocal of the dilution factor. This gave the number of fungal colony forming unit per gram of the breads and cake samples (CFU/g) (Oranusi and Wesley, 2012). The following formula was used to calculate the number of fungi colony forming units per gram of the samples.

Coliform Analysis

Nine (9) test tubes (3 each) with inverted Durham tubes containing lactose broth were labelled as 10 -1 for three sets of test tubes, 10 -2 for another set of three test tubes and 10 -3 for another set of three test tubes. 3ml of serial dilution (10^{-1}) was transferred

aseptically into the first three set of test tubes labelled as 10 -1 (1ml per test tube for the first three set). Another 3ml was taken from dilution factor 10^{-2} and transferred aseptically into the next three set of test tubes. Same process was carried out for the third dilution factor 10^{-3}. The test tubes were incubated at 35°C for 24-48 hours (Eaton *et al*., 2017).

Sub-Culturing

Some selective media such as EMB, SSA, MacConkey and Blood agar were prepared, poured into petri dishes and allowed to cool and solidify. The discrete colonies were sub-cultured by being inoculated onto the surface of those media using a sterile wire loop by streaking method. They were then incubated at 37°C or 24hrs in an inverted position. After incubation, distinctive morphology properties of each colony were formed and noted down for further study (Cheesbrough, 2012).

Gram Staining

A smear of bacteria was applied on a slide, air dried and heat fixed by passing through a flame a few times. 5 drops of crystal violet were added and allowed for 60seconds, bacteria were stained purple and then washed with distilled water and excess was shaken off. 5 drops of iodine solution (mordent) was added and then allowed for 30seconds and then washed away with distilled water. Then it was decolorized with solvent (acetone-alcohol) until purple color stops running, it was washed immediately and excess was shaken off. 5 drops of safranin were added and allowed for 60seconds, then washed with water and excess was shaken off. Then it was examined under microscope at 40x and 100x oil immersion. The purple color from a single colony of the slide under microscope indicated that the bacteria were gram positive and the pink color indicated negative. Microscopic investigation for gram reaction and morphological features of suspected colony was determined using standard method of Gram's staining (Cheesbrough, 2012).

Biochemical Test

Several biochemical tests were carried out in order to have a presumptive identification of the potential bacteria present. Most of the methods were done according to the microbiology laboratory manual. The biochemical tests performed were Indole production test, Methyl red test, Voges- Proskauer test, Citrate utilization test, Urease test, Catalase test and coagulase test.

Sub-Culturing of Fungi

After the incubation of the aerobic mesophilic fungal count (on PDA), the colonies were sub- cultured on plates containing sterile PDA. The colonies were picked using a sterile wire loop and transferred to the surface of the sterile agar plates aseptically using Bunsen burner flame to avoid contamination. The colonies were streaked uniformly on the surface of the agar. The agar plates were incubated in an inverted position at 25°C for five days for the development of the fungal colonies (Cheesbrough, 2012).

Identification of Fungal Isolates

The colonial and microscopic characteristics of the fungal isolates were determined using the lactophenol cotton blue staining method. The colony was picked with a sterile wire loop to a grease-free glass slide. One drop of lactophenol cotton blue was added to colony on the glass slide and covered with a cover slip and viewed under the microscope with x40 lens (Cheesbrough, 2012).

RESULTS

The following results were obtained from the analysis carried out on the *Garri* samples gotten from the sampling site (Wudil Market). The mean bacterial load of the samples ranged from 1.25x 10 4 CFU/g – 8.63 x 10 4 CFU/g. Sample P 10 has the highest mean bacterial load and sample P 9 having the least bacterial load. The mean fungal load of the samples ranged from 1.08 x 10 4 CFU/g – 5.01 x 10 4 CFU/g. Sample P 10 has the highest mean fungal load and sample P 4 having the least fungal load. The total Coliform count using Most Probable Number (MPN) ranged from 29 – 120. The bacterial load, the mean fungal load and the Total Coliform Count of the samples can be seen in (Table 1).

Table 1: The Mean bacterial, fungal load and total coliform count of the samples

Sample Code	Bacterial Counts	Fungal Counts	Coliform MPN/ml
P1	3.40×10^4	3.60×10^4	120
P2	7.06×10^4	4.83×10^4	93
P3	4.21×10^4	1.93×10^4	64
P4	2.43×10^4	1.08×10^4	120
P5	5.65×10^4	3.04×10^4	93
P6	4.49×10^4	2.25×10^4	35
P7	3.74×10^4	4.42×10^4	29
P8	4.40×10^4	1.09×10^4	75
P9	1.25×10^4	4.76×10^4	64
P10	8.63×10^4	5.01×10^4	120

Keys: S/NO – Serial Number, P 1 – P 10 – Sample Code, CFU – Colony Forming Unit, TCC – Total Coliform Count, MPN – Most Probable Number, ml – Millilitre

Morphological and Biochemical Characteristics of the Bacterial Isolates

The morphological and Biochemical characteristics of the isolates from the samples analyzed can be seen in (Table 2). The macroscopic and microscopic characteristics of fungal isolates is shown in (Table 3).

Table 2: Morphological and Biochemical Characteristics of the bacterial isolates from the samples

Macroscopy	Gram Stain	IND	CAT	COA	CIT	MR	VP	ISOLATES
Gray-whitish round, opaque colonies on Blood agar	+ve Rod	-	+	-	+	+	+	*Bacillus* spp.
Yellowish round, smooth colonies on M.S.A	+ve cocci	-	+	+	-	+	+	*Staphylococcus aureus*
Black centered colonies on S.S.A	-ve Rod	-	+	-	-	+	-	Salmonella *typhi*
Metallic sheen with dark centers on E.M.B agar	-ve Rod	+	+	-	-	+	-	*Escherichia coli*

Keys: S/NO – Serial Number, IN- Indole Test, CAT- Catalase Test, COA – Coagulase Test, CIT – Citrate Test, MR – Methyl-Red, VP – Voges Proskauer, + - Positive, - Negative

Table 3: Showing the cultural and morphological Characteristics of Fungal isolates

Cultural	Morphological	ISOLATES
Conidiophores are more or less distinct from the vegetative hyphae, are erect, straight or flexuous, unbranched or branched only in the apical region, with geniculate sympodial elongation in some species.	Colonies are rather slow growing, mostly olivaceous-brown but also sometime grey, buff or brown, suede like to floccose, often becoming powdery due to the production of abundant conidia	*Cladosporium* spp.
Non-branched conidiophore with bulb ends carries conidia like sun rays.	Pin-like black growth.	*Aspergillus niger*
Non-branched conidiophore with bulb ends carries conidia	Pin-like green growth.	*Aspergillus flavus*
Green or green-greyish color colonies grow over fruits especially citrus	Brush-like conidiophore carries conidia	*Penicillium* spp

Frequency Occurrence of the Bacterial and Fungal Isolates

The bacteria isolates identified from the samples analyzed were *Staphylococcus aureus*, *Escherichia coli, Salmonella* spp., and *Bacillus* spp. The highest isolates frequency from the research were *Escherichia coli* and *Staphylococcus aureus* (35%) and the least isolates frequency was *Bacillus* spp. (13%). While the fungal isolates identified were *Apergillus niger, Aspergillus flavus, Penicillium* spp. And *Cladosporium* spp. *Aspergillus niger* has the highest frequency (32%) with *Cladosporium* spp. and *Penicillium* spp. having the least occurrence (20%). The frequency of fungal occurrence of each isolates is shown in (Table 4).

Table 4: Frequency occurrence of the bacterial and fungal isolates from the samples

S/N	Bacterial Isolates	Frequency of Occurrence (%)	Fungal Isolates	Frequency of occurrence (%)
1.	*Staphylococcus aureus*	10 (34)	*Aspergullus niger*	8 (32%)
2.	*Escherichia coli*	10 (35%)	*Aspergillus flavus*	7 (28%)
3.	*Bacillus* spp.	4 (14)	*Penicillium* spp	5 (20%)
4.	Salmonella spp	5 (17%)	*Cladosporium* spp.	5 (20%)
5.	Total	29 (100%)	Total	25 (100%)

Key: S/NO – Serial Number, % - Percentage

DISCUSSION

The bacterial load of *Garri* samples in this research, ranging from 1.25 x 10^4 to 8.63 x 10^4 CFU/g, falls within the typical range of microbial counts reported in fermented food products. *Garri*, a staple food derived from fermented cassava, often harbors bacteria from both the fermentation process and environmental contamination. This findings align with other studies that have investigated the microbial content of *Garri*. Ijabadeniyi (2013) reported bacterial loads in *Garri* ranging from 1.0 x 10^4 to 9.0 x 10^4 CFU/g in samples collected from different markets. This is comparable to the results of this study, indicating that the bacterial load in *Garri* is influenced by post-processing handling and

environmental factors. The relatively high bacterial load may result from exposure to contaminated surfaces during processing, transportation, and storage. Ogiehor and Ikenebomeh (2006) found similar levels of microbial contamination in stored *Garri* samples, with bacterial counts ranging from 2.0 x 10^4 to 1.0 x 10^5 CFU/g. These authors also noted that the presence of bacteria in *Garri* is mainly due to improper handling during drying and packaging. In this study, the highest bacterial load (8.63 x 10^4 CFU/g) could be attributed to similar factors, including contamination from the environment during sun-drying or storage in non-hygienic conditions. However, variations in bacterial loads among different studies may also depend on the processing methods used. In some cases, bacterial loads as low as 1.0 x 10^3 CFU/g have been reported in *Garri* samples processed and stored under controlled, sanitary conditions (Amoa-Awua *et al*., 2007). This shows the importance of adopting hygienic practices during *Garri* production to minimize bacterial contamination.

In a study by Aboloma (2008), bacterial counts in *Garri* samples collected from Ekiti State, Nigeria, ranged from 1.0 x 10^3 to 5.5 x 10^4 CFU/g. This is slightly lower than the bacterial load found in this research, suggesting that factors such as regional differences in production practices, storage conditions, and climate may affect bacterial contamination levels. Aboloma also attributed higher bacterial loads to poor hygiene during sun-drying, where *Garri* is often exposed to dust and flies, contributing to increased microbial contamination. Another study by Ogugbue *et al*. (2011) reported bacterial loads in *Garri* samples ranging from 3.0 x 10^3 to 7.0 x 10^4 CFU/g, emphasizing the influence of market handling and packaging on contamination levels. In particular, *Garri* sold in open markets, where it is exposed to air, insects, and frequent human contact, showed higher bacterial loads compared to *Garri* stored in sealed containers.

This finding aligns with the upper limit of bacterial load (8.63 x 10^4 CFU/g) in this study, likely reflecting similar market and environmental exposure. Interestingly, Osundahunsi and Aworh (2003) reported that microbial loads in high-quality *Garri* (produced under controlled and sanitary conditions) were significantly lower, typically below 1.0 x 10^4 CFU/g. This finding reinforces the need for improved processing and storage techniques to reduce microbial contamination in *Garri*. This research results on the fungal load of *Garri* samples, ranging from 1.08 x 10^4 to 5.01 x 10^4 CFU/g, align with other studies investigating fungal contamination in *Garri*. Fungal contamination in food products, particularly starchy foods like *Garri*, is often attributed to improper processing, storage, or environmental factors such as humidity, which can promote the growth of fungi.

Olopade *et al*., (2014) found similar levels of fungal contamination in *Garri*, with counts ranging from 1.2 x 10^4 to 6.3 x 10^4 CFU/g. This study emphasized that poor storage conditions, especially in regions with high humidity, significantly increase the fungal load. Both studies indicate that the fungal load is within the range commonly found in stored *Garri*, suggesting that contamination often occurs post-production, particularly during storage in poorly ventilated environments. Ogiehor and Ikenebomeh (2006) reported lower fungal counts in *Garri* samples, with values ranging from 1.0 x 10^3 to 3.5 x 10^3 CFU/g. The discrepancy between their findings and this might be attributed to different handling and storage conditions. Ogiehor and Ikenebomeh noted that proper drying and packaging of *Garri* significantly reduced fungal contamination, showing the importance of these practices in maintaining food safety. Further comparison with Adejumo and Ojo (2012), who reported fungal loads of 1.5 x 10^4 to 4.8 x 10^4 CFU/g in *Garri*, shows that this results are within a comparable range. Their study concluded that fungal contamination in *Garri* is often due to post-processing exposure, and frequent fungal isolates include species of *Aspergillus* and *Penicillium*, which are known to thrive in improperly stored food products.

This research results on the total coliform counts in *Garri* samples, which range from 29 to 120 Most Probable Number (MPN)/g, indicate moderate contamination levels. Coliforms are typically used as indicators of hygiene and sanitation during food processing and handling, suggesting potential lapses in these areas. Adejumo *et al*., (2012) reported coliform counts in *Garri* samples from open markets ranging from 15 to 105 MPN/g. Their findings closely align with this research and suggest that contamination is often introduced during post-processing, particularly during packaging or from exposure to unsanitary environments. In contrast, a study by Ogiehor and Ikenebomeh (2006) recorded significantly lower coliform counts in well-packaged *Garri* stored under controlled conditions, with values as low as 5 to 25 MPN/g. These lower counts reflect the impact of proper hygienic practices, indicating that improved handling and packaging can minimize contamination. The disparity between their findings and this may stem from differences in storage conditions or market practices, where *Garri* is often exposed to environmental contaminants. Oranusi *et al*., (2013) found coliform levels in *Garri* samples ranging from 40 to 150 MPN/g, slightly higher than this results at the upper end. They attributed the contamination to poor hygiene in processing centers and improper storage, where exposure to rodents, insects, and contaminated water sources likely increased coliform presence.

This study also pointed out that the presence of coliforms, especially at higher levels, could lead to the growth of more pathogenic bacteria such as *Escherichia coli*. This research results on bacterial isolates from *Garri* samples identified *Staphylococcus aureus, Escherichia coli, Salmonella* spp., and *Bacillus* spp., with *Staphylococcus aureus* and *Escherichia coli*

exhibiting the highest frequency. This aligns with existing literature, which indicates that *Garri*, a popular fermented cassava product, can be a vehicle for foodborne pathogens due to improper processing and handling. Omoregie *et al*., (2020) reported similar findings, noting that *E. coli* and *S. aureus* were prevalent in *Garri* samples analyzed in Nigeria. The study showed that the presence of these pathogens is primarily linked to poor hygiene practices during preparation and post-processing contamination, which resonates with this findings. In contrast, while *Salmonella* spp. was also detected in this samples, Omoregie *et al*., (2020) reported lower occurrences of this pathogen, suggesting potential variability in contamination levels based on geographic location and processing methods. Abdu *et al*., (2021) found *Bacillus* spp. in *Garri* samples, although at lower frequencies compared to *E. coli* and *S. aureus*. *Bacillus* species are known to form spores, which can survive unfavorable conditions, making them a common contaminant in dry food products like *Garri*. This study indicated that *Bacillus* spp. could contribute to food spoilage and potential health risks, similar to the pathogens you identified. The predominance of *S. aureus* and *E. coli* in this samples may indicate a higher risk for consumers, as both are associated with serious foodborne illnesses. According to Kolo *et al*., (2023), *S. aureus* is particularly concerning due to its ability to produce enterotoxins, which can cause severe gastrointestinal symptoms. In contrast, while *E. coli* is a normal intestinal inhabitant, specific pathogenic strains can lead to severe diarrhea and abdominal pain (Sharma *et al*., 2022). This research results on fungal isolates from *Garri* samples indicate the presence of several significant fungal species, including *Aspergillus niger, Aspergillus flavus, Penicillium* spp., and *Cladosporium* spp., with *Aspergillus niger* exhibiting the highest frequency. This finding aligns with other studies that have documented similar fungal contamination in *Garri* and other starchy food products. *Aspergillus niger* is a common contaminant in many food products, particularly those high in carbohydrates.

A study by Adebayo-Tayo *et al*., (2020) reported that *A. niger* was the most frequently isolated fungus from various fermented foods, including cassava products like *Garri*. This organism is known for its ability to thrive in low moisture environments, which is typical of processed cassava products (Adebayo-Tayo *et al*., 2020). Additionally, *Aspergillus flavus*, another frequent isolate in this samples, is noteworthy due to its production of aflatoxins, which pose significant health risks when consumed (Patel *et al*., 2022). The presence of both *A. niger* and *A. flavus* in this study shows the potential for mycotoxin contamination, especially in improperly processed or stored *Garri*. The isolation of *Penicillium* spp. and *Cladosporium* spp. in this research also aligns with previous findings. Akinmoladun *et al*., (2018) noted that *Penicillium* species were prevalent in fermented cassava products, indicating that these fungi may play a role in the fermentation process, although they can also contribute to spoilage. *Cladosporium* spp., while less studied in the context of *Garri*, has been documented as a contaminant in other food products, where it can affect quality and safety (Nwinyi *et al*., 2019). In contrast, while this findings emphasize *Aspergillus* species, other studies have reported higher frequencies of *Penicillium* spp. in similar products. Ijato *et al*., (2021) found that *Penicillium* species dominated in fermented cassava products over *Aspergillus* species. This discrepancy may be attributed to differences in environmental conditions, methods of fermentation, and storage practices.

CONCLUSION

Based on the finding of the study it is concluded that the bacteria isolates identified from the samples analyzed were *Staphylococcus aureus*, *Escherichia coli, Salmonella* spp., and *Bacillus* spp. The highest isolates frequency from the research were *Escherichia coli* and *Staphylococcus aureus* and the least isolates frequency was *Bacillus* spp. while the fungal isolates identified were *Apergillus niger, Aspergillus flavus, Penicillium* spp. And *Cladosporium* spp. *Aspergillus niger* has the highest frequency with *Cladosporium* spp. and *Penicillium* spp. having the least occurrence.

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