Antimicrobial Resistance (AMR) in Low-Resource Settings: A Molecular And Public Health Investigation Into the Role Of Environmental Reservoirs And Over-The-Counter Antibiotic Use In South-South Nigeria

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Abstract. Antimicrobial resistance (AMR) is a significant public health challenge worldwide, particularly in underserved communities where access to healthcare is limited. Researchers are increasingly recognising that the clinical overuse and misuse of antibiotics drive antimicrobial resistance, and they also highlight habits such as the use of over-the-counter (OTC) antibiotics and environmental exposure as significant accelerators of resistance. People in underserved communities often buy antibiotics without prescriptions, misuse them or use them to treat non-bacterial sickness. Microbial resistance and resistance genes are spread due to poor sanitation and contaminated water. This study combines practical microbiological sampling and molecular analysis with public health surveys to investigate the interaction between OTC antibiotic use and environmental exposure. Common antibiotic resistance genes, such as blaTEM, tetM, and ermB, were tested for resistance genes in samples collected from household water, sewage drains, and clinic sources in South-South Nigeria.. The results showed that blaTEM was present in 47% of the samples, tetM in 38%, and ermB in 31%. Out of 45 environmental samples collected, 86% yielded growth of bacteria resistant to at least one antibiotic, 58% showed multi-drug resistance (MDR). Researchers surveyed 300 residents in selected communities across the Delta and Rivers States to assess their antibiotic practices and awareness of antimicrobial resistance. 78% of the participants reported buying antibiotics without a prescription, 66% admitted using antibiotics for fever, body pain, and infection before visiting a clinic, and 43% stopped their medication as soon as they felt better. Only 27% were aware of antimicrobial resistance. We found that environmental and clinical samples share the same resistance genes, particularly in areas with high rates of self-medication. People's habits and their environment play a significant role in the continued spread of antibiotic resistance. There is a clear connection between environmental risks and self-medication, even though the relationship is correlational.

Keywords: Antimicrobial resistance; over-the-counter antibiotics; environmental exposure; resistance genes; self-medication; public health; low-resource settings; sanitation; antibiotic awareness; microbiological sampling; Nigeria.

INTRODUCTION

One of the most serious health challenges facing Nigeria is antimicrobial resistance (AMR). Widespread antibiotic resistance has significantly reduced the effectiveness of antibiotics, rendering even common infections more difficult to treat. Antimicrobial resistance, a global issue, is considerably higher in developing countries, where access to clean water, equipped healthcare, and effective regulations is often limited [1].

Antimicrobial resistance is increasing quickly and quietly in Nigeria. Although national strategies are available, implementing them is inconsistent and slow, particularly in local communities. [2, 3]. The risk factors are more severe in the states of Rivers, Bayelsa, Delta, and Akwa Ibom, which comprise the South-South region of Nigeria. Easy access to antibiotics without prescriptions, poor sanitation, and limited access to healthcare in these States have created a conducive environment for antimicrobial resistance to thrive and spread [4, 5].

Resistance grows more in these communities due to the practice of Self-medication. People often purchase antibiotics over the counter without a prescription. These antibiotics are used in incorrect doses by people to treat fever, body pains and infections or conditions where antibiotics are not needed [6]. In many neighbourhoods in Nigeria, people often visit local chemists first when they are ill. Many of these chemists lack the knowledge and proper training on how to handle antibiotics, which makes it easier for antibiotic-resistant strains to develop and spread. Misuse of these drugs increases the spread of antibiotics in those communities [7].

Antimicrobial resistance (AMR) has spread beyond hospitals and is now prevalent in everyday life, particularly in low-resource communities. In places like South-South Nigeria, people live with its consequences daily, without knowing its impact on their health. The problem is not only its clinical misuse, but the way antibiotics are accessed, used, and how resistance quietly spreads through the environment.

Most studies on AMR focus on hospitals, where the misuse of antibiotics is easier to monitor and resistance is more visible. But the major misuse of antibiotics occurs outside formal healthcare systems. In many communities in Nigeria, people carry out self-medication using antibiotics bought over the counter without any prescription or diagnosis by a physician. They use them for everything, including for fever, stomach upset, menstruation problems, and so many others, which they usually stop midway as soon as they feel better [8–10]. These issues occur because clinics are often not affordable, far away, or unavailable, not because people don't care, while for some people, chemists and street vendors are the most accessible and only source of care at the point of need [11].

Waters used for drinking, bathing, or farming in many parts of South-South Nigeria are often contaminated by waste from clinics and homes, which are deposited directly into the river. Pathogenic bacteria and antibiotic resistance genes are primarily found in untreated water [12]. There can be an exchange of resistance genes between microbial species in the environment, making it difficult to trace their origin and introduce effective prevention strategies [13].

The most neglected yet critical discussion is the role of the environment in the spread of AMR resistance. Resistant bacteria and genes are constantly recycled in communities where untreated sewage passes through open drains and rivers, which serve as water sources [14]. Studies from southern Nigeria have found resistance genes, such as blaTEM, tetM, and ermB, in river water and wastewater, indicating that the environment itself has become a reservoir for resistance [15]. These genes don't just sit in the water-they spread, move, and evolve. People encounter these genes every day, without even knowing their health risk.

Hospitals often receive the majority of attention when antimicrobial resistance is discussed [16]. The role of environmental and community factors is also essential, and is usually neglected when studying antimicrobial resistance. There is a significant gap in States like South-South Nigeria, where antimicrobial resistance is present but not well understood by the community. Without evidence from local communities, it will be challenging to enforce policies and interventions that can address the issue [17].

Despite the evidence, most AMR policies and interventions continue to focus solely on previous health facilities, neglecting the fact that AMR resistance is also increasing in homes, on the streets, and in waterways. Emphasis on environmental surveillance remains rare, and few studies have attempted to link antibiotic behaviour in the community with the resistance patterns observed in the environment [18].

In South-South Nigeria, where sanitation is weak and non-prescription antibiotics use is widespread, both environmental exposure and drivers of AMR misuse exist together. Chemists without formal training, open defecation, polluted water sources, and a lack of awareness about antimicrobial resistance all feed into one another. It's a cycle: antibiotics are misused, resistance builds, waste from clinics, sewage reintroduces resistant bacteria into the environment, and exposure continues [19].

Researchers studied the relationship between environmental exposure to antimicrobial resistance and the use of over-the-counter antibiotics in Nigeria's South-South region. This research aims to provide a clear understanding of how antimicrobial resistance is growing not only within healthcare settings, but also in community environments such as homes, streets, and local water sources. Public health researchers can achieve this by combining molecular testing with environmental and clinical samples, as well as conducting surveys on antibiotic practices.

This research sheds more light on established knowledge of antimicrobial resistance by examining the combined impact of self-medication practices and environmental exposure in low-resource communities. Specifically, it combines microbiological sampling, molecular gene detection, and public health surveys, providing a holistic view of antimicrobial resistance beyond the hospital environment. It also identifies identical resistance genes (blaTEM, tetM, and ermB) in both environmental and clinical samples, suggesting that ecological reservoirs play an active role in the community transmission of antimicrobial resistance. Furthermore, it highlights the correlation between proximity to contaminated water sources and self-medication practices, offering practical insights for targeted interventions in underserved Nigerian communities.

The study provides new, localised insight data from the Rivers and Delta States region of Nigeria, which are often overlooked in national antimicrobial resistance frameworks. It emphasises the need for community-specific interventions that combine quality health education, environmental sanitation, and stronger pharmacy regulation.

METHODS

To assess recent trends in antimicrobial resistance in Nigeria, this review analyses literature from 2005 to 2025, using database sources such as PubMed, Google Scholar, and ScienceDirect. The research team chose this period to align with the post-implementation phases of Nigeria's National Action Plan on AMR, initiated in 2017 [20]. Following the WHO's Global Action Plan in 2015 [21]. Results from a cross-sectional study conducted in selected communities within urban and peri-urban areas of Rivers and Delta States in the South-South region are presented.

The study focuses on urban and peri-urban communities with high population density, informal medicine outlets, and exposure to untreated water sources.

The researchers chose these locations because of their high population density, observable environmental pollution, widespread informal medicine outlets, and reliance on untreated water sources for domestic use [22].

The research employed a combination of field sampling, laboratory-based molecular analysis and community survey. Samples, including wastewater and sewage from hospitals and pharmacies, water from wells and boreholes, and nearby rivers used for agricultural and household activities, were collected from various sources within the community. This research aims to understand the relationship between the use of over-the-counter antibiotics and environmental antibiotic resistance.

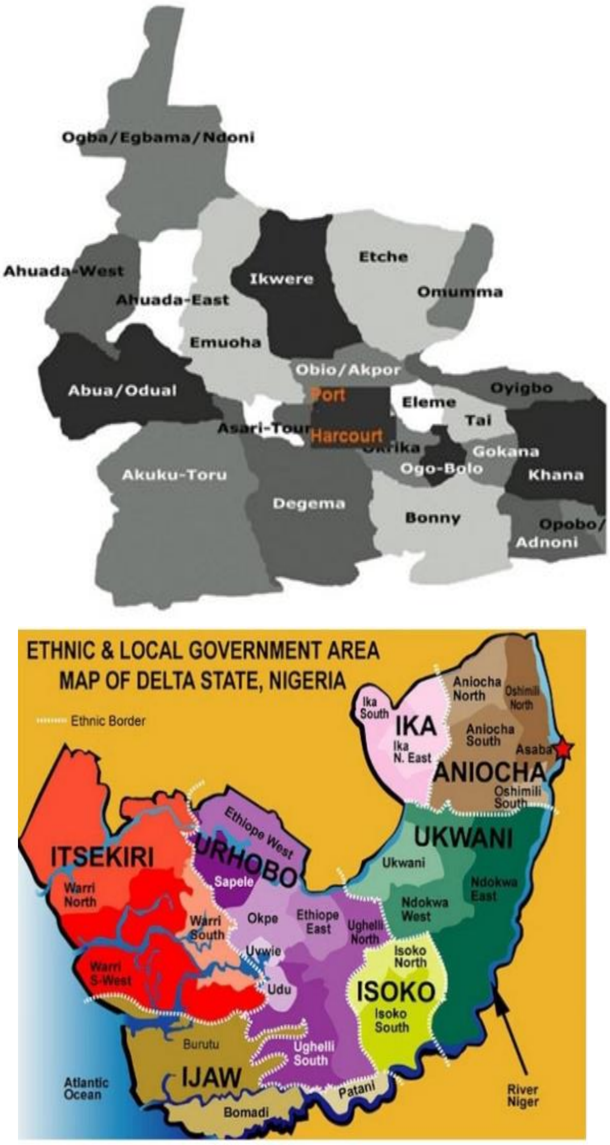

Figure 1 – Map of River and Delta State, Nigeria, showing selected sampling location for environmental and clinical data collection

The research team used 500 mL sterile bottles to collect samples from the environment and clinics. The samples were stored in coolers and transported to the laboratory within 6 hours. More than two samples were collected from each site to ensure reliability and accuracy.

We obtained non-identifiable bacterial isolates from the outpatient departments of two local hospitals: one in a private hospital in Port Harcourt and the other in Warri. These samples were obtained from patients diagnosed with urinary tract infections, wound infections, and gastrointestinal illnesses.

Standard biochemical tests, such as coagulase, indole, and catalase, were used to identify bacterial colonies after culturing environmental samples on selective media, including MacConkey, eosin methylene blue, and blood agar, to isolate both Gram-positive and Gram-negative bacteria. The Kirby-Bauer test method, also known as the disc diffusion test, is used for antibiotic susceptibility testing, following the guidelines of the Clinical and Laboratory Standards Institute (CLSI). Bacterial isolates obtained from environmental samples were tested against a panel of antibiotics, including levofloxacin, ciprofloxacin, Tetracycline, Chloramphenicol, amoxicillin, erythromycin, septrin, ampicillin, streptomycin, ceftriaxone, and ofloxacin. Zones of inhibition were measured and interpreted according to the CLSI standard to determine the antibiotic susceptibility profile of each isolate.

Molecular analysis, such as polymerase chain reaction (PCR), was used to detect resistance genes, including blaTEM, tetM, and ermB. The researchers used a 1.5% agarose gel to visualise the PCR products of the positive resistance genes, sequenced the selected gene products to determine their identity, and confirmed the results by comparing them with sequence data from the GenBank database. DNA of the confirmed isolates was extracted using the standard boiling method.

A questionnaire was structured and distributed to 300 homes across the communities where environmental samples were collected for this study. The survey focused on the reasons for practising self-medication, knowledge of antimicrobial resistance and its health implications, and how individuals obtain access to prescribed drugs. The researchers obtained consent from individuals aged 18 years and above before conducting the survey and used English and local dialects to carry out the study. The survey results were entered into the Statistical Package for the Social Sciences (SPSS) for descriptive analysis. Chi-square tests were used to assess the relationship between over-the-counter antibiotic use and the closeness to environmental sources that are positive for antimicrobial resistance. The researchers used laboratory results from isolates obtained from clinics and the environment to determine differences in their resistance mechanisms, setting a p-value of less than 0.05 ($p < 0.05$) as the benchmark for statistical significance.

All participants gave their consent, and the research team did not collect any personal information. The procedures used in this research followed established ethical standards for research involving human participation – all procedures involving sample collection and handling adhered to biosafety regulations. Samples obtained from clinics were de-identified before analysis. The research adhered to the principles outlined in the Declaration of Helsinki [23].

RESULTS AND DISCUSSION

Out of the 45 environmental samples collected, 86% yielded growth of bacteria resistant to at least one antibiotic, with 58% showing multidrug resistance (MDR). The most commonly isolated organisms were Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Pseudomonas aeruginosa, Clostridium perfringens, Enterococcus faecalis, Salmonella spp and Shigella spp. Researchers commonly found these organisms in open drains, shallow wells, and rivers near underserved communities.

As shown in Table 1, Escherichia coli isolated from clinic wastewater had the highest MDR rate of 80%, out of 10 samples, followed by Klebsiella pneumoniae from sewage and river water, with an MDR rate of 70% out of 10 samples.

Table 1 – Bacterial isolate from environmental samples (n=45)

Bacterial species	No of isolate	MDR Isolate (n)	MDR, %	Source
Escherichia coli	10	8	80	Clinic wastewater
Klebsiella pneumoniae	10	7	70	Sewage, river water
Staphylococcus aureus	7	4	57	Clinic wastewater
Pseudomonas aeruginosa	7	3	43	Stagnant water
Clostridium perfringens	3	1	33	Contaminated soil
Enterococcus faecalis	3	1	33	Open drains.
Salmonella spp	3	1	33	Untreated water
Shigella spp	2	1	50	Household wastewater
Total	45	26	58	

Staphylococcus aureus showed a 57% MDR rate, Shigella spp. had a 50% rate, Pseudomonas aeruginosa had a 43% rate, and Clostridium perfringens, Enterococcus faecalis, and Salmonella spp. all had a 33% rate.

Table 1 illustrates the percentage of MDR-resistant bacterial isolates from environmental samples. E. coli had a significant MDR rate (80%), while Klebsiella pneumoniae (70%) and Staphylococcus aureus (57%) also showed high MDR rates. Other isolates exhibited varying MDR resistance, ranging from 33% to 43%.

PCR analysis confirmed the presence of resistance genes in environmental isolates: blaTEM in 47%, tetM in 38%, and ermB in 31%. As shown in Table 2, blaTEM is associated with beta-lactam resistance, tetM shows resistance to tetracycline, and ermB is connected to macrolide resistance.

Table 2 – Prevalence of resistance genes detected in environmental isolate (n=45)

Resistance Gene	Positive samples, %	Prevalence or gene function
blaTEM	47	Beta-lactamase gene
tetM	38	Tetracycline resistance
ermB	31	Macrolide resistance

Twenty-five clinical samples were collected from outpatients who had infections at two hospitals. Isolates from both settings, such as Staphylococcus aureus, E. coli, and Klebsiella Pneumoniae, exhibited similar antibiotic resistance patterns and carried identical resistance genes found in the samples collected from the environment.

Out of 300 surveyed households, 78% of participants reported buying antibiotics without a prescription from a physician. Among them, 66% admitted using antibiotics for fever, body pain and infection before visiting a clinic, and 43% stopped their medication immediately when they felt better. Awareness about antimicrobial resistance was low, with only 27% of the population being aware of it, and even fewer understood its health implications, as shown in Table 3.

Statistical analysis revealed a highly significant relationship, indicated by a p-value below 0.05, between self-medication practices and residents living near contaminated water sources with high antimicrobial resistance loads; this suggests that communities with unsafe water sources are more likely to use antibiotics without a prescription from a physician, which contributes to the increase in resistance found in their environment.

Table 3 – Survey/Practice of antibiotic use among respondents (n=300)

Practice	% of participants
Buy antibiotics without a prescription.	78
Use antibiotics before visiting the clinic	66
Stop antibiotics when you feel better	43
Knowledge about AMR	27

This study reveals a concerning trend in the South-South region of Nigeria, where antimicrobial resistance is increasing in both environmental and community health settings, and these two factors exhibit a clear association. The high prevalence of multidrug-resistant bacteria in untreated water sources, frequently used daily by local communities, indicates that these environments serve as reservoirs and transmission points for antimicrobial resistance [22].

The primary concern is the overlap in resistance genes found in both environmental and clinical samples. The presence of genes such as blaTEM and tetM in non-hospital water sources suggests that antimicrobial-resistant bacteria are not confined to healthcare settings but are actively circulating in the community. These findings support earlier global studies suggesting that antimicrobial resistance is no longer restricted to hospital walls but is now deeply embedded in daily life, especially in communities with poor sanitation and inadequate antibiotic regulation [24].

The presence of identical resistance genes in both environmental and clinical samples indicates possible environmental-to-human or human-to-environment transmission. Poor hygiene practices may contribute to this, as well as the absence of waste treatment infrastructure and shared water sources [25, 26].

Although the researchers used a broad range of antibiotics for susceptibility testing in this study, they limited molecular analysis to selected resistance genes (blaTEM, tetM, and ermB). As a result, the researchers were unable to genetically characterise the resistance observed against other antibiotic classes, such as fluoroquinolones, sulfonamides, aminoglycosides, and chloramphenicol; this highlights the need for further molecular investigation to identify additional resistance mechanisms associated with these antibiotics.

Similar results have been reported from a study in the Edo State region of Nigeria, detecting blaTEM, tetM, ermB, and sul genes in sewage and surface water [27]. However, few studies in Nigeria have examined both environmental and clinical isolates obtained from the same communities. Among all the studies on AMR, this study is the first to be conducted in the South-South region of Nigeria, specifically in Rivers and Delta States, and it demonstrates the genetic relationship between AMR in clinical and non-clinical reservoirs.

Limited access to healthcare and inadequate awareness of antimicrobial resistance among community members contributed to the high demand for over-the-counter antibiotics and their frequent use without professional guidance. Although understandable in low-resource communities, this behaviour contributes profoundly to the selection and spread of antimicrobial resistance strains. When combined with exposure to environmental sources, the communities become trapped in a cycle where resistance is constantly reinforced and reintroduced [28].

This resistance has profound Public health implications. Many communities that depend on contaminated water, which they often use for household activities, are exposed to resistant bacteria [29]. Additionally, some individuals self-medicate with antibiotics frequently for minor sickness; unknowingly, they might take resistant strains which are already prevalent in the environment [8].

Urgent interventions are needed to improve public awareness, tighten pharmacy regulations and fix environmental sanitation. According to studies, adequate AMR awareness, combined with access to clean water and trained health personnel, can help to reduce the misuse of antibiotics in underserved communities such as those in the South-South region.

CONCLUSIONS

The two major causes of antimicrobial resistance in South-South Nigeria are inappropriate use of antibiotics and sustained environmental pollution. This study shows that resistant bacteria and resistance genes are not only found in hospitals but are also present in water sources and homes within local communities. The intersection between resistance patterns in environmental and clinical settings indicates the spread of antimicrobial resistance and challenges in managing infections.

Although only selected resistance genes were screened, the connection between environmental and clinical isolates highlights broader resistance issues that may extend beyond the genes detected.

Urgent and coordinated action is required to disrupt this cycle. Public education, stricter regulation of antibiotic access, and improved sanitation are not optional; they are essential components in addressing antimicrobial resistance. Antimicrobial resistance is no longer a hidden threat in these communities. Its presence has already been felt in daily life and must be addressed through intentional and timely action.

Local outreach programs on the dangers of self-medication and the basics of antimicrobial resistance should be integrated into community health initiatives to promote awareness and education. People need to understand not just that antimicrobial resistance exists, but how their daily actions contribute to it. Laws should be enforced by Local and state health authorities to limit the sale of antibiotics without prescriptions. Community pharmacies and patent medicine vendors must be monitored and trained. Government agencies should investigate and monitor water supply, waste disposal, and functional drainage systems to reduce environmental exposure to resistant bacteria. Furthermore, including environmental surveillance of antimicrobial resistance in Nigeria will help track and manage the spread of resistance, rather than focusing only on clinical data. Policymakers and stakeholders should promote collaboration among the public health, environmental, veterinary, and community development sectors to tackle antimicrobial resistance holistically.

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