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Research Article

Assessment of Detergent Residues and Microbial Contamination in Fermented Baked Cassava (Fufu) in Rivers State, Nigeria: Implications for Food Safety

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Abstract

Background: Fermented baked cassava (fufu) is a widely consumed staple food in Rivers State, Nigeria, and is predominantly produced using traditional processing methods. The study assessed the presence of detergent residues and determined the bacterial contamination of fermented baked cassava (fufu) produced in Rivers State, Nigeria. Methods: Four fufu samples were analyzed: Sample A (cassava soaked in borehole water) and Sample B (cassava soaked in distilled water) served as controls, while Sample C and Sample D were commercially processed fufu obtained from Umuanyagu and Okomoko villages in Etche, respectively. Detergent residues were analyzed using a titrimetric method to determine cationic and anionic surfactant concentrations. Microbial analysis was performed using serial dilution and culture plating techniques on agar for the enumeration of microorganisms. Data were statistically analyzed using one-way ANOVA at a 95% confidence level in SPSS version 27 and cross-validated in Python (scikit-learn library). Results: In the samples, cationic surfactant concentrations ranged from 1.1% to 2.0%, and anionic surfactant concentrations ranged from 3.1% to 4.2%, with the highest levels recorded in Sample D from Okomoko village. Significant ($P \leq 0.05$) differences were observed between the control and market samples. Microbial counts varied widely across samples: total heterotrophic bacterial counts ranged from $1.4 \pm 0.70 \times 10^9$ to $9.4 \pm 2.12 \times 10^9$ CFU/g, total coliform counts ranged from $1.1 \pm 2.82 \times 10^7$ to $8.2 \pm 2.12 \times 10^7$ CFU/g, and faecal coliform counts ranged from $0.8 \pm 1.41 \times 10^7$ to $3.0 \pm 0.70 \times 10^7$ CFU/g. *Staphylococcus aureus* counts ranged from $0.2 \pm 2.12 \times 10^7$ to $2.6 \pm 1.41 \times 10^7$ CFU/g. Codex-based interpretation revealed significant hygiene non-compliance in market-obtained fufu samples. PCA analysis further revealed clear separation between the market samples (C and D), which were dominated by pathogenic microbes, and the laboratory controls (A and B), characterised by fermentation-associated flora. The presence of surfactant residues and these microorganisms may pose chemical and increase microbiological exposure concerns, potentially contributing to mucosal irritation or other adverse health effects with repeated consumption. Conclusion: Detergent residues and microbial counts were observed in the market-obtained fufu samples. Regulatory agencies such as NAFDAC and the Ministry of Health should strengthen monitoring and enforcement of food hygiene standards among cassava processors. Education and training of local producers on safe fermentation techniques, use of clean water, and hygienic handling are urgently recommended to safeguard consumer health and ensure food safety.

Keywords

Cassava, Fufu, Detergent, Bacterial Screening, Fermentation

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1. Introduction

Cassava (*Manihot esculenta* Crantz) is one of the most important staple and major food crops in Nigeria [1-5]. Owing to its high carbohydrate content, cassava is processed into a variety of food products, including *fufu*, *garri*, flour, and tapioca Nigeria is the world's largest producer of cassava, with an estimated annual output of about 60 million metric tonnes The country's cassava transformation programme aimed at transitioning from subsistence to commercialized, high-yield, and diversified production systems, is among the most advanced in Africa Cassava tubers are perishable, and significant post-harvest losses often occur during storage. This is primarily due to the crop's high moisture content and its susceptibility to physiological deterioration and microbial invasion through harvest-induced bruises, which accelerate spoilage and undesirable biochemical changes [6, 7].

Fufu is a fermented cassava product processed through various traditional methods and local practices It is typically made by fermenting peeled or unpeeled cassava tubers to produce a soft, fermented pulp, followed by wet sieving and dewatering to obtain the fufu mash. The mash is then cooked and pounded into dough or dissolved in water and heated until it gelatinizes. Traditionally, fufu is marketed either in its wet form (containing approximately 50% moisture) or as cooked dough. The yield and quality of fufu depend largely on the efficiency of the fermentation process and the dry matter content of the cassava; poor fermentation often results in low mash yield. Fufu, also referred to as fermented baked cassava flour, remains a culturally and nutritionally significant food due to its ease of digestion and satisfaction derived by consumers [8, 9].

Previous studies on fermented cassava products have primarily centered on identifying and characterizing the microorganisms responsible for the fermentation process, particularly lactic acid bacteria, yeasts, and molds that contribute to the texture, flavour, and preservation of cassava-based foods such as fufu, gari, and lafun [3, 10, 11]. These beneficial microbes, including species of Lactobacillus, Leuconostoc, and Saccharomyces, play an important role in breaking down cyanogenic compounds, lowering the pH, and enhancing product safety during controlled fermentation [12, 13]. However, growing urbanization and commercialization have altered traditional processing methods, leading to increased risks of contamination from pathogenic microorganisms. Recent investigations have extended beyond fermentation studies to assess the microbial safety of cassava products available in open markets and supermarkets. For instance, Odu et al. [14] examined the microbial load of packaged and exposed cassava, yam, and plantain flours sold in Port Harcourt, Nigeria, and reported high counts of *Staphylococcus aureus*, *Escherichia coli*, and coliforms, indicators of poor hygiene and possible faecal contamination. Similar findings by Ngozi and Ndukwe [6] revealed that exposure during processing and storage promotes the proliferation of pathogenic bacteria and fungi, compromising food safety.

In recent times, the effects of climate change have made cassava fermentation more difficult, prompting some producers to adopt unconventional and potentially unsafe additives to accelerate the fermentation process. These additives include detergents, hypo (bleach), palm ash, bitter leaves, and *Jatropha* leaves used to enhance fermentation, whiteness, odor reduction, and product preservation at minimal cost [15, 16]. To maximize profit, some local producers reportedly add powdered detergents (such as Ariel and Omo), kerosene, hypo, and palm ash during fermentation [17, 18].

Detergents are surfactants or cleaning agents designed to remove grease and dirt from various surfaces [19-21]. They contain toxic substances that, when ingested, can cause severe health complications, including diarrhea, respiratory distress, vomiting, nausea, abdominal bloating, gastric mucosal damage, free radical generation, and blood pH imbalance leading to tissue injury [22, 23]. Research has shown that consumption of detergent-processed cassava can adversely affect kidney structure and function in animal studies. While these practices may improve yield and appearance, they introduce serious public health risks [18].

Although cassava fermentation has been widely studied, prior research has largely emphasized fermentative microorganisms and microbial safety, with limited focus on chemical contamination from unconventional processing aids. Empirical data quantifying detergent-derived surfactant residues in fufu remain scarce, and chemical and microbiological risks are rarely examined together. This lack of integrated evidence constrains understanding of potential dietary exposure and public health implications, particularly in informal production settings. Therefore, this study investigated the detergent levels and bacterial composition of fermented baked cassava (fufu) produced in two communities, Okomoko and Umuanyagu, in the Etche Local Government Area (LGA) of Rivers State, Nigeria, and compared the observed values with established international and national permissible limits.

2. Methods

2.1. Study Areas

This study was conducted in Okomoko and Umuanyagu communities, located within the Etche LGA of Rivers State, Nigeria. Etche LGA is predominantly rural and widely recognized for its extensive cassava cultivation and traditional processing of cassava-based foods, particularly fufu. Cassava farming and small-scale fermentation activities constitute major livelihood sources in these communities, making the area highly relevant for investigating food safety issues associated

with cassava processing. Okomoko and Umuanyagu were purposively selected due to their high levels of local cassava production, active household- and market-based fufu processing, and reliance on traditional fermentation practices. Informal reports and preliminary observations indicated the possible use of unconventional fermentation aids, including detergents and other additives, within these communities. Additionally, both locations host vibrant local markets where processed fufu is widely traded and consumed, allowing for comparison between laboratory-prepared controls and commercially available products. The selection of two communities within the same LGA enabled assessment of contamination patterns under similar agro-ecological and socio-cultural conditions while capturing variability in processing and handling practices.

2.2. Sample Collection and Preparation

Cassava tubers were purchased from Umuanyagu village market, peeled, washed, and divided into two equal portions. One portion was soaked in borehole water (Control A) and the other in distilled water (Control B), both left to ferment for seven (7) days. After fermentation, the softened cassava was separated from the water and manually mulched for about 30 minutes. The resulting pulp was allowed to settle to form starch, which was then collected and processed into baked cassava flour (fufu). This was done at ambient laboratory temperature (28 ± 2°C) using loosely covered plastic containers. Additionally, already processed baked cassava flour (fufu) samples were obtained from Umuanyagu village (Sample C) and Okomoko village (Sample D) in Etche Local Government Area. All samples (A, B, C, and D) were stored under refrigeration before analysis to prevent spoilage.

3. Detergent Analysis

3.1. Determination of Cationic Surfactants

The determination of cationic surfactants in the detergent was performed using the titrimetric method described by Ibiam et al. [24] 2 g of the sample were weighed into a 250 ml beaker, after which 50 ml of distilled water and 5 ml of citrate-phosphate buffer solution (pH 3.0) were added to obtain a homogeneous mixture. Subsequently, 30 ml of chloroform was introduced, followed by two drops of methyl orange indicator, which produced a yellow coloration. The mixture was then titrated with 0.010 M sodium tetraphenylboron solution until the endpoint was reached, indicated by the appearance of a red color in the aqueous layer. The percentage cationic surfactant was calculated using the formula:

$$\%\ \text{Cationic Surfactant} = \frac{\text{Titre value} \times \text{Sodium Terraphenyl Boron Equilvalent } 0.010}{\text{Weight of sample}} \times 100 \quad (1)$$

3.2. Determination of Anionic Surfactants

The determination of anionic surfactants was conducted using the titrimetric method described by Ibiam et al. [24], with slight modifications. 2.5 g of the sample was weighed into a 250 ml beaker, and 75 ml of distilled water was gently warmed and added. The mixture was stirred continuously until complete dissolution was achieved. It was then transferred into a 100 ml volumetric flask, and the beaker was rinsed thoroughly with distilled water. The rinsing water was added to the flask to make up the volume to the 100 ml mark. Subsequently, 20 ml of this solution was pipetted into a 100 ml stoppered measuring cylinder, to which 15 ml of chloroform and 10 ml of mixed indicator were added, producing a pink coloration. The mixture was titrated with 0.04 M hyamine until the pink color of the chloroform phase completely disappeared, indicating the endpoint. The anionic surfactant present was expressed as a percentage using the formula:

$$\%\ \text{Anionic Surfactant} = \frac{\text{Titre value} \times \text{Anionic surfactant equivalent } 0.040}{\text{Weight of sample}} \times 100 \quad (2)$$

4. Antimicrobial Analysis

4.1. Bacterial Enumeration

Sample preparation was carried out following the method described by Olopade et al. [25], with slight modifications. 10 g of each sample (A, B, C, and D) were accurately weighed using a digital balance and homogenized in 90 mL of normal saline. A ten-fold serial dilution was then performed, and aliquots from appropriate dilutions were inoculated in duplicates and spread-plated on solidified agar media. The media used included Nutrient Agar for total heterotrophic bacterial count, MacConkey Agar for total coliform count, Eosin Methylene Blue (EMB) Agar for total faecal coliform count, Salmonella-Shigella Agar for Salmonella and Shigella counts, Thiosulfate Citrate Bile Salts Sucrose (TCBS) Agar for Vibrio species, and Mannitol Salt Agar for Staphylococcus species. All plates were incubated for 24 hours at 37.2°C, except for faecal coliforms, which were incubated at 44.5°C. Colonies that developed were counted, and results were expressed as CFU/g using the formula described by Obadina et al. [26].

$$\text{CFU/mL} = \frac{\text{Number of colonies}}{\text{Dilution x volume plated}} \quad (3)$$

$$\text{CFU/g} = \text{CFU/mL}\ \frac{\text{Total homogenate volume (mL)umber of colonies}}{\text{Sample weight (g)}} \quad (4)$$

All culture media were sterilized using an autoclave at 121°C and 15 psi for 15 minutes. Heat-sensitive materials, such as plastic apparatus, were sterilized with 99.9% ethanol. Normal saline (0.85%) was used as the diluent. Nutrient Agar was employed for the enumeration of total heterotrophic bacteria, MacConkey Agar for total coliforms, Salmonella-Shigella Agar for *Salmonella* and *Shigella* species, Mannitol Salt Agar for *Staphylococcus aureus*, and Eosin Methylene Blue (EMB) Agar for faecal coliforms (*Escherichia coli*).

4.2. Detergent Contamination Index (DCI)

Detergent contamination in each sample was summarized using a Detergent Contamination Index (DCI), a composite metric combining measured cationic and anionic surfactant concentrations. DCI was calculated for each sample as the arithmetic mean of the cationic and anionic surfactant percentages:

$$\text{DCI} = \frac{\text{Cationic (\%)+Anionic (\%)}}{2}$$

4.3. Principal Component Analysis (PCA)

Principal Component Analysis (PCA) was performed to identify the microbial parameters that most strongly contributed to variations among the fufu samples and to determine patterns of similarity or differentiation between control and market-obtained samples. PCA was used to explore relationships among correlated microbial variables and identify the dominant factors driving sample variation. This multivariate approach enabled dimensionality reduction and clearer differentiation. The microbial parameters considered in the PCA included Total Heterotrophic Bacterial Count (THBC), Total Coliform, Faecal Coliform, and *Staphylococcus aureus* counts. These variables were selected because they represent the key microbial indicators of contamination, hygiene, and fermentation quality in food microbiology. Prior to analysis, microbial count data were standardized using z-scores to eliminate differences in units and magnitude across variables. PCA was conducted using SPSS version 27 and cross-validated in Python (scikit-learn library) to ensure computational accuracy. The analysis extracted principal components based on eigenvalues greater than 1, and varimax rotation was applied to improve interpretability of the factor loadings. The first two principal components (PC1 and PC2) were retained as they explained the highest proportion of variance in the dataset. PC1 represented microbial indicators associated with pathogenic contamination (*Staphylococcus aureus* and faecal coliforms*), while PC2 represented overall microbial load (driven primarily by THBC). The PCA loadings were used to determine which microbial parameters contributed most to sample separation, while the component scores were plotted in a biplot to visualize clustering patterns among samples (Control A, Control B, Sample C, and Sample D). Interpretation of the PCA biplot was based on the direction and magnitude of loadings along the principal components. Samples positioned closer together on the plot were considered to have similar microbial characteristics, whereas those farther apart indicated distinct contamination profiles. The differentiation along PC1 and PC2 was used to infer whether microbial variation was due to natural fermentation processes (as in control samples) or pathogenic contamination (as in market samples).

5. Data Analysis

Data obtained from the chemical and microbiological analyses of the fufu samples were statistically analyzed to determine variations among the different sample groups (Controls A and B, Samples C and D). The concentrations of cationic and anionic surfactants, as well as microbial counts, were expressed as mean ± standard deviation (SD). The data were subjected to Analysis of Variance (ANOVA) to test for statistically significant differences among samples at a 95% confidence interval ($P \leq 0.05$). All statistical analyses were performed using SPSS version 27 and Microsoft Excel 2019 for data entry, computation, and graphical representation. Mean separation was conducted using Duncan's Multiple Range Test (DMRT) to identify where significant differences occurred among treatment means. Results were presented in tables for clarity, with similar superscript letters indicating no significant difference and different superscripts showing significant variation among samples. All chemical and microbiological analyses were conducted in triplicate, and results are expressed as mean ± standard deviation (SD).

6. Results

This presents the findings from the analysis of detergent residues and microbial quality of fermented baked cassava (fufu) samples. The results are organized, detailing the levels of cationic and anionic surfactants as indicators of detergent contamination, followed by the microbial counts of various bacterial groups isolated from the samples. Both the chemical and microbiological parameters were statistically analyzed to determine variations among the control samples (A and B) and the locally processed samples (C and D). The results are summarized in tables and Figures below, highlighting differences in detergent residue concentrations, microbial load, and their compliance with Codex Alimentarius microbiological principles [27].

Table 1. *Detergent residue percentage.*

Sample Code	Cationic Surfactant (%)	Anionic Surfactant (%)
Control A	1.2	3.2
Control B	1.1	3.1
Sample C	2.0	4.0
Sample D	2.0	4.2

Sample A = Fresh cassava soaked with tap water; Sample B = Fresh cassava soaked with distilled water; Sample C = Processed cassava obtained from Umuanyagu village; Sample D = Processed cassava obtained from Okomoko village

Table 1 showed the percentage of detergent residues in the analyzed fufu samples. The cationic surfactant concentrations ranged from 1.1% to 2.0%, while the anionic surfactant concentrations ranged from 3.1% to 4.2%. The lowest levels were recorded in the control samples (A and B), which were laboratory-prepared under hygienic conditions, whereas higher concentrations were observed in the market samples (C and D), particularly in Sample D from Okomoko village. The elevated surfactant levels in market samples suggest possible use of detergents or chemical additives during cassava fermentation and processing, which may pose potential health risks to consumers. Table 1 presents the final calculated percentage detergent residues (%), while Table 2 reports the corresponding mean ± standard deviation (SD) values derived from triplicate titration measurements prior to percentage normalization. This dual presentation was adopted to distinguish between the direct analytical outputs and the standardized percentage expressions used for risk assessment.

Table 2. *Mean and Standard Deviation of Cationic and Anionic Surfactant Concentrations (mg/L) in Fufu Samples (ANOVA Test).*

Sample Code	Cationic Surfactant	Anionic Surfactant
Control A	24.6±0.566^{a}	19.8±0.141^{ab}
Control B	21.9±0.141^{b}	19.65±0.212^{ba}
Sample C	44.5±0.000^{c}	25.20±0.000^{c}
Sample D	39.55±0.495^{d}	26.25±0.354^{d}

Values with the same alphabet indicate no significant difference, while values with different alphabets indicate significant differences at $P \leq 0.05$ and a 95% confidence interval.

Table 2 showed the mean and standard deviation of cationic and anionic surfactant concentrations in the fufu samples. The results revealed significant variations ($P \leq 0.05$) among the samples. Cationic surfactant concentrations were highest in Sample C (44.5 ± 0.000) and Sample D (39.55 ± 0.495), while lower values were recorded in the control samples, particularly Control B (21.9 ± 0.141). Similarly, anionic surfactants were highest in Sample D (26.25 ± 0.354) and lowest in Control B (19.65 ± 0.212). The marked differences between market samples (C and D) and laboratory controls (A and B) indicate the likely introduction of detergent-related chemicals during local processing.

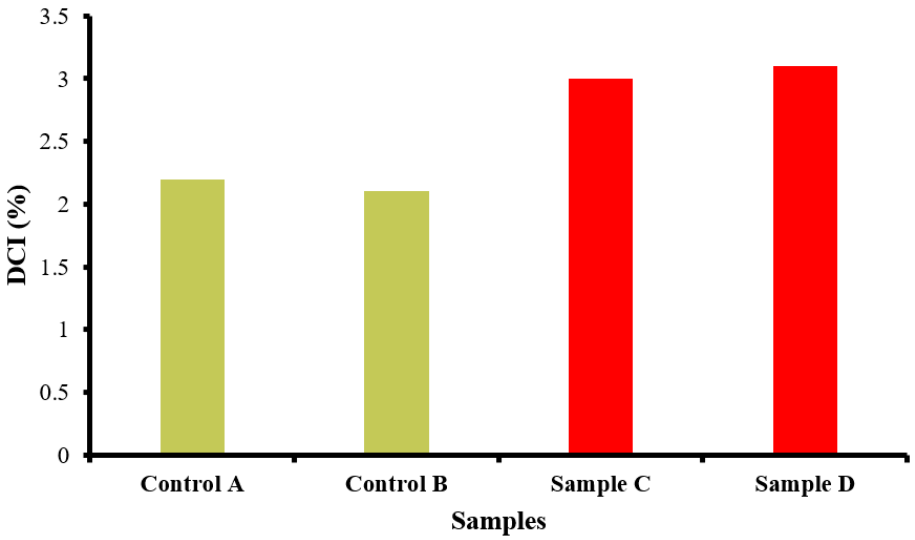

Figure 1. *Detergent contamination index (DCI) across fufu samples.*

Figure 1 showed the DCI across the analyzed fufu samples. The laboratory-prepared control samples (Controls A and B) recorded the DCI values, ranging from approximately 2.1% to 2.2%, indicating comparatively reduced levels of detergent-

derived surfactant residues under controlled fermentation conditions. In contrast, the market-obtained samples (Samples C and D) recorded higher DCI values, ranging from approximately 3.0% to 3.1%. These elevated values suggest greater detergent residue contamination in commercially processed fufu. The observed separation between control and market samples highlights potential differences in processing and handling practices, implying that local production methods may contribute to increased chemical contamination.

Table 3. *Mean and Standard Deviation of Microbial Counts (CFU/g) in Fufu Samples.*

Sample code	THBC (×10⁹) (CFU/g)	Total Coliform (×10⁷) (CFU/g)	Faecal Coliform (×10⁷) (CFU/g)	*Salmonella/Shigella* (CFU/g)	*Staphylococcus aureus* (×10⁷) (CFU/g)	*Vibrio* Count (CFU/g)
Sample D	2.2±1.41	5.7±0.70	1.1±2.12	Not detected	0.4±2.80	Not detected
Sample C	1.4±0.70	1.7±0.70	3.0±0.70	Not detected	1.6±1.41	Not detected
Control B	4.7±1.41	8.2±2.12	0.8±1.41	Not detected	0.2±2.12	Not detected
Control A	9.4±2.12	1.1±2.82	1.9±1.41	Not detected	2.6±1.41	Not detected
Codex-based criterion* [27].	Indicator organism (no fixed limit)	Indicator organism (low counts expected)	Absence required	Low counts expected; absence preferred	Absence in ready-to-eat foods	Absence in ready-to-eat foods

*Codex Alimentarius guidelines do not prescribe fixed numerical limits for all microbial indicators in ready-to-eat foods. Total heterotrophic bacteria and coliforms are used as hygiene indicators, where low counts are expected, while faecal coliforms (*Escherichia coli*), *Salmonella*, *Shigella*, and *Vibrio* species should be absent. *Staphylococcus aureus* should be present at low levels only, as elevated counts indicate poor hygiene and risk of toxin production.

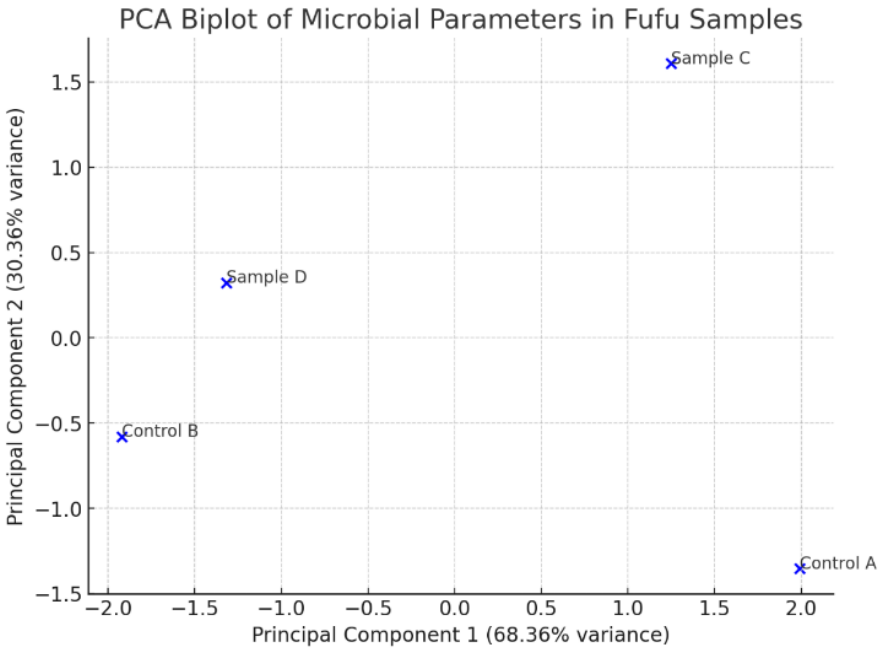

Figure 2. *PCA biplot illustrating the distribution of fufu samples based on microbial parameters.*

Table 3 presents the microbial counts of the fufu samples compared with Codex-based criterion. Total heterotrophic bacterial counts (THBC) ranged from 1.4×10^9 to 9.4×10^9 CFU/g, while total coliform and faecal coliform counts ranged from 1.1×10^7 to 8.2×10^7 CFU/g and 0.8×10^7 to 3.0×10^7 CFU/g, respectively. *Staphylococcus aureus* was present in all samples, whereas Salmonella, Shigella, and Vibrio species were absent. The presence of all bacterial counts showed poor hygienic conditions during fermentation and handling. The high microbial load poses potential public health risks to consumers of fufu in the study area.

PCA revealed the relative contributions of microbial parameters to variability among the fufu samples (Figure 2). The first principal component (PC1), explaining 68.36% of the total variance, was mainly associated with *Staphylococcus aureus* (loading = 0.59) and faecal coliforms (loading = 0.49), indicating that these pathogenic indicators were the primary drivers of sample differentiation. Samples with positive PC1 scores, particularly Sample C, were characterized by higher pathogenic contamination, whereas negative PC1 scores were associated with lower pathogen levels. The second principal component (PC2), accounting for 30.36% of the variance, was strongly influenced by total heterotrophic bacterial count (THBC) (loading = –0.82), reflecting differences in overall microbial load. The principal components (PC1 and PC2) explained 68.36% and 30.36% of the total variance, respectively, accounting for 98.72% of the cumulative dataset variability. Control samples aligned more closely with THBC, suggesting dominance of fermentation-associated microflora, while market samples clustered toward pathogenic indicators. The PCA biplot demonstrated clear separation between control and market-obtained samples, highlighting differences in microbial quality and hygiene status.

Table 4. *Comparison of PCA results.*

Category	Dominant Microbial Drivers	PCA Component Association	Interpretation	Risk Level
Control A & B	High THBC, Low *Staphylococcus aureus*, Low coliforms	High negative on PC2	Normal fermentation flora; minimal pathogen presence	Moderate (low risk)
Sample C & D	High *Staphylococcus aureus* and faecal coliforms	High positive on PC1	Pathogenic contamination from poor hygiene and handling	High (unsafe)

The PCA summary comparison in Table 4 showed clear differences between the control and market-obtained fufu samples. Controls A and B were associated with high total heterotrophic bacterial counts but low levels of *Staphylococcus aureus* and coliforms, indicating the presence of normal fermentation flora with minimal pathogenic contamination, thus posing a moderate or low health risk. In contrast, Samples C and D exhibited high *Staphylococcus aureus* and faecal coliform levels, loading positively on PC1, which reflects contamination from poor hygiene, unsafe handling, or use of contaminated water during processing.

7. Discussion

The findings of this study provide critical insight into the safety and quality of fermented baked cassava (fufu) produced and consumed in Etche. It revealed varying levels of detergent residues, both cationic and anionic surfactants, in the fufu samples analyzed. As presented in Table 1, cationic surfactant concentrations ranged from 1.1% to 2.0%, while anionic surfactant concentrations ranged from 3.1% to 4.2%, with the lowest levels observed in the control samples (A and B) and the highest in market samples (C and D). The ANOVA results (Table 2) further showed significant differences ($P \leq 0.05$) among the samples, confirming that detergent contamination levels were not uniform across all fufu samples. The low-to-moderate surfactant values detected in control samples may reflect background environmental contributions or matrix-related interferences rather than intentional detergent addition. Several plausible non-detergent sources of surface-active compounds can be identified from the literature. First, cassava tubers naturally contain phytochemicals including saponins and polar lipid fractions that share structural characteristics with anionic surfactants and are capable of reacting with titrimetric reagents such as hyamine and sodium tetraphenylboron employed in this study [1, 9]. Second, fermentation-associated lactic acid bacteria (LAB), including Lactobacillus and Leuconostoc species that are the dominant microflora of traditionally fermented cassava, are recognised producers of biosurfactants, lipopeptides, and exopolysaccharides during fermentation These biogenic compounds can generate measurable surfactant-equivalent signals in non-specific titrimetric assays and may account for a portion of the surfactant activity recorded in the control samples. Third, and most directly relevant, Hikon et al. [28] demonstrated through Fourier Transform Infrared Spectroscopy (FTIR) and flame photometric analyses that silicate, azide, and sodium compounds were present in both detergent-treated and untreated cassava flour samples. This finding confirms that certain surface-active chemical species are endogenous to the cassava matrix and are detectable regardless of deliberate detergent addition. Furthermore, procedural blanks consisting of distilled water combined with the full suite of analytical reagents but without any sample were analysed in parallel and yielded no detectable surfactant signal. This confirms that the observed DCI values in the control samples (2.1–2.2%) are attributable to the cassava matrix and fermentation-associated compounds rather than to background reagent contamination. The concentrations in Samples C and D, sourced from Umuanyagu and Okomoko villages, respectively, indicate that detergent-related compounds might have been introduced during cassava fermentation to accelerate the process or improve product appearance. These findings are consistent with the reports of Ibiam et al. [24] and

Hikon et al. [28], who observed detergent residues in cassava-based products and linked them to the intentional use of surfactants such as powdered detergents and bleach by local producers. Ibiam et al. [24] reported similar residue levels, suggesting that these additives are used to shorten fermentation time and enhance the whiteness of cassava products, particularly fufu. Likewise, the results revealed by Hikon et al. [28] showed that cassava flour samples processed with detergent exhibited varying fermentation times and sensory characteristics depending on the detergent concentration. Specifically, the sample with the lowest detergent concentration (0.05 g/L) fermented within 48 hours without any objectionable odour, while samples containing 0.1 g/L and 0.5 g/L of detergent fermented at 54 hours and 68 hours, respectively. In contrast, the control sample, which had no detergent, fermented only after 72 hours and produced an undesirable odour. Furthermore, Fourier Transform Infrared Spectroscopy (FTIR) and flame photometric analyses revealed the presence of silicate, azide, and sodium (Na) in both detergent-treated and untreated samples These findings indicate that some cassava flour products sold in Nigeria contain high residual concentrations of linear alkylbenzene sulfonate (LABS) and sodium, which are key chemical constituents of commercial detergent formulations, and are substances known to have adverse health effects on humans.

Comparing the present study with earlier work by Adebayo-Oyetoro et al. [3] and Ngozi and Ndukwe [6], the results align with the growing concern over poor food hygiene practices in cassava processing. Adebayo-Oyetoro et al. [3] found that microbial and chemical contamination in cassava products often stemmed from unhygienic fermentation environments and the addition of non-food-grade substances. Similarly, Ogbete et al. [17] reported that local processors sometimes use detergents, kerosene, or palm ash to enhance fermentation efficiency, which significantly increases the risk of chemical contamination in cassava-based foods.

The DCI results (Figure 1) further emphasize this trend. The DCI model, calculated as the mean of cationic and anionic surfactant concentrations, showed the surfactant levels for the different samples. This clearly indicates that locally sold fufu poses a greater contamination risk than laboratory-prepared samples. Additionally, Laitala & Jensen [20] and Oghobase et al. [22] reported that the toxicity of detergent residues depends on concentration, type of surfactant, and frequency of exposure, suggesting that the observed contamination levels in this study could have varying health implications depending on consumer exposure.

The results presented in Table 3 revealed substantial microbial contamination across all fufu samples analyzed. The total heterotrophic bacterial counts (THBC) ranged from 1.4×10^9 to 9.4×10^9 CFU/g, while total coliform counts varied between 1.1×10^7 and 8.2×10^7 CFU/g, and faecal coliform counts ranged from 0.8×10^7 to 3.0×10^7 CFU/g. *Staphylococcus aureus* was detected in all samples, whereas *Salmonella*, *Shigella*, and *Vibrio* species were not detected. Microbial results were interpreted using Codex Alimentarius microbiological principles for ready-to-eat foods, which emphasize the absence of enteric pathogens and low levels of hygiene indicator organisms [27]; however, the markedly elevated counts of total heterotrophic bacteria, coliforms, faecal coliforms, and *Staphylococcus aureus* observed in the market-obtained fufu samples indicate significant deviation from these food safety expectations. The elevated microbial counts indicate that the fufu samples, especially those obtained from local markets, were produced or handled under unhygienic conditions, posing potential public health risks to consumers. The findings from this study are consistent with those reported by Odu et al. [14], who observed high microbial loads, including coliforms and *Staphylococcus aureus*, in cassava, yam, and plantain flours sold in Port Harcourt markets. Their study attributed the contamination to poor sanitation, exposure of products during sales, and the use of contaminated water sources during processing. Similarly, Adebayo-Oyetoro et al. [3] found that fufu samples from Lagos markets contained high bacterial counts, exceeding food safety limits, and linked the contamination to open-air drying and inadequate storage practices. The current study supports these findings, that market-sourced fufu samples are exposed to multiple contamination pathways, including handling by food vendors without proper hygiene and environmental exposure to dust, flies, and unsanitary processing environments.

However, an interesting contrast emerges when comparing the control samples (A and B) with the market samples (C and D). The control samples, which were prepared under laboratory conditions, still exhibited high THBC values but relatively lower coliform and faecal coliform counts. This suggests that while microbial growth occurs naturally during cassava fermentation, it is primarily due to non-pathogenic fermentative bacteria such as *Lactobacillus* and *Leuconostoc* species, as reported by Odetokun et al. [29]. These beneficial bacteria contribute to acid production, lowering the pH of fermenting cassava and inhibiting pathogen growth. Therefore, the high THBC observed in the control samples likely reflects normal fermentation flora rather than contamination. In contrast, the presence of *Staphylococcus aureus* and coliforms in market samples suggests secondary contamination after fermentation, often caused by poor handling, use of dirty utensils, and contaminated water during washing or packaging. The detection of *Staphylococcus aureus* in all samples is of particular concern. *Staphylococcus aureus* is an indicator of human handling contamination and can cause food poisoning through the production of enterotoxins. Odetokun et al. [29] similarly reported *Staphylococcus aureus* contamination in market-sold fufu samples, confirming that improper personal hygiene among food handlers is a major source of contamination. The absence of *Salmonella*, *Shigella*, and *Vibrio* species in this study, however, aligns with findings of Oghobase et al. [22], who noted that these pathogens are often less common in fermented cassava products due to the acidic conditions of fermentation, which inhibit their growth.

The Principal Component Analysis (PCA) results revealed a clear separation pattern between the control and market-obtained fufu samples, reflecting differences in microbial contamination sources and hygiene practices. The first two components (PC1 and PC2) accounted for most of the variability in microbial profiles, highlighting how different bacterial parameters influence contamination patterns. PC1 was mainly driven by *Staphylococcus aureus* and faecal coliforms two key indicators of pathogenic contamination, while PC2 was influenced by total heterotrophic bacterial count (THBC), which represents general microbial load linked to fermentation or handling quality. The distinct distribution of the control (A and B) and market (C and D) samples across these axes underscores the difference between natural fermentation-associated microbes and contamination from poor hygiene or unsafe processing conditions. The control samples, prepared under laboratory conditions, were associated with higher THBC but low *Staphylococcus aureus* and coliform counts, signifying the presence of normal fermentation flora such as *Lactobacillus* and *Leuconostoc* species. These bacteria are non-pathogenic and beneficial to the fermentation process, contributing to the texture and characteristic aroma of fufu. This finding aligns with the reports of Adebayo-Oyetoro et al. [3], who noted that well-controlled cassava fermentation is dominated by lactic acid bacteria that suppress pathogenic organisms through acid production. Similarly, Olopade et al. [25] observed that hygienically processed cassava flour had low pathogenic contamination, further supporting the interpretation that the microbial load in the control samples reflects safe and desirable fermentation rather than external contamination. The negative loading of THBC on PC2 in the PCA indicates that while total microbial presence was high, the nature of these microbes was largely non-pathogenic.

Conversely, the market samples (C and D), obtained from Umuanyagu and Okomoko villages, displayed high *Staphylococcus aureus* and faecal coliform counts, which strongly influenced PC1 and clearly separated them from the controls. This contamination pattern suggests post-fermentation or post-processing contamination, most likely introduced through poor personal hygiene, the use of unclean water, or exposure during open-air storage and sales. This agrees with the findings of Odu et al. [14], who reported elevated coliform and *Staphylococcus aureus* levels in packaged cassava, yam, and plantain flours sold in Port Harcourt markets. Similarly, Ogbete et al. [18] documented that fufu producers often rely on unsafe processing practices, including the use of detergents, poor water quality, and unsanitary environments, all of which elevate microbial contamination risks. These observations are further supported by Ngozi and Ndukwe [6], who linked microbial proliferation in cassava products to poor post-harvest handling and high moisture retention.

The biological implications of these findings are significant. The dominance of *Staphylococcus aureus* and faecal coliforms in market samples signifies possible faecal contamination and poor sanitation, representing a public health hazard. These pathogens can cause gastrointestinal illnesses, food poisoning, and other infections when consumed. In contrast, the THBC-driven component in the controls represents natural fermentative microbes that enhance product quality and safety when fermentation is properly managed. Bamidele et al. [30] emphasized that fermentation under controlled conditions is critical for cassava safety, as it reduces cyanogenic glycosides and pathogenic load simultaneously. Therefore, PCA confirms that the contamination in market samples is extrinsic, arising from unsafe environmental and handling practices, whereas the microbial population in control samples is intrinsic and associated with safe fermentation. The PCA highlights that while all samples contained microbial activity, their nature and origin differ significantly. Laboratory-prepared controls showed microbial profiles consistent with natural fermentation and low public health risk, while market samples were dominated by pathogenic bacteria, reflecting external contamination. This finding corroborates earlier studies on cassava fermentation hygiene and reinforces the need for improved sanitary practices in local cassava processing and sales to minimize contamination risks and protect consumers' health.

This study is strengthened by its combined chemical and microbiological assessment, which provides a comprehensive evaluation of the safety of fermented baked cassava (fufu). The inclusion of both laboratory-prepared controls and market-obtained samples enabled direct comparison between hygienic processing conditions and real-world practices. The application of multivariate tools (PCA) further enhanced the robustness and interpretability of the findings. However, the study has some limitations. Sampling was limited to two communities, which may affect the generalizability of the results. In addition, the titrimetric methods employed to quantify detergent residues are inherently non-specific: both the methyl orange–sodium tetraphenylboron titration for cationic surfactants and the hyamine titration for anionic surfactants respond to any molecule bearing appropriate ionic or amphiphilic properties, not exclusively to synthetic detergent compounds. The DCI, derived as the arithmetic mean of these two measurements, therefore represents overall surfactant-like activity in the sample matrix rather than a selective measure of exogenous detergent residues. Naturally occurring matrix constituents such as cassava saponins, polar lipids, fermentation-derived organic acids, and biogenic surfactants produced by LAB may contribute to the cationic and anionic surfactant signals, particularly in the control samples. Procedural blank analysis confirmed that analytical reagents introduced no detectable background; however, the non-zero DCI values in control samples are most plausibly explained by these matrix-related interferences. Compound-specific instrumental confirmation such as FTIR or liquid chromatography-mass spectrometry was not performed in this study, and this represents a recognised methodological limitation. Future investigations should incorporate blank-corrected reporting and instrumental validation to improve chemical specificity, and should also assess fungal toxins and a broader range of communities to enhance generalisability.

8. Public Health Implications

The findings of this study raise important public health concerns regarding the safety of fufu consumed in the study area. The detection of detergent-derived surfactant residues in both control and market-obtained samples indicates potential dietary exposure to non-food-grade chemical contaminants. Chronic ingestion of such residues, even at low concentrations, may contribute to adverse health outcomes, including gastrointestinal irritation, mucosal damage, and possible systemic toxicity, as suggested by previous toxicological studies. The DCI values observed in market samples highlight the chemical risk associated with informal cassava processing practices. In addition to chemical hazards, the microbial loads recorded, particularly the presence of faecal coliforms and *Staphylococcus aureus*, indicate substantial hygiene deficiencies during fermentation, handling, and post-processing stages. These microorganisms are widely recognized indicators of faecal contamination and poor personal hygiene, and their presence in ready-to-eat foods increases the risk of foodborne illnesses, including diarrhoeal diseases and staphylococcal food poisoning. The coexistence of chemical residues and pathogenic bacteria suggests a compounded exposure risk, which may disproportionately affect vulnerable populations such as children, the elderly, and immunocompromised individuals.

9. Conclusions

The study showed that fufu samples produced in Etche, Rivers State, contained concentrations of detergent residues, indicating possible use of detergents during fermentation. The high counts of heterotrophic bacteria, coliforms, faecal coliforms, and *Staphylococcus aureus* suggest poor hygiene practices during production, handling, and storage. Although *Salmonella*, *Shigella*, and *Vibrio* species were not detected, the presence of other pathogenic bacteria and chemical contaminants poses potential health risks to consumers. Therefore, it is recommended that public health authorities strengthen surveillance of local fufu production and enforce food safety regulations. Producers should be sensitized on hygienic fermentation techniques and the health dangers of using detergents and other harmful additives. Regular laboratory monitoring and consumer awareness campaigns are also essential to ensure the safety of cassava-based foods.

Abbreviations

ANOVA	Analysis of Variance
CFU/g	Colony Forming Units per Grams
DCI	Detergent Contamination Index
DMRT	Duncan's Multiple Range Test
EMB	Eosin Methylene Blue
LABS	Linear Alkylbenzene Sulfonate
NAFDAC	National Agency for Food and Drug Administration and Control
PCA	Principal Component Analysis
PL	Permissible Limit
RDCI	Relative Detergent Contamination Index
SD	Standard Deviation
SPSS	Statistical Package for the Social Sciences
TCBS	Thiosulfate Citrate Bile Salts Sucrose
THBC	Total Heterotrophic Bacterial Count
WHO	World Health Organization

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Author Contributions

Alozie Chidinma Obumneke: Conceptualization, Methodology, Project administration, Supervision, Validation, Writing – review & editing

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Data Availability Statement

The datasets generated and/or analysed during the current study are available on request from the corresponding author.

Conflicts of Interest

The authors declare no competing interests.

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