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## A review of antimicrobial resistance challenges in Nigeria: The need for a one health approach

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### ABSTRACT

The discovery of penicillin and other antibiotics has revolutionized modern medicine. However, overreliance on antibiotics has led to a global antimicrobial resistance (AMR) crisis, jeopardizing progress made over the past decades. Antimicrobial resistance poses a critical public health challenge, affecting humans, animals, and the environment. The AMR challenge is particularly dire in Nigeria owing to the extensive antibiotic use across various sectors and ineffective antimicrobial stewardship programs. This narrative review summarizes the literature from January 2018 to December 2023, focusing on the current trends in AMR in Nigeria, including knowledge of antimicrobial usage, prescription patterns, and adherence to guidelines for humans, animals, and their shared environments. High antibiotic resistance patterns were detected in isolates recovered from healthcare settings, food supply chains, companion animals, wildlife, and the environment. Factors exacerbating the AMR crisis in Nigeria include poor regulation of antimicrobial agents, improper empirical prescriptions, inadequate infection prevention practices, arbitrary and prophylactic use of antibiotics in food-producing animals, environmental contamination, and insufficient surveillance programs. To effectively mitigate this crisis, it is essential to adopt the One Health approach, which prioritizes collaborative efforts among stakeholders, including governmental agencies, healthcare institutions, veterinary experts, farmers, and the scientific community, to address the convergence of human, animal, and environmental health. These efforts will promote transdisciplinary surveillance approaches and the establishment of policies aimed at ameliorating the impact of AMR on the Nigerian economy, the well-being of its population, and diverse ecosystems.

### 1. Introduction

The discovery of penicillin by Sir Alexander Fleming in 1928 revolutionized modern medicine, heralding the era of antibiotics and significantly enhancing our ability to combat bacterial infections [1]. Fleming reported that the misuse of antibiotics could lead to the emergence and spread of antibiotic-resistant bacterial species within a decade [2]. By the 1950s, antimicrobial resistance (AMR) emerged as a global challenge, jeopardizing much of the progress made in the past decades [3]. AMR occurs when microorganisms evolve mechanisms to resist or evade the effects of antimicrobial agents, making infections more difficult to treat [4]. The increase in antibiotic-resistant bacteria (ARB) complicates disease management, leading to increased morbidity, prolonged hospital stays, increased healthcare costs, and reduced life expectancy, particularly in low-and middle-income countries (LMICs) [5].

In 2019, AMR was linked to approximately 1.27 million deaths

worldwide, attributed to multiple antibiotic-resistant bacterial infections. Should these trends persist, annual deaths from untreatable ARB infections could reach up to 10 million by 2050 [6,7]. Western sub-Saharan Africa bore the greatest burden of AMR in 2019, with approximately 27.3 deaths per 100,000 people directly attributed to AMR and a staggering 114.8 deaths per 100,000 people linked to AMR complications [6]. Nigeria faces developmental and resource (mis)allocation challenges that have dovetailed into widespread poverty and poor growth indices, as reflected in its limited access to potable water, poor hygiene and sanitation, and minimal infection control measures [8]. Of Nigeria's population of over 203 million people, 71 million lack access to clean water, while 130 million do not have basic sanitation [9]. Although water scarcity is a widespread challenge in Nigeria, the rural population faces the greatest impact [10]. Currently, only 61 % of Nigerians have access to safe water: 41 % within a 30-min round trip from their homes, 31 % directly on their premises, and just 7 % with

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pipe-borne water inside their households [11]. However, as of 2019, the mortality rate linked to unsafe water, poor hygiene, and inadequate sanitation exceeded 70 % per 100,000 people in various regions of Africa, including Lesotho, Somalia, Chad, Nigeria, Sierra Leone, and Niger, significantly higher than the global average of 18 % [12].

The Nigerian AMR crisis has been linked to extensive antibiotic use and misuse across various sectors, including healthcare, veterinary medicine, food production, and environmental contamination [13–16]. One of the challenges in addressing the AMR crisis in LMICs is the lack of accurate information regarding the scope of the problem, particularly in areas with limited surveillance and sparse data. This makes it difficult to grasp the extent of the challenge and develop effective strategies to combat it. Further, limited access to advanced medical care and diagnostic tools hinders accurate diagnosis and treatment [6]. This underscores the need for a One Health approach to address the AMR challenge across human, animal, and environmental health sectors [17]. This narrative review summarizes the current patterns of AMR across healthcare, food supply chain, and environmental sectors, focusing on the need for a One Health approach in tackling the challenge across various sectors in Nigeria.

#### 2. Methods

This narrative review was based on a comprehensive search of major databases, including PubMed, ScienceDirect, Google Scholar, ResearchGate, and African Journals Online for peer-reviewed research articles as well as web reports on antimicrobial resistance in Nigeria published between January 1, 2018, and December 31, 2023. The choice of the time frame (2018-2023) for reviewing the AMR crisis in Nigeria was based on the fact that Nigeria's National Action Plan on AMR was launched in 2017 in response to the WHO Global Action Plan (2015). Studies from 2018 onward reflect its impact, highlighting progress or gaps. Given the rapid evolution of AMR due to changing prescribing practices and bacterial adaptation, selecting studies from 2018 to 2023 ensures the inclusion of the most recent data. Additionally, the past five years have seen an increased adoption of molecular techniques (e.g., whole-genome sequencing and PCR-based resistance detection) in Nigerian AMR studies, enhancing data quality and comparability. We conducted this study following the guidelines recommended by Gregory and Denniss [18] that prescribed PRISMA for systematic review, but not a narrative review. The search utilized the Boolean operators "AND" and "OR" with keywords including "antibiotic resistance OR antimicrobial resistance", "antibiotic stewardship" AND "One Health System" in combination with terms "healthcare system," "agriculture" "veterinary medicine," "environment," "companion animals," and "wildlife." Specific bacterial species (that is, "Escherichia coli," OR "Staphylococcus aureus," OR "Klebsiella pneumoniae," OR "Acinetobacter baumannii," OR "Pseudomonas aeruginosa," OR "Enterobacter," OR "Enterococcus species") were included in the search terms.

Qualitative and quantitative data from observational studies published in English were included, whereas review articles and encyclopedic content were excluded. Also excluded from the review are articles published by journals listed in Beall's list of predatory journals [19]. The African Journals Online (AJOL) was selected as the primary source for identifying relevant studies because of its extensive collection of peerreviewed African research, including a wide range of Nigerian journals covering medical, microbiological, and public health disciplines. AJOL provides access to regionally published studies that may not be widely indexed in global databases, ensuring a comprehensive and contextually relevant literature search.

The results of the searches were first screened by titles before considering the abstract and reviewing the whole manuscript. As for relevant articles, we extracted data, including the authors' names, year of publication, article title, microbial isolation source, and detected antimicrobial resistance phenotypes and genotypes into Microsoft Excel 2018. Duplicate entries were removed before proceeding with the

remaining articles.

### 3. Results and discussion

### 3.1. Antimicrobial resistance in healthcare delivery settings

Several studies conducted in Nigeria between January 2018 and December 2023 reported a high prevalence of WHO-listed 'priority bacteria' in clinical samples from secondary and tertiary healthcare facilities. Between 2019 and 2021, 5606 isolates were subjected to antimicrobial susceptibility testing as part of the national human health sentinel surveillance system. During this period, the prevalence of carbapenem-resistant Enterobacteriaceae ranged from 20 to 30 %, while extended-spectrum  $\beta$ -lactamase (ESBL) producers accounted for 60 to 80 % of cases. Amikacin-resistant Enterobacteriaceae remained at 20 % or lower throughout the time frame. Methicillin-resistant Staphylococcus aureus (MRSA) exceeded 80 %, and Streptococcus pneumoniae accounted for 90 % of the resistance. Fluoroquinolone resistance in Salmonella was notably high (70-90 %), whereas cephalosporin resistance was reported to be 20–30 %. This trend is particularly concerning, as these multidrugresistant (MDR) bacteria not only exhibit resistance to multiple antibiotics but also harbor mobile genetic elements (MGEs) that mediate the transfer of resistance traits to other bacterial species. These elements, including plasmids and integrons, facilitate the horizontal transfer of antibiotic resistance genes (ARGs), further exacerbating the challenge of antimicrobial resistance [20-22].

Gram-negative bacteria were the most dominant isolates recovered from the clinical samples, often harboring genes encoding ESBLs and New Delhi metallo-β-lactamases (NDM), such as *bla<sub>TEM</sub>*, *bla<sub>CTX-M</sub>*, *bla<sub>SHV</sub>*, bla<sub>OXA</sub>, and bla<sub>NDM</sub>. Conversely, the Gram-positive isolates carried the vanA and mecA genes, conferring resistance to glycopeptides and penicillin, respectively (Table 1). Alabi et al. [23] reported that MDR S. aureus was the predominant bacterium isolated from highly touched surfaces in selected hospitals in Northwest Nigeria. A study conducted in Kebbi State, Northwest Nigeria, reported a 14.6 % methicillin-resistant S. aureus (MRSA) colonization rate among veterinarians, highlighting the high risk of livestock-acquired methicillin-resistant S. aureus (LA-MRSA) infection due to close contact with livestock. These MRSA isolates exhibited resistance to various classes of antibiotics, with approximately 60 % harboring mecA [24]. These trends have raised concerns about the public health risks of MDR infections, particularly among immunocompromised individuals.

### 3.2. Challenges in controlling AMR in healthcare settings

Nigerian healthcare systems face several challenges in controlling AMR. The most notable driver is the lack of regulatory oversight on the sale of antibiotics, which are readily available without prescription [41]. In addition, poor antimicrobial stewardship programs [42,43], irrational antibiotic prescriptions [31,44], inadequate infection prevention and control (IPC) practices [23], low public awareness of the AMR crisis [45], insufficient clinical waste disposal management, and environmental contamination [8,22]. Surveys revealed that approximately 59.9 % of patent medicine vendors and up to 97 % of pharmacists in Nigeria dispense antibiotics without a prescription [46,47]. Furthermore, antibiotics from the Watch category are frequently prescribed, with third-generation cephalosporins and fluoroquinolones accounting for approximately 66 % of antibiotics administered after consultation. In contrast, antibiotics from the 'access group', such as amoxicillin, are more commonly prescribed for outpatients [48].

Joy-Okwor and colleagues [49] assessed infection prevention and control (IPC) preparedness across 461 Nigerian healthcare facilities, comprising 350 (75.9 %) private and 111 (24.1 %) public institutions. Public facilities demonstrated greater IPC preparedness, with 69.7 % having an IPC focal point and 59.6 % having an IPC work plan, compared to 32.3 % and 26.8 % in private facilities, respectively.

 Table 1

 Antibiotic Resistance Patterns and Resistance Genes in Clinical Isolates

### Table 1 (continued)

Sources	Isolates	Resistance	ARGs	References	Sources	Isolates	Resistance Patterns	ARGs	References
Urine, Intra- abdominal, and blood	E. coli	Patterns  AMP, SXT, CIP, CTM	bla <sub>CTX-M</sub> -	Seni et al., 2018 [25]	stool, semen, sputum, endocervical swab, ear			bla <sub>SHV</sub> , bla <sub>CTX-M</sub> .	
samples Urine, high vaginal swabs, ear and wound swabs	S. aureus	AMP, GEN, LEV, CIP, ERY, OXA, RIF, CLD, SXT, S	тесА	Angel et al., 2019 [26]	swab urethral swab, throat swab, and abdominal abscess		AMP, ERY,		
Stool	Enterococcus sp.	PEN, CIP, GEN, S, TET, NIT,	vanA	Shettima et al., 2019 [27]	Yo Cooke d		TET, DOX, VAN, CLD, MOX,*SHL-		
Nasal swab	Methicillin- resistant <i>S. aureus</i>	LIN OXA, TET, GEN, VAN, PEN, ERY, NEO, SXT	тесА	Gaddafi et al., 2020 [24]	Infected surgical incisions, urine, skin burns, and	S. aureus, P. aeruginosa, K. kristinae, P.	R, FOX, CFR, NIT, AMP/ SULBA, SXT, CIP,	No ARG	Alabi et al.,
Stool	E. coli	AMP, AMC, FOX, CIP, LEV	No ARG reported	David et al., 2020 [28]	wound pus Stool, urine,	mirabilis	OXA AMC, AMX, CTM, CXM,	reported bla <sub>TEM</sub> , bla <sub>SHV</sub> ,	2023 [23]
Urine	E. coli, Klebsiella sp., Morganella sp., Providencia sp., Proteus sp., Yersinia sp., Serratia sp.	CDZ, CRX, GEN, CFR, ERY, OFX, AMC	No ARG reported	Kayode et al., 2020 [29]	catheter tips, wound swabs, and ear swabs	E. coli	FOX, CFR, CDZ, CIP, TET, SXT	bla <sub>CTX-M</sub> , aac-lb-6- cr bla <sub>CTX-M</sub> . 15, bla <sub>OXA-1</sub> ,	Egwu et al., 2023 [33]
Urine	Proteus sp. Klebsiella sp., E. coli, Enterobacter sp., Citrobacter sp., Providencia sp., S. aureus, Enterococcus sp., Corynebacterium sp., P. aeruginosa, and Salmonella sp.	AMX, NIT, CFX, CXM	No ARG reported	Okwume et al., 2021 [30]			SXT, MPM, CEFOL, TZB, COL, TGC, FOS, CDZ, AVB,	bla <sub>OXA</sub> . 320· bla <sub>OXA</sub> . 534· bla <sub>OXA</sub> . 181· bla <sub>NDM-1</sub> . bla <sub>TEM</sub> . 1A· bla <sub>TEM-1b</sub> . aph(3")-	
Urine, sputum, blood, swabs, aspirates, biopsies, seminal fluids and cerebrospinal	P. aeruginosa	CIP, LEV, CDZ, GEN, CAR	No ARG reported	Manga et al., 2021 [31]	Blood, urine, wound swabs	E. coli, C. freundii, K. pneumoniae, E. cloacae subsp. Cloacae, S. ureilytica, K. quasipneumoniae	CEFEP, CFR, CDZ, AKN, GEN, ARM, AMP, SBT, PIP, TZB, CTM.	Ib, catB3, aac(3)- IIa, sul2, tet(A,), aac(6')- Ib-cr CTX-M-	Medugu et al., 2023 [34]
fluids Urine, blood, non-blood, throat, ocular, stool and	K. pneumoniae, K. quasipneumoniae	CBM, PNC, TET, SUL, TMP, BLA	bla <sub>NDM-1</sub> , bla <sub>NDM-5</sub> , bla <sub>CTX-M-</sub>	Afolayan et al., 2021 [21]	Stool and rectal swab	Enterobacteriaceae	Not reported	1, CTX- M-9, bla <sub>NDM</sub> optrA, poxtA,	Edwards et al., 2023 [35] Ngbede
rectal swabs			bla <sub>SHV</sub> , dfrA14, tetD,		Fecal samples	E. faecalis, E. faecium	FF, TZD, VAN CFR, NAL,	cfr, rplD, rplC, rplV	et al., 2023 [36]
Blood	E. coli	CEF, SUL, SXT, AMP, CIP, AMG	qnrS, oqxAB gyrA, parC, parE, aac (6')-lb- cr5, bla <sub>TEM-1</sub> , bla <sub>TEM-</sub>	Afolayan et al., 2022 [22]	Slaughtered cattle, poultry, and at-risk humans Urine, blood, sputum, urethral swab, wound	Campylobacter sp.	CTM, EFL, CIP, S, GEN, ERY, AZM, CPC, TET	aadE-1, aphA- 3–1, tetO, cmeB, bla <sub>oxa-61</sub>	Njoga et al., 2023 [37]
			40, bla <sub>TEM</sub> . 84, bla <sub>TEM</sub> . 135, bla <sub>OXA-2</sub> , bla <sub>VEB-1</sub> , bla <sub>CMY-42</sub>		swabs, skin, ear swabs, high vaginal swabs, endocervical swabs, throat swabs, eye swabs, and stool samples	S. aureus	AMC, ERY, QD, CLD, TGC, TET, RIF, FOX, VAN, CIP, GEN	No ARG reported	Akpudo et al., 2023 [38]
Urine, high vaginal swab, wound swab,	E. coli, Klebsiella sp.	CBM, CPS, QNL, AMG, MRD	bla <sub>TEM</sub> , bla <sub>VEB</sub> , mecA,	Chukwu et al., 2022 [32]	Clinical specimens	K. pneumoniae, P. aeruginosa	AMC, CDZ	bla <sub>TEM</sub> , bla <sub>SHV</sub> , bla <sub>CTX-M</sub>	Daam et al., 2023 [39] ed on next page)

Table 1 (continued)

Sources	Isolates	Resistance Patterns	ARGs	References
Urine samples, nasal and wound swabs	S. aureus	GEN, PEN, VAN, CIP, NFX, FOX, CFR	vanA, mecA	Abdulrahim et al., 2023 [40]

KEYS: CBM- Carbapenems; PNC- Phenicols; TMP-Trimethoprim; CPS- cephalosporins; AMG- aminoglycosides; CPC- chloramphenicol; TET- tetracycline; MRDmacrolides; FQL- Fluoroquinolones; QNL- Quinolone; AMP-Ampicillin; AMC-Amoxicillin-clavulanic acid: AMX-Amoxicillin: OFX- Ofloxacin: CDZ-Ceftazidime; CIP-Ciprofloxacin; GEN-Gentamicin; NIT-Nitrofurantoin; RIF-Rifampicin; CFR-Ceftriaxone; SXT-Sulphamethoxazole/trimethoprim; TET-Tetracycline; FF-florfenicol; S-streptomycin; CPC-chloramphenicol; NEO-Neomycin; CXM-Cefuroxime; CEF- ceftiofur; PIP-Piperacillin; LEV-Levofloxacin; CEFAZ- Cefazolin; FOX-Cefoxitin; CEFEP- Cefepime; MER-Meropenem; TBR-Tobramycin; IMI-imipenem; CPD-Cefpodoxime; CTM-Cefotaxime; OXA-Oxacillin; LIN-Linezolid; CAR-Carbenicillin; ERY-Erythromycin; CLD-Clindamycin; CFX-Cefixime; DOX-Doxycycline; TGC-Tigecycline; QD-Quinupristin-Dalfopristin; ERT-Ertapenem; CPZ-Cefoperazone; SBT-Sulbactam; NFX-Norfloxacin; MOX- Moxifloxacin; \*SHL-R- Streptomycin High Level (synergy); PEN-Penicillin G; AKN- Amikacin; FF-Florfenicol; TZD-Tedizolid; AZM-Azithromycin; EFL-enrofloxacin; OQX - Oxyimino-cephalosporins; PNC -Phenicols, ARM-Aztreonam; TZB-Tazobactam; CEFOL- Cefolozane; AVB- Avibactam; ARGs -Antibiotic Resistance Genes.

However, both sectors lacked trained staff and essential equipment [49]. Evidence in the literature also points to a gap in the utilization of advanced diagnostic technologies, such as next-generation sequencing (NGS), for the surveillance, characterization, and subtyping of clinically relevant isolates [21,22,34,36]. Although genomics and bioinformatics are crucial for improving public health delivery in Nigeria, expertise shortages, the high cost of whole-genome sequencing, and the lack of available resources limit the use of this technology in the region. To enhance public health responses to AMR and guide evidence-based treatment policies, affordable, user-friendly tools and interfaces to simplify genomic and bioinformatics technologies for non-experts are needed [50,51].

### 3.3. Antimicrobial resistance in the environment, companion animals, and wildlife

The interplay between humans, animals, and the environment in driving AMR is a complex and interconnected process, as evidenced by studies conducted across Nigeria. These studies collectively highlight how the interactions among these three components facilitate the spread of ARB and resistance genes, posing significant risks to public health and food safety. For instance, Nyandjou et al. [52] isolated Salmonella sp. exhibiting resistance to multiple antibiotics in waste dumps in Northwest Nigeria, while Adesoji et al. [53] reported the recovery of MDR P. aeruginosa in household sewage, highlighting the risk of water source contamination. These findings illustrate how environmental contamination, driven by improper waste disposal and inadequate sanitation, serves as a critical pathway for the dissemination of ARB into water sources used for irrigation, aquaculture, and recreational activities. Adesoji and Call [16] further emphasized this issue by detecting MDR bacteria, including Pseudomonas sp. and Proteus sp. carrying floR, in treated water distribution systems in Southwest Nigeria. This persistence of resistance genes even after water treatment highlights the resilience of ARB in the environment and their potential to enter the food supply chain.

Animals, both domestic and wildlife, also play a pivotal role in this dynamic as reservoirs of ARB. Falodun et al. [54] identified ESBL-producing *E. coli* in fecal samples from healthy dogs in Ibadan, demonstrating that companion animals can harbor and spread ARB. Similarly, Obodoechi et al. [55] isolated MDR, ESBL-producing *E. coli* from frugivorous and insectivorous bats in Southeast Nigeria, revealing

that wildlife also contributes to the maintenance and dissemination of ARGs. Kabantiyok et al. [56] expanded on this by reporting ARB in barn owls in North-Central Nigeria, where zoonotic bacterial pathogens, including *Leptospira* species, antibiotic-resistant *Corynebacterium amy-colatum*, and *E. coli* were recovered (Table 2). These findings underscore the role of animals in bridging the gap between environmental contamination and human exposure, as ARB from animals can enter the food chain through direct contact, consumption of contaminated animal products, or environmental contamination.

Human practices further exacerbate this cycle by driving the selection and spread of ARB. The extensive use of antibiotics in aquaculture and veterinary practices, such as the misuse of florfenicol, contributes to the emergence of resistant strains, as evidenced by the high minimum inhibitory concentrations (MICs) to florfenicol observed in bacterial isolates recovered from water distribution systems [16]. Additionally, inadequate waste management and poor sanitation practices allow ARB and resistance genes to persist in the environment, creating a continuous loop of contamination. The interconnectedness of humans, animals, and the environment creates a multifaceted challenge in addressing AMR within the food supply chain, as contaminated water sources, soil, and animals directly impact food safety. This complex interplay underscores the need for a holistic, One Health approach to tackle AMR. Without addressing the contributions of all three components, efforts to mitigate AMR in the Nigerian food supply chain will remain incomplete, leaving public health and food safety at continued risk.

### 3.4. Antimicrobial resistance in the food supply chain

Antimicrobial resistance presents significant challenges in Nigeria's food supply chain because of extensive antimicrobial use (AMU) practices in food-producing animals. In the poultry industry, a knowledge gap among farmers regarding proper AMU has led to the unregulated prophylactic use of antibiotics. This non-adherence to veterinary guidelines has increased the risk of ARB in food-producing animals and public health. Chah et al. [57] reported that all poultry farmers in Enugu State, Southeast Nigeria use antibiotics for growth promotion, disease prevention, and treatment. The mean knowledge index of antibiotic use (KABU) was 0.54, indicating moderate knowledge among farmers, whereas the mean knowledge index of antibiotic resistance (KABR) was 0.65, with 70.5 % of farmers demonstrating good knowledge. However, 83 % of the respondents practiced inappropriate antibiotic use, highlighting the need for training to improve poultry farmers' AMR knowledge and practices.

Furthermore, Alhaji et al. [13] investigated the practices and perceptions of 151 fish farmers regarding AMU and its implications for AMR and residual antibiotics in freshwater fish farms in North-Central Nigeria. The authors assessed the risk status of AMU and AMR using a traffic light model and detected antibiotic residues in fish organs and pond water samples. This study revealed that widespread antibiotic misuse and residue spread through the consumption of residual antibiotics in fish and contact with wastewater released from fish farms into the environment. Similarly, Smith et al. [58] surveyed antibiotic prescription habits among Nigerian veterinarians and their potential contribution to AMR. Most veterinarians acknowledge the over prescription and overuse of antibiotics, and a significant portion do not perform culture or antibiotic susceptibility testing (AST) before antibiotics are prescribed. The authors recommend laboratory reliance on antibiotic prescriptions [57]. Consequently, a high prevalence of MDR bacterial strains such as MRSA, MDR Campylobacter sp., extensively resistant E. coli, linezolid-resistant enterococci, and MDR non-typhoidal Salmonella serovars has been reported in poultry, underscoring the high risk of zoonotic transmission of ARB in the food supply chain and farm environment.

Aworh et al. [59] reported zoonotic transmission of ESBL-producing  $E.\ coli$  among beef cattle, abattoir workers, and abattoir environments in Abuja and Lagos, Nigeria, and the circulation of the  $bla_{CTX-M-55}$  gene

 Table 2

 Antimicrobial Resistance Patterns and Antibiotic Resistance Genes in the Environment, Companion Animals, and Wildlife.

Sources	Isolates	Resistance Patterns	ARGs	References
*** . 1		AMP, AMC, OFX, SXT, CEF,	V 400	Nyandjou et al.,
Waste dumps	Salmonella sp.	TET, CIP CDZ, CRX, GEN, CPR, OFX,	No ARG reported	2019 [52] Adesoji et al.,
Residential sewage	P. aeruginosa	AUG, NIT, AMP	No ARG reported	2023 [53]
Drinking water distribution	Pseudomonas sp., Serratia sp., Proteus sp., Acinetobacter sp.,	FF, TET, S, GEN, KAN, CPC,		Adesoji and
systems	P. rettgeri	CEF, SXT, AMC,	floR	Call, 2020 [16]
	S. aureus, P. aeruginosa, E. gallinarum, O. anthropi, S. thoraltensis,			
	C. violaceum, S. paucimobilis, E. cloacea subsp. dissolvens, S.	AMP, PIP, LEV, CIP, CFX,		
Highly touched surfaces in selected	haemolyticus, Pantoea sp., E. cloacea, S. vitulinus, E. faecalis, P.	CEFAZ, GEN, NIT, FOX,		Alabi et al.,
hospital wards	stuartii	CEFEP, CDZ, MRP, SXT, TBR	No ARG reported	2023 [23]
		TET, SXT, AMP, CIP, CFX,	bla <sub>SHV</sub> , bla <sub>TEM</sub> ,	Falodun et al.,
Dog fecal samples (Pets)	E. coli	CDZ AMC, IPM, CPD	bla <sub>CTX-M</sub>	2022 [54]
Liver, spleen, and intestines of fruit			bla <sub>CTX-M-15</sub> , bla <sub>TEM</sub> ,	
(Eidolon helvum) and insect-		AMP, AMC, CTX, CDZ, SXT,	aac(3)-II, tetA, tetB,	Obodoechi
eating (Nycteris hispida) bats	E. coli	TET, S, GEN	int1(Integron)	et al., 2021 [55]
Blood samples, Oropharyngeal and				
cloacal swabs from Barn Owls	L. enterohaemorrhagica. L. grippotyphosa, L. mini (zoonotic	QNL, TET, CPS, SUL, PEN,		Kabantiyok
(Tyto alba)	bacterial pathogens), C. amycolatum, M. sciuri, and E. coli	BLA	No ARG reported	et al., 2023 [56]

KEYS: QNL- Quinolone; CPS- cephalosporins; SUL-sulphonamides; BLA- β-Lactam; PEN- Penicillins; AMP-Ampicillin, AMC- Amoxicillin-clavulanic acid, OFX-Ofloxacin, CDZ, Ceftazidime; CRX, Cefuroxime; CPR, Ciprofloxacin; GEN, Gentamicin; NIT, Nitrofurantoin; CIP-Ciprofloxacin; CFX-Ceftriaxone; SXT-Sulfamethoxazole/trimethoprim; TET-Tetracycline; FF-florfenicol; S-streptomycin; CPC-chloramphenicol; N-Nalidixic acid; CEF- ceftiofur; PIP-Piperacillin; LEV-Levofloxacin; CEFAZ- Cefazolin; FOX-Cefoxitin; CEFEP- Cefepime; MRP: Meropenem; TBR-Tobramycin; IPM-imipenem; CPD- cefpodoxime; CTX-Cefotaxime; CLX-cloxacillin; KAN-Kanamycin; AUG-Augmentin; NIT-Nitrofurantoin; ARGs -Antibiotic Resistance Genes.

among abattoir workers and beef cattle via MGEs. In a similar study following the One Health approach, Olorunleke et al. [14] collected fecal and cecal samples from slaughtered cattle, abattoir environments, and abattoir workers in southeastern Nigeria. The authors also sampled livestock from farms, animal markets, environmental samples, and hand swabs from humans in contact with the animals. The findings revealed a widespread prevalence of extended-spectrum cephalosporin-resistant

*E. coli* in livestock and humans, with a high prevalence of *bla<sub>CTX-M</sub> genes*, particularly *bla<sub>CTX-M-15</sub>*. Notably, a plasmid harboring *bla<sub>CTX-M-15</sub>* recovered from livestock showed high sequence identity with a plasmid recovered from river water in India [60], suggesting the global dissemination of this ESBL plasmid. In contrast, Ajuzieogu et al. [61] examined the bacteriological quality of ready-to-eat African salads in Enugu, Nigeria, and the antibiogram patterns of the associated bacteria.

**Table 3**Antimicrobial Resistance Patterns and Antibiotic Resistance Genes in Poultry, Aquaculture, and Food Supply Chains.

Sources	Isolates	Resistance Patterns	ARGs	References
Fish and water samples	Antibiotic residue in fish organs and water samples	CIP, EFL, COL, ERY, No ARGs reported AMP, NEO, PEN, TET, S, SUL		Alhaji et al., 2021 [13]
Beef cattle, abattoir environments, and abattoir workers	E. coli	TET, FPA, PEN, QNL, AMG, PNC, MRD, NTF, CBM, CPS	bla <sub>TEM-1</sub> , bla <sub>OXA-1</sub> , bla <sub>CTX-M-14</sub> , bla <sub>CTX-M-15</sub> , bla <sub>CTX-M</sub> , 55, sul1, sul2, sul3, dfrA1, dfrA7, dfrA12, dfrA14, dfrA17, aadA1, aadA2, aadA5, aac(3)-Ila, aac(6)-Iaa, aac(6)-Ib3, aac(6)-Ib-cr, aph(3)-Ia, aph(3)-Ib, aph(3)-Id, aph(6)-Id	Aworh et al., 2022 [59]
Livestock on farms, abattoirs, and animal markets, and in-contact humans	E. coli	CBM, 3rd generation CPS, AMG, TET, FPA, PEN, MBM, BLI, QNL, FQL	blaCTX-M-15, blaCTX-M-55, blaCTX-M-64, blaTEM-1b, blaOXA-1, blaACT-25, blaSHV-28, blaCTX-M-65, StrA, StrB, qnrS1, tet(A)-v2, tet(A), tet(D), tet-AB, sul2, dfrA14	Olorunleke et al., 2022 [14]
Ready-to-eat African salad	Salmonella sp., S. aureus, Klebsiella sp., E. coli, V. mimicus, V. fluvialis, V. cholerae, V. parahaemolyticus and V. hollisae	BLI, BLA	No ARGs reported	Ajuzieogu et al., 2022 [61]
Freshly dressed chicken, Frozen/ imported chicken, Processors, Consumers, Knives and Tables	Methicillin-resistant S. aureus	BLA, FQL, AMG, TET, FPA, MRD,	mecA, dfrG, tet(38), blaZ, fosB, aacA-aphD, MSR(A), aphA3, mph(C), dfrS1, sat4 tet(K), SCCmec type IVa, V, Vc	Ogundipe et al., 2020 [62]
Poultry droppings	Salmonella sp.	AMP, GEN, KAN, CTX, CIP, SUL, TET, CPC, TMP, NAL, MEM	blaTEM, tet(R), aac(3)-II, aph (3")-I, aph (6)-Ic sul1, sul2, sul3, tet (A), tet (M), qnrS1, qnrB19	Jibril et al., 2021a [63]
Poultry meat samples	Salmonella sp.	AMP, PIP, AZM, ERY, TET, CPC, TMP, SUL, CIP, KAN, S, CDZ, CFZ	sul1, sul2, strA, floR, $bla_{CTX}$	Igbinosa et al., 2022 [64]
Broiler caecal samples	E. coli	FQL, FOS, SXT, AMP and CPS, AMG, CPC, TET, MRD	bla <sub>TEM-106</sub> , bla <sub>TEM-126</sub> , bla <sub>CTX-M-14</sub> , bla <sub>CTX-M-55</sub> , fosA3, qnrS1, qnrB19 tet(M), aph(3)-lb, mef(B), qacE, sul1, sul2, sul3, catA1, qacE, sitABCD	Al-Mustapha et al., 2022 [65]
Poultry	Salmonella sp.	CIP, GEN, NAL, SXT, TET	pmrA, gyrA, parC, qnr, tem, catA1, cmlA1, floR, dfrA5–14, sul2, aac (3)-le, tetA	Fagbamila et al., 2023 [66]

KEYS: FOS- fosfomycin; CPS- cephalosporins; AMG- aminoglycosides; CPC- chloramphenicol; TET- tetracycline; MRD- macrolides; FQL- Fluoroquinolones; BLA- $\beta$ -Lactam; FPA- Folate pathway antagonist; BLI-  $\beta$ -Lactam inhibitor; QNL- Quinolone; PEN- Penicillins; CDZ-Ceftazidime; CFZ- Cefazolin; EFL-enrofloxacin; NEO-neomycin; CIP-ciprofloxacin; COL-colistin; ERY-erythromycin; S-streptomycin; SUL-sulphonamides; AMP-ampicillin; GEN-gentamicin; KAN-kanamycin; CTX-cefotaxime; SUL-sulphonamides; CPC-chloramphenicol; TMP-trimethoprim; NAL-nalidixic acid; MEM-meropenem; PIP-Piperacillin; AZM-Azithromycin; MBM-Monobactam; CBM- Carbapenems; PNC- Phenicols; NTF- Nitrofurans; ARGs -Antibiotic Resistance Genes.

This study revealed high bacterial counts and the presence of various pathogenic bacteria, including  $\beta$ -lactam-resistant *Vibrio* sp., *Salmonella* sp., and *E. coli*. They recommended improved hygiene, regular cleaning, and disinfection of food-contact surfaces (Table 3).

Antimicrobial resistance (AMR) in Nigeria's food supply chain is a complex issue driven by systemic failures, including inadequate regulatory oversight, economic constraints, and a gap between knowledge and practice. Despite moderate awareness of antibiotic resistance among some farmers, irresponsible practices persist. Antibiotics are often used for growth promotion or prophylactically without proper diagnosis or adherence to dosage guidelines, highlighting the need for targeted education and training programs that promote alternatives and better farm management practices. Economic barriers further exacerbate the issue, as farmers and veterinarians frequently rely on antibiotics as a low-cost solution due to limited access to diagnostic testing and financial resources. Thus, addressing AMR in the food supply chain requires systemic changes, including the implementation and enforcement of stricter regulations, investment in affordable diagnostic tools, and financial incentives for antimicrobial stewardship programs to enhance food security.

### 3.5. Nigeria's AMR crisis: a need for one health transdisciplinary response

Although Gram-negative bacterial infections are globally dominant [67], Nigeria's healthcare delivery systems, food supply chains, companion animals, wildlife, and environments are threatened by the spread of MDR Gram-negative bacteria. Antimicrobial resistance poses a significant threat to global public health [68], with Nigeria being no exception. In Nigeria, AMR challenges are driven largely by weak regulatory frameworks and inadequate enforcement mechanisms [69]. Despite existing policies, the over-the-counter sale of antibiotics without prescriptions remains widespread, contributing to their misuse in both human and veterinary medicine. Additionally, the unregulated use of antibiotics in livestock, often as growth promoters or feed additives, further exacerbates the problem, leading to the emergence of resistant bacterial strains that can spread through the food chain [70].

Regulatory agencies such as the National Agency for Food and Drug Administration and Control (NAFDAC) face significant challenges in monitoring and enforcing compliance. The proliferation of substandard and counterfeit antibiotics further complicates efforts to contain resistance, highlighting the urgent need for more stringent regulatory oversight [71]. While NAFDAC has a legal mandate, the penalties for noncompliance, as well as the regulation of the importation and distribution of counterfeit antibiotics, are sometimes seen as insufficient or not strictly applied, reducing their deterrent effect. On the other hand, many farmers in Nigeria lack awareness of the risks associated with the misuse of antibiotics in aquaculture and livestock [13,57,70]. Collaborating with agricultural extension services and veterinary professionals to disseminate best practices and farmer education programs is essential to promote responsible antibiotic use and alternative practices, such as improved animal husbandry, vaccination, and biosecurity measures.

In June 2017, Nigeria underwent its Joint External Evaluation (JEE) to assess its core capacities under the International Health Regulations (IHR). While strengths were noted in the One Health framework, significant gaps remain, particularly in surveillance and outbreak response. The evaluation also highlighted the absence of a well-coordinated, institutionalized long-term strategy for One Health as a critical area requiring attention. Further complicating these challenges is the limited government funding allocated to the sector, inadequate routine sharing of laboratory information or specimens related to zoonotic diseases among relevant agencies, and weak intersectoral collaboration in surveillance activities. Additionally, Rapid Response Teams (RRTs) in rural and Local Government Areas (LGAs) are underperforming, further hindering effective disease control and response efforts [72].

Thus, proactive stakeholder engagement and the formulation of a

cohesive national framework aimed at strengthening antimicrobial stewardship programs (ASPs) are urgently needed. Such efforts would enhance a comprehensive, transdisciplinary One Health surveillance system capable of addressing the multifaceted challenges of AMR while mitigating its adverse effects on Nigerian society.

### 3.6. Interconnectedness and multi-sectoral collaboration: the one health perspective

The One Health framework underscores the intricate interconnectedness of human, animal, and environmental health, particularly in the context of antimicrobial resistance (AMR). The overuse of antibiotics in livestock, for instance, not only impacts animal health but also contributes to the emergence and spread of ARB, which can be transmitted to humans through the food supply chain [73,74]. Furthermore, environmental contamination with residual antibiotics exacerbates this problem by promoting the proliferation of antibiotic-resistant strains, posing significant health risks to humans, wildlife, and ecosystems [75–78]. These complex interactions highlight the interconnected drivers of AMR, necessitating a unified approach to address the issue holistically [79,80]. A cornerstone of the One Health approach is its emphasis on multisectoral collaboration, which is essential for effectively managing AMR [81]. Tackling AMR requires coordinated efforts across diverse sectors, including human healthcare, veterinary medicine, agriculture, and environmental science. By integrating public health initiatives, veterinary practices, agricultural policies, and environmental management strategies, stakeholders can develop cohesive and comprehensive interventions to combat AMR [82]. This collaborative approach ensures that all potential sources of AMR are addressed, from clinical settings and livestock production to environmental reservoirs, and safeguards the health of humans, animals, and ecosystems.

### 3.7. Addressing antimicrobial usage

Antibiotics are often prescribed indiscriminately in Nigerian healthcare settings, and their use is imprudently prevalent in foodproducing animals for growth promotion and disease prevention, leading to unchecked misuse of antibiotics because of a lack of regulatory oversight and ASPs [31,41,57,83]. The pharmaceutical sector faces significant challenges in regulation due to the vast number of products, practitioners, and premises (both registered and unregistered) that require oversight. Issues such as the prevalence of fake and counterfeit drugs, a disorganized distribution system, insufficient infrastructure, limited enforcement capabilities, and a lack of collaboration with other law enforcement agencies further complicate matters. Additionally, regulators struggle with inadequate human resources, insufficient funding, heavy dependence on imported pharmaceuticals, and substandard facilities for quality control, all of which hinder effective regulation and control of the sector [48]. Additional challenges in managing AMR include the absence of dedicated antimicrobial stewardship (AMS) teams in many hospitals across the country, as well as insufficient training and support for AMS initiatives from hospital management [84]. The One Health approach recognizes responsible antibiotic stewardship as a core principle [17], which involves a thorough and tailored strategy for managing antimicrobial use, considering not only the amount used but also how, why, and by whom they are used. This approach considers the diverse perspectives and practices of various stakeholders, including healthcare providers, patients, and others, as well as the specific circumstances that influence the decision to prescribe antimicrobial agents [85]. However, public awareness of ASPs in Nigeria remains alarmingly low, as evident by the routine and often inappropriate use of antibiotics. The One Health approach can target these practices by promoting the responsible use of antibiotics across various sectors.

### 3.8. Surveillance and monitoring

Effective surveillance and monitoring are essential for understanding and controlling AMR [86-88]. Many initial obstacles encountered in establishing a national AMR surveillance system in Nigeria have been resolved by integrating national reference laboratory (NRL) functions backed by genomics [51]. Nonetheless, challenges persist and continue to arise when applying this approach in the Nigerian context. The NRLs face significant challenges, including understaffing and difficulty retaining skilled professionals in clinical laboratory science, sequencing, and bioinformatics [51]. Compounding these issues, Nigeria's primary healthcare systems remain weak, and there is a notable absence of antimicrobial stewardship programs in both public and private healthcare sectors. Additionally, the lack of coordination, comprehensive data, and national reports on antibiotic consumption across human and animal health sectors continues to hinder progress. Despite these challenges, the Federal Government of Nigeria has taken steps to address AMR, such as launching the National Action Plan for Antimicrobial Resistance in 2017 [48]. However, there is a critical need for integrated, cross-sectoral monitoring and surveillance systems that enable the comprehensive collection and analysis of AMR data across human, animal, and environmental sectors in rural and urban areas across States

The One Health approach enhances these efforts by integrating human, animal, and environmental data. Implementing a unified national surveillance system can facilitate real-time monitoring of AMR patterns and inform targeted interventions. Data-driven decision-making, supported by robust surveillance frameworks, allows for timely responses to address this public health threat [89,90].

### 3.9. Education and awareness

Education and awareness are pivotal components of the One Health System [91]. During the 2020 World AMR Awareness Week, a diverse panel of experts from various sectors came together to address critical issues surrounding antibiotic use in Nigeria. The panel included representatives from national government agencies, research institutions, academia, and the World Health Organization, all operating within the Nigerian One Health framework. They identified widespread lack of awareness and a weak regulatory framework as key drivers of inappropriate antibiotic use across the country, further compounded by both technical and socio-economic challenges [92].

Raising awareness of the public health dangers of AMR and promoting the responsible use of antimicrobial agents is crucial for all stakeholders. In Nigeria, this includes educating healthcare providers about proper prescription practices, informing farmers about the risks of antibiotic overuse in livestock, and engaging the public in understanding the importance of adherence to prescribed drugs [13,31,58]. Educational campaigns and training programs can empower individuals and communities to make informed decisions on antibiotic use.

### 3.10. Environmental considerations

Environmental contamination is often a neglected yet critical driver of AMR in Nigeria. Antibiotics can enter the environment through waste from healthcare facilities, agricultural runoff, improper clinical and farm waste disposal practices, poor sanitation, and the release of unmetabolized antibiotics or their residues into the environment through animal manure. On the other hand, releasing pharmaceutical industrial effluents into the environment has exacerbated this crisis [93]. These factors are closely linked and significantly contribute to the spread of AMR in the environment. These environmental pathways can spread ARB in the water, soil, and air [94]. The One Health approach advocates for environmental safety and management practices that minimize the release of antibiotics and their residues into the environment, thereby reducing selective pressure.

### 3.11. Cultural sensitivity

A recent study revealed significant gaps in antimicrobial prescriptions among Nigerian tertiary hospital physicians, with 68 % of respondents prescribing antibiotics on the WHO reserved list [95]. Another prevalent cultural practice that significantly contributes to the AMR challenges in Nigeria is self-medication, where individuals use antibiotics without a prescription or medical supervision, leading to the overuse of antibiotics [96]. The One Health approach emphasizes the need for culturally sensitive solutions that consider local practices and beliefs. Nigeria can mitigate these cultural drivers of AMR by addressing the root causes of inappropriate prescriptions and self-medication and by promoting alternative health-seeking behaviors.

### 4. Conclusion

This study revealed high resistance to β-lactam antibiotics in both clinical and food-related bacterial isolates, with MecA, AmpC \beta-lactamases, and ESBLs being the predominant resistance mechanisms. However, there is a paucity of data on the virulence determinants in these isolates across various sectors. To address the growing threat of AMR in Nigeria, it is imperative to strengthen antimicrobial stewardship programs across the healthcare and veterinary sectors, including livestock production and aquaculture. A unified national strategy, aligned with global initiatives and supported by robust surveillance systems, is essential to mitigate AMR risks in healthcare delivery and food supply chains. Sustained efforts are needed to enhance research and data collection on antibiotic usage, resistance patterns, and virulence factors in food-producing animals, particularly in rural areas, to enable realtime monitoring of AMR patterns and guide targeted interventions. Cross-sector collaboration is critical to reducing extensive antibiotic use in humans and animals, promoting effective alternative treatment options, improving farm hygiene, and strengthening surveillance systems. Embracing a One Health approach will foster transdisciplinary research and partnerships across human, veterinary, and environmental health sectors, address the root causes of AMR, safeguard public health, and protect Nigeria's ecosystems.

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### CRediT authorship contribution statement

**Emmanuel Dayo Alabi:** Writing – original draft, Data curation, Conceptualization. **Akeem Ganiyu Rabiu:** Writing – review & editing, Methodology, Formal analysis. **Ayodele Timilehin Adesoji:** Writing – review & editing, Supervision, Methodology, Formal analysis.

### Declaration of competing interest

Following the Journal's policy on conflicts of interest, the authors declare no conflicts of interest.

### Data availability

Data will be made available on request.

### References

- S. Sengupta, M.K. Chattopadhyay, H.P. Grossart, The multifaceted roles of antibiotics and antibiotic resistance in nature, Front. Microbiol. 4 (2013) 38490, https://doi.org/10.3389/fmicb.2013.00047.
- [2] N. Rosenblatt-Farrell, The Landscape of Antibiotic Resistance, 2009, pp. A244–A250, https://doi.org/10.1289/ehp.117-a244.

- [3] B. Spellberg, D.N. Gilbert, The future of antibiotics and resistance: a tribute to a career of leadership by John Bartlett, Clin. Infect. Dis. 59 (suppl\_2) (2014) S71–S75, https://doi.org/10.1093/cid/ciu392.
- [4] World Health Organization, Worldwide Country Situation Analysis: Response to Antimicrobial Resistance; Geneva, Switzerland. https://iris.who.int/bitstream/h andle/10665/163468/9789241564946\_eng.pdf?sequence=1, 2015 (Accessed 14 December 2023).
- [5] J. Frean, O. Perovic, V. Fensham, et al., External quality assessment of national public health laboratories in Africa, 2002-2009, Bull. World Health Organ. 90 (3) (2012) 191–199. https://www.scielosp.org/pdf/bwho/v90n3/v90n3a11.pdf (Accessed 14 December 2023).
- [6] C.J. Murray, K.S. Ikuta, F. Sharara, et al., Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis, Lancet 399 (10325) (2022) 629–655, https://doi.org/10.1016/S0140-6736(21)02724-0.
- [7] J. O'Neill, Antimicrobials in agriculture and the environment: reducing unnecessary use and waste, the review on antimicrobial resistance, London. https://edepot.wur.nl/365663, 2015.
- [8] C.O. Iheanacho, U.I. Eze, Antimicrobial resistance in Nigeria: challenges and charting the way forward, Eur. J. Hosp. Pharm. 29 (2) (2022) 119, https://doi.org/ 10.1136/ejhpharm-2021-002762.
- [9] RTI International, Effective Water, Sanitation, and Hygiene Services in Nigeria (E-WASH). https://www.rti.org/impact/effective-water-sanitation-and-hygiene-services-nigeria-e-wash, 2018. Accessed 12 March 2025.
- [10] H.O. Nwankwoala, Localizing the strategy for achieving rural water supply and sanitation in Nigeria, Afr. J. Environ. Sci. Technol. 5 (13) (2011) 1170–1176, https://doi.org/10.5897/AJESTX11.011.
- [11] A. Alao, J. Garrett, How Can Nigeria Fill the Funding Gap to Address Its State of WASH Emergency? WASH Matters. https://www.wateraid.org/ng/blog/how-cannigeria-fill-the-funding-gap-to-address-its-state-of-wash-emergency, 2019. Accessed 12 March 2025.
- [12] World Health Organization, Improving Access to Water, Sanitation, and Hygiene Can Save 14 Million Lives Per Year, Says New WHO Report. https://www.who.in t/news/item/28-06-2023-improving-access-to-water-sanitation-and-hygiene-can-save-1.4-million-lives-per-year-says-new-who-report, 2023 (Accessed 12 March 2005).
- [13] N.B. Alhaji, B.V. Maikai, J.K. Kwaga, Antimicrobial use, residue and resistance dissemination in freshwater fish farms of north-Central Nigeria: one health implications, Food Control 130 (2021) 108238, https://doi.org/10.1016/j. foodcont.2021.108238.
- [14] S.O. Olorunleke, M. Kirchner, N. Duggett, et al., Molecular characterization of extended-spectrum cephalosporin-resistant *Escherichia coli* isolated from livestock and in-contact humans in Southeast Nigeria, Front. Microbiol. 13 (2022) 937968, https://doi.org/10.3389/fmicb.2022.937968.
- [15] A.A. Ajayi, G.O. Onipede, B.C. Okafor, et al., Phenotypic identification of soil bacterial and fungal communities inhabiting an archaeological monument at Augustine University, Ilara Epe, Southwest Nigeria, Afr. J. Clin. Exp. Microbiol. 22 (4) (2021) 473–479, https://doi.org/10.4314/ajcem.v22i4.7.
- [16] A.T. Adesoji, D.R. Call, Molecular analysis of florfenicol-resistant bacteria isolated from drinking water distribution systems in southwestern Nigeria, J. Glob. Antimicrob. Res 23 (2020) 340–344, https://doi.org/10.1016/j.jgar.2020.10.005.
- [17] W.B. Adisasmito, S. Almuhairi, C.B. Behravesh, et al., One health: a new definition for a sustainable and healthy future, PLoS Pathog. 18 (6) (2022) e1010537, https://doi.org/10.1371/journal.ppat.1010537.
- [18] A.T. Gregory, A.R. Denniss, An introduction to writing narrative and systematic reviews - tasks, Tips and Traps for Aspiring Authors, Heart, lung & circulation 27 (7) (2018) 893–898, https://doi.org/10.1016/j.hlc.2018.03.027.
- [19] J. Beall, Beall's list of potential predatory journals and publishers. https://beallslist.net/, 2021.
- [20] Nigeria Centre for Disease Control and Prevention, Antimicrobial resistance: factsheet. https://ncdc.gov.ng/diseases/factsheet/70, 2023 (Accessed 13 March 2024)
- [21] A.O. Afolayan, A.O. Oaikhena, A.O. Aboderin, et al., Clones and clusters of antimicrobial-resistant *Klebsiella* from southwestern Nigeria, Clin. Infect. Dis. 73 (Supplement\_4) (2021) S308–S315, https://doi.org/10.1093/cid/ciab769.
- [22] A.O. Afolayan, A.O. Oaikhena, A.O. Aboderin, et al., An ST131 clade and a phylogroup A clade bearing an O101-like O-antigen cluster predominate among bloodstream *Escherichia coli* isolates from South-West Nigeria hospitals, Microb. Genom 8 (12) (2022), https://doi.org/10.1099/mgen.0.000863.
- [23] E.D. Alabi, B.L. Bindawa, I. Mzungu, et al., Characterization of selected multidrugresistant bacteria from clinical and hospital environmental sources using the Vitek 2 compact system, Appl. Microbiol: Open Access. 9 (2023) 258, https://doi.org/ 10.35248/2471-9315.23.9.258.
- [24] M.S. Gaddafi, Y. Yakubu, B. Garba, et al., Occurrence and antimicrobial resistant patterns of methicillin-resistant Staphylococcus aureus (MRSA) among practicing veterinarians in Kebbi state, Nigeria, Folia Vet 64 (4) (2020) 55–62, https://doi. org/10.2478/fv:2020-0038
- [25] J. Seni, G. Peirano, K.O. Okon, et al., The population structure of clinical extraintestinal *Escherichia coli* in a teaching hospital from Nigeria, Diagn. Microbiol. Infect. Dis. 92 (1) (2018) 46–49, https://doi.org/10.1016/j. diagmicrobio.2018.04.001.
- [26] O.D. Angel, P.S. Kadarko, J.S. Muazu, et al., Antimicrobial resistance profile and molecular detection of *MecA* gene in methicillin resistant *Staphylococcus aureus* from patients in selected general hospitals in Abuja municipal, Nigeria, GSC Biol Pharm. Sci 7 (2019) 3, https://doi.org/10.30574/gscbps.2019.7.3.0090.

- [27] S.A. Shettima, K.C. Iregbu, Antimicrobial resistance pattern of enterococci isolated from stool samples in a tertiary hospital in Nigeria, Annals Trop. Path 10 (2) (2019) 126, https://doi.org/10.4103/atp.atp.1\_19.
- [28] E.E. David, M.A. Yameen, I.O. Igwenyi, et al., The frequency of virulent genes and antimicrobial resistance patterns of diarrheagenic *Escherichia coli* isolated from stools of children presenting with diarrhea in a tertiary hospital in Abakaliki, Nigeria, int'l J one, Health 6 (2) (2020) 147–152, https://doi.org/10.14202/ JJOH.2020.147-152.
- [29] A. Kayode, P. Okunrounmu, A. Olagbende, et al., High prevalence of multiple drug resistant enteric bacteria: Evidence from a teaching hospital in Southwest Nigeria, J. Infect. Pub. Health 13 (4) (2020) 651–656, https://doi.org/10.1016/j. iiph.2019.08.014.
- [30] C.C. Okwume, N.F. Onyemelukwe, I.N. Abdullahi, et al., Prevalence of symptomatic urinary tract infection and bacterial spectrum of diabetic and nondiabetic patients at the two teaching hospitals in Enugu, Nigeria, Afr. J. Clin. Exp. Microbiol. 22 (4) (2021) 480–488, https://doi.org/10.4314/ajcem.v22i4.8.
- [31] M.M. Manga, M. Ibrahim, E.W. Isaac, et al., Antibiogram of *Pseudomonas* species: an important tool to combat antibiotic resistance for patient safety in Gombe, Nigeria, Afr. J. Clin. Exp. Microbiol. 22 (2) (2021) 279–283, https://doi.org/10.4314/aicem.v2212.21.
- [32] E.E. Chukwu, O.B. Awoderu, C.A. Enwuru, et al., High prevalence of resistance to third-generation cephalosporins detected among clinical isolates from sentinel healthcare facilities in Lagos, Nigeria, Antimicrob. Resist. Infect. Control 11 (1) (2022) 134, https://doi.org/10.1186/s13756-022-01171-2.
- [33] E. Egwu, F.A. Ibiam, I.B. Moses, et al., Antimicrobial susceptibility and molecular characteristics of beta-lactam-and fluoroquinolone-resistant *E. coli* from human clinical samples in Nigeria, Sci. Africa 21 (2023), https://doi.org/10.1016/j. sciaf.2023.e01863 e01863.
- [34] N. Medugu, I.A. Tickler, C. Duru, et al., Phenotypic and molecular characterization of beta-lactam resistant multidrug-resistant Enterobacterales isolated from patients attending six hospitals in northern Nigeria, Sci. Report. 13 (1) (2023) 10306, https://doi.org/10.1038/s41598-023-37621-z.
- [35] T. Edwards, C.T. Williams, M. Olwala, et al., Molecular surveillance reveals widespread colonisation by carbapenemase and extended spectrum beta-lactamase producing organisms in neonatal units in Kenya and Nigeria, Antimicrob. Resist. Infect. Control 12 (1) (2023) 14, https://doi.org/10.1186/s13756-023-01216-0.
- [36] E.O. Ngbede, I. Sy, C.A. Akwuobu, et al., Carriage of linezolid-resistant enterococci (LRE) among humans and animals in Nigeria: coexistence of the cfr, optrA, and poxtA genes in Enterococcus faecium of animal origin, J. Glob. Antimicrob. Res 34 (2023) 234–239, https://doi.org/10.1016/j.jgar.2023.07.016.
- [37] E.O. Njoga, J.A. Nwanta, K.F. Chah, Detection of multidrug-resistant *Campylobacter* species from food-producing animals and humans in Nigeria: public health implications and one health control measures, Comp. Immunol. Microbiol. Infect. Dis. 103 (2023) 102083, https://doi.org/10.1016/j.cimid.2023.102083.
- [38] M.O. Akpudo, O. Jimoh, G.O. Adeshina, et al., Biofilm formation and antimicrobial susceptibility pattern of Staphylococcus aureus clinical isolates from two healthcare facilities in Zaria, Niger. J. Pharm. Res. 19 (1) (2023) 59–70, https://doi.org/ 10.4314/nipr.y1911.6.
- [39] K.C. Daam, D.A. Samuel, U. Nwokoro, et al., Detection of CTX-M and SHV genes in extended Spectrum Beta-lactamase producing *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* in a tertiary hospital in north-Central Nigeria, Nig. Med. Journal 64 (2) (2023) 196–204, https://doi.org/10.60787/NMJ-64-2-159.
- [40] U. Abdulrahim, D.A. Oche, M. Kachallah, et al., Emergence of clinical vanA-type vancomycin-resistant Staphylococcus aureus isolates in National Orthopaedic Hospital Dala, Kano Nigeria, Afr. J. Clin. Exp. Microbiol. 24 (3) (2023) 250–257, https://doi.org/10.4314/aicem.v24i3.4.
- [41] C.M. Chukwuani, M. Onifade, K. Sumonu, Survey of drug use practices and antibiotic prescribing pattern at a general hospital in Nigeria, Pharm. World Sci. 24 (2020) 188–195, https://doi.org/10.1023/A:1020570930844.
- [42] C.D. Umeokonkwo, U.C. Madubueze, C.K. Onah, et al., Point prevalence survey of antimicrobial prescription in a tertiary hospital in south East Nigeria: a call for improved antibiotic stewardship, J. Glob. Antimicrob. Res 17 (2019) 291–295, https://doi.org/10.1016/j.jgar.2019.01.013.
- [43] J.O. Obasanya, O. Ogunbode, V. Landu-Adams, An appraisal of the contextual drivers of successful antimicrobial stewardship implementation in Nigerian health care facilities, J. Glob. Antimicrob. Res 31 (2022) 141–148, https://doi.org/ 10.1016/j.jgar.2022.08.007.
- [44] J.O. Fadare, O. Ogunleye, G. Iliyasu, et al., Status of antimicrobial stewardship programmes in Nigerian tertiary healthcare facilities: findings and implications, J. Glob. Antimicrob. Res 17 (2018) 132–136, https://doi.org/10.1016/j. jgar.2018.11.025.
- [45] E.E. Chukwu, D.A. Oladele, O.B. Awoderu, et al., A national survey of public awareness of antimicrobial resistance in Nigeria, Antimicrob. Resist. Infect. Control 9 (2020) 1, https://doi.org/10.1186/s13756-020-00739-0.
- [46] K.J. Awosan, P.K. Ibitoye, A.K. Abubakar, Knowledge, risk perception and practices related to antibiotic resistance among patent medicine vendors in Sokoto metropolis, Nigeria, Niger. J. Clin. Pract. 21 (11) (2018) 1476–1483, https://doi. org/10.4103/jicp.picn.60.18
- [47] A.D. Batista, A. Rodrigues, D. Figueiras, et al., Antibiotic dispensation without a prescription worldwide: a systematic review, Antibiotics 9 (11) (2020) 786, https://doi.org/10.3390/antibiotics9110786.
- [48] Nigerian Center for Disease Control, Antimicrobial use and resistance in Nigeria: situation analysis and recommendations. https://ncdc.gov.ng/themes/common/ docs/protocols/56\_1510840387.pdf, 2017 (Accessed 18 March 2025).
- [49] T. Joy-Okwor, J. Gatua, C.D. Umeokonkwo, et al., An assessment of infection prevention and control preparedness of healthcare facilities in Nigeria in the early

- phase of the COVID-19 pandemic (February–may 2020), J. Infect. Prev. 23 (3) (2022) 101–107, https://doi.org/10.1177/17571774211060418.
- [50] W. Calero-Cáceres, J.L. Balcázar, Leveraging genomic surveillance for public health: insights from Latin America, The Lancet Microb 5 (2024) 11, https://doi. org/10.1016/S2666-5247(24)00159-9.
- [51] I.N. Okeke, A.O. Aboderin, A. Egwuenu, et al., Establishing a national reference laboratory for antimicrobial resistance using a whole-genome sequencing framework: Nigeria's experience, Microbiol 168 (8) (2022) 001208, https://doi. org/10.1099/mic.0.001208.
- [52] Y.M.C. Nyandjou, S.E. Yakubu, I.O. Abdullahi, et al., Multidrug resistance patterns and multiple antibiotic resistance index of *Salmonella* species isolated from waste dumps in Zaria Metropolis, Nigeria, J. Appl. Sci. Env. Mgt 23 (1) (2019) 41–46, https://doi.org/10.4314/jasem.v23i1.6.
- [53] A.T. Adesoji, J.P. Onuh, I.P. Palang, et al., Prevalence of multi-drug resistant Pseudomonas aeruginosa isolated from selected residential sewages in Dutsin-ma, Katsina state, Nigeria, J. Pub. Health Afr 14 (2023) 2, https://doi.org/10.4081/ iphia.2023.2152
- [54] O.I. Falodun, M.C. Afolabi, A.G. Rabiu, Detection of extended Spectrum β-lactamase (ESBL) genes in *Escherichia coli* isolated from fecal samples of apparently healthy dogs in Ibadan Nigeria, Animal Gene 26 (2022) 200133, https://doi.org/10.1016/j.angen.2022.200133.
- [55] L.O. Obodoechi, I. Carvalho, N.S. Chenouf, et al., Antimicrobial resistance in Escherichia coli isolates from frugivorous (Eidolon helvum) and insectivorous (Nycteris hispida) bats in Southeast Nigeria, with detection of CTX-M-15 producing isolates, Comp. Immunol. Microbiol. Infect. Dis. 75 (2021) 101613, https://doi. org/10.1016/j.cimid.2021.101613.
- [56] D. Kabantiyok, L.E. Logyan, A.O. Ogundeji, et al., Peri-urban wildlife as sentinels for antimicrobial resistance: insights from owlets (*Tyoto alba*) in Jos, Nigeria. Sok. J. Vet. Sci 21 (3) (2023) 151–154, https://doi.org/10.4314/sokjvs.v21i3.7.
- [57] J.M. Chah, S.C. Nwankwo, I.O. Uddin, et al., Knowledge and practices regarding antibiotic use among small-scale poultry farmers in Enugu state, Nigeria, Heliyon 8 (4) (2022), https://doi.org/10.1016/j.heliyon.2022.e09342.
- [58] S.I. Smith, J.K. Kwaga, S.S. Ngulukun, et al., Antibiotic prescription practices amongst veterinarians in Nigeria, Res. Vet. Sci. 152 (2022) 219–227, https://doi. org/10.1016/j.rvsc.2022.07.028.
- [59] M.K. Aworh, E. Ekeng, P. Nilsson, et al., Extended-spectrum & lactamase-producing Escherichia coli among humans, beef cattle, and abattoir environments in Nigeria, Front. Cell. Infect. Microbiol. 12 (2022) 869314, https://doi.org/10.3389/ frimb 2022 869314
- [60] M. Akiba, T. Sekizuka, A. Yamashita, et al., Distribution and relationships of antimicrobial resistance determinants among extended spectrum-cephalosporinresistant or carbapenem-resistant *Escherichia coli* isolates from rivers and sewage treatment plants in India, Antimicrob. Agents Chemother. 60 (5) (2016) 2972–2980. https://doi.org/10.1128/aac.01950-15.
- [61] C.A. Ajuzieogu, I.C. Dyboh, D.C. Nwobodo, Culture-dependent examination of the bacteriological quality of ready-to-eat African salads in Enugu metropolis, Nigeria and antibiotic resistance profile of associated bacteria, Heliyon 8 (2022) 10, https://doi.org/10.1016/j.heliyon.2022.e10782.
- [62] F.O. Ogundipe, O.E. Ojo, A.T. Feßler, et al., Antimicrobial resistance and virulence of methicillin-resistant Staphylococcus aureus from human, chicken and environmental samples within live bird markets in three Nigerian cities, Antibio 9 (9) (2020) 588, https://doi.org/10.3390/antibiotics9090588.
- [63] A.H. Jibril, I.N. Okeke, A. Dalsgaard, et al., Genomic analysis of antimicrobial resistance and resistance plasmids in *Salmonella* serovars from poultry in Nigeria, Antibio 10 (2) (2021) 99, https://doi.org/10.3390/antibiotics10020099.
- [64] E.O. Igbinosa, A. Beshiru, I.H. Igbinosa, et al., Antimicrobial resistance and genetic characterisation of Salmonella enterica from retail poultry meats in Benin City, Nigeria, LWT 169 (2022) 114049, https://doi.org/10.1016/j.lwt.2022.114049.
- [65] A.I. Al-Mustapha, S.A. Alada, I.A. Raufu, et al., Co-occurrence of antibiotic and disinfectant resistance genes in extensively drug-resistant *Escherichia coli* isolated from broilers in Ilorin, north Central Nigeria, J. Glob. Antimicrob. Resist 31 (2022) 337–344, https://doi.org/10.1016/j.jgar.2022.11.002.
- [66] I.O. Fagbamila, E. Ramon, A.A. Lettini, et al., Assessing the mechanisms of multidrug resistant non-typhoidal *Salmonella* (NTS) serovars isolated from layer chicken farms in Nigeria, PLoS One 18 (9) (2023) e0290754, https://doi.org/10.1371/ journal.pone.0290754.
- [67] S.L. Gu, Y. Gong, J. Zhang, et al., Effect of the short-term use of fluoroquinolone and β-lactam antibiotics on mouse gut microbiota, Infect. Drug Res (2020) 4547–4558, https://doi.org/10.2147/IDR.S281274.
- [68] F. Ferrara, T. Castagna, B. Pantolini, et al., The challenge of antimicrobial resistance (AMR): current status and future prospects, Naunyn-Schmiedeberg's Arch. Pharm 1 (2024) 3, https://doi.org/10.1007/s00210-024-03318-x.
- [69] V.O. Ajekiigbe, I.J. Ogieuhi, T.A. Odeniyi, et al., Understanding Nigeria's antibiotic resistance crisis among neonates and its future implications, Dis. Pub. Health 22 (1) (2025) 28, https://doi.org/10.1186/s12982-025-00422-y.
- [70] N.B. Alhaji, T.O. Isola, Antimicrobial usage by pastoralists in food animals in north-Central Nigeria: the associated socio-cultural drivers for antimicrobials misuse and public health implications, One Health 6 (2018) 41–47, https://doi.org/10.1016/j.onehlt.2018.11.001.
- [71] M.A. Eruaga, T. Bature, E.O. Itua, Pharmacovigilance in Nigeria: addressing challenges in ensuring drug safety and monitoring adverse effects, GSC Adv. Res. Rev 18 (3) (2024) 078–082, https://doi.org/10.30574/gscarr.2024.18.3.0093.

- [72] Nigerian Center for Disease Control, One Health Strategic Plan, 2019–2023. https://ncdc.gov.ng/themes/common/docs/protocols/93\_1566785462.pdf, 2019.
- [73] R.L. Finley, P. Collignon, D.J. Larsson, et al., The scourge of antibiotic resistance: the important role of the environment, Clin. Infect. Dis. 57 (5) (2013) 704–710, https://doi.org/10.1093/cid/cit355.
- [74] Q. Tang, P. Song, J. Li, et al., Control of antibiotic resistance in China must not be delayed: the current state of resistance and policy suggestions for the government, medical facilities, and patients, Biosci. Trends 10 (1) (2016) 1–6, https://doi.org/ 10.5582/bst.2016.01034.
- [75] F.C. Cabello, H.P. Godfrey, A.H. Buschmann, et al., Aquaculture as yet another environmental gateway to the development and globalisation of antimicrobial resistance, The Lancet Infect. Dis 16 (7) (2016) e127–e133, https://doi.org/ 10.1016/51473-3099(16)00100-6.
- [76] C. Manyi-Loh, S. Mamphweli, E. Meyer, et al., Antibiotic use in agriculture and its consequential resistance in environmental sources: potential public health implications, Molecules 23 (4) (2018) 795, https://doi.org/10.3390/ molecules23040795.
- [77] P.K. Thai, V.N. Binh, P.H. Nhung, et al., Occurrence of antibiotic residues and antibiotic-resistant bacteria in effluents of pharmaceutical manufacturers and other sources around Hanoi, Vietnam, Sci. Total Environ. 645 (2018) 393–400, https://doi.org/10.1016/j.scitotenv.2018.07.126.
- [78] P. Taylor, R. Reeder, Antibiotic use on crops in low and middle-income countries based on recommendations made by agricultural advisors, CABI Agric. Biosci. 1 (1) (2020) 1, https://doi.org/10.1186/s43170-020-00001-y.
- [79] P.J. Collignon, S.A. McEwen, One health—its importance in helping to better control antimicrobial resistance, Trop. Med. Infect. Dis 4 (1) (2019) 22, https://doi.org/10.3390/tropicalmed4010022.
- [80] M.E. Velazquez-Meza, M. Galarde-López, B. Carrillo-Quiróz, et al., Antimicrobial resistance: one health approach, Vet. World 15 (3) (2022) 743, https://doi.org/ 10.14202/yetworld.2022.743-749.
- [81] J. Zinsstag, E. Schelling, K. Wyss, et al., Potential of cooperation between human and animal health to strengthen health systems, Lancet 366 (9503) (2005) 2142–2145, https://doi.org/10.1016/S0140-6736(05)67731-8.
- [82] D.E. Lucero-Prisno III, G.A. Owhor, A. Olayemi, et al., Addressing one health in Nigeria; challenges and recommendations, PAMJ-One Health (2023) 10, https://doi.org/10.11604/pamj-oh.2023.10.3.38072.
- [83] M.O. Emeje, S. Oloye, M. Bubakari, et al., Use of antibiotics in livestock in Nigeria: curbing antimicrobial resistance and developing a national regulatory guideline towards monitoring antibiotic use in animal and animal foods, Int. Res. J. Pub. Env. Health 9 (2) (2022) 55, https://doi.org/10.15739/iripeh.22.007.
- [84] U. Abubakar, B. Tangiisuran, Nationwide survey of pharmacists' involvement in antimicrobial stewardship programs in Nigerian tertiary hospitals, J. Glob. Antimicrob. Res 21 (2020) 148–153, https://doi.org/10.1016/j.jgar.2019.10.007.
- [85] R. Hibbard, M. Mendelson, S.W. Page, et al., Antimicrobial stewardship: a definition with a one health perspective, Npj Antimicrob. Res 2 (1) (2024) 15, https://doi.org/10.1038/s44259-024-00031-w.
- [86] I. Frost, G. Kapoor, J. Craig, et al., Status, challenges and gaps in antimicrobial resistance surveillance around the world, J. Glob. Antimicrob. Res 25 (2021) 222–226. https://doi.org/10.1016/j.jegr.2021.03.016
- 222–226, https://doi.org/10.1016/j.jgar.2021.03.016.
   [87] O.J. Dyar, B. Huttner, J. Schouten, et al., What is antimicrobial stewardship? Clin, Microbiol. Infect 11 (2017) 793–798, https://doi.org/10.1016/j.cmi.2017.08.026.
- [88] D.H. Lloyd, S.W. Page, Antimicrobial stewardship in veterinary medicine, in: Antimicrobial Resistance in bacteria from livestock and companion animals, American Society for Microbiol. (2018) 675–697, https://doi.org/10.1128/9781555819804 ch31
- [89] M. Sharan, D. Vijay, J.P. Yadav, et al., Surveillance and response strategies for zoonotic diseases: a comprehensive review, Sci. One Health 2 (2023) 100050, https://doi.org/10.1016/j.sob.2023.100050
- [90] S. Singh, P. Sharma, N. Pal, et al., Holistic one health surveillance framework: synergizing environmental, animal, and human determinants for enhanced infectious disease management, ACS Infect. Dis 10 (3) (2024) 808–826, https://doi.org/10.1021/acsinfecdis.3c00625.
- [91] S.A. McEwen, P.J. Collignon, Antimicrobial resistance: a one health perspective, Microbiol. Spectr 521-547 (2018), https://doi.org/10.1128/9781555819804.
- [92] C.R. Achi, O. Ayobami, G. Mark, et al., Operationalising one health in Nigeria: reflections from a high-level expert panel discussion commemorating the 2020 world antibiotics awareness week, Front. Public Health 9 (2021) 673504, https://doi.org/10.3389/fpubh.2021.673504.
- [93] I. Ahmad, H.A. Malak, H.H. Abulreesh, Environmental antimicrobial resistance, and its drivers: a potential threat to public health, J. Glob. Antimicrob. Res 27 (2021) 101–111, https://doi.org/10.1016/j.jgar.2021.08.00.
- [94] N. Sharda, D. Kumar, R. Thakur, et al., Environmental antibiotic resistance: recent trends, scope, and relevance, Water Air Soil Pollut. 234 (11) (2023) 683, https://doi.org/10.1007/s11270-023-06695-w.
- [95] D. Ogoina, G. Iliyasu, V. Kwaghe, et al., Predictors of antibiotic prescriptions: a knowledge, attitude, and practice survey among physicians in tertiary hospitals in Nigeria, Antimicrob. Resist. Infect. Control 10 (2021) 1–7, https://doi.org/ 10.1186/s13756-021-00940-9.
- [96] W. Akande-Sholabi, A.T. Ajamu, Antimicrobial stewardship: assessment of knowledge, awareness of antimicrobial resistance and appropriate antibiotic use among healthcare students in a Nigerian university, BMC Med. Edu 21 (2021) 1–8, https://doi.org/10.1186/s12909-021-02912-4.