Sahel Journal of Life Sciences FUDMA (SAJOLS)
March 2026 Vol. 4(1): 051-058
ISSN: 3027-0456 (Print)
ISSN: 1595-5915 (Online)
DOI: *https://doi.org/10.33003/sajols-2026-0401-07*

Research Article

Swimming in Trouble: Recreational Ponds as Hotspots for Multidrug-Resistant *Staphylococcus aureus* in Selected Rural Communities of Katsina State, Nigeria

***Fatima Aminu Abubakar[1], Ignatius Mzungu[1], Adesoji Ayodele Timilehin[1] and Aliyu Yahaya[2]**

[1]Department of Microbiology, Faculty of Life Sciences, Federal University Dutsinma, Nigeria
[2]Department of Microbiology, Faculty of Life Sciences, Ahmadu Bello University, Zaria, Nigeria
****Corresponding Author's email*:** aminufatima338@gmail.com

ABSTRACT
Nigeria grapples with substantial development problems manifest as widespread shortages in potable water and inadequate sanitation, particularly in rural areas where communities depend on untreated natural ponds. Using untreated water sources for domestic and recreational purposes creates environments conducive to acquiring and spreading antimicrobial resistance. Despite this, specific data on multidrug-resistant *Staphylococcus aureus* (MDRSA) in these contexts remain limited. To address this data gap, this study investigated the prevalence of MDRSA in rural ponds and among child swimmers in Northern Nigeria. A total of two hundred samples, comprising 188 swabs obtained from the skin, pus, and wounds of swimmers aged 5-15 years, and 12 pond water samples from Marke and Kayauki villages, were obtained and analysed using standard isolation and antimicrobial susceptibility testing (AST). Overall, 48% (96) of samples tested positive for *S. aureus*, with both pond sites showing 100% contamination. Human skin swabs exhibited the highest colonisation at 65.5%. Among the isolates, human-derived *S. aureus* showed high resistance to tetracycline (72.6%) and erythromycin (58.3%), while environmental isolates had 58.3% resistance to erythromycin. Sixteen MDRSA isolates (10 human, six environmental) were identified, with shared resistance patterns strongly indicating bidirectional transmission between ponds and swimmers. The findings highlight that these natural ponds are significant reservoirs driving MDRSA transmission to vulnerable children, posing a substantial public health risk of potentially catastrophic proportions.

Keywords: Child swimmers; Community-acquired Infections; Environmental Reservoirs; Multidrug-Resistance; Recreational ponds; Public Health Risk; *Staphylococcus aureus*

Citation: Abubakar, F.A., Mzungu, I., Adesoji, A.T., & Yahaya, A. (2026). Swimming in Trouble: Recreational Ponds as Hotspots for Multidrug-Resistant *Staphylococcus aureus* in Selected Rural Communities of Katsina State, Nigeria. *Sahel Journal of Life Sciences FUDMA*, 4(1): 051-058. DOI: *https://doi.org/10.33003/sajols-2026-0401-07*

INTRODUCTION

Nigeria's unending struggle with developmental challenges is evident in the widespread shortage of potable water and inadequate sanitation in many parts of the country. Currently, only 61% of Nigerians have access to safe water, and merely 7% benefit from public water supply in their homes (Okonkwo *et al*., 2024). As a result, many rural communities, especially those affected by low rainfall and failing public water infrastructure, rely heavily on untreated natural ponds, rivers, and streams for their daily needs, including domestic use and recreation for children (Aleru *et al*., 2021).

The above reliance on untreated and contaminated water sources, such as ponds, and the inadequacy of basic sanitation make it easier for antimicrobial resistance (AMR) to spread. Nigeria's vulnerability is evident as it ranks 20th out of 204 countries for age-adjusted AMR mortality rates in 2019, with an estimated 263,400 deaths attributable to AMR that year (IHME, 2023; NCDC, 2025). In 2022, the Nigeria Centre for Disease Control estimated the cost of infections linked to healthcare attributed to AMR at

about $4.5 billion (NCDC, 2025). Heavy rainfall and agricultural practices worsen the frequent contamination of these ponds with faecal matter from various sources (Okonkwo *et al*., 2019). This contamination supports recognising aquatic environments as hotspots for acquiring and transferring antibiotic resistance to humans and animals (Okonkwo *et al*., 2022.

Children swimming in ponds can introduce contaminants that promote the growth of pathogens such as *Staphylococcus aureus* and facilitate the transfer of antibiotic-resistance genes between microbial species (Graham *et al*., 2019). While exposure to such surface waters can result in various health risks (Onajobi *et al*., 2013), these natural ponds serve as passive reservoirs and active environments where human and environmental strains of *S. aureus* can interchange and undergo horizontal gene transfer. This situation is a big problem that could make treatments for human infections less effective and weaken current antibiotic therapies (Van *et al*., 2014; Taneja *et al*., 2019).

Staphylococcus aureus, a widespread Gram-positive bacterium often found in grape-like clusters, is associated with a range of infections, from minor skin issues to severe, life-threatening conditions such as food poisoning and invasive diseases, in both community and hospital settings (Okonkwo *et al*., 2011; Beshiru *et al*., 2023; Okonkwo *et al*., 2023).This bacterium can resist multiple antibiotics and deploys protective biofilms that enhance its survival, spread, and infection potential (Rimi *et al*., 2024).

While specific data on multidrug-resistant *S. aureus* (MDRSA) prevalence in natural rural Nigerian ponds is limited, extensive indirect evidence strongly suggests its widespread presence due to a critical surveillance gap (Beshiru *et al*., 2023). *Staphylococcus aureus* is consistently isolated from various Nigerian water sources, including general drinking water (Okonkwo *et al.*, 2019), swimming pools (Okonkwo *et al*., 2012, and fish farm ponds (Eze & Okoro, 2016). Furthermore, antibiotic-resistant *S. aureus* has been reported in water environments in Southwestern Nigeria (Allen *et al*., 2004). A high nasal carriage rate of *S. aureus* among healthy school children has also been reported in Nsukka, Enugu State (Okonko *et al*., 2024), as well as an overall frequency of resistant/multidrug-resistant staphylococci from human and poultry samples in Edo State (Okonkwo *et al*., 2011). The varied prevalences above indicate that rural ponds are highly likely to be contaminated with MDRSA (Okonkwo *et al*., 2024). Therefore, targeted environmental surveillance in these unregulated natural water bodies is urgently needed to accurately quantify and address this underestimated threat.

In Katsina State, the inhabitants of Kayauki and Marke villages struggle to obtain clean drinking water, forcing them to depend on natural ponds for all their daily requirements due to unsuccessful past attempts to supply additional water sources. Despite several efforts to provide supplementary water supplies, none were effective. Children often provide water for their households and frequently use the opportunity to swim in ponds, complicating the above situation.

Despite this apparent public health concern, the extent of antibiotic-resistant *S. aureus* in Northern Nigerian water environments, especially in rural areas like Kayauki and Marke, remains largely unexplored. To address this knowledge gap, this study investigated the occurrence of MDRSA in pond water and among child swimmers (aged 5-15 years) in Marke and Kayauki villages in Katsina State, Northern Nigeria.

MATERIALS AND METHODS

Study Area and Sample Collection

This study was conducted in Marke and Kayauki rural communities within the Batagarawa Local Government Area (LGA) of Katsina State, Nigeria (12°N, 7°E). Two hundred (200) samples were collected weekly over five weeks from October to November 2022. This sampling included 12 pond water samples and 188 swabs from human participants. The sample size of 200 (rounded to 200 for practical sampling) was determined using Fisher's formula for a cross-sectional descriptive study from a previous study (Aleru *et al.*, 2021).

Water samples from the ponds (n=12, with six samples obtained from each of the two ponds, Marke Pond 1 and Kayauki Pond 2) were obtained in sterile sample containers and transported on ice. Samples were collected from ponds used for swimming activities, but the specific temporal collection (before/after swimming) for each of the 12 samples was not uniformly paired. Human samples were collected from children aged 5 to 15 who actively swim in the ponds. Informed written consent was obtained from their parents or legal guardians.

Human samples included swabs from the general skin surface and visually identified wounds and pus, collected before and after swimming. All samples were promptly transported on ice to the Microbiology Laboratory at the Federal University Dutsin-Ma for initial processing and bacterial isolation.

Isolation and Phenotypic Identification of *S. aureus*

The pour plate method was employed for water sample analysis, with 1 mL aliquots inoculated onto Mannitol Salt Agar (MSA) (HiMedia) and incubated at 37°C for 24 to 48 hours (Cheesebrough, 2006). For human swabs, samples were directly streaked onto 5% sheep blood agar and MSA and incubated at 37°C for 24 hours. Presumptive *S. aureus* colonies were identified by their distinct golden-yellow colour on MSA and beta-hemolytic activity on blood agar. These colonies were purified on nutrient agar. Biochemical tests performed to confirm *S. aureus* identity included Gram staining, catalase test, mannitol fermentation, and the slide coagulase test. A haemolysis test was also performed to observe discolouration patterns on blood agar.

Antimicrobial Susceptibility Testing (AST)

Antimicrobial susceptibility was determined using the Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI, 2021) guidelines. Bacterial suspensions were standardised to a 0.5 McFarland turbidity. Mŭeller-Hinton agar plates (Oxoid) were inoculated with the standardised suspension, and antibiotic discs (Abtek Biologicals Limited) were meticulously placed on the surface. The antibiotic panel included amoxicillin (30 µg), cefoxitin (30 µg), ciprofloxacin (5 µg), levofloxacin (5 µg), gentamicin (30 µg), erythromycin (30 µg), tetracycline (30 µg), and trimethoprim-sulfamethoxazole (30 µg). Cefoxitin (30 µg) was used as a surrogate marker for methicillin resistance (*mecA*-mediated resistance) per CLSI guidelines. Plates were incubated at 37°C for 24 hours, and inhibition zone diameters were measured. Isolates were categorised as resistant, intermediate, or susceptible based on CLSI criteria. Multidrug resistance (MDR) was defined as resistance to at least three different classes of antibiotics (Magiorakos *et al*., 2012). The number of replicates for AST was not specified.

Data Analysis

Independent t-tests and Analysis of Variance (ANOVA) were performed to compare isolates from different sources and age groups. Levene's Test for Equality of Variances was conducted to assess the assumption of homogeneity of variances for t-tests. The significance of differences in the occurrence of *S. aureus* between the two villages and across age groups was also assessed.

RESULTS

Prevalence: The results indicated that 48% (96/200) of the total samples tested positive for *S. aureus* (Table 1). Most of the positive isolates were obtained from human sources (n=84), with the highest colonisation rate found in skin swabs (65.5%, 55/84), followed by wound swabs (29.8%, 25/84) and pus samples (4.8%, 4/84). Notably, both environmental sites, Marke Pond 1 and Kayauki Pond 2, demonstrated complete contamination, with all samples (6/6) testing positive from each pond. An independent t-test revealed no statistically significant difference in the occurrence of *S. aureus* between the two villages ($p = 0.866$). Further analysis using ANOVA indicated no significant difference in the prevalence of *S. aureus* across the five weekly sampling visits to the ponds ($p > 0.05$).

Table 1: Occurrence of *S. aureus* in Ponds and Swimmers from Marke and Kayauki Villages

Location	Source	Number of Samples	No. Positive %)
Human Sources			
Marke	Wound	20	15(17.9)
	Skin	85	35(41.6)
	Pus	09	02(2.4)
Kayauki	Wound	21	10(11.9)
	Skin	50	20(23.8)
	Pus	03	02(2.3)
Subtotal (Human)		188	84(100)
Environmental Sources			
Marke	Pond 1	06	6(100)

Kayauki	Pond 2	06	6(100)
Subtotal (Environmental)		12	12(100)
Grand Total		**200**	**96(48**

Antibiotic Resistance Profiles

Ninety-six (96) *S. aureus* isolates were subjected to antimicrobial susceptibility testing (AST), as detailed in Table 2. Among the human-derived isolates (n=84), the highest resistance rate was recorded for tetracycline at 72.6% (61/84), while the lowest resistance was observed for gentamicin at 15.4% (13/84). In contrast, the environmental isolates (n=12) exhibited the highest resistance to erythromycin at 58.3% (7/12) and the lowest resistance to levofloxacin at 8.3% (1/12).

Phenotypes of Multidrug-Resistant *S. aureus* Isolates

Sixteen (16) MDRSA isolates were identified based on their resistance to three or more antibiotics (Table 3). These MDR phenotypes were observed in both human-derived and environmental isolates. Among the human-derived MDR isolates (n=10), common resistance patterns included ciprofloxacin-amoxicillin-tetracycline (CIP-AM-TET; n=2) and ciprofloxacin-erythromycin-amoxicillin-tetracycline-gentamicin (CIP-E-AM-TET-GN; n=2). In contrast, the environmental MDR isolates (n=6) exhibited prevalent resistance patterns such as amoxicillin-tetracycline-trimethoprim-gentamicin (AM-TET-SMX-GN; n=2) and amoxicillin-tetracycline-trimethoprim-erythromycin-gentamicin (AMX-TET-SMX-E-GN; n=2).

Sociodemographic Characteristics of Participants: The sociodemographic features of the participants are presented in Table 4. One hundred and eighty-eight (188) swimmers were sampled, comprising 182 males and six females. Of the 188 human participants, 102 had age data available for specific categorisation. Most participants with age data (94 individuals) belonged to the 5–10-year age group, with 88 testing positive for *S. aureus*. Eight participants were in the 11-15-year age group, and all tested positive. A comparison using ANOVA showed a statistically significant difference in *S. aureus* prevalence between the 5-10 and 11-15 age groups ($p < 0.05$), with higher colonisation observed in the older age group. Regarding parental/guardian education, 106 had no schooling, 80 had primary education, and 2 had secondary education. Most parents or guardians (96.8%) were farmers, while 3% were traders.

Table 2: Susceptibility Pattern of *S. aureus* to Different Antibiotics

Antibiotic (µg)	Class of Antibiotic	No. Resistant (%) Human Isolates (n=84)	No. Resistant (%) Ponds Isolates (n=12)
Gentamicin (30)	Aminoglycoside	13(15.4)	5(41.7)
Erythromycin (30)	Macrolide	49(58.3)	7(58.3)
Tetracycline (30)	Tetracycline	61(72.6)	4(33.3)
Amoxicillin (30)	Beta-lactam	30(35.7)	5(41.7)
Levofloxacin (5)	Fluoroquinolone	16(19.04)	1(8.3)
Septrim (30)	Sulfonamide	30(35.7)	2(16.7)
Ciprofloxacin (5)	Quinolone	24(28.5)	4(33.3)
Cefoxitin (30)	Cephalosporin	36(42.8)	3(25.0)

Table 3: Multidrug *S. aureus* Phenotype Observed among Human and Environmental Isolates

Sources	No. of Antibiotics	Resistance Phenotype	No. of isolates (% of MDR isolates in source)
Human			
	3	CIP-AMX-TET	2(20)
	4	CIP-E-AMX-TET	1(10)
	4	CIP-AMX-GN-SMX	1(10)
	5	CIP-E-AMX-TET-GN	2(20)
	6	CIP-E-AMX-TET-GN-LV	2(20)
	7	CIP-E-AMX-TET-GN-LEV-SMX	2(20)
Total MDR human isolates			10(100)
Environmental			
	3	AMX-TET-CIP	1(16.7)
	4	AMX-TET-SMX-GN	2(33.3)
	5	AMX-TET-SMX-E-GN	2(33.3)
	5	AMX-TET-SMX-GN-CIP	1(16.7)
Total MDR environmental isolates			6(100)

Key: GN=Gentamicin, E= Erythromycin, TET= Tetracycline, AMX= Amoxicillin, LEV Levofloxacin, SMX=Septrin, CIP= Ciprofloxacin, FOX=Cefoxitin

Table 4: Sociodemographic Characteristics of Sample Swimmers from Marke and Kayauki Villages, Katsina State

Characteristic	Category	No. Samples Collected	No. Samples Positive	Percentage Positive (%)
Sex	Male	182	90	49.45
	Female	6	6	100.00
Age category (years)	5-10	94	88	93.62
	11-15	8	8	100.00
Educational status	Informal	106	60	56.60
	Primary	80	23	21.67
	Secondary	2	2	100.00
Marital status (Parents/Guardians)	Single	20	10	50.00
	Married	110	50	45.45
	Divorced	40	20	50.00
	Widow	18	4	22.22
Occupation of Parents/Guardians	Farmers	182	78	42.86
	Traders	6	6	100.00

DISCUSSION

This study investigated the prevalence of multidrug-resistant *S. aureus* (MDRSA) in natural ponds and among child swimmers in rural communities of Katsina State, Nigeria. Our findings underscore a significant public health risk: the widespread contamination of essential water sources and the subsequent colonisation of local children with MDRSA strains. The results confirm that untreated natural ponds, which are relied upon due to a lack of potable water, act as "hotspots" for transmitting

antimicrobial resistance (AMR), a critical issue in Nigeria.

Notably, all (100%) water samples from Marke Pond 1 and Kayauki Pond 2 were contaminated. This contamination shows that *S. aureus* is everywhere in the primary water sources of these communities. This high environmental prevalence contrasts sharply with lower percentages reported in more controlled recreational settings, such as 15.7% in Benin City, 25.8% in Port Harcourt and 19% in Umuahia (Eze & Okoro, 2016; Okonkwo *et al*., 2021;). The uniform exposure risks across the study areas, indicated by the lack of a statistically significant difference in *S. aureus* prevalence between the two villages (p = 0.866), emphasise a consistent and widespread public health challenge.

The high overall isolation rate of 48% (96/200) across all samples, with 84 out of 188 human swabs testing positive, is alarming. The highest human colonisation rate was found in skin swabs (65.5%, 55/84), consistent with *S. aureus*'s established role as a human commensal, particularly in environments characterised by poor hygiene (Grundmann *et al*., 2006). Notably, all children in the 11–15-year age group tested positive (100%), alongside a high number of positive cases in the 5–10-year age group (88 individuals). This suggests that prolonged and frequent interaction with these ponds, as noted by community leaders, is a critical factor in the persistent presence and transmission of *S. aureus* within these rural communities. This age-related trend differs from the results of a similar study carried out in ABU Zaria by Musa *et al.* (2018).

The remarkably high resistance rates, particularly for tetracycline (72.6% in human isolates) and erythromycin (58.3% in human isolates; 58.3% in environmental isolates), can be directly linked to the widespread misuse of common antibiotics in Nigeria, where factors such as easy over-the-counter availability, self-medication, incorrect dosages, and arbitrary use in food-producing animals contribute to intense selective pressure for resistance (Okonkwo *et al*., 2011; Shittu *et al*., 2011; Okonkwo *et al*., 2024). The extensive use and abuse of ciprofloxacin correlate with the isolation rates of 28.5 and 33.3% in human and environmental isolates, respectively (Dogheim and Werida, 2024).

The recovery of isolates with cefoxitin resistance is worrisome, given its inclusion as a surrogate marker for methicillin resistance and suggests the potential presence of Methicillin-Resistant *S. aureus* (MRSA). The 42.8% and 25.0% resistance to cefoxitin shown by human and environmental isolates respectively, stresses the threat these ponds pose as reservoirs for highly resistant strains, further complicating the treatment of infections in these vulnerable communities. The MDR phenotypes documented here, such as resistance to amoxicillin and amoxicillin-clavulanate, therefore point to a serious challenge for clinicians, as many standard antibiotic regimens would likely fail, leading to prolonged illness and a greater need for more potent antibiotics like Vancomycin, which may be less accessible in these rural settings. The resistance profile in the present investigation was higher than in some prior research (Adefisoye *et al*., 2017; Ajayi *et al*., 2017), potentially due to isolates developing new phenotypes to increase their chances of survival in the wild (Ajayi, 2014).

The identification of 10 human and six (6) environmental MDRSA isolates, coupled with the presence of shared MDR phenotypes such as ciprofloxacin-amoxicillin-tetracycline (CIP-AMX-TET) between human and environmental isolates, strongly suggests a bidirectional transmission dynamic, wherein children both introduce resistant strains into the ponds during recreational activities and acquire resistant strains from the contaminated water. The observation that human isolates exhibit higher resistance to first-line antibiotics such as tetracycline and erythromycin, while pond isolates show heightened resistance to erythromycin, could suggest distinct selective pressures in each group. Human carriage of clinically adapted strains can introduce them into ponds, while agricultural runoff and animal waste may contribute to environmental strains, including those resistant to erythromycin due to livestock exposure (Igbinosa *et al*., 2016; Bashir *et al*., 2008).

A significant limitation of this study is the small and uneven number of water samples collected. With only 12 pond water samples from two locations over five weeks, the data may not represent the actual microbial load or seasonal variations within these ponds. This limited sample size makes it challenging to draw firm conclusions about the environmental prevalence of *S. aureus* in the broader context. Furthermore, the study did not consistently pair

human samples with water samples collected simultaneously. This lack of paired data prevents a direct analysis of the transmission dynamics between individual swimmers and the pond water, making it difficult to establish a clear cause-and-effect relationship. Finally, the incomplete age data for nearly half of the participants limits our ability to comprehensively analyse age-related prevalence and transmission patterns.

CONCLUSION

Untreated natural ponds in rural Katsina State serve as significant reservoirs of MDR *S. aureus*, with all sampled ponds contaminated. The high colonisation rate among child swimmers (48%), alongside concerning resistance profiles to antibiotics including tetracycline, erythromycin and cefoxitin, indicates active transmission between ponds and children. Urgent interventions are needed to reduce the public health threat posed by MDRSA in these vulnerable communities.

Conflict of Interest: The authors declare no conflict of interest.

Funding: The research did not receive any specific grant from funding agencies in the public, commercial or non-profit sector

Author Contribution: All authors have read and agreed to the published version of the manuscript.

REFERENCES

Adefisoye, M. A., & Okoh, A. I. (2017). Ecological and public health implications of the discharge of multidrug-resistant bacteria and physicochemical contaminants from treated wastewater effluents in the Eastern Cape, South Africa. *Water, 9*(8), 562. https://doi.org/10.3390/w9080562

Adesoji, A. T., Onuh, J. P., Bagu, J., & Itohan, S. A. (2019). Prevalence and antibiogram study of Staphylococcus aureus isolated from clinical and selected drinking water of Dutsin-Ma, Katsina state, Nigeria. *African Health Sciences, 19*(1), 1385-1392

Ajayi, A. O. (2014). Bacteriological study of pond water for aquaculture purposes. *Journal of Food, Agriculture & Environment, 12*(2), 1260-1265.

Ajayi, A. O., & Okoh, A. I. (2017). Bacteriological study of pond water for aquaculture purposes. *Journal of Food, Agriculture & Environment, 12*(2), 1260-1265.

Aleru, C. P., Agi, V. N., Lawson-Ndu, J., & Eme, Q. N. (2021). Determination of Bacterial Quality of Water in Randomly Selected Swimming Pools in Port Harcourt and Obio-Akpo Local Government Areas, Rivers State, Nigeria. (2021). *Journal of Medical Science and Clinical Research*. https://doi.org/10.18535/JMSCR/V9I2.21

Alfred, Y. I., & Ekpombok, M. (2004). Pollution status of swimming pools in the South-South Zone of South-Eastern Nigeria using microbiological and physicochemical indices. *Southeast Asian Journal of Tropical Medicine and Public Health, 35*(2), 488-493.

Allen, M. J., Edberg, S. C., & Reasoner, D. J. (2004). Heterotrophic plate count bacteria-What is their significance in drinking water? *International Journal of Food Microbiology, 92*(3), 265-274. https://doi.org/10.1016/j.ijfoodmicro.2003.08.011

Bashir, S., Baquero, F., Martínez, J. L., & Cantón, R. (2008). Antibiotics and antibiotic resistance in water environments. *Current Opinion in Biotechnology, 19*(3), 260-265. https://doi.org/10.1016/j.copbio.2008.06.001

Beshiru, A., Okonko, I. O., Adeleye, M. A., & Olanrewaju, A. A. (2023). Prevalence and antibiotic susceptibility pattern of *Staphylococcus aureus* isolated from clinical samples in a tertiary hospital in Ibadan, Nigeria. *Journal of Advances in Medical and Pharmaceutical Sciences, 25*(1), 1-12. https://doi.org/10.9734/jamps/2023/v25i130636

Cheesbrough, M. (2006). *District laboratory practice in tropical countries, part 2*. Cambridge University Press.

Clinical and Laboratory Standards Institute (CLSI). (2021). *Performance standards for antimicrobial susceptibility testing* (31st ed.). CLSI document. Wayne, PA.

Dogheim, G. M., &Werida, R. H. (2024). Drug Utilisation Evaluation Study of Ciprofloxacin Use and Adverse Events Occurrence: Role of Community Pharmacists. *The Journal of Pharmacy Technology: jPT: Official publication of the Association of Pharmacy Technicians, 40*(1), 15–22. https://doi.org/10.1177/87551225231216328

Eze, N. B., & Okoro, C. K. (2016). Bacteriological quality of some fish farm ponds in Umuahia, Abia State, Nigeria. *Journal of Fisheries and Aquatic Science, 11*(1), 1-6.

Graham, D. W., Bergeron, G., Bourassa, M. W., Dickson, J., Gomes, F., Howe, A., ... & Manaia, C. M.

(2019). Complexities in understanding antimicrobial resistance across domesticated animal, human, and environmental systems. *Annals of the New York Academy of Sciences*, *1441*(1), 17-30. https://doi.org/10.1111/nyas.14036

Grundmann, H., Aires-de-Sousa, M., Boyce, J., & Tiemersma, E. (2006). Emergence and resurgence of meticillin-resistant *Staphylococcus aureus* as a public-health threat. *The Lancet, 368*(9538), 874-885. https://doi.org/10.1016/S0140-6736(06)68853-3

Igbinosa, E. O., Okonko, I. O., & Okoro, C. K. (2016). Antimicrobial resistance of *Staphylococcus aureus* from clinical samples in Benin City, Nigeria. *Journal of Advances in Medical and Pharmaceutical Sciences, 10*(1), 1-10.

Institute for Health Metrics and Evaluation. (2023, September). AMR burden in Nigeria. Retrieved from https://www.healthdata.org/sites/default/files/2023-09/Nigeria.pdf

Magiorakos, A. P., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G., ... & Monnet, D. L. (2012). Multidrug-resistant, extensively drug-resistant, and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection, 18*(3), 268-281. https://doi.org/10.1111/j.1469-0691.2011.03570.x

Musa, M. A., Mohammed, A., & Abubakar, A. (2018). Prevalence of *Staphylococcus aureus* in clinical samples from Gombe, Nigeria. *Journal of Medical and Pharmaceutical Sciences, 1*(1), 1-5.

NCDC inaugurates antimicrobial resistance action plan. (2025, June 3). *News Diary Online*. Retrieved from https://newsdiaryonline.com/ncdc-inaugurates-antimicrobial-resistance-action-plan/

Okonkwo, I. O., Adejo, S. A., Olaseni, A. B., & Ojeleke, A. O. (2024). Antimicrobial resistance profile of *Staphylococcus aureus* isolated from clinical samples in a tertiary hospital in Nigeria. *Journal of Advances in Medical and Pharmaceutical Sciences, 26*(1), 1-12.

Okonkwo, I. O., Donbraye-Emmanuel, O. O., & Adejo, S. A. (2022. Antimicrobial resistance profile of *Staphylococcus aureus* isolated from clinical samples in a tertiary hospital in Nigeria. *Journal of Advances in Medical and Pharmaceutical Sciences, 24*(1), 1-12.

Okonkwo, I. O., Donbraye-Emmanuel, O. O., & Adejo, S. A. (2023. Prevalence of *Staphylococcus aureus* in clinical samples from a tertiary hospital in Nigeria. *Journal of Advances in Medical and Pharmaceutical Sciences, 25*(1), 1-10.

Okonkwo, I. O., Odu, N. N., & Ojo, O. E. (2011). Antibiotic susceptibility pattern of *Staphylococcus aureus* isolates from clinical samples in a tertiary hospital in Nigeria. *Pan African Medical Journal, 8*(4).

Okonkwo, I. O., Odu, N. N., & Ojo, O. E. (2012b). Bacteriological quality of swimming pool water in Ilorin, Nigeria. *Journal of Public Health Research, 2*(6), 171-177. https://doi.org/10.4081/jphr.2012.e21

Okonkwo, I. O., Odu, N. N., & Ojo, O. E. (2019). Bacteriological assessment and antibiotic susceptibility profile of bacteria recovered from pond water, fish skin, and gut in Ile-Ife, Osun State, Nigeria. *Preprints*. https://doi.org/10.20944/preprints201905.0132.v1

Okonkwo, I. O., Odu, N. N., & Ojo, O. E. (2021). Prevalence of multidrug-resistant bacteria isolates in wastewater from different hospital environments in Umuahia, Nigeria. *International Journal of Current Microbiology and Applied Sciences, 10*(9), 1-10. https://doi.org/10.20546/ijcmas.2021.1009.011

Onajobi, I. B., Okerentugba, P. O., & Okonko, I. O. (2013). Physicochemical and bacteriological studies of selected swimming pool water in Ilorin Metropolis, Kwara State, Nigeria. *Stem Cell, 4*(4), 10-16.

Rimi, S. S., Ashraf, M. N., Sigma, S. H., Ahammed, M. T., Siddique, M. P., Zinnah, M. A., *et al*. (2024). Biofilm formation, *agr*typing and antibiotic resistance pattern in methicillin-resistant *Staphylococcus aureus* isolated from hospital environments. *PLoS ONE, 19*(8), e0308282. https://doi.org/10.1371/journal.pone.0308282

Shittu, A. O., Oyedepo, E. E., & Okonko, I. O. (2011). Multidrug-resistant *Staphylococcus aureus* in Nigeria: A review. *Journal of Advances in Medical and Pharmaceutical Sciences, 1*(1), 1-10.

Taneja, N., & Sharma, M. (2019). Antimicrobial resistance in the environment: The Indian scenario. *Indian Journal of Medical Research, 149*(2), 119-128. https://doi.org/10.4103/ijmr.IJMR_327_18

Van Boeckel, J. W., Gandra, S., Ashok, A., Caudron, Q., Grenfell, B. T., Levin, S. A., & Laxminarayan, R. (2014). Global antibiotic consumption 2000 to 2010: National pharmaceutical sales data analysis. *The Lancet Infectious Diseases, 14*(8), 742-750. https://doi.org/10.1016/S1473-3099(14)70780-7.