African Journal of Life Sciences Research (AJLSR)
E-ISSN 2978-3496 (Online); ISSN 2978-3488 (Print)

Indexed by SABINET

Volume 1, Number 1, June 2025

Pp 9-36

Molecular Characterization and Antibiotic Susceptibility of Bacteria Associated with Cassava Farmlands from Igbariam Rural Communities in Anambra State, Nigeria

DOI: https://doi.org/10.31920/2978-3496/2025/v1n1a1

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Abstract

Cassava (*Manihot esculenta Crantz*) is a key staple crop for millions of people worldwide, particularly in tropical and subtropical regions. It is well-known for its ability to thrive in poor soil and drought conditions, making it a vital resource for food security especially in third world nations. However, the economic viability of cassava farming is frequently threatened by microbial pathogens that lead to diseases like cassava bacteria blight and root rot. The aim of this study is to carry out molecular characterization and antibiotic characterization of bacteria associated with cassava tubers in the rural communities at Igbariam, Anambra state, Nigeria. Cassava tubers were collected from five different farmlands and were processed by fermentation. The fermented cassava tubers were cultured in MacConkey, cetrimide, and mannitol salt agars. The isolates were identified by their morphological features, biochemical tests, DNA analysis and sequencing. Antibiotic susceptibility testing was performed on Mueller-Hinton agar after standardizing to 0.5 McFarland standard. The diameter of the zones of inhibition was measured (in mm) after incubation and the results interpreted by EUCAST charts. A total of 42 isolates comprising *Alcaligenes faecalis* (14) 33.3%, *Pseudomonas*

aeruginosa (13) 30.95% and *Pseudomonas putida* (15) 35.71% were identified. The isolates were resistant to cefixime, nitrofurantoin, ampicillin, amoxicillin-clavulanate, ceftriaxone, imipenem, and cefuroxime. The isolates showed sensitivity to gentamicin, azithromycin, ofloxacin and levofloxacin. The findings contribute to the understanding of some microorganisms that make up the microbiome associated with cassava tubers. By studying these bacteria, beneficial microorganisms that promote plant health, enhance nutrient uptake, or provide natural resistance against pathogens can be identified.

Keywords: *Cassava, Bacteria, Disease, PCR, DNA analysis*

Introduction

Food security remains a pressing issue in both developed and developing nations, intensifying global focus on agriculture. Beyond food production, agriculture promotes environmental sustainability, biodiversity, and economic growth, contributing to hunger eradication, resource management, and job creation (*Alabi et al., 2011; Obi et al., 2022; Yadav et al., 2022; Younas et al., 2022; Chinyere et al., 2022*).

Cassava (*Manihot esculenta* Crantz or *Manihot utilissima* Phol), a key crop in Africa, Asia, and Latin America, plays a vital role in food and economic security (*Bayata, 2019; Halake & Chinthapalli, 2020; Simonyan, 2015; Zhou et al., 2023*). It is widely processed into food products—flour, garri, fufu, sweeteners—and industrial items like textiles and adhesives (*Adebayo-Oyetoro et al., 2013; Ono & Taniwaki, 2021*). Despite its utility, cassava contains toxic compounds such as linamarin and cyanogenic glycosides, which require proper processing to avoid health risks (*Adebayo-Oyetoro et al., 2013*).

Cassava is commercially cultivated due to its nutritional value and adaptability for food processing (*Balogun et al., 2021; Simonyan, 2015*). Its high demand underscores the need to understand the microbial communities associated with cassava tubers, as these can influence both crop health and food safety. Advanced molecular tools like high-throughput sequencing and metagenomics allow in-depth analysis of microbial populations, revealing both culturable and non-culturable species (*Bokulich et al., 2023; Koren et al., 2023., De Souza et al., 2023; Singh et al., 2021*).

Molecular characterization identifies both pathogens and beneficial microbes involved in spoilage, storage, and disease resistance. This information supports improved breeding and disease management

strategies (*Oduor et al., 2022; Wu et al., 2023*). Integrating techniques such as PCR, NGS, and metagenomics is key to sustainable cassava production.

This study aims to characterize bacterial isolates and their antibiotic resistance profiles in cassava tubers from Igbariam, Awkuzu, Ukwulu, Umudioka, and Otoko. It will expand the limited data on cassava's microbial ecology and guide future agricultural practices (*Marín et al., 2023*).

Materials and Methods

Study Area

The survey was conducted across five different zones within the Awkuzu metropolis and its environs in Anambra State, Nigeria. These zones include the cassava farmlands located in Chukwuemeka Odumegwu Ojukwu University (COOU), Igbariam; as well as in the communities of Awkuzu, Ukwulu, Umudioka, and Otoko. The study area lies within the geographical coordinates of latitudes 5°59.99'–6°00.00'N and longitudes 6°13'–6°56'E (Ezenwaji *et al.*, 2017). This region is situated in Southeastern Nigeria and is known for its significant cassava production, owing to its fertile soils and favourable tropical climate. The study was carried out between June and August 2024 at the Pharmaceutical Microbiology and Biotechnology Laboratory of the Faculty of Pharmaceutical Sciences in the University.

Sample Collection and Processing

Ten cassava tubers were collected from five zones—COOU Igbariam, Awkuzu, Ukwulu, Umudioka, and Otoko—in Anambra East LGA, Anambra State, Nigeria. Only healthy, insect-free tubers were selected. Samples were placed in sterile bags, labeled, and transported to the Pharmaceutical Microbiology and Biotechnology Laboratory, COOU (Renner et al., 2024). Tubers were aseptically peeled, washed, and cut into approximately 3 cm pieces, then fermented in sterile vessels with distilled water for four days at 25 °C (Balogun et al., 2022). The samples from the soaked cassava water were serially diluted to give tenfold (10^{-3}) dilutions. Each 1 ml of the cassava water sample was agitated with 9 ml of distilled water to ensure a homogenous mixture. Subsequently, a tenfold serial dilution of the homogenates was made in nutrient broth such that each

broth diluent test tube contained 9 ml. Afterwards, the broth sample tubes were incubated at 35 °C for 24–48 hours (Chetan et al., 2017).

Preparation of Culture Media

All media used in this study were prepared and sterilized according to the manufacturer's instructions. The media used are Nutrient broth, Nutrient Agar, MacConkey Agar, Mannitol Salt Agar, Cetrimide Agar and Mueller-Hinton Agar.

Microbiological analysis

With the aid of sterile syringes, 0.2 ml of the respective diluents of broth-cultured specimens were aseptically collected and inoculated onto the surfaces of the various solidified Nutrient agar plates. Thereafter, it was incubated for 24 hours at 37°C. The number of colonies on the plates with distinct characteristics after incubation were noted and counted (Nwakoby *et al.,* 2021).

Isolation of the Pure Cultures of Bacteria

With the aid of a sterile wire loop, a colony from each respective Nutrient agar plates was picked and streaked accordingly in a series of parallel and non-overlapping lines on the surfaces of the well-groomed and labeled sterile petri dishes containing MacConkey Agar, Mannitol Salt Agar, and Cetrimide Agar, and incubated for 24–48 hours at 35°C (Chetan *et al.*, 2017).

Identification of Bacteria Isolates

The pure bacterial isolates were identified based on their morphological and biochemical analysis. Morphological tests like color, shape, height, consistency, and margin assessments as well as biochemical tests were conducted to confirm the results obtained from the examination of the pure culture isolates (Parija, 2012).

Indole Test

The indole test involved incubating isolates in peptone water at 37 °C for 24 hours, adding Kovac's reagent, and observing colour change. A red ring indicated a positive result (Chinyere *et al.*, *2022*).

Citrate Utilization Test

The isolates were inoculated by stab technique onto a slope of Simmons's citrate solid media and incubated at 37°C for 24 hours. Growth with a blue colour on the slant indicates a positive test and no growth or growth without any colour change indicates a negative test (Nwakoby*et al.,* 2021; Parija, 2012).

Oxidase Test

A 1% solution of oxidase reagent, freshly prepared was soaked onto a piece of filter paper and then moistened with sterile distilled water. A sterile wire loop was used to pick isolates and spread them over the filter papers. Formation of deep purple colour change within 10 seconds (an indophenol blue), indicates a positive test for oxidation complement (Chinyere *et al.,* 2022; Parija, 2012).

Catalase Test

About 5 drops of 3% hydrogen peroxide (H_2O_2) were emulsified with a 24-hour-old sample colony on a sterile test slide. The slides were placed against a dark background and observed for immediate effervescence or bubbles representing a positive test because of the breakdown of H_2O_2 by the catalase enzyme to produce oxygen bubbles (Chinyere *et al.,* 2022; Parija, 2012).

Antibiotics Susceptibility Testing (AST)

Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method. Standardized bacterial inoculum was swabbed on Mueller-Hinton agar plates. Antibiotic-impregnated discs were placed on the surface and incubated at 37°C for 18–24 hours. The susceptibility of each isolate to each antibiotic was shown by a clear zone of growth inhibition measured millimeters and they were interpreted using a standard chart, EUCAST 2023 (European Committee on Antimicrobial Susceptibility Testing).

Molecular Characterization of Bacteria Isolates

Bacterial DNA Extraction

Bacterial cells were pelleted by centrifuging 5 mL of culture at 10,000 x g for 12 minutes and re-suspended in 500 µL of guanidine hydrochloride. Proteinase K was added for protein digestion and equal volume ethanol was added to the lysate, and the solution was transferred to a spin column. Centrifugation at 10,000 x g allowed DNA to bind to the column. Purified DNA was eluted by adding 70 µL of TE buffer and centrifuging.

PCR Amplification

Universal bacterial primers 27F and 1492R, which target the 16S rRNA gene, were prepared in a cocktail 27F (5'- **GAGTTTGATCMTGGCTC AG-3'**) and 1492R (5'**TACGGYTACCTTGTTACGACTT-**3'**)**. The total reaction volume was 25 µL, including template DNA, primers, and PCR Master Mix. The thermal cycling conditions were set as follows: Initial denaturation at 94°C for 5 minutes, 35 cycles of denaturation at 94°C for 30 seconds, annealing at 56°C for 30 seconds, and extension at 72°C for 45 seconds and Final extension at 72°C for 7 minutes, followed by an indefinite hold at 4°C (Green & Sambrook, 2012).

Agarose Gel Electrophoresis

A 2% agarose gel was prepared by dissolving agarose in TAE buffer and adding ethidium bromide for DNA visualization. PCR products were loaded into the gel and electrophoresed at 100V for 35 minutes. A 100-bp DNA ladder was used as a marker. DNA bands were visualized under UV light using an Accuris UV Transilluminator (Green & Sambrook, 2012).

Sequencing

PCR products were cleaned enzymatically using EXOSAP and sequenced using the Brilliant Dye™ Terminator Cycle Sequencing Kit V3.1. The sequences were analyzed using a BLAST search to identify the bacterial species (Green & Sambrook, 2012).

Results

Identified Bacteria Isolates from Specimens Cultures

A total of 42 strains of bacteria isolates were obtained from the fermented cassava tubers and identified as *Alcaligenes faecalis* (14) 33.3%, *Pseudomonas aeruginosa* (13) 30.95% and *Pseudomonas putida* (15) 35.71% *as* shown on tables 1.

TABLE 1: Morphological and Biochemical Features of Bacteria Isolates from sample

MEDIUM	COLONY FEATURES	IND	CIT	CAT	NUMBER OF ISOLATES
Macconkey agar	Red, Solitary, Sticky, Convex, Non-hemolytic, Slimy	+	+	-	14
Mannitol salt agar	Yellow, entire, smooth, shiny, solitary, convex	+	-	+	13
Cetrimide agar	Green, Shiny, Mucoid, Convex	–	+	+	15

Key:
IND = Indole test
CIT = Citrate test
CAT = Catalase test
CT= Cassava Tubers
+ = Positive
–=Negative

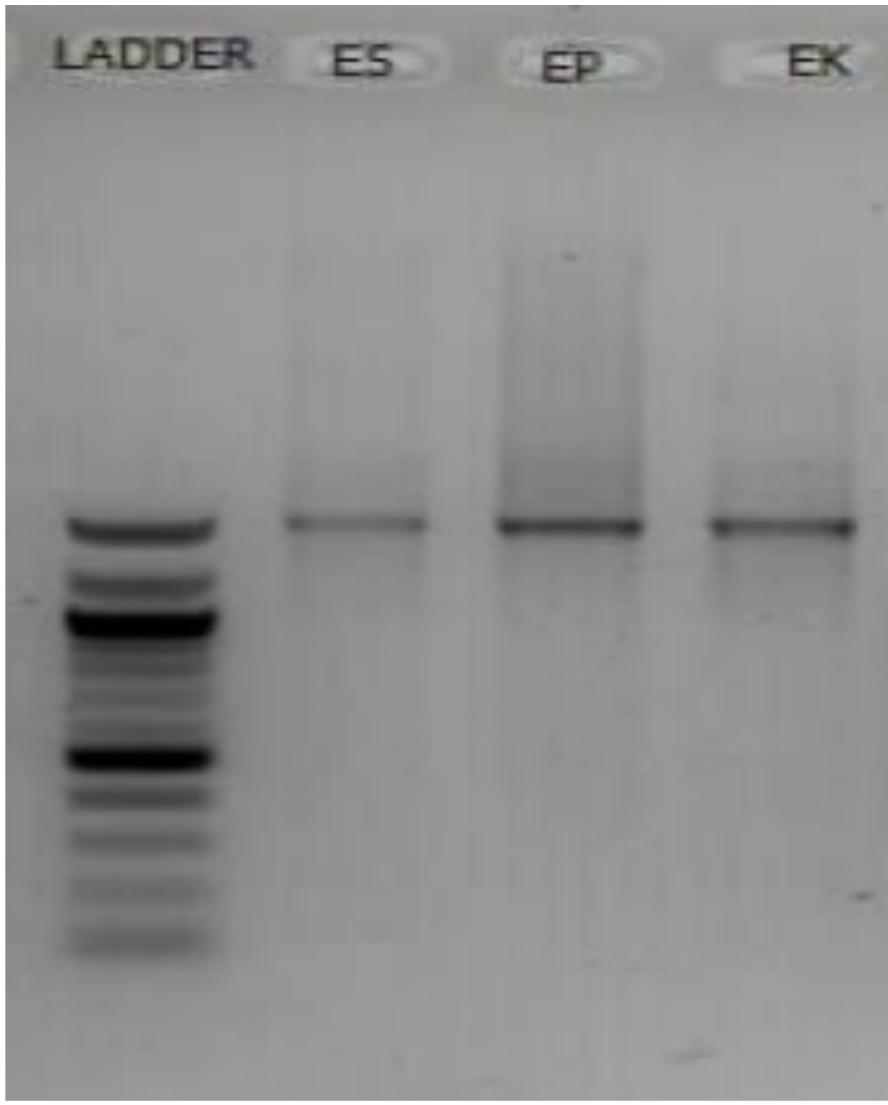

Figure 1: *Agarose gel electrophoresis showing PCR amplification of the 16S rRNA gene (~1500 bp) from bacterial isolates obtained from cassava tuber samples. Lane* ***L****: DNA ladder (molecular weight marker); Lane* ***ES****: amplified product from sample ES; Lane* ***EP****: amplified product from sample EP; Lane* ***EX****: amplified product from sample EX. All samples showed distinct bands at approximately 1500 bp, indicating successful amplification of the 16S rRNA gene region.*

Table 2: Antibiotics susceptibility test results of *Pseudomonas aeruginosa* with the Inhibition Zone Diameter measured in mm

Isolates	AZN	AUG	CXM	CIP	CRO	GN	LBC	IMP	ZEM	OFX
Pseudomonas aeruginosa	0	0	0	19	0	12	0	0	0	0
Pseudomonas aeruginosa	09	0	0	0	0	0	15	0	0	0
Pseudomonas aeruginosa	0	0	18	0	0	14	25	0	0	0
Pseudomonas aeruginosa	0	0	0	0	0	0	0	0	0	19
Pseudomonas aeruginosa	0	0	0	0	0	0	15	15	0	0
Pseudomonas aeruginosa	12	0	0	19	0	17	16	0	0	0
Pseudomonas aeruginosa	19	0	15	21	0	13	27	20	0	20
Pseudomonas aeruginosa	19	0	0	12	0	12	10	0	0	0
Pseudomonas aeruginosa	0	0	0	0	0	0	17	0	0	09
Pseudomonas aeruginosa	0	0	0	17	0	0	15	0	0	0
Pseudomonas aeruginosa	21	0	15	0	0	14	15	0	0	0
Pseudomonas aeruginosa	15	0	0	0	0	0	20	0	0	0
Pseudomonas aeruginosa	0	0	0	0	0	16	16	0	0	0

Keys *→AZN– Azithromycin (15 µg), AUG– Amoxicillin-clavulanic acid (30 µg), CXM– Cefuroxime (30 µg), CIP– Ciprofloxacin (5 µg), CRO– Ceftriaxone (30 µg), GN– Gentamycin (10 µg), LBC– Levofloxacin (5 µg), IMP– Imipenem (10 µg), ZEM– Cefixime (5 µ), OFX–Ofloxacin (5 µg)*

Isolated bacteria	AUG	CRO	ACX	IMP	GN	CXM	NF	LBC	ZEM	OFX
Alcaligenes faecalis	0	0	0	0	0	0	0	23	0	15
Alcaligenes faecalis	0	0	0	0	17	0	0	16	0	0
Alcaligenes faecalis	0	0	0	0	0	0	0	0	0	22
Alcaligenes faecalis	0	0	0	0	10	0	0	21	0	10
Alcaligenes faecalis	0	0	0	0	21	0	0	29	0	0
Alcaligenes faecalis	0	0	0	0	15	0	0	18	10	0
Alcaligenes faecalis	0	0	0	0	0	0	0	25	10	15
Alcaligenes faecalis	0	0	0	0	0	0	0	22	15	0
Alcaligenes faecalis	0	0	0	0	12	0	0	15	0	0
Alcaligenes faecalis	0	0	0	0	14	0	0	17	0	0
Alcaligenes faecalis	0	0	0	0	0	0	0	26	0	15
Alcaligenes faecalis	0	0	0	0	0	0	0	22	0	0
Alcaligenes faecalis	0	0	0	0	0	0	0	21	0	10
Alcaligenes faecalis	0	0	0	0	15	0	0	18	0	12
Pseudomonas putida	0	0	0	0	0	0	0	10	0	18
Pseudomonas putida	0	0	0	0	0	0	0	20	0	12
Pseudomonas putida	0	0	0	0	0	0	0	10	0	17
Pseudomonas putida	0	0	0	0	14	0	0	22	0	16
Pseudomonas putida	0	0	0	0	0	0	0	20	0	0
Pseudomonas putida	0	0	0	0	0	0	0	10	0	0
Pseudomonas putida	0	0	0	0	0	0	0	0	0	0

Pseudomonas putida	0	0	0	0	0	0	0	0	0	15
Pseudomonas putida	0	0	0	0	0	0	0	16	0	0
Pseudomonas putida	0	0	0	0	10	0	0	0	0	17
Pseudomonas putida	0	0	0	0	0	0	0	19	0	10
Pseudomonas putida	0	0	0	0	15	0	0	0	0	0
Pseudomonas putida	0	0	0	0	11	0	0	0	0	19
Pseudomonas putida	0	0	0	0	17	0	0	0	0	0
Pseudomonas putida	0	0	0	0	17	0	0	0	0	0

Table 3: Antibiotics susceptibility test results of *Alcaligenes faecalis* with the Inhibition Zone Diameter measured in mm

Keys *→AZN– Azithromycin (15 µg), AUG–Amoxicillin-clavulanic acid (30 µg), CXM–Cefuroxime (30 µg), CIP–Ciprofloxacin (5 µg), CRO– Ceftriaxone (30 µg), GN– Gentamycin (10 µg), LBC– Levofloxacin (5 µg), IMP– Imipenem (10 µg), ZEM– Cefixime (5 µ), OFX– Ofloxacin (5 µg)*

Discussion

This study investigated the microbial composition of cassava farmlands in Anambra State, Nigeria, identifying three major bacteria: *Alcaligenes faecalis*, *Pseudomonas aeruginosa*, and *Pseudomonas putida*. The microbial isolation was conducted in two phases: biochemical tests (indole, catalase, oxidase, coagulase) and molecular studies using 16S rRNA sequencing for definitive identification. The isolates comprised *Pseudomonas putida* (36%), *Alcaligenes faecalis* (33%), and *Pseudomonas aeruginosa* (31%), consistent with previous findings in Benin and Delta State (*Dike et al., 2022; Igbinosa & Igiehon, 2015; Adomi et al., 2020*).

A similar study by *Kandasamy et al. (2015)* identified *Pseudomonas putida* in cassava wastewater. *Pseudomonas* spp. are frequently associated with cassava fermentation due to their enzymatic role in cyanide reduction (*Balogun et al., 2021; Bankole et al., 2022*). *Aremu et al. (2010)* demonstrated that *Pseudomonas aeruginosa* utilizes cassava-derived reducing sugars for polyhydroxy butyrate production during fermentation. The presence of

Pseudomonas spp. in cassava tubers may also stem from farmland contamination with cassava effluents, influencing soil microbial diversity and pH (*Igbinosa & Igiehon, 2015*). *Alcaligenes faecalis* was also isolated, in agreement with *Obire et al. (2021)*, and its occurrence in cassava and plantain flours was also reported by *Oyeyinka & Oyeyinka (2018)*.

Molecular techniques have increasingly been used to study microbial communities in agricultural environments. For instance, *Orji et al. (2019)* and *Okonko et al. (2020)* used 16S rRNA sequencing to detect *Pseudomonas aeruginosa* in food and water samples, affirming its prevalence in environmental matrices. *Babalola et al. (2018)* also identified *Pseudomonas putida* in cassava effluents and soils, reinforcing its relevance in bioremediation. Likewise, *Singh et al. (2021)* and *Biswas et al. (2017)* identified *Alcaligenes faecalis* in agricultural soils using molecular methods, emphasizing its nitrogen-cycling role and bioremediation potential.

Antibiotic susceptibility testing followed EUCAST (2025) guidelines to evaluate resistance profiles of *Pseudomonas aeruginosa*, *Pseudomonas putida*, and *Alcaligenes faecalis*. *Pseudomonas aeruginosa* exhibited 100% resistance to cefixime, amoxicillin-clavulanic acid, ceftriaxone, cefuroxime, ciprofloxacin, ofloxacin, and azithromycin; 92.4% resistance to imipenem and gentamicin; and 76.9% to levofloxacin. Minor susceptibility was noted to levofloxacin (7.6%) and gentamicin (7.6%), with intermediate response to imipenem. These findings align with *Urganci et al. (2022)* and *Pang et al. (2019)*.

Alcaligenes faecalis showed 100% resistance to amoxicillin-clavulanic acid, ceftriaxone, azithromycin, imipenem, cefuroxime, cefixime, ofloxacin, and ciprofloxacin; 92.8% resistance to gentamicin; and 42.8% to levofloxacin. *Huang (2020)* and *Moscoso et al. (2023)* similarly reported multidrug resistance in *Alcaligenes faecalis*.

Pseudomonas putida demonstrated 100% resistance to amoxicillin-clavulanic acid, ceftriaxone, imipenem, cefuroxime, levofloxacin, cefixime, ofloxacin, ciprofloxacin, and azithromycin, and 93% resistance to gentamicin.

Pseudomonas aeruginosa showed notable resistance to multiple antibiotics including azithromycin, beta-lactams, and fluoroquinolones. However, some sensitivity was noted to ciprofloxacin (12–21 mm), gentamicin (12–17 mm), and levofloxacin (10–27 mm). These findings reflect earlier studies which report resistance of *Pseudomonas aeruginosa* to beta-lactams and partial susceptibility to aminoglycosides and fluoroquinolones.

Alcaligenes faecalis demonstrated relatively lower resistance, with notable sensitivity to levofloxacin (15–29 mm), gentamicin (10–21 mm), and

ofloxacin (10–22 mm). Resistance to beta-lactam antibiotics was consistent with its known intrinsic resistance profile.
Pseudomonas putida was resistant to most antibiotics, yet showed moderate sensitivity to levofloxacin (10–22 mm), ofloxacin (10–19 mm), and gentamicin (10–17 mm), suggesting fluoroquinolones, particularly ofloxacin, may be viable for treatment.

Antibiotic resistance was further evaluated by counting the number of antibiotics each organism resisted. *Pseudomonas aeruginosa* and *Pseudomonas putida* resisted five antibiotics and were sensitive to three, while *Alcaligenes faecalis* also resisted five but was sensitive to four, indicating slightly lower resistance overall. The ability to survive antibiotic-exposed environments suggests an adaptive advantage. Studies by *Odu & Adeniji (2013)* and *Nwancho et al. (2014)* similarly reported widespread antibiotic resistance in cassava ecosystems, emphasizing the broader implications for food safety and public health.

Conclusion

The presence of *Pseudomonas aeruginosa*, *Pseudomonas putida*, and *Alcaligenes faecalis* in cassava farmlands poses serious health and economic risks. These opportunistic pathogens can cause infections, particularly in vulnerable individuals, and exhibit high antibiotic resistance. Contaminated cassava may threaten food safety and reduce product shelf life, resulting in financial losses. *Alcaligenes faecalis*, though useful in waste treatment, is emerging as a public health concern. These findings highlight the need for improved agricultural practices, regular microbial monitoring, and further research on resistance mechanisms to ensure the safety and quality of cassava products in Nigeria.

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Appendix

16S rRNA GENE SEQUENCING RESULTS

Sample EK
Organism: *Alcaligenes faecalis* strain LCU-MCB-22-001
GenBank Accession Number: OP114642.1
Sequence Identity: 100%
Partial 16S rRNA Sequence:
AAGTCGAACGGCAGCGCGAGAGAGCTTGCTCTCTTGGCGGC
GAGTGGCGCACGGGTGAGTAATATATCGGAACGTGCCCGAT
AGCGGGGGATAACTACTCGAAACAGTGGCTAATACCGCATA
CGCCCTACGGGGGAAAGGGGGGGATCGCAAGACCTCTCACT
ATTGGAGCGGCCGATATCGGATTAGCTAGTTGGTGGGGTAA
AGGCTCACCAAGGCTACGATCCGTAGCTGGTTTGAGAGGAC
GACCAGCCACACTGGGACTGAGACACGGCCCAAACTCCTAC
GGGAGGCAGCAGTGGGGAATTTTGGACAATGGGGGAAACC
CTGATCCAGCCATCCCGCGTGTATGATGAAGGCCTTCGGGTT
GTAAAGTACTTTTGGCAAAGAATAAAAGGTATCCCCTAATAC
GGGATACTGCTGACGGTATCTGCAGAATAAGCACCGGCTAA
CTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGT
TAATCGGAATTACTGGGCGTAAAGCGTGTGTAGGCGGTTCG
GAAAGACAGATGTGAAATCCCAGGGCTCAACCTTGGAACTG
CATTTTTAACTGCCGAGCTAGAGTATGTCAGAGGGGGGTAG
AATTCCACGTGTAGCAGTGAAATGCGTAGATATGTGGAGGA
ATACCGATGGCGAAGGCAGCCCCCTGGGATAATACTGACGC
TCAGACACGAAAGCGTGGGGAGCAAACAGGATTAGATACCC
TGGTAGTCCACGCCCTAAACGATGTCAACTAGCTGTTGGGG
CCGTTAGGCCTTAGTAGCGCAGCTAACGCGTGAAGTTGACC
GCCTGGGCAGTACGGTCGCAAGATTAAAACTCAAAGGAATT
GACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTC
GATGCAACGCGAAAAACCTTACCTACCCTTGACATGTCTGGA
AAGCCGAAGAGATTTGGCCGTGCTCGCAAGAGAACCGGAAC
ACAG

Sample ES
Organism: *Pseudomonas aeruginosa strain PsADMC09*
GenBank Accession Number: MK598336.1
Sequence Identity: 87.93%
Partial 16S rRNA Sequence:
TTATAGATTTTTGTCCTCTGATATGAGCGGCGGGTATGCCTA
CTAAATGCAAATCGAGGGGCGGAGAGAGAGTACTCTCCTGT
TGTCAGCGGCGGCGGGGTGAGTTATTTATTGGGATCTGCCT
GATAGGGGGGAAAAACGTCCGGAAACGGGCGCTAATACCG
CATAAGTCCTGTGGGGGGAAGGGGGGGGTTTTCGGACCTT
TCGCTATCAGATGAGCCCATGTGCGATTAGTTAGTTGGTGG
GGTAAAGGCTTACCTAGGCGACGATCCGTAACTGGTTTGAG
AGGATGATCAGCCACCCTGGAACTGAGACACGGTCCCGACT
CCTACGGGAGGCA
GCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCA
GCCATCCCGCGTGTGTGAAGAAGGCCTTTGGGTTGTAAAGT
ACTTTAAGTTGGGAGGAAGGGCAGTAAGTTAATACCGTGGT
CTTTTGACGTTTCCAACAAAAAAAGCACCGGCTAATTTCTTGC
CACCAGCCCCGGTAATACTAAGGGGGCAAGGGTTTATTGGA
ATTTTTGGGGGTAAAAAGGGGGTAGGGGGTTTATCAATTTG
GATGTGAAAACCTCGGGCCTAACCTGGGAAATGCATCCAAA
ACTGGTGAGCTAGAGTCAGGTAGAGGGAGGTAGAATTTCAT
GTGTAGCGGTGAAATGGGTAAAATTTGGGAGGAAAACCGG
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ACAAACCGCCCGTCACCCCATGGGAGTGGGTTGCTACAAAA

GCACTAATTTAACCGTCACGAGGACGGCTCCCACGATGTGAT
TCTTGACTGCGGTGACCCAAACAAGGCC

Sample EP
Organism: *Pseudomonas putida strain SB19*
GenBank Accession Number: MZ430405.1
Sequence Identity: 84.82%
Partial 16S rRNA Sequence:
GCGTTAGCTGCGGACTGAGGGAGACCCACCGGCTATCGACA
TCGTTTACCGGGGACTACCAGGGAACTAATCCTGGTTGGTCC
CCACGCTTTCCCACCTCAGTGCAGTATGTCCAGGGGGCCCTT
CCCACGGGTTCCTTCCTATTTTACCATTTCCCGTACCCAGAAA
TTCCACCCCCTTCCATACTTAGCTTCGGTTTTGGATGTTCCCG
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GACCGTGTCTCAGTCCAGGTGACTGATCATCCTCTCAACAGT
ACGGATCGTCGCTAGGTAGCATTACCTCACCTACTACTAATC
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CCCACTACAGGCAGATCCTATGATTACTCACCCGTCCGCCGC
TACAAGGAAATCCCGTCTCCGTCCTGCAGTGTAGCCTGACCA
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