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Antimicrobial Pollution in Tanzanian Surface Waters: Sources, Environmental Risks, and Public Health Implications

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Abstract

Antimicrobial pollution in surface waters has become an urgent environmental issue globally, yet few studies have specifically focused on the prevalence and impacts of antimicrobial contaminants in Tanzanian surface waters. This review article presents a comprehensive assessment of antimicrobial pollutants in Tanzania's aquatic ecosystems, filling a critical gap in the current literature. The findings reveal widespread contamination of surface waters, primarily with antibiotics, from diverse sources, including domestic sewage, agricultural runoff, industrial effluents, and healthcare facilities. This work integrates findings from a range of disciplines, including environmental monitoring, public health, and agricultural practices, to provide a holistic understanding in the Tanzanian context. The presence of antimicrobial pollutants may lead to the promotion of antimicrobial resistance, disruption of microbial communities, and risks to human health through food chain. Therefore, there is a call for further studies to assess the extent of antimicrobial pollution in Tanzania and its broader implications for both environmental and public health.

Keywords

Antimicrobial Pollution, Antibiotics, Environmental Implications, Tanzania, Waters

1. Introduction

In recent decades, the pervasive presence of antimicrobial pollutants in aquatic environments has emerged as a pressing global concern, with profound implications for environmental sustainability and public health (Hossein & Ripanda, 2025). Antimicrobial pollution, refers to the environmental contamination resulting from the release of ntimicrobial agents such as antibiotics, antiviral, or antifungal in active form, their metabolites or transformational products into natural ecosystems as a result of anthropogenic activities including pharmaceutical industry, agriculture, aquaculture, healthcare systems, households and release of produced effluents (Hossein et al., 2025; Ripanda, 2024). A recent study from East Africa indicated that Inadequate policy enforcement has been reported to result into improper disposal of pharmaceuticals, their metabolites and transformational products leading to, antibiotic resistance risks to human, other animal, and entire ecology (Karungamye et al., 2022). Previous research examining trends in emerging pollution in Tanzania, noted preliminary studies on pharmaceuticals, endocrine-disrupting hormones, and disinfection by-products (Miraji et al., 2016). These studies underscored the urgent need to expand monitoring efforts, enhance analytical infrastructure, and establish clear policies for managing emerging contaminants.

In Tanzania, a country with abundant freshwater resources critical for livelihoods, agriculture, and biodiversity conservation, the issue of antimicrobial contamination in surface waters (Marijani, 2022; Ripanda et al., 2023c), demands immediate attention. This work delves into the burgeoning problem of antimicrobial pollutants in Tanzania's surface waters, shedding light on their occurrence, sources, and far-reaching environmental implications. Tanzania, like many developing countries, grapples with a myriad of challenges (Achankeng, 2003; Zohoori & Ghani, 2017), ranging from rapid urbanization to inadequate waste management infrastructure. These challenges exacerbate the release of antimicrobial pollutants into surface waters through various pathways, including domestic, agricultural, industrial, and healthcare-related sources. A recent study by Kundu et al. (2024), reported occurences of high levels of pharmaceuticals in the station downwards of a wastewater stabilization pond, discharging its partially treated effluent into the river, followed by stations whose rivers flowed through informal areas. Further sampled points' located near the river's water sources had fewer compounds with values below the detection limits, including amoxicillin, doxycycline, and sulfamethoxazole (94 ng/L) in the borehole, most of the concentrations detected in rivers were ten times higher than in boreholes (Kundu et al., 2024). Even trace levels of antimicrobial pollutants pose public health risks by creating selective pressure that fosters the emergence and spread of antimicrobial-resistant pathogens through the food chain and clinical settings, impairing ecological health.

A study by Ripanda et al. (2023c), revealed a significant role of urban wastewater as a reservoir of resistant bacteria and genes, particularly in resource limited settings including Tanzania. The prevalence of multidrug resistance (MDR) bacteria, especially *E. coli*, and the presence of resistance genes such as Sul and Tet families highlight a growing threat of resistant infections (Ripanda et al., 2023c). The detection of β-lactamase-producing isolates further complicates treatment options, given their ability to deactivate critical antibiotic classes.

Antimicrobial pollutants such as antibiotics from human and veterinary use, and agricultural runoff from livestock farming and crop cultivation practices introduces pollutants into rivers and lakes (Mdegela et al., 2021; Mwega et al., 2020). Similarly, industrial effluents from pharmaceutical manufacturing and healthcare facilities discharge potent antimicrobial compounds into water bodies (Adeola & Forbes, 2022; Ripanda et al., 2025), compounding the contamination burden. The impacts of antimicrobial pollution in Tanzanian surface waters are far-reaching, extending beyond ecological harm to include significant public health and economic consequences. A particularly concerning outcome is the intensification of antimicrobial resistance (AMR), a global health threat undermining the effectiveness of life-saving antibiotics. The continuous exposure of aquatic microorganisms to sub-lethal concentrations of antimicrobial agents fosters the selection of resistant strains, potentially compromising the effectiveness of medical treatments and increasing healthcare costs. A study by Hounmanou et al. (2019), revealed the presence of toxigenic *Vibrio cholerae* O1 strains in Lake Victoria during a non-outbreak period, demonstrating their environmental persistence and pathogenic potential. Identified strains harbored major virulence genes (like *ctxA*, *ctxB*, *zot*, *tcpA*) and pathogenicity islands (like VPI-1, VPI-2, VSP-1, VSP-2) (Hounmanou et al., 2019), which are critical for disease causation. The identified strains possessed genes for biofilm formation, stress response, and quorum sensing, enhancing survival in aquatic environments. The genes carried the SXT integrative conjugative element, conferring MDR to aminoglycosides, sulfamethoxazole, trimethoprim, phenicol, and quinolones (Hounmanou et al., 2019). This indicates dual threats of cholera outbreaks and AMR posed by these persistent environmental strains, requiring intervention.

Figure 1 presents structures of selected antimicrobial pollutants and other reported pharmaceutical contaminants. A study by Kimera et al. (2021), revealed that among recovered isolates, 45.5% were *Klebsiella pneumoniae* and 29.6% were *Escherichia coli*. Resistance patterns varied across different environments. For instance, *K. pneumoniae* showed higher resistance in effluent (27.9%) compared to *E. coli* (26.6%), while *E. coli* exhibited greater resistance in river water, sediment, and crop soil (35% vs. 25%) (Kimera et al., 2021). Notably, *K. pneumoniae* showed high resistance to nalidixic acid (54.6%) and ciprofloxacin (33.3%), whereas *E. coli* displayed significant resistance to ciprofloxacin (39.7%) and trimethoprim/sulfamethoxazole (38%) (Kimera et al., 2021). Resistance levels increased downstream, from 28.3% in Kisarawe to 66.7% in Upanga West. About 53.2% isolates possessed MDR genes, especially extended-spectrum beta-lactamase (ESBL), quinolone-resistant, and carbapenem-resistant strains (Kimera et al., 2021).

A study by Marijani (2022) highlighted a significant bacterial contamination in fish from botopen-air markets and supermarkets, with *E. coli* being the most prevalent species (40% in open-air markets, 37% in supermarkets), followed by

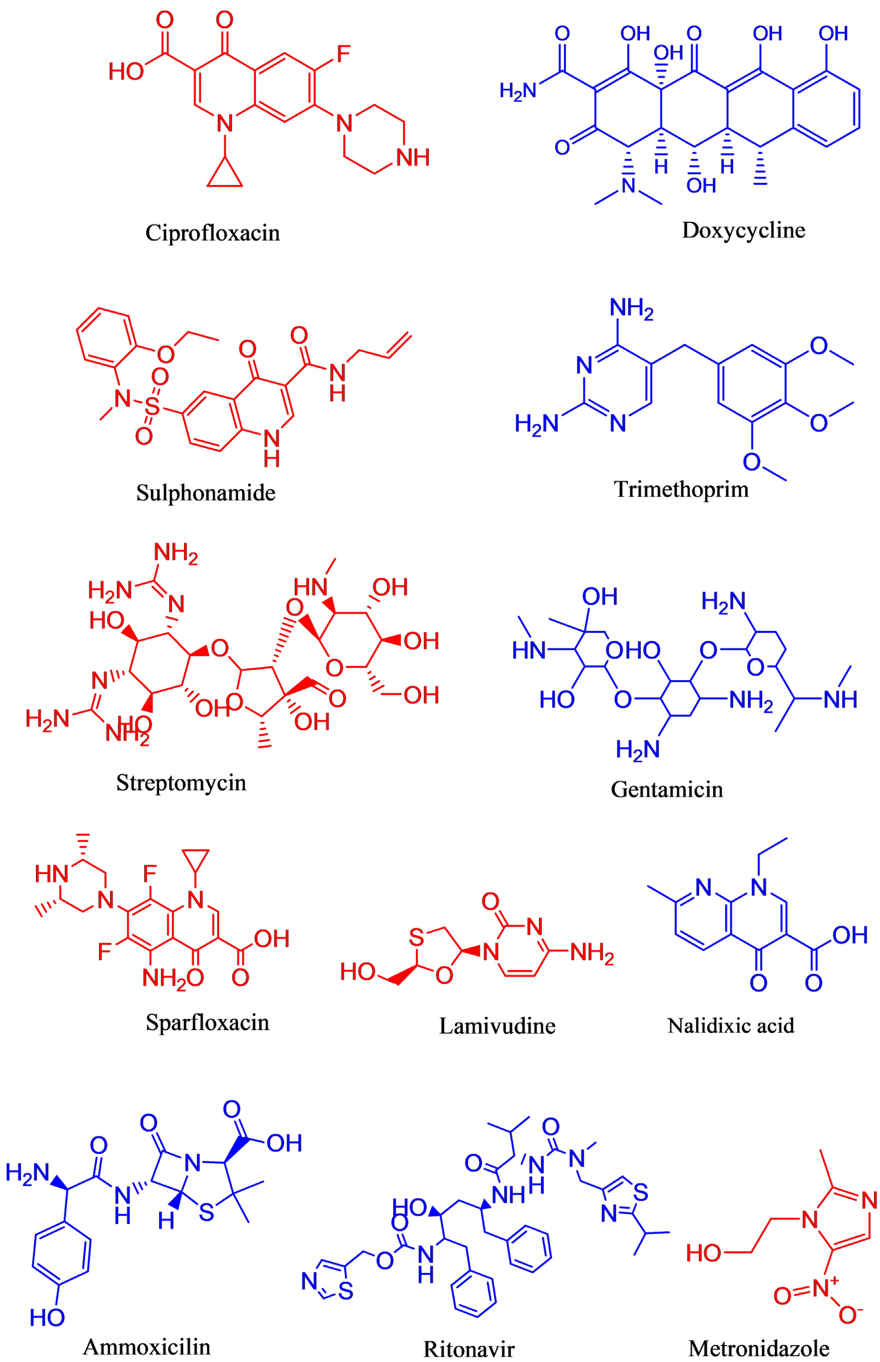


Figure 1. The structures of selected antimicrobials (Source: Prepared using ChemDraw).

Klebsiella spp., *Salmonella* spp., and other pathogens like *Shigella* spp., *Citrobacter* spp., and *Pseudomonas* spp. While 58.7% of the samples met the International Commission on Microbiological Specifications for Foods criteria as "good," 41.3% were only marginally acceptable (Marijani, 2022). Particularly, isolates of *E. coli* and *Salmonella* spp. exhibited resistance to multiple antibiotics (Marijani, 2022), including penicillin, erythromycin, gentamicin, and tetracycline, threatening public health. A study by Moremi et al. (2016b) revealed the presence of multiple antibiotic resistance genes such as sulfonamides (sul1/sul2), tetracyclines (tet(A)/tet(B)), fluoroquinolones (aac(6′)-Ib-cr, qnrS1), aminoglycosides (aac(3)-lld, strA, strB), and trimethoprim (dfrA14) in bacterial isolates from the environment and fish. Notably, *E. coli* sequence types ST-38 and ST-5173 were detected in isolates from the environment and fish, suggesting a potential link between environmental and food-chain contamination, threatening public health. The identification of IncY plasmids carrying key resistance genes (blaCTX-M-15, qnrS1, strA, strB) in environmental isolates and fish (Moremi et al., 2016b), highlighting the role of plasmid-mediated dissemination in spreading resistance as reported by Hossein and Ripanda (2025). This suggests that resistant *E. coli* from Mwanza city's sewage system may be entering Lake Victoria, highlighting the close link between human activities, environmental contamination, and the food chain.

The continued presence of bla_{CTX-M-15} in this ecosystem is driven by both the clonal spread of resistant strains and horizontal gene transfer via IncY plasmids, underscoring the urgent need for integrated strategies to combat antibiotic resistance, Further studies indicated growing trends of bacterial infections in fish farms and will continue to be an issue of concern into the future (Marijani, 2022; Mdegela et al., 2021; Mzula et al., 2019, 2021), which may increase the use of antimicrobial agents requiring intervention. These findings pose a public health risk, particularly to immunocompromised individuals, emphasizing the need for improved food safety measures, regular AMR monitoring, and consumer education on safe handling practices to mitigate health hazards.

In Tanzania AMR pollution is a significant issue, driven by widespread use of antibiotics in healthcare, agriculture, and community settings. Recent data indicates that in 2019, Tanzania reported approximately 12,500 deaths attributable to AMR and 54,000 deaths associated with drug-resistant infections (Evaluation, 2023). The primary pathogens contributing to these outcomes include *Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus pneumoniae*, *Escherichia coli, and Salmonella Typhi,* which are linked to respiratory, bloodstream, and intra-abdominal infections (Camara et al., 2023; Evaluation, 2023; Mbwasi et al., 2020; Mdegela et al., 2021). Tanzania ranks 30th globally for AMR-related age-standardized mortality rates, highlighting its substantial burden compared to other regions (Evaluation, 2023). Efforts are underway to address the issue through national AMR action plans, though challenges remain in data collection, surveillance, and resource allocation. Moreover, the presence of antimicrobial pollutants can disrupt aquatic ecosystems, leading to biodiversity loss, altered nutrient cycling (Bashir et al., 2020; Wang et al., 2023), and the proliferation of harmful algal blooms. These ecological disruptions cascade through food webs, affecting fisheries, agriculture, and tourism-dependent livelihoods, thus underscoring the interconnectedness of environmental health and socio-economic well-being (Achankeng, 2003; Bashir et al., 2020; Wang et al., 2023).

Additionally, the contamination of surface waters poses direct risks to human health, as communities reliant on these water sources for drinking, cooking, and irrigation may be exposed to antimicrobial residues and resistant bacteria, leading to waterborne diseases and treatment challenges. Addressing the complex challenge of antimicrobial pollution in Tanzanian surface waters necessitates a multifaceted approach encompassing scientific research, policy interventions, community engagement, and capacity-building initiatives. Robust monitoring programs are essential to assess the extent of contamination, identify hotspots, and track temporal trends, enabling evidence-based decision-making and targeted mitigation efforts. The findings emphasize the urgent need for improved wastewater management, monitoring of AMR genes in environmental reservoirs, strengthened antibiotic stewardship and surveillance programs to curb AMR transmission to humans and other animals. Appendix **Table A1** presents selected employed antimicrobial agents during this period in Tanzania, category, structure, reported environmental effects and its implications, in some cases combinations of these agents are employed (Sangeda et al., 2021). Together, sulphonamides and trimethoprim are often used in combination (e.g., co-trimoxazole) because they act synergistically to inhibit folic acid synthesis at two different points in the pathway, making the treatment more effective and reducing the likelihood of resistance development.

Origin of antimicrobial pollution

The release of effluents containing antimicrobial agents such as such as penicillin and erythromycin for bacterial infections (Pérez-Legaspi & Rico-Martínez, 2023; Rugumisa et al., 2016), antivirals such as lamivudine and oseltamivir for viral infections (Huang et al., 2021), antifungals such as fluconazole for fungal infections (Lu et al., 2021), and antiparasitic drugs such as chloroquine for malaria (Meo et al., 2020) is of public health concern, referred to antimicrobial pollution. These drugs are crucial in the treatment and prevention of various infectious diseases (Pérez-Legaspi & Rico-Martínez, 2023; Rugumisa et al., 2016). Report indicate an increase in global antibiotic consumption rate by 46% in 2018 compared to that of 2000 (Browne et al., 2021). Studies indicate that 30 to 90% of consumed drug is excreted through urine or faeces (Bamfo et al., 2021; Daghrir & Drogui, 2013; Egan et al., 2000), indicating that approximately more than 90 thousand tons may end up in the environment especially aquatics. Further, between 2010 and 2017, Tanzania utilized a cumulative total of 13390.32 tonnes of antibiotics (Hamim et al., 2021), equivalent to about 1675 tonnes per year. This indicates introduction of more than 500 tonnes of antibiotics per year in the environment especially water bodies, which may impact ecological health. **Table A2** showcases comprehensive data on AMR pollution in various environmental compartments in Tanzania. This includes the concentrations of antimicrobials where available, the presence of antimicrobial-resistant microbes, and the detection of resistance genes. The table highlights findings from wastewater, surface waters, urban receiving waters, effluents, and the food chain. This data is crucial for understanding the extent of antimicrobial contamination and the spread of resistance. The table underlines the pervasive nature of antimicrobial pollution and its potential public health impacts. The presence of resistant microbes and genes in these environments indicates the ongoing risk of AMR spreading through environmental and food pathways. This information is vital for developing strategies to mitigate AMR and safeguard environmental and human health.

Similarly, over the course of eight years (2010 to 2017), there was a significant level of systemic antivirals usage, reaching 367.1 and antifungals 10.8 defined daily doses (DDD), per 1000 inhabitants per day (Hamim et al., 2021). This indicates introduction of more than 110 defined daily doses of antiviral and 3 defined daily doses of antifungal per 1000 inhabitants per day into the environment. A similar study reported average daily defined dose (DDD) per 1,000 inhabitants for all antimicrobials was 80.8 ± 39.35. The DDD per 1,000 inhabitants per day (DDD/1000/D) decreased significantly from 136.41 in 2017 to 54.98 in 2018 and further to 51.02 in 2019 (Mbwasi et al., 2020). Doxycycline, amoxicillin, and trimethoprim-sulfamethoxazole were the most used antibiotics during this period, with DDD/1,000/D values of 20.01, 16.75, and 12.42, respectively (Mbwasi et al., 2020).

Most recommendations of antimicrobial agents use in Tanzania is done by the private medical sector, this is evidenced by an annual increase in its share from 2017 to 2019 (Mbwasi et al., 2020). Over 90% of the antimicrobials consumed were classified as access class medications, while class medications made up less than 10% and 1% of reserve class medications. The private sector use of antimicrobials is rising significantly and needs to be closely monitored in line with national policies to ensure ecological safety and sustainability. Report indicates lack of information on antimicrobial consumption patterns in sub-Saharan Africa, this requires intervention. On the other hand, guidelines for disposal of expired or unused medication are only available for public premises and hospitals dis regarding households, leading to pollution as people discards together with domestic wastes or pit latrines (Karungamye et al., 2022; Banaga, 2020). AMR pollution not only poses a direct threat to ecosystems and human health but also exacerbates the problem of AMR in clinical settings.

2. Methodology

This narrative literature review examines antimicrobial pollution in Tanzanian surface waters, focusing on regions with available data on the prevalence of resistance and associated genes in various environmental matrices, including surface water, groundwater, wastewater effluents, sediments, soils, and the food chain, as detailed in **Table A2**. The review draws on journal articles sourced from multiple databases, including Web of Science, Scopus, Google Scholar, Wiley Online Library, ScienceDirect, Taylor & Francis Online, Sage Publishing, and PubMed. By compiling and analyzing data from studies across Tanzania, this review provides insights into the antimicrobial pollution in Tanzanian surface waters focusing on the sources, environmental risks, and public health implications, an area that remains underexplored in existing literature.

3. Environmental Occurrences of Antimicrobial Pollutants

The global nature of AMR pollution means that resistant microorganisms, along with resistance genes, can traverse borders, posing a transboundary threat to public health. The interconnectedness of ecosystems and the movement of people and goods make this issue difficult to contain within national boundaries. The prevalence of AMR in the environment ultimately affects clinical care, as infections caused by resistant pathogens become harder to treat. There is limited data highlighting the status of AMR pollution on Tanzania aquatic environments (Joachim et al., 2023; Kimera et al., 2021; Subbiah et al., 2020), but AMR pollution is transboundary and there are reports of diseases as a result of resistant strains of microbs. A study by Kimera and Coallegues reported that among the recovered isolates, 45.5% were *Klebsiella pneumoniae* and 29.6% were *Escherichia coli*. *K. pneumoniae* showed greater resistance in effluent (27.9%) compared to *E. coli* (26.6%) (Kimera et al., 2021). However, *E. coli* exhibited higher resistance in river water, sediment, and crop soil compared to *K. pneumoniae* (35% vs. 25%, respectively) (Kimera et al., 2021). *K. pneumoniae* had the highest resistance to nalidixic acid (54.6%) and ciprofloxacin (33.3%), while *E. coli* was most resistant to ciprofloxacin (39.7%) and trimethoprim/sulfamethoxazole (38%) (Kimera et al., 2021). Resistance increased from 28.3% in Kisarawe, where the river originates, to 59.9% in Jangwani (middle section) and 66.7% in Upanga West, where the river enters the Indian Ocean (Kimera et al., 2021). Further, of the *E. coli* and *K. pneumoniae* isolates, 53.2% were resistant to more than three classes of antibiotics, with higher occurrence among ESBL producers, quinolone-resistant, and carbapenem-resistant strains.

A study by Silago and Colleagues investigated multidrug-resistant uropathogens causing community acquired urinary tract infections among patients attending health facilities in Mwanza and Dar es Salaam, and reported that *Staphylococcus aureus* and *Staphylococcus haemolyticus* were the predominant (Silago et al., 2022). *Escherichia coli* exhibited resistance ranging from 0.7% (meropenem) to 86.0% (ampicillin), while other *Enterobacterales* showed resistance from 0.0% (meropenem) to 75.6% (ampicillin). Multidrug resistance was observed in 45.4% of *Enterobacterales* and 22.4% of Gram-positive bacteria p-value = 0.008 (Silago et al., 2022). Overall, sulfamethoxazole emerged as the most frequently identified compound in surface water across Africa, ranging from 0.00027 to 39 μg/L (Faleye et al., 2018), in recent study sulfamethoxazole (94 ng/L) was identified in the borehole, with most detected pollutants in rivers being ten times higher than in boreholes (Kundu et al., 2024), including report of resistance to sulfamethoxazole (Baniga et al., 2020; Ripanda, 2024; Ripanda et al., 2023c). Further, Efavirenz and nevirapine exhibit notable persistence in effluents and are prevalent in surface water based on environmental concentrations. Elevated levels of resistance to penicillin G, chloramphenicol, streptomycin, and oxytetracycline have been documented, among pathogenic microbial communities in dairy cattle suffering from mastitis (Mdegela et al., 2021). Similar patterns are observed in poultry, where both eggs and meat are contaminated with *Escherichia coli* strains resistant to amoxicillin + clavulanate, sulphamethoxazole, and neomycin (Mdegela et al., 2021). Furthermore, a growing trend of emerging multidrug-resistant *E. coli*, and *Klebsiella pneumoniae,* has been observed in food animals. Reports also indicate an uptick in methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum beta-lactamase (ESBL) in the livestock sector in Tanzania (Mdegela et al., 2021).

4. Antimicrobial Pollutants Load, and Flow

Antimicrobial pollutants enter and circulate in the environment, potentially bioaccumulate in living tissues, bioconcentrates in living organisms and biomagnifies through food chain (Hossein et al., 2023), while creating harm to exposed organism. The presence of antimicrobial pollutants in the environment is linked to deterioration of ecosystem health and increased diseases (Martins et al., 2012; Omotola et al., 2021). Other pathways by which antimicrobials are introduced into the environment include improper disposal of leftover and expired drugs in water stream or down the toilet, chemical waste from manufacturing facilities, and municipal landfill leachates (Miraji et al., 2016; Sorensen et al., 2014), aquaculture, and animal systems (Gwenzi et al., 2020). Less-explored yet potentially significant sources include non-engineered landfills, on-site sanitation facilities, funeral parlors, and gravesites (Gwenzi et al., 2020). Once these chemicals are in the environment, they can flow from one compartment to another while creating harm. However, the drawbacks of antimicrobials in the environment extend beyond acute effects to delayed effects from bioaccumulation, amplified effects from drug-drug interactions, aggravation of drug resistance, and reduction in aquatic and terrestrial food production (Kamba et al., 2017). **Figure 2**

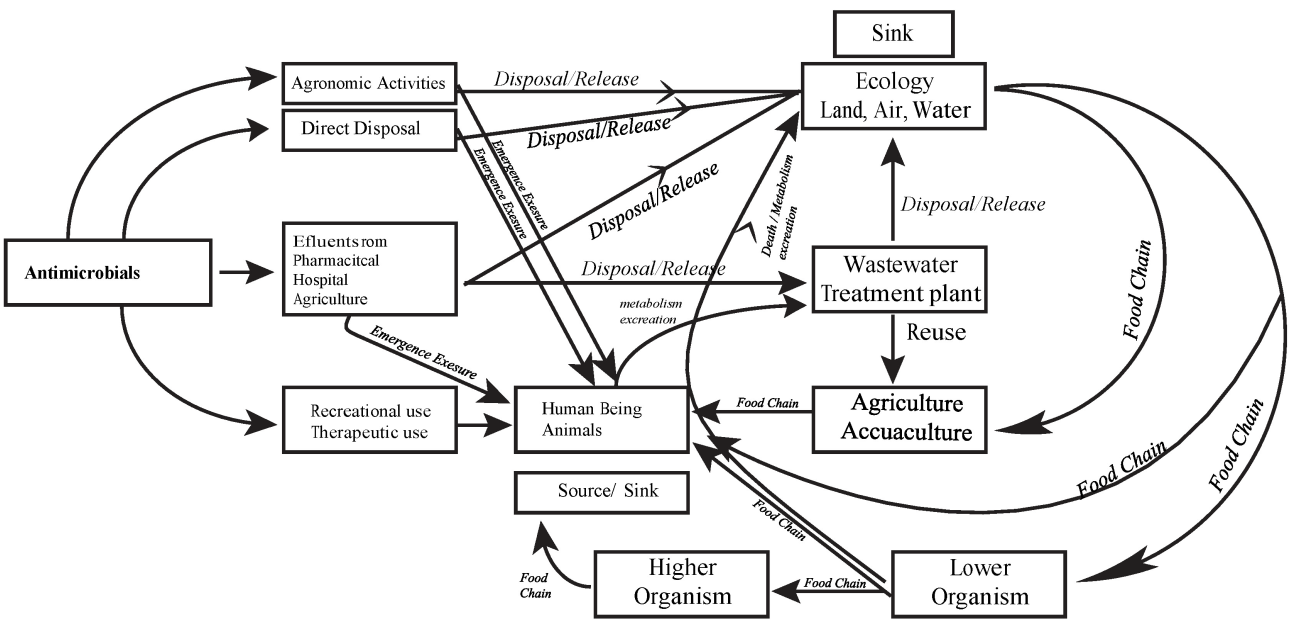


Figure 2. Flow of antimicrobial pollutants in different environmental compartments, and through food chain (Source: Ripanda (2024)).

presents reported sources of antimicrobial pollutants including agronomic activities (Mdegela et al., 2021), direct disposal (Chengula et al., 2015; Kihampa, 2013), effluents (Bidu et al., 2021; Miraji et al., 2016), therapeutic use including disposal practices (Gwenzi et al., 2023; Millanzi et al., 2023; Minzi & Manyilizu, 2013), indicating human is the source and sink of antimicrobial and other emerging pollutants.

This may lead to antimicrobial pollution and dissemination of antimicrobial resistant pathogens leading to increased hospitalization (Kumburu et al., 2017; Mikomangwa et al., 2020; Moremi et al., 2016a; Seni et al., 2019b), mortality rates (Blomberg et al., 2007; Manyahi et al., 2020; Seni et al., 2019a; Seni et al., 2019b), and overall degradation of ecological balance (Karungamye et al., 2023; Kümmerer, 2009, 2011; Miraji et al., 2016; A. Ripanda et al., 2023b; Ripanda et al., 2024; Ripanda et al., 2023c). After their introduction into the environment (Ripanda et al., 2023c; Subbiah et al., 2020), they persist while circulating in environmental compartments such as soil , water (Hossein et al., 2018; Ripanda et al., 2023c), sediments (Kimera et al., 2021; Sabatino et al., 2024), crops (Kimera et al., 2021), creating harm and flow including through good chain (Azabo et al., 2022; Ripanda et al., 2022; Sonola et al., 2021a; Sonola et al., 2021b; Subbiah et al., 2020). Further the results of environmental risk assessment and routine environmental monitoring regulations do not include antimicrobial pollutants, simply because acute risk assessments show insignificant human health hazards, this may lead to antimicrobial pollution. The presence of antimicrobial pollutants in waters, aquatic ecosystems, and other environmental compartment have been reported globally (Atnafie et al., 2021), with scarcity of information from developing countries as a result of limited fund to purchase or manage the state of art equipment necessary for their isolation, identification, and quantification.

5. Environmental Effects of Antimicrobial Pollutants

Most reported antimicrobial pollutants include antibiotics such as ciprofloxacin (Ripanda et al., 2024), and anti-retroviral drugs such as lamivudine (Ripanda et al., 2023a, 2023b), are considered active once in the environment. A load of antimicrobial residues released into the environment after anthropogenic usage has been linked to both human and environmental health degradation. Although antimicrobials are of public health concern, they are currently neither monitored nor included in the environmental guidelines in most countries. These chemicals are environmentally persistent and have tendency to bioconcentrate, bioaccumulate and biomagnify through food chain while causing potential environmental risk especially when such chemicals come into contact with drinking water supplies and the food chain (Abelkop et al., 2018).

Robinson H. Mdegela et al. (2021), reported that microorganisms, including bacteria, along with their residues, can disseminate through food, water, and the environment, creating a One Health risk pathway that connects other animals, humans, and ecosystems. This pathway also facilitates the potential spread of resistance through travel, trade, and interactions at the interfaces between domestic animals, wildlife, and humans. A recent survey in Tanzania found residues of the human designated antiviral agent lamivudine in animal feeds and tissues of domestic pigs and broiler chickens (Kimera et al., 2025). This indicates the potential for these pollutants to be disseminated through the food chain, impairing ecological and public health. Antimicrobial agents such as lamivudine and ciprofloxacin and their residues can exert a wide range of ecotoxicological effects on aquatic organisms, influencing physiological, biochemical, and community-level processes as a result of single or mixture of drugs (Alderton et al., 2021; Fernandez et al., 2021; Michael et al., 2014).

In the treatment of medical conditions antimicrobials, including antibiotics, play a vital role, but, according to WHO, AMR has been declared a major threat to public health and is predicted to cost about 10 million lives a year by 2050. Reports of occurrences of substances such as antimicrobial pollutants, and other emerging contaminants in the environment including surface waters are globally available (Groot & van't Hooft, 2016; Hong et al., 2013; Wu et al., 2016), including Tanzania (Hossein et al., 2018; Hounmanou et al., 2019; Kimera et al., 2021; Marijani, 2022; Moremi et al., 2016b; Mzula et al., 2019), this calls for remediation of these contaminants for ecological safety.

Research laboratories demonstrated growth inhibition in microalgae *Pseudokirchneriella subcapitata* sunder short-term exposures to ciprofloxacin than *Daphnia magna* and *Gambusia holbrooki* (Martins et al., 2012), reduced reproduction in crustaceans *Daphnia magna* (Martins et al., 2012), and oxidative stress in fish species such as *Danio rerio* (Batir-Marin et al., 2025). Report of adverse impact on the root lengths on exposure to lamivudine was recorded for *Allium cepa*, evidenced by chromosomal aberration in the exposed *Allium cepa* root tips (Omotola et al., 2021). These effects collectively indicate the potential of antimicrobials to disrupt aquatic food webs, nutrient cycling, and ecosystem resilience. However, most ecotoxicological data are derived from temperate model organisms that may not accurately represent tropical aquatic systems.

According to Moffo et al. (2024), the use of antimicrobial agents in production systems and resistance in African fish present a growing public health challenge with direct implications for the One Health framework. The meta-analysis revealed higher pooled prevalence of resistance among bacterial isolates, particularly *Escherichia coli* showing 87.1% resistance to ampicillin, with widespread multidrug resistance to commonly used antimicrobials including cotrimoxazole, gentamicin, tetracycline, and amoxicillin (Moffo et al., 2024). Such resistant strains can be transmitted to humans through the consumption of contaminated fish, contact with aquaculture water, or their environmental dissemination through effluents, thereby undermining the efficacy of critical antibiotics used in clinical settings leading to health degradation. Poor adherence to withdrawal periods and off-label antimicrobial use which increase the likelihood of drug residues in fish and aquatic environments was also highlighted, indicating the potential for consumers to be exposed to the residues and associated health impact.

These residues not only pose toxicological risks but also create selective pressure that drives the persistence of resistant bacteria in natural environments. Results of surveillance of Msimbazi River Basin in Tanzania, revealed widespread antimicrobial resistance among Enterobacteriaceae, particularly *E. coli* and *K. pneumoniae* (Kimera et al., 2021), isolates were multidrug-resistant, with high prevalence of ESBL, quinolone, and carbapenem resistance. This indicates potential for degradation of ecological health, highlighting critical environmental dissemination of AMR and underscore the urgent need to control antimicrobial pollution within the basin. In Tanzania (Kilusungu et al., 2024; Mramba & Kahindi, 2023) and other Sub-Saharan African countries, where aquaculture contributes substantially to food security and livelihoods, this situation threatens both public health and economic stability, emphasizing the urgent need for integrated antimicrobial use (AMU) and AMR surveillance, regulatory enforcement, and responsible antimicrobial stewardship in line with One Health principles to ensure ecological safety.

Furthermore, antimicrobial pollutants may induce selective pressure on microbial communities, promoting the proliferation of resistant microorganism such as antibiotic-resistant bacteria and genes within sediments and water columns. This process creates a feedback loop that links environmental health to human and animal health a central concern under the One Health framework. Considering limited wastewater treatment capacity and the close human, livestock, wildlife-water interface, the ecological risks associated with antimicrobial pollution are particularly pronounced. Therefore, localized ecotoxicological studies using native species and realistic environmental concentrations are essential to assess ecological vulnerability and to guide mitigation and policy interventions.

The environmental AMR pollution, including resistance genes are linked to clinical outcomes, and in Tanzania is becoming increasingly evident. Studies have revealed that resistance determinants such as bla-CTX-M, bla-SHV, and bla-NDM detected in *Escherichia coli* and *Klebsiella spp*. isolated from rivers, wastewater, and livestock environments are genetically similar to those identified in clinical isolates from major hospitals in Dar es Salaam, Mwanza, and Arusha. This overlap suggests continuous exchange of resistance genes between environmental reservoirs and human populations through contaminated water, food, and direct contact. The persistence of these resistance elements in surface waters and sediments not only heightens infection risks but also complicates treatment outcomes in healthcare settings, requiring intervention. Strengthening integrated AMR surveillance that links environmental sampling with hospital microbiology data is therefore vital to fully operationalize One Health AMR framework in Tanzania, enabling timely, evidence-based interventions across sectors.

6. Regulatory and Management Framework

In Tanzania, the regulatory and management framework for AMR is designed to address the growing threat through a coordinated, multi-sectoral approach. The framework is guided by the National Action Plan (NAP), which aligns with the Global Action Plan on AMR endorsed by the WHO (Munkholm & Rubin, 2020; Neale & Cullen, 2024). The key elements of the AMR framework include the NAP, first NAP on AMR was launched its in 2017, covering a five-year period (2017-2022), with ongoing efforts to update and extend the plan (Frumence et al., 2021). The NAP focuses on improving awareness and understanding of AMR, strengthening knowledge through surveillance and research, reducing the incidence of infection, optimizing the use of antimicrobial agents, and ensuring sustainable investment in AMR initiatives (Frumence et al., 2021). Tanzania Medicines and Medical Devices Authority (TMDA) is responsible for regulating the quality, safety, and efficacy of medicines, including antimicrobials (Mbwasi et al., 2020). TMDA oversees the registration, distribution, and use of antibiotics in both human and veterinary medicine. Whereas the Ministry of Health (MoH) oversees the implementation of AMR policies and strategies (Frumence et al., 2021), including infection prevention and control (IPC) programs in healthcare settings. Tanzania Veterinary Laboratory Agency (TVLA) is involved in the regulation of antimicrobial use in animals and ensuring compliance with veterinary guidelines (Mkopi et al., 2024). Tanzania has established an integrated surveillance system for AMR, which includes the collection and analysis of data from both human health and animal health sectors. This system is critical for tracking resistance patterns and informing policy decisions.

Similarly, the country has developed a network of laboratories capable of detecting AMR, which plays a key role in monitoring resistance trends and guiding treatment protocols (Camara et al., 2023). The implementation of IPC programs in hospitals and clinics to reduce the spread of infections and promote the rational use of antimicrobials, will be of help to mitigate the negative effects on these substances on environment and health. Public health campaigns and community outreach programs aim to educate the public on the risks of AMR and promote good hygiene practices (Ashley et al., 2016; Mudenda et al., 2023). Tanzania has laws and regulations that control the sale and use of antibiotics, particularly focusing on preventing over-the-counter sales without a prescription (Chuwa et al., 2024; Ndaki et al., 2021). Also, there are specific guidelines for the prudent use of antimicrobials in animals to prevent the emergence of resistance in zoonotic pathogens. In Tanzania AMR framework is built on a One Health approach, involving collaboration between human health, animal health, and environmental sectors. This approach ensures that AMR is addressed comprehensively across different sectors. Further, universities and research institutions in Tanzania contribute to the AMR framework by conducting studies on resistance mechanisms, developing new diagnostics, and evaluating the effectiveness of AMR interventions. Tanzania collaborates with international organizations such as WHO, the Food and Agriculture Organization (FAO), and the World Organisation for Animal Health (OIE) to strengthen its AMR response and align with global best practices to ensure ecological health and sustainability.

7. Curbing AMR Pollution through Behavior Change

Curbing AMR pollution in Tanzania requires not only scientific and policy interventions but also a transformative behavior change across communities (Durrance-Bagale et al., 2021; Frumence et al., 2021). Through the World AMR Awareness Week (WAAW), Tanzania has amplified national efforts to educate the public on the prudent use of antimicrobials in human, animal, and environmental health sectors (Fuller et al., 2023; Mathobela, 2025; Mramba et al., 2025). The Tanzania Parliamentarian Alliance for AMR has been instrumental in driving political commitment and advocating for evidence-based policies that strengthen antimicrobial stewardship and environmental protection. Complementing these initiatives, grassroots campaigns such as "Healthy Farming-No AMR" promote responsible antibiotic use among livestock farmers by encouraging biosecurity, hygiene, and vaccination as alternatives to routine antimicrobial use. Similarly, the "Holelaholela Itakucost" campaign uses culturally resonant messaging to warn against careless antibiotic consumption and disposal, linking everyday behavior to the growing AMR crisis. Together, these efforts underscore the power of coordinated awareness, policy advocacy, and behavioral change in reducing AMR pollution and safeguarding public health in Tanzania.

8. World AMR Awareness Week (WAAW) in Tanzania

Tanzania has emerged as a continental leader in promoting antimicrobial resistance (AMR) awareness through the annual commemoration of World AMR Awareness Week (WAAW), coordinated by the Ministry of Health in collaboration with key One Health partners. The country's role as host of the 7th Africa Continental WAAW Campaign, planned for November 2025 in Dar es Salaam, underscores its growing regional influence in AMR advocacy and policy dialogue. WAAW events in Tanzania bring together diverse stakeholders—including human and animal health professionals, environmental experts, researchers, policymakers, and the public to promote responsible antimicrobial use, infection prevention, and biosecurity best practices. This multi-sector engagement not only reinforces Tanzania's One Health approach but also translates global AMR commitments into community-level action and behavioural change. Through such sustained annual campaigns, Tanzania continues to demonstrate how coordinated public awareness can catalyse national and regional progress in AMR mitigation.

9. The "Healthy Farming-No AMR" Campaign

The "Healthy Farming-No AMR" campaign, organised by the One Health Society, Tanzania and supported by the Trinity Challenge, is one example of a community-driven effort to combat AMR focusing on the livestock, environment-human interface. This campaign was conducted between June and November 2025 across the Dar es Salaam and Pwani regions in the eastern costal part of Tanzania, using integrated One Health approach to transform livestock production practices through behaviour change, education, and innovation. The campaign engaged livestock farmers, veterinarians, feed suppliers, and community leaders, to promote prudent antimicrobial use, improved biosecurity, and environmentally sustainable farming. The campaign focus on co-designing solutions with farmers showing workable alternatives like improved record-keeping, vaccination, and hygiene lessen reliance on antibiotics. The campaign further links farm-level stewardship with environmental protection by addressing antimicrobial pollutants in effluents and animal waste, reinforcing that responsible farming is not only vital for animal health and productivity but also for safeguarding ecosystems and public health. These locally tailored, evidence-informed interventions can operationalize One Health principles for real-world AMR mitigation in Tanzania.

10. The Tanzania Parliamentarian Alliance for AMR

The Tanzania Parliamentarian Alliance for AMR, an initiative led by the One Health Society-Tanzania (OHS), marks a transformative step toward embedding antimicrobial resistance (AMR) governance into the country's political and legislative framework. By strategically engaging Members of Parliament, the initiative fosters political will, policy coherence, and resource mobilization to strengthen Tanzania's multisectoral AMR response. Drawing on OHS's advocacy evidence and the National Action Plan on AMR (2017-2022), the alliance empowers legislators to champion laws that regulate antimicrobial use across human health, veterinary, and environmental sectors aligning with the Global Action Plan on AMR (WHO, FAO & OIE). Its innovation lies in bridging the gap between science and policy, ensuring parliamentary committees integrate AMR oversight within public health, agriculture, and environmental governance agendas. This political stewardship model demonstrates how Tanzania is institutionalizing the One Health approach through legislative engagement, fostering accountability and sustainability in AMR mitigation.

11. The "Holelaholela Itaku-Cost" Campaign

In Tanzania, the "Holela-holela Itakukosti" campaign literally translated as "Recklessness Will Cost You", which is most creative and impactful public health initiatives addressing AMR. This is collaborative campaign between the Government of Tanzania through Office of the Prime Minister, One Health Section, Ministries of Health, Livestock, Fisheries, and Environment, United States Agency for International Development (USAID), and the Johns Hopkins Center for Communication Programs (CCP) (Desmon, 2024), launched under the One Health framework. The campaign blends science-based messaging with culturally resonant communication strategies to shift public behaviour around antibiotic usage. The campaign reframes AMR as not only a medical but also social and economic issue that affects families, farmers, and entire ecosystems, through the use of mass media, social influencers, community dialogues, and an engaging mascot representing "responsible medicine". "Holela-holela Itakukosti" is an example of innovation in public engagement that integrates messages on human, animal, and environmental health to transform AMR into relatable everyday actions such as completing prescriptions, avoiding self-medication, and maintaining hygiene in livestock management, aiding in the combat to ensure ecological safety.

This participatory approach empowers communities to become stewards of antimicrobial stewardship, making it a model for AMR mitigation efforts across Africa. Preliminary descriptive data suggest that the 'Holela-Holela Itakukosti' campaign engaged a broad audience: for example, media reports cite approximately 24.7 million listeners reached and over 23 million social-media account users exposed to campaign content. Although these figures point to high reach and favourable expert endorsement, many countries within the East, Central and Southern African region have expressed interest in emulating it, rigorous publicly-available evaluation data on sustained behaviour change, antimicrobial consumption or reduction in misuse remain limited.

12. Challenges and Future Directions

Tanzania faces significant challenges in combating AMR, primarily due to inadequate regulation, overuse of antibiotics, and limited public awareness (Camara et al., 2023; Mbwasi et al., 2020; Ndaki et al., 2021). A key issue is the widespread use of antibiotics in agriculture (Mdegela et al., 2021), and human health (Mbwasi et al., 2020; Mdegela et al., 2021; Ndaki et al., 2021), without proper oversight, contributing to the rapid emergence of resistant strains. Studies have shown that antibiotic residues are prevalent in the environment (Ripanda & Miraji, 2022; Ripanda, 2024), particularly in wastewater (Ripanda et al., 2023c; Ripanda et al., 2021), and agricultural runoff (Hossein et al., 2023; Miraji et al., 2021; Ripanda et al., 2021), exacerbating the spread of resistance genes. The healthcare infrastructure struggles with inconsistent antibiotic stewardship, and diagnostic capacities are often insufficient, leading to the misuse of antibiotics. For example, antibiotics are frequently prescribed without confirming bacterial infections, driven by limited access to diagnostic tools (Doern & Brecher, 2011). Additionally, counterfeit and substandard medications (Al-Worafi, 2020; Kelesidis et al., 2007), further contribute to resistance.

Future efforts must focus on strengthening regulatory frameworks, improving antibiotic stewardship, and enhancing public education on the prudent use of antibiotics. The implementation of robust surveillance systems is critical to monitor AMR patterns and guide targeted interventions. Moreover, integrating AMR strategies into the broader public health agenda, including water, sanitation, and hygiene (WASH) initiatives, is vital for controlling the spread of resistance. Collaboration between government, healthcare providers, and international organizations will be essential to build capacity and ensure sustainable solutions to the growing AMR challenge in Tanzania.

While Tanzania has made commendable strides in addressing AMR, significant research gaps remain that prospective researcher must address to strengthen the country's AMR response. The limited scope and geographic coverage of AMR surveillance systems, necessitating studies that leverage innovative, cost-effective technologies such as genomic sequencing or AI-driven analytics to monitor resistance patterns in underrepresented regions. Additionally, the long-term ecological and human health impacts of antimicrobial pollutants in Tanzanian waterways and agricultural soils are poorly understood, highlighting the need for investigations into how these pollutants contribute to resistance gene proliferation. Research into the effectiveness of specific water, sanitation, and hygiene (WASH) interventions in mitigating AMR transmission dynamics is also essential. Furthermore, there is a pressing need to explore the cultural, economic, and behavioral drivers of antibiotic misuse, particularly in rural and underserved areas, to inform targeted public health campaigns. Alternative antimicrobial strategies, such as plant-based treatments or phage therapy, require further study to reduce reliance on conventional antimicrobials including antibiotics. Finally, while regulatory frameworks exist, their implementation and efficacy remain underexplored, creating opportunities for research into enforcement mechanisms and their outcomes. Addressing these gaps will provide critical insights to guide sustainable, evidence-based strategies in the fight against AMR in Tanzania.

13. Conclusion

Antimicrobial pollution in Tanzania poses an escalating threat at the nexus of public health, agriculture, and environmental sustainability. High levels of antimicrobial residues and resistant bacteria, particularly *E. coli* and *Klebsiella* spp. have been detected indicating contamination from human and animal waste streams. Unregulated antibiotic use continues to drive the emergence of multidrug-resistant pathogens, with residues often exceeding recommended limits in animal products and sediments. While One Health commitment and national action plan mark substantial progress in Tanzania, addressing AMR pollution demands enhanced environmental monitoring, strict enforcement of antimicrobial stewardship, and community-level awareness. Leveraging digital technologies, local research innovations, and community education can transform current efforts into data-driven, sustainable solutions. The stakes are high, but with strategic investments and a concerted national effort, Tanzania can mitigate the impact of AMR, safeguarding the health and well-being of its population for generations to come.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

Abelkop, A. D., Graham, J. D., & Royer, T. V. (2018). *Persistent, Bioaccumulative, and Toxic (PBT) Chemicals: Technical Aspects, Policies, and Practices.* CRC Press.

Achankeng, E. (2003). Globalization, Urbanization and Municipal Solid Waste Management in Africa. In *Proceedings of the African Studies Association of Australasia and the Pacific 26th Annual Conference* (pp. 1-22). African Studies Association of Australasia and the Pacific.

Adeola, A. O., & Forbes, P. B. C. (2022). Antiretroviral Drugs in African Surface Waters: Prevalence, Analysis, and Potential Remediation. *Environmental Toxicology and Chemistry, 41,* 247-262. https://doi.org/10.1002/etc.5127

Adeyemo, O., Shogbanmu, T., Alarape, S., & Denslow, N. (2021). Biomonitoring of Aquatic Pollution: Status and Trends from Genomics to Populations. *Proceedings of the Nigerian Academy of Science, 13,* No 2s. https://doi.org/10.57046/yujf3797

Akenga, P., Gachanja, A., Fitzsimons, M. F., Tappin, A., & Comber, S. (2021). Uptake, Accumulation and Impact of Antiretroviral and Antiviral Pharmaceutical Compounds in Lettuce. *Science of the Total Environment, 766,* Article ID: 144499. https://doi.org/10.1016/j.scitotenv.2020.144499

Alderton, I., Palmer, B. R., Heinemann, J. A., Pattis, I., Weaver, L., Gutiérrez-Ginés, M. J. et al. (2021). The Role of Emerging Organic Contaminants in the Development of Antimicrobial Resistance. *Emerging Contaminants, 7,* 160-171. https://doi.org/10.1016/j.emcon.2021.07.001

Al-Worafi, Y. M. (2020). Counterfeit and Substandard Medications. In Y. Al-worafi (Ed.), *Drug Safety in Developing Countries* (pp. 119-126). Elsevier. https://doi.org/10.1016/b978-0-12-819837-7.00010-8

Amangelsin, Y., Semenova, Y., Dadar, M., Aljofan, M., & Bjørklund, G. (2023). The Impact of Tetracycline Pollution on the Aquatic Environment and Removal Strategies. *Antibiotics, 12,* Article 440. https://doi.org/10.3390/antibiotics12030440

Ashley, E., Recht, J., Chua, A., Dance, D., Dhorda, M., Thomas, N., Ranganathan, N., Turner, P., Guerin, P., & White, N. (2016). *Antimicrobial Resistance in Low and Middle Income Countries: An Analysis of Surveillance Networks.* IDDO.

Atnafie, S. A., Muluneh, N. Y., Getahun, K. A., Tsegaw Woredekal, A., & Kahaliw, W. (2021). Pesticide Residue Analysis of Khat Leaves and Health Risks among Khat Chewers in the Amhara Region, Northwestern Ethiopia. *Journal of Environmental and Public Health, 2021,* Article ID: 4680573. https://doi.org/10.1155/2021/4680573

Azabo, R. R., Mshana, S. E., Matee, M. I., & Kimera, S. I. (2022). Antimicrobial Resistance Pattern of Escherichia Coli Isolates from Small Scale Dairy Cattle in Dar Es Salaam, Tanzania. *Animals, 12,* Article 1853. https://doi.org/10.3390/ani12141853

Bamfo, N. O., Hosey-Cojocari, C., Benet, L. Z., & Remsberg, C. M. (2021). Examination of Urinary Excretion of Unchanged Drug in Humans and Preclinical Animal Models: Increasing the Predictability of Poor Metabolism in Humans. *Pharmaceutical Research, 38,* 1139-1156. https://doi.org/10.1007/s11095-021-03076-y

Banaga, D. K. (2020). *Assessment of Knowledge, Attitude and Practice of Household Disposal of Unused and Expired Medications in Dodoma City.* Doctoral Dissertation, The Open University of Tanzania.

Baniga, Z., Hounmanou, Y. M. G., Kudirkiene, E., Kusiluka, L. J. M., Mdegela, R. H., & Dalsgaard, A. (2020). Genome-based Analysis of Extended-Spectrum β-Lactamase-Producing *Escherichia coli* in the Aquatic Environment and Nile Perch (Lates Niloticus) of Lake Victoria, Tanzania. *Frontiers in Microbiology, 11,* Article 108. https://doi.org/10.3389/fmicb.2020.00108

Baraka, V., Andersson, T., Makenga, G., Francis, F., Minja, D., Overballe-Petersen, S. et al. (2023). Unveiling Rare Pathogens and Antibiotic Resistance in Tanzanian Cholera Outbreak Waters. *Microorganisms, 11,* Article 2490. https://doi.org/10.3390/microorganisms11102490

Bashir, I., Lone, F. A., Bhat, R. A., Mir, S. A., Dar, Z. A., & Dar, S. A. (2020). Concerns and Threats of Contamination on Aquatic Ecosystems. In K. Hakeem, R. Bhat, & H. Qadri (Eds.), *Bioremediation and Biotechnology* (pp. 1-26). Springer. https://doi.org/10.1007/978-3-030-35691-0_1

Batir-Marin, D., Boev, M., Cioanca, O., Lungu, I., Marin, G., Burlec, A. F. et al. (2025). Exploring Oxidative Stress Mechanisms of Nanoparticles Using Zebrafish (*Danio rerio*): Toxicological and Pharmaceutical Insights. *Antioxidants, 14,* Article 489. https://doi.org/10.3390/antiox14040489

Bidu, J. M., Van der Bruggen, B., Rwiza, M. J., & Njau, K. N. (2021). Current Status of Textile Wastewater Management Practices and Effluent Characteristics in Tanzania. *Water Science and Technology, 83,* 2363-2376. https://doi.org/10.2166/wst.2021.133

Blomberg, B., Manji, K. P., Urassa, W. K., Tamim, B. S., Mwakagile, D. S., Jureen, R. et al. (2007). Antimicrobial Resistance Predicts Death in Tanzanian Children with Bloodstream Infections: A Prospective Cohort Study. *BMC Infectious Diseases, 7,* Article No. 43. https://doi.org/10.1186/1471-2334-7-43

Browne, A. J., Chipeta, M. G., Haines-Woodhouse, G., Kumaran, E. P. A., Hamadani, B. H. K., Zaraa, S. et al. (2021). Global Antibiotic Consumption and Usage in Humans, 2000-18: A Spatial Modelling Study. *The Lancet Planetary Health, 5,* e893-e904. https://doi.org/10.1016/s2542-5196(21)00280-1

Camara, N., Moremi, N., Mghamba, J., Eliakimu, E., Shumba, E., Ondoa, P. et al. (2023). Surveillance of Antimicrobial Resistance in Human Health in Tanzania: 2016-2021. *African Journal of Laboratory Medicine, 12,* Article 2053. https://doi.org/10.4102/ajlm.v12i1.2053

Chadha, J., & Khullar, L. (2021). Subinhibitory Concentrations of Nalidixic Acid Alter Bacterial Physiology and Induce Anthropogenic Resistance in a Commensal Strain of *Escherichia coli in Vitro. Letters in Applied Microbiology, 73,* 623-633. https://doi.org/10.1111/lam.13550

Chakraborty, A., Adhikary, S., Bhattacharya, S., Dutta, S., Chatterjee, S., Banerjee, D. et al. (2023). Pharmaceuticals and Personal Care Products as Emerging Environmental Contaminants: Prevalence, Toxicity, and Remedial Approaches. *ACS Chemical Health & Safety, 30,* 362-388. https://doi.org/10.1021/acs.chas.3c00071

Chengula, A., Lucas, B. K., & Mzula, A. (2015). Assessing the Awareness, Knowledge, Attitude and Practice of the Community towards Solid Waste Disposal and Identifying the Threats and Extent of Bacteria in the Solid Waste Disposal Sites in Morogoro Municipality in Tanzania. *Journal of Biology, Agriculture and Healthcare, 5,* 54-65.

Chota, A., Kitojo, O., & Ngongolo, K. (2021). Knowledge on Diseases, Practices, and Threats of Drugs Residues in Chicken Food Chains in Selected Districts of Dodoma Region, Tanzania. *Journal of Applied Poultry Research, 30,* Article ID: 100186. https://doi.org/10.1016/j.japr.2021.100186

Chuwa, L., Metta, E., & Frumence, G. (2024). Inspection Practices for Regulating Prescription Handling and Antibiotics Control in Ilala Community Pharmacies of Dar Es Salaam, Tanzania: Qualitative Assessment. *Tanzania Journal of Health Research, 25,* 1163-1175. https://doi.org/10.4314/thrb.v25i3.14

Daghrir, R., & Drogui, P. (2013). Tetracycline Antibiotics in the Environment: A Review. *Environmental Chemistry Letters, 11,* 209-227. https://doi.org/10.1007/s10311-013-0404-8

Desmon, S. (2024). *New Campaign Aims to Reduce Antimicrobial Resistance, Zoonotic Diseases.* Johns Hopkins Center for Communication Programs. https://ccp.jhu.edu/2024/07/08/campaign-tanzania-amr-zoonotic-diseases/

Diogo, B. S., Rodrigues, S., Golovko, O., & Antunes, S. C. (2024). From Bacteria to Fish: Ecotoxicological Insights into Sulfamethoxazole and Trimethoprim. *Environmental Science and Pollution Research, 31,* 52233-52252. https://doi.org/10.1007/s11356-024-34659-y

Dionísio, R., Daniel, D., Alkimin, G. D. d., & Nunes, B. (2020). Multi-Parametric Analysis of Ciprofloxacin Toxicity at Ecologically Relevant Levels: Short- and Long-Term Effects on Daphnia Magna. *Environmental Toxicology and Pharmacology, 74,* Article ID: 103295. https://doi.org/10.1016/j.etap.2019.103295

Doern, G. V., & Brecher, S. M. (2011). The Clinical Predictive Value (or Lack Thereof) of the Results of *in Vitro* Antimicrobial Susceptibility Tests. *Journal of Clinical Microbiology, 49,* S11-S14. https://doi.org/10.1128/jcm.00580-11

Durrance-Bagale, A., Jung, A., Frumence, G., Mboera, L., Mshana, S. E., Sindato, C. et al. (2021). Framing the Drivers of Antimicrobial Resistance in Tanzania. *Antibiotics, 10,* Article 991. https://doi.org/10.3390/antibiotics10080991

Efthimiadou, E. K., Karaliota, A., & Psomas, G. (2010). Metal Complexes of the Third-Generation Quinolone Antimicrobial Drug Sparfloxacin: Structure and Biological Evaluation. *Journal of Inorganic Biochemistry, 104,* 455-466. https://doi.org/10.1016/j.jinorgbio.2009.12.019

Egan, W. J., Merz, K. M., & Baldwin, J. J. (2000). Prediction of Drug Absorption Using Multivariate Statistics. *Journal of Medicinal Chemistry, 43,* 3867-3877. https://doi.org/10.1021/jm000292e

Evaluation, I. F. H. M. A. (2023). The Burden of Antimicrobial Resistance (AMR) in United Republic of Tanzania. In I. F. H. M. A. Evaluation (Ed.), *Healthdata.org* (pp. 1-4). University of Washington.

Faleye, A. C., Adegoke, A. A., Ramluckan, K., Bux, F., & Stenström, T. A. (2018). Antibiotic Residue in the Aquatic Environment: Status in Africa. *Open Chemistry, 16,* 890-903. https://doi.org/10.1515/chem-2018-0099

Felis, E., Kalka, J., Sochacki, A., Kowalska, K., Bajkacz, S., Harnisz, M. et al. (2020). Antimicrobial Pharmaceuticals in the Aquatic Environment—Occurrence and Environmental Implications. *European Journal of Pharmacology, 866,* Article ID: 172813. https://doi.org/10.1016/j.ejphar.2019.172813

Fernandez, R., Colás-Ruiz, N. R., Bolívar-Anillo, H. J., Anfuso, G., & Hampel, M. (2021). Occurrence and Effects of Antimicrobials Drugs in Aquatic Ecosystems. *Sustainability, 13,* Article 13428. https://doi.org/10.3390/su132313428

Frumence, G., Mboera, L. E. G., Sindato, C., Katale, B. Z., Kimera, S., Metta, E. et al. (2021). The Governance and Implementation of the National Action Plan on Antimicrobial Resistance in Tanzania: A Qualitative Study. *Antibiotics, 10,* Article 273. https://doi.org/10.3390/antibiotics10030273

Fuller, W., Kapona, O., Aboderin, A. O., Adeyemo, A. T., Olatunbosun, O. I., Gahimbare, L. et al. (2023). Education and Awareness on Antimicrobial Resistance in the WHO African Region: A Systematic Review. *Antibiotics, 12,* Article 1613. https://doi.org/10.3390/antibiotics12111613

Granja, R. H. M. M., Niño, A. M. M., Zucchetti, R. A. M., Niño, R. E. M., Patel, R., & Salerno, A. G. (2009). Determination of Streptomycin Residues in Honey by Liquid Chromatography-Tandem Mass Spectrometry. *Analytica Chimica Acta, 637,* 64-67. https://doi.org/10.1016/j.aca.2009.01.006

Groot, M. J., & van't Hooft, K. E. (2016). The Hidden Effects of Dairy Farming on Public and Environmental Health in the Netherlands, India, Ethiopia, and Uganda, Considering the Use of Antibiotics and Other Agro-Chemicals. *Frontiers in Public Health, 4,* Article 12. https://doi.org/10.3389/fpubh.2016.00012

Gwenzi, W., Musiyiwa, K., & Mangori, L. (2020). Sources, Behaviour and Health Risks of Antimicrobial Resistance Genes in Wastewaters: A Hotspot Reservoir. *Journal of Environmental Chemical Engineering, 8,* Article ID: 102220. https://doi.org/10.1016/j.jece.2018.02.028

Gwenzi, W., Simbanegavi, T. T., & Rzymski, P. (2023). Household Disposal of Pharmaceuticals in Low-Income Settings: Practices, Health Hazards, and Research Needs. *Water, 15,* Article 476. https://doi.org/10.3390/w15030476

Hamim, H., Sangeda, R. Z., Bundala, M., Mkumbwa, S., Bitegeko, A., Sillo, H. B. et al. (2021). Utilization Trends of Antiviral and Antifungal Agents for Human Systemic Use in Tanzania from 2010 to 2017 Using the World Health Organization Collaborating Centre for Drug Statistics Methodology. *Frontiers in Tropical Diseases, 2,* Article 723991. https://doi.org/10.3389/fitd.2021.723991

Hong, P., Al-Jassim, N., Ansari, M., & Mackie, R. (2013). Environmental and Public Health Implications of Water Reuse: Antibiotics, Antibiotic Resistant Bacteria, and Antibiotic Resistance Genes. *Antibiotics, 2,* 367-399. https://doi.org/10.3390/antibiotics2030367

Hossein, M., & Ripanda, A. S. (2025). Pollution by Antimicrobials and Antibiotic Resistance Genes in East Africa: Occurrence, Sources, and Potential Environmental Implications. *Toxicology Reports, 14,* Article ID: 101969. https://doi.org/10.1016/j.toxrep.2025.101969

Hossein, M., Chande, O., Faustin, N., & Erwin, M. (2018). Spatial Occurrence and Fate Assessment of Potential Emerging Contaminants in the Flowing Surface Waters. *Chemical Science International Journal, 24,* 1-11. https://doi.org/10.9734/csji/2018/44211

Hossein, M., Makaye, A., Dadi, S., Ripanda, A., Rwiza, M. J., Nyanza, E. C. et al. (2025). Opportunities and Adoptive Challenges of Pharmaceuticals and Personal Care Products in Wastewater Treatment Schemes in Developing Countries. In A. K. Thakur, R. Kumar, N. A. Khan, A. H. Khan, R. Shankar, & N. Pervez (Eds.), *Advanced Oxidation Process-Based Integrated and Hybrid Technologies for Degradation of Pharmaceuticals and Personal Care Products* (pp. 377-398). Elsevier. https://doi.org/10.1016/b978-0-443-21887-3.00024-9

Hossein, M., Ripanda, A., Eunice, M., Chande, O., Ngassapa, F., & Mahmoud, A. E. D. (2023). Monitoring of Contaminants in Aquatic Ecosystems Using Big Data. In A. El Din Mahmoud, M. Fawzy, & N. A. Khan (Eds.), *Artificial Intelligence and Modeling for Water Sustainability* (pp. 129-157). CRC Press. https://doi.org/10.1201/9781003260455-7

Hounmanou, Y. M. G., Leekitcharoenphon, P., Hendriksen, R. S., Dougnon, T. V., Mdegela, R. H., Olsen, J. E. et al. (2019). Corrigendum: Surveillance and Genomics of Toxigenic Vibrio Cholerae O1 from Fish, Phytoplankton and Water in Lake Victoria, Tanzania. *Frontiers in Microbiology, 10,* Article 2974. https://doi.org/10.3389/fmicb.2019.02974

Huang, P., Chiu, C., Hsiao, M., Yow, J., Tzang, B., & Hsu, T. (2021). Potential of Antiviral Drug Oseltamivir for the Treatment of Liver Cancer. *International Journal of Oncology, 59,* No. 6. https://doi.org/10.3892/ijo.2021.5289

Ighalo, J. O., Igwegbe, C. A., Adeniyi, A. G., Adeyanju, C. A., & Ogunniyi, S. (2020). Mitigation of Metronidazole (Flagyl) Pollution in Aqueous Media by Adsorption: A Review. *Environmental Technology Reviews, 9,* 137-148. https://doi.org/10.1080/21622515.2020.1849409

Joachim, A., Manyahi, J., Issa, H., Lwoga, J., Msafiri, F., & Majigo, M. (2023). Predominance of Multidrug-Resistant Gram-Negative Bacteria on Contaminated Surfaces at a Tertiary Hospital in Tanzania: A Call to Strengthening Environmental Infection Prevention and Control Measures. *Current Microbiology, 80,* Article No. 148. https://doi.org/10.1007/s00284-023-03254-8

Kamba, P. F., Kaggwa, B., Munanura, E. I., Okurut, T., & Kitutu, F. E. (2017). Why Regulatory Indifference Towards Pharmaceutical Pollution of the Environment Could Be a Missed Opportunity in Public Health Protection. A Holistic View. *Pan African Medical Journal, 27,* Article 77. https://doi.org/10.11604/pamj.2017.27.77.10973

Karungamye, P., Rugaika, A., Mtei, K., & Machunda, R. (2022). The Pharmaceutical Disposal Practices and Environmental Contamination: A Review in East African Countries. *HydroResearch, 5,* 99-107. https://doi.org/10.1016/j.hydres.2022.11.001

Karungamye, P., Rugaika, A., Mtei, K., & Machunda, R. (2023). Physicochemical and Microbiological Characterization and of Hospital Wastewater in Tanzania. *Total Environment Research Themes, 8,* Article ID: 100075. https://doi.org/10.1016/j.totert.2023.100075

Kelesidis, T., Kelesidis, I., Rafailidis, P. I., & Falagas, M. E. (2007). Counterfeit or Substandard Antimicrobial Drugs: A Review of the Scientific Evidence. *Journal of Antimicrobial Chemotherapy, 60,* 214-236. https://doi.org/10.1093/jac/dkm109

Kihampa, C. (2013). Environmental Exposure and Public Health Concerns of Municipal Solid Waste Disposal in Dar es Salaam, Tanzania. Sustain Dev Africa. *Electronic Journal, 15,* 198-208.

Kihampa, C. (2014). *β*-Lactams and Fluoroquinolone Antibiotics in Influents and Effluents of Wastewater Treatment Plants, Dar es Salaam, Tanzania. *Research Journal of Chemical Sciences, 2231,* 606.

Kilusungu, Z. H., Kassam, D., Kimera, Z. I., Mgaya, F. X., Nandolo, W., Kunambi, P. P. et al. (2024). Tetracycline and Sulphonamide Residues in Farmed Fish in Dar Es Salaam, Tanzania and Human Health Risk Implications. *Food Additives & Contaminants: Part B, 17,* 161-170. https://doi.org/10.1080/19393210.2024.2331106

Kimera, Z. I., Mgaya, F. X., Mshana, S. E., Karimuribo, E. D., & Matee, M. I. N. (2021). Occurrence of Extended Spectrum Beta Lactamase (ESBL) Producers, Quinolone and Carbapenem Resistant *Enterobacteriaceae* Isolated from Environmental Samples along Msimbazi River Basin Ecosystem in Tanzania. *International Journal of Environmental Research and Public Health, 18,* Article 8264. https://doi.org/10.3390/ijerph18168264

Kimera, Z. I., Mgaya, F. X., Mshana, S. E., Karimuribo, E. D., & Matee, M. I. N. (2024). Occurrence of Extended-Spectrum *β*-Lactamase and Quinolone Resistance Genes among Escherichia Coli and Klebsiella Pneumoniae Isolated from Poultry, Domestic Pigs and Environ in Msimbazi River Basin in Tanzania. *Journal of Applied Sciences and Environmental Management, 28,* 37-47. https://doi.org/10.4314/jasem.v28i1.5

Kimera, Z. I., Shimo, P., Balandya, E. C., Matee, M. I. N., & Adams, L. V. (2025). Survey on Human-Designated Antiretroviral (ARV) Drug Residues in Broiler Chicken, Domestic Pigs, and Animal Feeds In, Tanzania. *Bulletin of the National Research Centre, 49,* Article No. 21. https://doi.org/10.1186/s42269-025-01314-6

Kitamura, R. S. A., Marques, R. Z., Kubis, G. C., Kochi, L. Y., Barbato, M. L., Maranho, L. T. et al. (2023). The Phytoremediation Capacity of Lemna Minor Prevents Deleterious Effects of Anti-HIV Drugs to Nontarget Organisms. *Environmental Pollution, 329,* Article ID: 121672. https://doi.org/10.1016/j.envpol.2023.121672

Kumburu, H. H., Sonda, T., Mmbaga, B. T., Alifrangis, M., Lund, O., Kibiki, G. et al. (2017). Patterns of Infections, Aetiological Agents and Antimicrobial Resistance at a Tertiary Care Hospital in Northern Tanzania. *Tropical Medicine & International Health, 22,* 454-464. https://doi.org/10.1111/tmi.12836

Kümmerer, K. (2009). Antibiotics in the Aquatic Environment—A Review—Part I. *Chem-*

osphere, 75, 417-434. https://doi.org/10.1016/j.chemosphere.2008.11.086

Kümmerer, K. (2011). Antibiotics in the Aquatic Environment. In *Antimicrobial Resistance in the Environment* (pp. 325-335). https://doi.org/10.1002/9781118156247.ch18

Kundu, M. N., Komakech, H. C., & Sang, J. (2024). Spatial Occurrence and Variation of the Active Pharmaceutical Compounds in Rivers and Groundwater Systems in Arusha City, Tanzania. *Heliyon, 10,* e32681. https://doi.org/10.1016/j.heliyon.2024.e32681

Lee, S., Kim, C., Liu, X., Lee, S., Kho, Y., Kim, W. et al. (2021). Ecological Risk Assessment of Amoxicillin, Enrofloxacin, and Neomycin: Are Their Current Levels in the Freshwater Environment Safe? *Toxics, 9,* Article 196. https://doi.org/10.3390/toxics9080196

Li, J., Wang, Y., Fan, Z., Tang, P., Wu, M., Xiao, H. et al. (2023). Toxicity of Tetracycline and Metronidazole in *Chlorella pyrenoidosa*. *International Journal of Environmental Research and Public Health, 20,* Article 3623. https://doi.org/10.3390/ijerph20043623

Lu, H., Shrivastava, M., Whiteway, M., & Jiang, Y. (2021). *Candida albicans* Targets That Potentially Synergize with Fluconazole. *Critical Reviews in Microbiology, 47,* 323-337. https://doi.org/10.1080/1040841x.2021.1884641

Mabilika, R. J., Shirima, G., & Mpolya, E. (2022). Prevalence and Predictors of Antibiotic Prescriptions at Primary Healthcare Facilities in the Dodoma Region, Central Tanzania: A Retrospective, Cross-Sectional Study. *Antibiotics, 11,* Article 1035. https://doi.org/10.3390/antibiotics11081035

Makokola, S., Ripanda, A., & Miraji, H. (2019). Quantitative Investigation of Potential Contaminants of Emerging Concern in Dodoma City: A Focus at Swaswa Wastewater Stabilization Ponds. *Egyptian Journal of Chemistry, 62,* 427-436. https://doi.org/10.21608/ejchem.2019.11764.1772

Manyahi, J., Kibwana, U., Mgimba, E., & Majigo, M. (2020). Multi-Drug Resistant Bacteria Predict Mortality in Bloodstream Infection in a Tertiary Setting in Tanzania. *PLOS ONE, 15,* e0220424. https://doi.org/10.1371/journal.pone.0220424

Marijani, E. (2022). Prevalence and Antimicrobial Resistance of Bacteria Isolated from Marine and Freshwater Fish in Tanzania. *International Journal of Microbiology, 2022,* Article ID: 4652326. https://doi.org/10.1155/2022/4652326

Martins, N., Pereira, R., Abrantes, N., Pereira, J., Gonçalves, F., & Marques, C. R. (2012). Ecotoxicological Effects of Ciprofloxacin on Freshwater Species: Data Integration and Derivation of Toxicity Thresholds for Risk Assessment. *Ecotoxicology, 21,* 1167-1176. https://doi.org/10.1007/s10646-012-0871-x

Matee, M., Mshana, S. E., Mtebe, M., Komba, E. V., Moremi, N., Lutamwa, J. et al. (2023). Mapping and Gap Analysis on Antimicrobial Resistance Surveillance Systems in Kenya, Tanzania, Uganda and Zambia. *Bulletin of the National Research Centre, 47,* Article No. 12. https://doi.org/10.1186/s42269-023-00986-2

Mathobela, C. K. K. (2025). The Use of Antimicrobial Agents and Smart Regulations to Prevent Antimicrobial Resistance in Poultry Farms: Towards One Health. Ph.D. Thesis, University of Limpopo.

Mbwasi, R., Mapunjo, S., Wittenauer, R., Valimba, R., Msovela, K., Werth, B. J. et al. (2020). National Consumption of Antimicrobials in Tanzania: 2017-2019. *Frontiers in Pharmacology, 11,* Article 585553. https://doi.org/10.3389/fphar.2020.585553

Mdegela, R. H., Mwakapeje, E. R., Rubegwa, B., Gebeyehu, D. T., Niyigena, S., Msambichaka, V. et al. (2021). Antimicrobial Use, Residues, Resistance and Governance in the Food and Agriculture Sectors, Tanzania. *Antibiotics, 10,* Article 454. https://doi.org/10.3390/antibiotics10040454

Meo, S., Klonoff, D., & Akram, J. (2020). Efficacy of Chloroquine and Hydroxychloro-

Quine in the Treatment of COVID-19. *European Review for Medical and Pharmacological Sciences, 24,* 4539-4547.

Michael, I., Vasquez, M. I., Hapeshi, E., Haddad, T., Baginska, E., Kümmerer, K., & Fatta-Kassinos, D. (2014). Metabolites and Transformation Products of Pharmaceuticals in the Aquatic Environment as Contaminants of Emerging Concern. In D. A. Lambropoulou, & L. M. L. Nollet (Eds.), *Advanced Mass Spectrometry-Based Techniques for the Identification Structure Elucidation of Transformation Products of Emerging Contaminants* (pp. 413-459). Wiley.

Mikomangwa, W. P., Bwire, G. M., Kilonzi, M., Mlyuka, H., Mutagonda, R., Kibanga, W. et al. (2020). the Existence of High Bacterial Resistance to Some Reserved Antibiotics in Tertiary Hospitals in Tanzania: A Call to Revisit Their Use. *Infection and Drug Resistance, 13,* 1831-1838. https://doi.org/10.2147/idr.s250158

Millanzi, W. C., Herman, P. Z., & Mtangi, S. A. (2023). Knowledge, Attitude, and Perceived Practice of Sanitary Workers on Healthcare Waste Management: A Descriptive Cross-Sectional Study in Dodoma Region, Tanzania. *SAGE Open Medicine, 11,* 1-16. https://doi.org/10.1177/20503121231174735

Minzi, O., & Manyilizu, (2013). Application of Basic Pharmacology and Dispensing Practice of Antibiotics in Accredited Drug-Dispensing Outlets in Tanzania. *Drug, Healthcare and Patient Safety, 5,* 5-11. https://doi.org/10.2147/dhps.s36409

Miraji, H., Othman, O. C., Ngassapa, F. N., & Mureithi, E. W. (2016). Research Trends in Emerging Contaminants on the Aquatic Environments of Tanzania. *Scientifica, 2016,* Article ID: 3769690. https://doi.org/10.1155/2016/3769690

Miraji, H., Ripanda, A., & Moto, E. (2021). A Review on the Occurrences of Persistent Organic Pollutants in Corals, Sediments, Fish and Waters of the Western Indian Ocean. *Egyptian Journal of Aquatic Research, 47,* 373-379. https://doi.org/10.1016/j.ejar.2021.08.003

Mkopi, J., Mushi, J., & Mzula, M. (2024). Occurrence and Antimicrobial Resistance Pattern of *Escherichia coli* and *Salmonella* Species Isolated from Domestic and Peridomestic Rodents. *German Journal of Microbiology, 4,* 15-28.

Moffo, F., Ndebé, M. M. F., Tangu, M. N., Noumedem, R. N. G., Awah-Ndukum, J., & Mouiche, M. M. M. (2024). Antimicrobial Use, Residues and Resistance in Fish Production in Africa: Systematic Review and Meta-Analysis. *BMC Veterinary Research, 20,* Article No. 307. https://doi.org/10.1186/s12917-024-04158-w

Mongi, R. J., Meshi, E. B., & Ntwenya, J. E. (2022). Consumer Awareness and Production Practices of Farmers on Antimicrobial Residues in Chicken Eggs and Chinese Cabbage in Dodoma, Central Tanzania. *PLOS ONE, 17,* e0272763. https://doi.org/10.1371/journal.pone.0272763

Moremi, N., Claus, H., & Mshana, S. E. (2016a). Antimicrobial Resistance Pattern: A Report of Microbiological Cultures at a Tertiary Hospital in Tanzania. *BMC Infectious Diseases, 16,* Article No. 756. https://doi.org/10.1186/s12879-016-2082-1

Moremi, N., Manda, E. V., Falgenhauer, L., Ghosh, H., Imirzalioglu, C., Matee, M. et al. (2016b). Predominance of CTX-M-15 among ESBL Producers from Environment and Fish Gut from the Shores of Lake Victoria in Mwanza, Tanzania. *Frontiers in Microbiology, 7,* Article 1862. https://doi.org/10.3389/fmicb.2016.01862

Mramba, R. P., & Kahindi, E. J. (2023). Pond Water Quality and Its Relation to Fish Yield and Disease Occurrence in Small-Scale Aquaculture in Arid Areas. *Heliyon, 9,* e16753. https://doi.org/10.1016/j.heliyon.2023.e16753

Mramba, R. P., Mbinda, A. G., & Massawe, J. I. (2025). Assessment of Public Awareness on Antimicrobial Resistance and Practices for Antimicrobial Use in Dodoma Region of

Tanzania. *Discover Social Science and Health, 5,* Article No. 25. https://doi.org/10.1007/s44155-025-00171-y

Mudenda, S., Chabalenge, B., Daka, V., Mfune, R. L., Salachi, K. I., Mohamed, S. et al. (2023). Global Strategies to Combat Antimicrobial Resistance: A One Health Perspective. *Pharmacology & Pharmacy, 14,* 271-328. https://doi.org/10.4236/pp.2023.148020

Munkholm, L., & Rubin, O. (2020). The Global Governance of Antimicrobial Resistance: A Cross-Country Study of Alignment between the Global Action Plan and National Action Plans. *Globalization and Health, 16,* Article No. 109. https://doi.org/10.1186/s12992-020-00639-3

Mwanga, I., Mzula, A., Mwega, E., Chota, A. C., & Wambura, P. N. (2024). Virulence Attributes and Antimicrobial Profile of *Pasteurella multocida* Isolated from Pneumonic Goats in Northern Tanzania. *Scientific African, 26,* e02490. https://doi.org/10.1016/j.sciaf.2024.e02490

Mwega, E., Chengula, A., Colquhoun, D., Mutoloki, S., Mdegela, R., Evensen, Ø., & Wasteson, Y. (2020). *Antimicrobial Susceptibility of Flavobacteriaceae Isolates from Nile tilapia (Oreochromis niloticus) in Tanzania.* Zenodo.

Mzula, A., Wambura, P. N., Mdegela, R. H., & Shirima, G. M. (2019). Phenotypic and Molecular Detection of Aeromonads Infection in Farmed Nile Tilapia in Southern Highland and Northern Tanzania. *Heliyon, 5,* e02220. https://doi.org/10.1016/j.heliyon.2019.e02220

Mzula, A., Wambura, P. N., Mdegela, R. H., & Shirima, G. M. (2021). Present Status of Aquaculture and the Challenge of Bacterial Diseases in Freshwater Farmed Fish in Tanzania; A Call for Sustainable Strategies. *Aquaculture and Fisheries, 6,* 247-253. https://doi.org/10.1016/j.aaf.2020.05.003

Ndaki, P., Mushi, M., Mwanga, J., Konje, E., Ntinginya, N., Mmbaga, B. et al. (2021). Dispensing Antibiotics without Prescription at Community Pharmacies and Accredited Drug Dispensing Outlets in Tanzania: A Cross-Sectional Study. *Antibiotics, 10,* Article 1025. https://doi.org/10.3390/antibiotics10081025

Neale, D., & Cullen, L. (2024). Evaluating the National Action Plan (NAP) on Antimicrobial Resistance, and Recommendations for the Next 5-Year NAP: A Roundtable Discussion. *Sustainable Microbiology, 1,* qvad001. https://doi.org/10.1093/sumbio/qvad001

Nugnes, R., Orlo, E., Russo, C., Lavorgna, M., & Isidori, M. (2024). Comprehensive Eco-Geno-Toxicity and Environmental Risk of Common Antiviral Drugs in Aquatic Environments Post-Pandemic. *Journal of Hazardous Materials, 480,* Article ID: 135947. https://doi.org/10.1016/j.jhazmat.2024.135947

Omotola, E. O., Genthe, B., Ndlela, L., & Olatunji, O. S. (2021). Environmental Risk Characterization of an Antiretroviral (ARV) Lamivudine in Ecosystems. *International Journal of Environmental Research and Public Health, 18,* Article 8358. https://doi.org/10.3390/ijerph18168358

Pérez-Legaspi, I. A., & Rico-Martínez, R. (2023). Antibiotics as Contaminants of Aquatic Ecosystems: Antibiotic-Resistant Genes and Antibiotic-Resistant Bacteria. In P. Singh, & M. Sillanpää (Eds.), *Degradation of Antibiotics and Antibiotic-Resistant Bacteria from Various Sources* (pp. 143-157). Elsevier. https://doi.org/10.1016/b978-0-323-99866-6.00011-8

Ripanda, A. (2024). *Emerging Pollution, Antimicrobial Resistance, and the Applicability of Biochar Adsorbents: A Comprehensive Study in African Water Systems.* Doctoral dissertation, NM-AIST. http://repository.costech.or.tz/handle/20.500.14732/95840

Ripanda, A. S., Rwiza, M. J., Nyanza, E. C., Machunda, R. L., & Vuai, S. H. (2022). Contribution of Illicit Drug Use to Pharmaceutical Load in the Environment: A Focus on Sub-Saharan Africa. *Journal of Environmental and Public Health, 2022,* Article ID: 9056476. https://doi.org/10.1155/2022/9056476

Ripanda, A. S., Rwiza, M. J., Nyanza, E. C., Njau, K. N., Vuai, S. A. H., & Machunda, R. L. (2021). A Review on Contaminants of Emerging Concern in the Environment: A Focus on Active Chemicals in Sub-Saharan Africa. *Applied Sciences, 12,* Article 56. https://doi.org/10.3390/app12010056

Ripanda, A., & Miraji, H. (2022). A Review on the Occurrence and Impacts of Nutrient Pollution in the Aquatic Ecosystem of Sub-Saharan Countries. *Journal of Biodiversity and Environmental Sciences, 20,* 154-165.

Ripanda, A., Rwiza, M. J., Nyanza, E. C., Bakari, R., Miraji, H., Njau, K. N. et al. (2023a). Data from the Batch Adsorption of Ciprofloxacin and Lamivudine from Synthetic Solution Using Jamun Seed (*Syzygium cumini*) Biochar: Response Surface Methodology (RSM) Optimization. *Data in Brief, 47,* Article ID: 108975. https://doi.org/10.1016/j.dib.2023.108975

Ripanda, A., Rwiza, M. J., Nyanza, E. C., Bakari, R., Miraji, H., Njau, K. N. et al. (2023b). Removal of Lamivudine from Synthetic Solution Using Jamun Seed (*Syzygium cumini*) Biochar Adsorbent. *Emerging Contaminants, 9,* Article ID: 100232. https://doi.org/10.1016/j.emcon.2023.100232

Ripanda, A. S., Rwiza, M. J., Nyanza, E. C., Miraji, H., Bih, N. L., Mzula, A. et al. (2023c). Antibiotic-Resistant Microbial Populations in Urban Receiving Waters and Wastewaters from Tanzania. *Environmental Chemistry and Ecotoxicology, 5,* 1-8. https://doi.org/10.1016/j.enceco.2022.10.003

Ripanda, A., Rwiza, M. J., Nyanza, E. C., Bih, L. N., Hossein, M., Bakari, R. et al. (2024). Optimizing Ciprofloxacin Removal from Water Using Jamun Seed (*Syzygium cumini*) Biochar: A Sustainable Approach for Ecological Protection. *HydroResearch, 7,* 164-180. https://doi.org/10.1016/j.hydres.2024.03.001

Ripanda, A., Rwiza, M. J., Nyanza, E. C., Hossein, M., Alfred, M. S., El Din Mahmoud, A. et al. (2025). Ecological Consequences of Antibiotics Pollution in Sub-Saharan Africa: Understanding Sources, Pathways, and Potential Implications. *Emerging Contaminants, 11,* Article ID: 100475. https://doi.org/10.1016/j.emcon.2025.100475

Rugumisa, B. T., Call, D. R., Mwanyika, G. O., Mrutu, R. I., Luanda, C. M., Lyimo, B. M. et al. (2016). Prevalence of Antibiotic-Resistant Fecal *Escherichia coli* Isolates from Penned Broiler and Scavenging Local Chickens in Arusha, Tanzania. *Journal of Food Protection, 79,* 1424-1429. https://doi.org/10.4315/0362-028x.jfp-15-584

Sabatino, R., Sbaffi, T., Corno, G., Cabello-Yeves, P. J., & Di Cesare, A. (2024). The Diversity of the Antimicrobial Resistome of Lake Tanganyika Increases with the Water Depth. *Environmental Pollution, 342,* Article ID: 123065. https://doi.org/10.1016/j.envpol.2023.123065

Sangeda, R. Z., Baha, A., Erick, A., Mkumbwa, S., Bitegeko, A., Sillo, H. B. et al. (2021). Consumption Trends of Antibiotic for Veterinary Use in Tanzania: A Longitudinal Retrospective Survey from 2010-2017. *Frontiers in Tropical Diseases, 2,* Article 694082. https://doi.org/10.3389/fitd.2021.694082

Scotti, C., & Barlow, J. W. (2022). Natural Products Containing the Nitrile Functional Group and Their Biological Activities. *Natural Product Communications, 17,* 1-24. https://doi.org/10.1177/1934578x221099973

Seguni, N. Z., Kimera, Z. I., Msafiri, F., Mgaya, F. X., Joachim, A., Mwingwa, A. et al. (2023). Multidrug-Resistant *Escherichia coli* and *Klebsiella pneumoniae* Isolated from Hospital Sewage Flowing through Community Sewage System and Discharging into the Indian

Ocean. *Bulletin of the National Research Centre, 47,* Article No. 66. https://doi.org/10.1186/s42269-023-01039-4

Seni, J., Mwakyoma, A. A., Mashuda, F., Marando, R., Ahmed, M., DeVinney, R. et al. (2019a). Deciphering Risk Factors for Blood Stream Infections, Bacteria Species and Antimicrobial Resistance Profiles among Children under Five Years of Age in North-Western Tanzania: A Multicentre Study in a Cascade of Referral Health Care System. *BMC Pediatrics, 19,* Article No. 32. https://doi.org/10.1186/s12887-019-1411-0

Seni, J., Tito, J. N., Makoye, S. J., Mbena, H., Alfred, H. S., van der Meer, F. et al. (2019b). Multicentre Evaluation of Significant Bacteriuria among Pregnant Women in the Cascade of Referral Healthcare System in North-Western Tanzania: Bacterial Pathogens, Antimicrobial Resistance Profiles and Predictors. *Journal of Global Antimicrobial Resistance, 17,* 173-179. https://doi.org/10.1016/j.jgar.2018.12.024

Shao, S., & Wu, X. (2020). Microbial Degradation of Tetracycline in the Aquatic Environment: A Review. *Critical Reviews in Biotechnology, 40,* 1010-1018. https://doi.org/10.1080/07388551.2020.1805585

Silago, V., Moremi, N., Mtebe, M., Komba, E., Masoud, S., Mgaya, F. X. et al. (2022). Multidrug-Resistant Uropathogens Causing Community Acquired Urinary Tract Infections among Patients Attending Health Facilities in Mwanza and Dar Es Salaam, Tanzania. *Antibiotics, 11,* Article 1718. https://doi.org/10.3390/antibiotics11121718

Sodhi, K. K., Kumar, M., & Singh, D. K. (2021). Insight into the Amoxicillin Resistance, Ecotoxicity, and Remediation Strategies. *Journal of Water Process Engineering, 39,* Article ID: 101858. https://doi.org/10.1016/j.jwpe.2020.101858

Sonola, V. S., Katakweba, A. S., Misinzo, G., & Matee, M. I. N. (2021a). Occurrence of Multi-Drug-Resistant *Escherichia coli* in Chickens, Humans, Rodents and Household Soil in Karatu, Northern Tanzania. *Antibiotics, 10,* Article 1137. https://doi.org/10.3390/antibiotics10091137

Sonola, V. S., Misinzo, G., & Matee, M. I. (2021b). Occurrence of Multidrug-Resistant *Staphylococcus aureus* among Humans, Rodents, Chickens, and Household Soils in Karatu, Northern Tanzania. *International Journal of Environmental Research and Public Health, 18,* Article 8496. https://doi.org/10.3390/ijerph18168496

Sorensen, J., Lapworth, D., Nkhuwa, D., Stuart, M., Bell, R., Chirwa, M., & Kabika, J. (2014). Emerging Organic Contaminants in Urban and Peri-Urban Groundwater Sources in Sub-Saharan Africa. In *Proceedings of the International Association of Hydrogeologists IAH* (pp. 15-19). NERC Open Research Archive. https://nora.nerc.ac.uk/id/eprint/508955

Subbiah, M., Caudell, M. A., Mair, C., Davis, M. A., Matthews, L., Quinlan, R. J. et al. (2020). Antimicrobial Resistant Enteric Bacteria Are Widely Distributed Amongst People, Animals and the Environment in Tanzania. *Nature Communications, 11,* Article No. 228. https://doi.org/10.1038/s41467-019-13995-5

Wang, W., Weng, Y., Luo, T., Wang, Q., Yang, G., & Jin, Y. (2023). Antimicrobial and the Resistances in the Environment: Ecological and Health Risks, Influencing Factors, and Mitigation Strategies. *Toxics, 11,* Article 185. https://doi.org/10.3390/toxics11020185

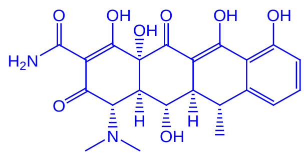
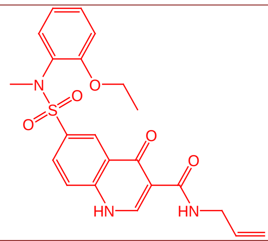
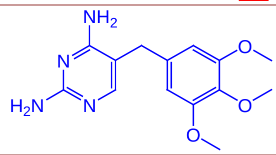
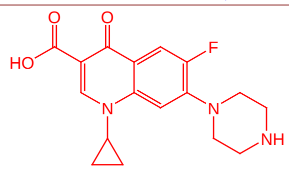
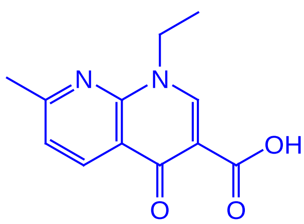
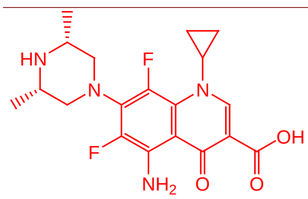
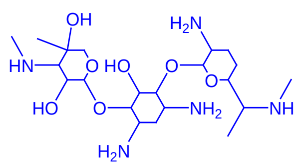
Wu, M., Que, C., Xu, G., Sun, Y., Ma, J., Xu, H. et al. (2016). Occurrence, Fate and Interrelation of Selected Antibiotics in Sewage Treatment Plants and Their Receiving Surface Water. *Ecotoxicology and Environmental Safety, 132,* 132-139. https://doi.org/10.1016/j.ecoenv.2016.06.006

Zhang, H., Quan, H., Yin, S., Sun, L., & Lu, H. (2022). Unraveling the Toxicity Associated with Ciprofloxacin Biodegradation in Biological Wastewater Treatment. *Environmental Science & Technology, 56,* 15941-15952. https://doi.org/10.1021/acs.est.2c04387

Zohoori, M., & Ghani, A. (2017). Municipal Solid Waste Management Challenges and Problems for Cities in Low-Income and Developing Countries. *International Journal of Science and Engineering Applications, 6,* 39-48. https://doi.org/10.7753/ijsea0602.1002

Appendix

Table A1. Selected antimicrobial agents used in Tanzania.

Antimicrobial used	Type	Structure	Reported environmental effects	Implication	References
Doxycycline	Tetracyclines, broad-spectrum antibiotics		Can accumulate in the food chain, leading to toxicity in microbial communities, promoting antibiotic resistance, contaminating drinking and irrigation water, and disrupting the microbial balance in the human intestine	This indicates the need for careful management of antibiotic use and waste to prevent environmental contamination and protect public health	(Amangelsin et al., 2023; Shao & Wu, 2020)
Sulphonamides	Antimetabolite antibiotics		The species tested displayed varying levels of acute sensitivity to SMX (*A. fischeri* < *D. magna* < *E. coli* < *L. minor*) and TRIM (*L. minor* < *A. fischeri* < *D. magna* < *E. coli*). TRIM generally exhibited lower toxicity than SMX, except in the case of *E. coli*. Both antibiotics impacted *L. minor, D. magna*, and *D. rerio* at both individual levels (e.g., growth and survival) and sub-individual levels.	The varying sensitivities of species to SMX and TRIM, indicating potential ecological disruption, environmental risk, and the need for monitoring to prevent antibiotic resistance and long-term ecosystem damage.	(Diogo et al., 2024; Felis et al., 2020)
Trimethoprim					
Ciprofloxacin	Quinolones, broad-spectrum antibiotics		Even ecologically relevant concentrations of ciprofloxacin may cause oxidative stress in individuals of *D. magna* and in catfish *Rhamdia quelen*	This indicates potential exposure to ciprofloxacin, which may impar ecological health	(Dionísio et al., 2020; Zhang et al., 2022)
Nalidixic Acid			Results indicated significant changes in the growth profile of commensal *E. coli* upon exposure to NA at sub-MICs.	This demonstrates how antibiotics play an important role as signalling molecules or elicitors in driving the pathogenicity of commensal bacteria *in vitro*	(Chadha & Khullar, 2021)
Sparfloxacin			The highest concentration of ofloxacin, ciprofloxacin, sparfloxacin and gemifloxacin were found to be 66, 18, 58 and 0.2 μg/L respectively. Which may impact ecological health	Potential degradation to ecological health	(Efthimiadou et al., 2010)
Gentamicin	Aminoglycosides, antibiotics		Gentamicin can be toxic to certain aquatic organisms, such as fish and invertebrates. Exposure to sub-lethal concentrations can impact their growth, reproduction, and overall health, potentially leading to declines in population and biodiversity	There is the need for managing the use and disposal of gentamicin and other antibiotics to mitigate their impact on ecosystems and public health	(Adeyemo et al., 2021; Chakraborty et al., 2023)

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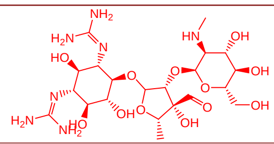
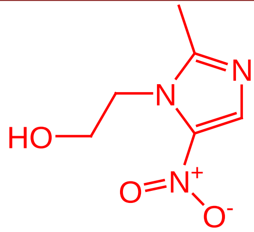
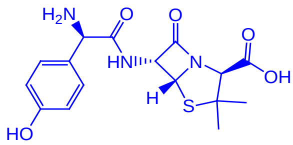
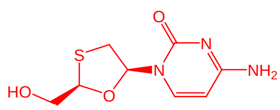
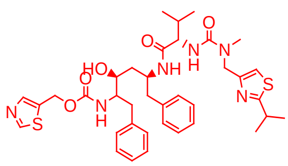
Strepto-mycin			Potential for bioaccumulation, bio-concentration and biomagnifica-tion through food chain while cause resistance and complication.	Measures are required for ecological safety	(Granja et al., 2009)
Metronidazole	Beta-lactams, antibi-otics		Toxic to aquatic organisms, including fish, invertebrates, and algae. Exposure can lead to changes in growth, reproduction, and survival rates, potentially affecting aquatic biodiversity and ecosystem health.	Measures are required for ecological safety	(Ighalo et al., 2020; Li et al., 2023)
Amoxicillin	Penicillin class of		Toxic to aquatic organisms such as fish, invertebrates, and algae. This can lead to reduced growth, reproductive issues, and potential declines in aquatic biodiversity.	Measures are required for ecological safety	(Lee et al., 2021; Sodhi et al., 2021)
Lamivudine	Nucleoside reverse transcriptase inhibitors (NRTIs)		Lamivudine can be harmful to aquatic flora and fauna. Ecotoxicity bioassays have shown that lamivudine can have an adverse effect on the germination rate and hypocotyl lengths of seeds	Lamivudine is ecotoxic, with potential to disrupt aquatic ecosystems by impairing plant development, affecting biodiversity, and altering food chains. Requiring improved wastewater treatment and stricter regulations to mitigate antimicrobial pollution and its broader ecological impacts.	(Akenga et al., 2021; Hamim et al., 2021; Kitamura et al., 2023; Omotola et al., 2021; Scotti & Barlow, 2022)
Ritonavir	Protease inhibitors		Given the limited data on ritonavir's direct effects on terrestrial and aquatic plants, further research is necessary to understand its environmental impact fully	Monitoring and mitigating the release of ritonavir into the environment are crucial steps to protect the environment	(Nugnes et al., 2024)

Table A2. Representative data on antimicrobial pollution, levels of antimicrobials where available, antimicrobial resistant microbes, and resistant genes in surface and, ground water, and food chain reported in Tanzania.

Study	Type of study	year	Matrix or Site	Results	ARGs	Levels	Implication	References
Investigation of AMR, and virulence genes in *P. multocida* isolated from goats with pneumonic pasteurellosis	Experimental	2024	*Pasteurella multocida* isolated from pneumonic goats	Results revealed high resistance against antimicrobials, including cefotaxime, sulfamethoxazole/trimethoprim, amoxicillin, erythromycin, ampicillin, chloramphenicol, tetracycline, and pefloxacin. However, they remained 100 % susceptible to gentamicin and ciprofloxacin	ErmX, blaTEM and sul1	-	This may significantly impact animal health and productivity, leading to substantial economic losses for producers	(Mwanga et al., 2024)
Investigation of the prevalence and AMR patterns of *E. coli and Salmonella spp.* isolated from rodents	Experimental	2024	Domestic and peri-domestic rodents	This study provides preliminary data on the prevalence and antimicrobial resistance characteristics of *E. coli* isolated from rodents in Iringa municipality, shedding light on the resistance profiles of these pathogens within their respective reservoirs	BlaCTX-M, sul1, sul2, tetA, acrA, and aac (3)-1, where the acr (A)	-	Potential exposure through food chain	(Mkopi et al., 2024)
Presence and distribution of genes encoding ESBL and quinolone resistance in multi-drug-resistant in *microbs*	Experimental	2024	Poultry, domestic pig and environmental samples along Msimbazi River	Resistance genes were highest in isolates from the environmental samples (86%, n = 33), followed by poultry 72.5% (n = 29), and domestic pigs 21.4%, (n = 9).	BlaCTX-M, blaTEM, qnrS, qnrB and aac (6)-lb-cr	-	Potential exposure to aquatics	(Kimera et al., 2024)
Investigation of antimicrobials in surface and ground waters	Experimental	2024	Surface and ground water	Report indicates the presence of amoxicillin, doxycycline and other pharmaceuticals.	-	Except for sulfamethoxazole (94 ng/L) in the borehole, most of the concentrations detected in rivers were ten times higher than in boreholes	Potential harm to the entire ecology through the food chain	(Kundu et al., 2024)
Investigation of composition of Cholera Outbreak Waters	Experimental	2023	Water sources	Multiple antibiotic resistance genes were detected in both the bacterial and bacteriophage fractions of water sources	BlaOXA-48, tetA, tetM, and blaCTX-M9, blaCTX-M1	-	Wastewater is the potential hotspot for contamination of surface waters	(Baraka et al., 2023)

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Investigation of composition of Cholera Outbreak Waters	Experimental	2023	Water sources	Multiple antibiotic resistance genes were detected in both the bacterial and bacteriophage fractions of water sources	BlaOXA-48, tetA, tetM, and blaCTX-M9, blaCTX-M1	-	Wastewater is the potential hotsport for contamination of surface waters	(Baraka et al., 2023)
Assessment of antibiotic use practices	Retrospective cross-sectional study	2023	Dodoma region, Central Tanzania	The prevalence of self-medication with antibiotics was 23.6% (38/161) among rural respondents and 23.4% (63/269) among urban respondents.	-	-	Antibiotics were dispensed without requiring a prescription, highlighting potential gaps in antibiotic regulation and oversight	(Mabilika et al., 2022)
Investigation of AMR in urban receiving and wastewaters	Experimental	2023	Surface water, wastewater	*E. coli* had an 83% higher proportion of multi-drug resistance (MDR) than Klebsiella spp.., which had 68.5%, and no MDR was shown by P. aeruginosa isolates.	Tet A, Tet B – 1, Tet D, β-lactamases (bla CTX-M, bla SHV), Sul and Sul 2	-	Potential transmission of resistant diseases to humans and animals	(Ripanda, 2024; Ripanda et al., 2023c)
Determination of the performance in addressing AMR in Tanzania and other countries	Experimental	2023	Theoretical study	Few well-established laboratories in tertiary hospitals, both private and public hospitals. The animal, environment and agricultural sectors had limited capacity for AMR surveillance	-	-	Possibility of ecosystem injury	(Matee et al., 2023)
Investigated multidrug-resistant *Escherichia coli* and *Klebsiella pneumoniae* in sewage from a referral hospital, tracing their presence through the urban sewage system to the discharge point in the Indian Ocean.	Experimental	2023	Hospital sewage flowing through community sewage system and discharging into the Indian Ocea	Multidrug resistance (MDR) was seen in 80.9% (186/230) *E. coli* and 71.6% (101/141) *K. pneumoniae*. Of the MDR isolates, 27.2% (78/287) were resistant to four different classes of antibiotics, while 6.9% (20/287) exhibited resistance to eight classes. The most frequent MDR pattern was PEN/CEP/TET/QNL/SUL	-	-	Possibility of ecosystem injury	(Seguni et al., 2023) (Seguni et al., 2023)

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Assessment of awareness and production practices from 420 consumers, 30 chicken egg farmers, and 30 Chinese cabbage	A cross-sectional study	2022	Chicken farm	About 42% of consumers of eggs and Chinese cabbages were not aware of the likelihood of antimicrobial residues in these foods. The awareness was significantly influenced by the consumer's educational level ($p = 0.001$) and geographical location ($p = 0.045$), with educated and urban consumers being 7.7 and 1.6 times more informed	-	-	Potential exposure through food chain	(Mongi et al., 2022)
Investigation were carried out to establish farmers' awareness of diseases, drugs, and withdrawal times.	A cross-sectional questionnaire survey and on-field clinical and postmortem diagnoses	2021	Chicken farm	Oxytetracycline in 62 and 43.5%, enrofloxacin in 9 and 19.5%, and tylosin in 5 and 26.5% of local chickens and layer keepers respectively, were the most commonly used drugs. High mortality, mean 94.79 (SE; 86.05–103.53) per flock life span was observed in layers	-	-	The observed higher mortality rate may be due to drug resistant infections	(Chota et al., 2021)
Identification ESBL-producing *Escherichia coli* in Nile perch and water	Experimental	2020	Nile perch and water (Lake Victoria)	The isolates exhibited complete resistance to sulfamethoxazole–trimethoprim and ampicillin/cloxacillin (100%), along with resistance to erythromycin (72.7%, 8/11), tetracycline (90.9%, 10/11), and nalidixic acid (63.6%, 7/11	Sulfonamides (sul1 and sul2), trimethoprim (dfrA and dfrB), aminoglycosides (aac(3)-IId, strA, and strB), tetracyclines (tet(B) and tet(D)), and fluoroquinolones (qepA4). IncF, IncX, IncQ, and Col, with blaCTX-M-15 and blaTEM-1B and IncF.	-	Potential harm to the ecosystems	(Baniga et al., 2020)
Investigation of emerging pollution in wastewater	Experimental	2019	Wastewater	Presence of antibiotics	-	Metronidazole in the range of 0.065-0.104 ppm	Potential for AMR development, dissemination in the environment	(Makokola et al., 2019)

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Investigated the occurrence of CEC in flowing Surface Waters	Experimental	2018	Flowing Surface Waters	Presence of pharmaceuticals including antibiotics	-	Cetirizine (0.0073 ppm), and metronidazole (0.0024 ppm)	Potential for exposure of these chemicals and ecosystem injury	(Hossein et al., 2018)
Investigated occurrences of antibiotics in the wastewater effluents	Experimental	2014	Wastewater effluents	The presence of antibiotics	-	Ciprofloxacin, and ampicillin in influents ranging from BDL to 0.367 mg/l) and effluents ranging from BDL to 0.037 mg/L	Potential for exposure of these chemicals and ecosystem injury	(Kihampa, 2014)