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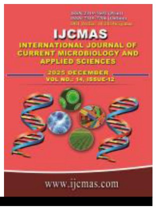

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Prevalence and Antibiotic Resistance Profiles of Bacterial Contaminants in Rural Drinking Water Sources - A One Health Study of Rural Drinking Water Sources

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ABSTRACT

Keywords

Antibiotics, β-lactams, tetracyclines, fluoroquinolones, Antimicrobial resistance (AMR)

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Rural drinking water sources are a key link between human, animal, and environmental health, and they may operate as reservoirs for antibiotic-resistant bacteria. This review presents current research on the incidence, variety, and antibiotic resistance profiles of bacterial contamination found in rural drinking water sources. Resistance to antibiotics including β-lactams, tetracyclines, and fluoroquinolones is common among both Gram-positive and Gram-negative bacteria, including opportunistic and pathogenic strains. Factors such as poor sanitation, agricultural runoff, and livestock interactions all lead to contamination and resistance spread. The research identifies surveillance limitations and underscores the importance of integrated One Health strategies for reducing antibiotic resistance in rural water systems.

Introduction

Antimicrobial resistance (AMR) describes that bacteria, viruses, parasites, and fungi that resist antimicrobials. Drug-resistant bacteria currently cause an estimated 700, 000 deaths per year, with a projected increase to 10 million fatalities per year. Water act as main reserviour that transfer drug resistant bacteria to human by in taking contaminated drinking water. Resistance to standard fecal indicator bacteria (FIB), including *E. coli and enterococci*, as well as bacterial diseases, is of interest in recreational waterways. Bacterial pathogens found in ambient waters include *Enterobacteriaceae* (pathogenic *E. coli, Klebsiella spp., Salmonella spp., Shigella spp., and Yersinia pestis)* and *Staphylococcus aureus* (MRSA). Intrinsic resistance refers to structural or functional features shared by a bacterial species, regardless of previous antibiotic exposure. Antibiotics must penetrate bacterial cell walls to reach their target and other mechanisms through which resistant is acquire antibiotics. Resistance mechanisms include decreased cell permeability, increased efflux pump expression, genetic or post-translational target change, and enzymatic blockage or degradation of antibiotics (Ana catarina Duarte *et al.,* 2022).

Poor sanitation is the primary source of drinking water problems in the 21st century, resulting in water borne illnesses and diarrhea. This causes nearly half a million fatalities annually, primarily in developing nations. However, UNICEF (2015) reports that over 30% of people in undeveloped regions still lack access to safe drinking water. The World Health Organization (WHO) reports that at least 2 billion people globally, primarily in developing countries, ingest water polluted with feces, resulting in 485, 000 deaths from diarrheal diseases each year (IHSAN T *et al.,* 2024). India comprises 16% of the world's population and 4% of its freshwater resources. According to estimates, the availability of surface and ground water is around 1, 869 billion cubic meters. 40% is unable for usage because of geological and geographical considerations. Surface water is mostly used by agriculture (89%), followed by the industrial and home sectors (2% and 9%, respectively) (Vidyadhara, 2024). Waterborne infections afflict approximately 37.7 million Indians annually, resulting in 1.5 million infant deaths from diarrhea and 73 million lost working days. Water-borne infections have a high disease burden and have a major influence on the country's economic growth. These infections occur annually during the summer and rainy seasons due to poor water supply management, particularly for drinking water and sanitation. Water-borne infections are prevalent in urban slums due to weak governance, rapid economic growth, dense population, and inadequate housing and sanitation (Pradeep kumar *et al.,* 2022). This review article highlights about antimicrobial resistant in environment especially in drinking water and multi drug bacteria in drinking water and its impact on public health.

Conceptual Framework of One Health in Waterborne Antimicrobial Resistance

The notion of One Health originated in the early 20th century, when contagious diseases between animals and humans were detected. However, it was not until the 1990s that the term "One Health" was coined, resulting in a legal definition. The principle of One Health, which emphasizes the interconnections of human, animal, and environmental health, has recently gained prominence. This approach to health emphasizes treating all three components for optimal health results. The One Health concept is based on a few basic elements such as Recognizing the connection between human, animal, and environmental health, Recognize that the health of one component can affect the health of the other two, Highlighting the importance of teamwork and communication among healthcare professionals across sectors, Promoting an interdisciplinary approach involving professionals in medical, veterinary medicine, public health, environmental science, and social sciences (Dr. Abbas Kazim., 2023).

Animals play a significant part in this cycle since antibiotics used in livestock, poultry, and fish can be released into the water, resulting in the creation of resistance strains. This resistant bacteria can be released into nearby water sources through a variety of means, including farm runoff and animal waste. Different bacteria interface with one another in environmental sources such as water, and as they do, antibiotic resistance genes propagate to one another, similar to how AMR spreads. When humans ingest contaminated water, resistant bacteria enter their bodies and cause a variety of illnesses.

Rural Drinking Water Sources and Vulnerability to Microbial Contamination

For drinkable water, in India 2% of households depend upon surface water, while 53% dependent on groundwater. There are eight categories of drinking water sources: tap water, well water, hand pumps, tube/bore water, spring water, river water, tank/pond water, and others. Approximately 43.5% of households have both treated and untreated tap water (Siroop Chaudhuri *et al.,* 2017). Water can include several kinds of microorganisms, including viruses, bacteria, and protozoa. Surface water typically contains greater amounts of microbes than groundwater (Farhat Nabeela *et al.,* 2014). Water microorganisms can enter through contaminated water supply pipelines and inadequately treated water. Contaminated water supply pipelines and inadequately treated water can introduce microbes into drinking water. In 2022, feces contaminated the drinking water of around 1.7 billion people worldwide (WHO). Additionally, parasites can contaminate drinking water. The intestinal protozoa that spread through contaminated feces are helminthus and protozoa. *Entamoeba histolytoica, Giardia intestinalis, and Toxoplasma gondii* are common protozoan pathogens that can contaminate water and cause serious sickness in people. Heavy rains can create flooding and surface runoff, which can contaminate the water that transports feces, as well as dilute the concentrations of fecal matter in drinking water sources. Few research investigations discovered that heavy rain fall can induce a rise in *E.coli*, which is a fecal indicator bacteria levels in drinking water and also in stored household water (Julie E. Powers *et al.,* 2023). Alage blooms can potentially contaminate water. *Caynobacteria* will cause an algea bloom in fresh water. Cyanobacterial blooms in untreated water sources pose a threat to Drinking Water Treatment Plants (DWTPs), which rely on them for drinking water (Marlena piontek *et al.,* 2023). The most frequent viruses that can infect drinking water are *novirus, astrovirus, hepatitis A and E viruses, rotavirus, norovirus, and other caliciviruses, as well as enteroviruses such as coxsackieviruses and polioviruses*. Inadequate disinfection of feces-contaminated drinking water can quickly lead to massive outbreaks of viral gastroenteritis by ingestion. Drinking water can transmit viruses by inhalation (e.g., showering) or skin/eye contact (e.g., swimming), resulting in respiratory and ocular disorders (Aimee M. Gali *et al.,* 2015).

Common Bacterial Contamination of Drinking Water

Surface water is contaminated by the bacteria chlera and *Clostridium perfringes. Vibrio* are short, curved Gram-negative rods. *Vibrio* belong to aquatic microorganisms. *Vibrio* causes chlorea, which is a water-borne infectious disease. *Vibrio* can live in contaminated water, sewage, and food and its can exist in biofilms. The most common mode of transmission is fecal contamination of water systems. May survive in water for a long period of time (R. Sujatha lakshmi *et al.,* 2025). Escherichia species include *Escherichia coli, Escherichia albertii, Escherichia fergusonii, and Escherichia hermannii. Escherichia coli (E. coli*) was the most prevalent Escherichia strain discovered in drinking water. There are four forms of harmful *E. coli*: enterotoxigenic (ETEC), enteropathogenic (EPEC), enterohemorrhagic (EHEC), and enteroinvasive (EIEC). ETEC can be found commonly in both cow and human feces. ETEC contamination can take place when feces are released into water sources. (Evariste Bako *et al.,* 2017). *Salmonella* is a rod-shaped, gram-negative bacteria. *Salmonella* bacteria can cause salmonellosis infection which is of two types such as paratyphoid fever, and gastroenteritis and Symptomatic infection. The Salmonella genus had only two species: *Salmonella enterica (S. enterica) and Salmonella bongori*. *Salmonella* can be found in several environments. As a result, it could spread to people in many different kinds of ways, including water tainted with animal excrement.

Shigella was a gram-negative, rod-shaped bacteria. It can lead to bacillary dysentery (commonly known as shigellosis) in humans. The genus *Shigella* contained four species: *Shigella dysenteriae, Shigella flexneri, Shigella boydii, and Shigella sonei. Shigella flexneri* is the most commonly encountered species globally, followed by S. sonnei. *Shigella* species were mostly transmitted among individuals by feces or drinking water contaminated with the bacteria (Risky Ayu Kristanti *et al.,* 2022).

Bacterial Indicator for Drinking Water

Coliform bacteria, often known as total coliforms or simply coliforms, are Gram-negative, facultatively anaerobic, non-spore-forming, rod-shaped bacteria that can ferment lactose to acid and gas at ~37 ◦C within 48 h. They constitute around 10% of gut microbes. Traditionally, total coliforms consisted of four closely related organisms from the Enterobacteriaceae family: *Escherichia, Enterobacter, Klebsiella, and Citrobacter*. Coliform bacteria presently include species from 19 genera, including Hafnia, Serratia, and Raoultella. Escherichia coli functions as a fecal indicator to evaluate the quality of drinking water.

Clostridium perfringens is a Gram-positive, spore-forming, biofilm-forming, anaerobic, pathogenic species found in feces. It is one of the first fecal indicators in aquatic environments.*C. perfringens* spores have a thick peptidoglycan cortex that protects them from environmental stresses like chlorination, heat, and UV radiation, as well as toxins from industrial waste. This allows them to survive longer in polluted waters than other FIB, particularly in freshwater. *C. perfringens* is a more reliable sign of accumulated fecal contamination (Enze Li *et al.,* 2021). *Enterococci* are opportunistic bacteria that cause millions of infections every year and are significant members of gut communities. They are widely used as probes for evaluating recreational water quality throughout the world due to their abundance in human and animal excrement, their simplicity of culture, and their association with human health effects in fresh and marine waters. The most common role for *enterococci* is as general indicators of fecal contamination, or fecal indicator bacteria (FIB) (N. Byappanahalli *et al.,* 2012).

MDR Bacteria and Its Antibiotic Resistant Profiles in Waterborne Bacteria

Antibiotic-resistant genes (ARGs) are becoming more prevalent in the aquatic environment, complicating the worldwide waterborne disease burden. Antibiotic resistance genes (ARGs) have been found in drinking water in both developed and developing countries. ARGs pose an important danger to public health as they can spread from the environment to infections in animals and humans. Antibiotic-resistant bacteria (ARBs) and ARGs are common environmental contaminants found in water and drinking water systems (Tsegahun Asfaw Abebe *et al.,* 2024). Environmental water sources act as important reservoirs and transmission routes for pathogenic bacteria and antibiotic-resistance genes (ARGs). Contaminated water treatment plants release effluent containing residues such as resistant bacterial cells, antibiotics, disinfectants, and ARGs into rivers, lakes, and other natural water sources. ARGs are transmitted in the water environment by a variety of mechanisms, including direct contact in the water, movement and migration of microorganisms in the water, and interactions between microorganisms in the water and their hosts. Furthermore, human activities such as the discharge of hospital, municipal, and animal wastewater contribute significantly to the spread of antibiotic resistance (Yiwen Yang *et al.,* 2025). The most frequent bacteria that cause infection are drug-resistant coliforms, which can be contracted through unsanitary food and drink. Overuse of antibiotics can harm beneficial bacteria, leading to the emergence of resistant diseases. Consuming less than the suggested dosage of antibiotics does not kill the pathogen, but instead increases resistance. In both circumstances, treating MDR bacteria can be difficult and even dangerous (Meerambika Mishra *et al.,* 2018).

E. *coli* were isolated from several environments, including surface water and feces samples. Environmental isolates have higher levels of resistance to cephalothin and tetracycline. *Klebsiella spp*. was the most frequent organism found in the water samples, followed by *E.coli*. Other bacteria obtained from water were *P. aeruginosa, Enterobacter spp., Proteus vulgaris, and Enterococcus faecalis. Vibriocholerae and Shigella spp*. were the least isolated organisms. The most resistant *E. coli* strains were to penicillin, followed by cefuroxime, erythromycin, tetracycline, and ampicillin. Few isolates exhibit resistance to chloramphenicol and pipemidic acid (Stephen T. Odonkor *et al.,* 2018). *Enterococcus* isolated from diverse surface waters is highly resistant to most antibiotics, including erythromycin, tetracycline, and fluoroquinolones. *Enterococcus* strains are resistant to ampicillin (A. Łuczkiewicz *et al.,* 2010). *Bacillus spp*. are resistant to Ciprofloxacin, Chloramphenicol, Streptomycin, and Amoxicillin. *S. faecium* is resistant to Erythromycin, Ciprofloxacin, Cotrimoxazole, Pefloxacin, Ceftriazone, Chloramphenicol, Streptomycin, and Amoxicillin. *Micrococcus spp*. were resistant only to the antibiotic Ofloxacin, whereas *S. aureus* was resistant to Ciprofloxacin, Cotrimoxazole, Pefloxacin, Gentamicin, Ceftriazone, Chloramphenicol, Streptomycin, and Amoxicillin. *Pseudomonas spp* isolated from water shows resistant to most antibiotic which is tested (T. A. Ayandiran *et al.,* 2014). *Salmonella* isolated from different kind of water which shows highest resistant to linezolid which is 90.6% and gatifloxacin antibiotics (D. H. Tambekar *et al.,* 2007).

Extended-Spectrum β-Lactamase (ESBL), AmpC and Carbapenemase Producing Bacteria

Bacteria produce beta-lactamases that make them resistant to beta-lactam antibiotics such as cephalosporins, carbapenems, penicillins, and monobactams. AmpC beta-lactamases play a crucial role in Enterobacteriaceae's resistance to beta-lactam antibiotics. These enzymes, present in Gram-negative bacteria such as *K. pneumoniae and E. coli,* are resistant to most beta-lactam antibiotics, with the exception of carbapenems and fourth-generation cephalosporins. AmpC beta-lactamases may be encoded on chromosomes or plasmids. AmpC beta-lactamases are chromosomally encoded in the majority of Gram-negative bacteria, specifically Enterobacterales. Plasmids propagate AmpC genes from their chromosomal origin, leading to widespread drug resistance due to plasmid-mediated AmpC beta-lactamase (pAmpC) function. AmpC variants mediated by plasmids are classified into five evolutionary groups:

CIT (CMY-2 kinds), EBC (ACT-1 and MIR-1), DHA, ACC, and FOX and MOX. These categories are based on sequence similarities with AmpC enzymes native to each species. Enterobacteriaceae include numerous AmpC genes, with blaCMY-2 and blaDHA-1 being the most frequent in E. coli and K. pneumoniae strains, respectively (Saba Gebremichael Tekele *et al.,* 2025).

ESBLs are β-lactamases that can break down extended-spectrum β-lactam antibiotics like cephalosporins and monobactams. However, β-lactamase inhibitors, such as clavulanate, can suppress their activity. ESBLs have been observed in various Enterobacteriaceae strains. Most ESBLs are variations of TEM, SHV, or CTX-M enzymes. The initial TEM and SHV enzymes were β-lactamases, with point mutations resulting in the ESBL phenotype. CTX-M enzymes are the most frequent ESBLs, with 251 family members classified into five groups: CTX-M-1, CTX-M-2, CTX-M-8, CTX-M-9, and CTX-M-25.ESBL-producing *Enterobacteriaceae* have been found in the population and environment, including healthy individuals, wastewater, water sources, wild animals, cattle, companion animals, and food-related products (Sohyun Cho *et al.,* 2023).

Carbapenemases are classified as Ambler classes A, B, or D. Class A and D enzymes use a serine-based hydrolytic mechanism, while class B enzymes require one or two zinc ions for catalytic activity. *Klebsiella pneumoniae* carbapenemase (KPC) is found in other gram-negative organisms, including *Pseudomonas aeruginosa*. *A. baumannii* frequently exhibits acquired class D carbapenem-hydrolyzing β-lactamases, specifically OXA [oxacillinase]-23, OXA-24/40, and OXA-58-like enzymes. OXA-48 and its derivatives (e.g., OXA-181 and OXA-232) are found in Enterobacteriaceae and can break down narrow-spectrum β-lactams and carbapenems, but not broad-spectrum cephalosporins (ceftazidime and cefepime) (Robert A. Bonomo *et al.,* 2018).

Molecular Dermenatives of Antibiotic Resistance in Rular Water Sources

ARGs related to tetracycline: Tetracycline-resistant bacteria have been found in the enviroments. There have been at least 38 distinct tetracycline resistance (tet) genes and three oxytetracycline resistance (otr) genes reported to date. These genes comprise 23 genes that code for effluxproteins (effluxpump mechanism), 11 genes for ribosomal protection proteins (target modification mechanism), three genes for an inactivating enzyme, and one gene with an unknown resistance mechanism. More than 22 tet or otr genes have been identified in bacterial isolates from aquatic settings. Tetracycline resistance genes consisting of tetM, O, S, Q, and W, that encode for ribosome protective proteins, have recently been discovered in microbial communities of sewage treatment systems (Auerbach *et al.,* 2007).

ARGs in sulfonamides and trimethoprim - Mutations in DHPS and DHFR genes can cause resistance to sulfonamides and trimethoprim. Sulfonamide resistance can be acquired through a variety of mechanisms, including alterations in sul genes and mobile elements.The important main trimethoprim resistant mechanisms is that plasmid or transposon will replace trimethoprim-sensitive (DHFR), trimethoprim Resistant (DHFR). There are four different types of sul genes that is sul1, sul3 and sulA this are genes discovered in bacteria from environment origins in this sul1 and sul2 have been observed in bacteria which is isolated from water and also in the sediments of aquaculture (Xu-Xiand *et al.,* 2009).

β lactamase ARGs - β lactams are the most used antibiotics but most of the isolates resistant to β lactam. In gram negative bacteria the most common resistance mechanisms is enzymatic inactivation through the cleavage of β lactam ring by beta lactamases. A wide range of ARGs (bla) founded in water and aquaculture areas. The bla genes are commonly dectected in most of the enviroment pathogens such as Aeromonas, *Enterobacter, Salmonella, Staphylococcus and Vibrio*. Beta lactamases amp c gene obtained in bacteria which is isolates from surface water and in drinking water films. From hospital wastewater (mec A gene) isolated from Methicillin Resistant *Staphylococci*. The bla gene which contains plasmids isolated from wastewater plant also carry other resistant elements encoding aminoglycoside, nucleotidyl transferase (acetyltransferase) and chloramphenicol efflux protein (cml).

ARGs encoding resistance to aminoglycoside, β-lactam, tetracycline, and trimethoprim-sulfamethoxazole were discovered in E. coli bacteria isolated from drinking water (Sengul Alpay-Karaoglu *et al.,* 2007). Study shows that the vanA and ampC genes are present in both wastewater and drinking water biofilms. *Listeria monocytogenes* isolated from dairy farm drinking water have been discovered to carry the floR and penA resistance genes (Xu-Xiang Zhang *et al.,* 2009).

Environmental Drivers of Antibiotic Resistance in Rural Water Sources

Antibiotic resistance may originate from mutations in bacteria's pre-existing genome as well as the uptake of foreign DNA. Some resistant bacteria may colonize or infect hosts through these settings. A single transmission event to another individual has a limited impact on a resistant pathogen that is already widely circulating among humans, unlike an evolutionary event that results in the emergence of a successful resistance genotype in pathogens, which can have global consequences (Joakim Larsson *et al.,* 2022). The ecosystem connects animals, soil, water, sand, and sewage. The environment serves as a reservoir for mobile genetic elements, which spread to different sections or human and animal hosts. Antibiotics enter the environment through several sources, include municipal and hospital waste, animal husbandry, manufacturing, agricultural areas with livestock dung, and landfill leachates. Antibiotics have a half-life ranging from hours to hundreds of days, but their remnants remain as persistent pollutants in the environment. Pharmaceutical substances and old antibiotics are discarded in the garbage, contaminating groundwater and aquatic systems during wastewater treatment. A very low concentration of these discarded antibiotics can cause selective pressure via horizontal gene transfer or target site modification. One of the main reasons for antibiotic resistant genes in the environment is through diverse waste in water, such as agricultural and industrial waste. Increased levels of ARGs in pharmaceutical wastewater have been linked to the use of therapeutically relevant antibiotics during treatment stages and subsequent released in enviroment. Hospitals and healthcare facilities generate antimicrobial waste, either from patient secretions or abandoned drugs (Samreen *et al.,* 2020). Municipal waste water is a major source of carry resistant organisms or genes, as 30-90% of all antimicrobials are excreted intact through human feces and urine. Only 20-30% of municipal waste water is treated at treatment plants, which is insufficient to remove resistant microbes.

Human Health Implication of Antibiotic Resistant in Waterborne Pathogens

The direct health impacts of Antibiotic resistant bacteria in drinking water is the spread of resistant bacteria that causes water borne diseases. The common waterborne outbreaks are diarrhea caused by various multi-drug resistant bacteria such as *E.coli, Shigella and Salmonella*. Acute diarrheal diseases outbreaks poses a significant public health challenge especially in india that mainly affect children due to intake of contaminate drinking water. In rural areas where only limited medical serves it more challenging to diagnosis and treat waterborne infections. The World health organization (WHO) detected that nearly 600 million people suffer from waterborne infection that is out of 10 people 1 gets affect by waterborne diseases (Tapan Majumdar *et al.,* 2024). Vibrio cholera causes cholera infection which is major waterborne diseases. Annualy it is estimated that nearly 3 to 5 million cholera cases occurs in which nearly 200, 000 death. This cholera outbreaks is due following factors such as improper chlorination of drinking water, poor quality of piped water systems, not proper cleaning of water pipelines, break or leakage of drinking water pipelines which leads to cross contamination with sewage water. Cholera affects mainly for both children as well as adults. The main reasons for this illness is uptaking contaminated water or cooked food that is contaminated wateer. There are 2 serotypes that is 01 and 0139 are major strains for major outbreaks (Tony Fredrick *et al.,* 2015). Through enviroment multi drug resistant bacteria enter into human as it shows resistant to most commonly used antibiotics it is diffcult to treat infection and also prolong treatment is needed.

Hepatitis A virus, Norovirus, Adenovirus, Enteroviruses are common viruses that causes outbreaks by contaminated drinking water. Most of the groundwater are contaminated with viruses. Water borne viral infection can be more fatal and causes more outbreaks in children, elderly people and immune compromised patients (A. G. Nerkar *et al.,* 2021).

Animal-Human-Environment Interface in Rural Settings

Antibiotic resistance (AR) is a complex issue that threatens the health of cattle, humans, and the environment (soil, air, water). AR is one of the most critical global health challenges, exemplifying the One Health idea. This is because antibiotic-resistant bacteria such as Escherichia coli, Salmonella, and Campylobacter can spread among cattle, humans, and the environment. The One Health concept acknowledges the interconnectedness and reciprocal influence of these three domains. One Health is a collaborative endeavor amongst health science professionals, associated disciplines, and institutions to attain maximum health for animals, humans, wildlife, plants, and the environment. Interactions between animals, humans, and the environment can lead to the spread of bacteria, mobile genetic elements (MGEs), and antibiotics. These channels enable the migration of entities between compartments, increasing the spread of AR.AR spreads due to poor antibiotic use, polluted settings, and ineffective infection control practices. Humans' careless use of antibiotics contributes to the emergence and spread of antibiotic-resistant bacteria (ARBs) and antibiotic resistance genes. Resistant bacteria can spread among humans through direct contact, food, water, and environmental surfaces. Environmental pollution contributes significantly to the spread of antibiotic-resistant bacteria and genes. Antibiotic-resistant bacteria may thrive in soil and water, potentially spreading to animals and humans when they come into touch with polluted environmental sources (Sriniwas Pandey *et al.,* 2024). Livestock farms are an important source of ARB and ARGs. ARBs are resistant to multiple antibiotic classes, including aminoglycosides, tetracyclines, sulfonamides, chloramphenicols, and β-lactams. Livestock farms can have harmful zoonotic bacteria, including *S. aureus, Salmonella, Campylobacter, E. coli, and Listeria species*. Pathogens from animals can spread into the environment via air, slurry, and excrement, potentially causing outbreaks and a source of ARGs (Maria Angeles Argudín *et al.,* 2017). AR evolves in a complex parameter space, making it difficult to explain its spread and direction. However, it has been discovered that the spread of AR at the human-animal-environment interface is caused by AR bacterial clones, MGEs, and ARGs. MGEs function as vehicles for the spread of resistance at the human-animal-environment interface. They are divided into two groups: intracellular MGEs (such as transposons and integrons) and intercellular MGEs (such as plasmids).Humans and other mammals can get leptospirosis, a zoonotic illness caused by the spirochete bacterium Leptospira. Leptospirosis is one of the most common zoonotic illnesses in the world, with over 1, 000, 000 cases and an estimated 50, 000 human deaths annually1–4. When a wound or mucous membrane is exposed to the bacteria, humans can get contact with bacteria and causes this infection. Both direct interaction with animals and indirect contact after coming into contact with water or soil tainted by the urine of diseased animals can result in this exposure (Udomsak Narkkul *et al.,* 2021).

Surveillance and Monitoring Strategies for Antibiotic Resistance in Drinking Water

The World Health Organization launched the Global Action Plan on Antimicrobial Resistance (GAP) in 2015 to address antibiotic resistance in humans, animals, and the environment using a One Health approach. The One Health conceptual framework takes into account the links between humans, animals, and the environment, as well as how resistance can transcend social, ecological, and habitat borders. The WHO's GAP has five key objectives: (1) increasing awareness and understanding, (2) boosting surveillance and research, (3) lowering the frequency of illness, (4) optimizing the use of antimicrobial drugs, and (5) assuring long-term investment in resistance management (WHO GLOBAL ACTION PLAN ON AMR 2015). There are various method to monitor and detect antibiotic resistance in drinking water such as culture depended method, traditional phenotype method, PCR. The identification of AMBs in water samples relies primarily on culture-dependent techniques. Using a variety of methods, this strategy enables researchers to discover resistant strains based on their phenotypic traits and growth patterns. By preventing the development of non-target bacteria, selective media are intended to isolate particular microorganisms, particularly those that might contain ARGs. Evaluating water samples for antimicrobial resistance (AMR) usually use two primary methods: (i) media designed for initial generic bacterial differentiation and (ii) media particularly designed to target resistant species. This technique aids in the primary detection of the antibiotic-resistant gene in water.The examples for selective media to detect Antibiotic resistant in water such as CHROM agar for recovery of CRE and other example are ESBL agar which is use to isolate extended spectrum beta-lactamase (ESBL) producing bacteria (Zina Alfahl *et al.,* 2024). In molecular biology, PCR has become a fundamental method, especially for identifying ARGs in a variety of settings, including water. The detection and monitoring of ARGs in aquatic environments is crucial for understanding the dissemination and impact of resistance on public health. Antibiotic-resistant genes, such as bla, mecA, vanA, sul1, tetA, and qnr, can be found in water bodies such as surface water, groundwater, and wastewater. These genes can originate from various sources, including agricultural runoff, industrial discharge, and municipal wastewater. Therefore, PCR plays an essential role in detecting these kinds of genes. PCR is frequently employed to identify and quantify ARGs in diverse water matrices, including surface, groundwater, wastewater, and drinking water, due to its high sensitivity, specificity, quantitative capabilities, and quick findings. Advancements in sequencing technologies have expanded bacterial sequence data availability and reduced prices, making it a feasible tool for antibiotic resistance surveillance. In recent years, several approaches have been developed to identify genetic determinants of antibiotic resistance in whole-genome sequencing (WGS) and whole-metagenome sequencing (WMS) data sets (Manish Boolchandan *et al.,* 2019).

Prevention, Mitigation and Policy Implication from a One Health Prerspective

The Indian government formed a Core Working Group on AMR to develop a national action plan (NAP). The NAP identifies six strategic targets that address AMR in the environment, whether directly or indirectly. Each strategic goal includes defined interventions, actions, and outputs, with a predicted schedule for the following five years. The present NAP is comprehensive and well-aligned with the World Health Organization's (WHO) GAP for AMR. The plan aligns with the GAP's five primary objectives and includes a goal to strengthen India's leadership in AMR. The initiative aims to address AMR across multiple areas, including agriculture, fisheries, animal husbandry, and the environment, using a 'one health approach' (Neelam Taneja *et al.,* 2019). In health research, implementation research (IR) focuses on putting policies, programs, or individual habits into action (together known as interventions). Adapted for AMR, IR can validate processes for systematic and sustainable absorption of evidence-based interventions into normal practice, using both quantitative and qualitative methods (Mark P. Khurana *et al.,* 2023). Improving water sanitation and hygiene (WASH) and wastewater management in all sectors is crucial to preventing infections and lowering the spread of antimicrobial resistance (AMR), according to the Global Action Plan to Combat AMR. Ensuring widespread access to sanitation, hygiene, and potable water in homes, health facilities, and schools is also a top goal for preventing many diseases that would otherwise require antimicrobial treatment. WHO partners with the WASH sector to promote AMR-sensitive programming aimed at universal WASH in families, health care facilities, and schools (WHO). The prevention method for Antibiotic resistant in water is to reduce overuse of antibiotic, wastewater management system need to be improved and proper drinking water sanitation procedures need to followed such as chlorination of drinking water to avoid spreading resistant bacteria to human.

Research Gaps, Future Directions and Conclusion

Significant gaps persist despite increasing proof of antibiotic-resistant microorganisms in rural water sources. To evaluate seasonal fluctuations and long-term trends in contamination and resistance profiles, there is a shortage of longitudinal data. Furthermore, a lot of research concentrates on the existence of bacteria without sufficiently connecting contamination levels to real health consequences in communities that are exposed. There are also gaps in the assessment of how well inexpensive, locally relevant water treatment and sanitation measures work to lower bacterial load and antibiotic resistance. Additionally, there are gaps in the assessment of how well inexpensive, locally relevant water treatment and sanitation measures work to lower bacterial load and antibiotic resistance. Future research should routinely test rural drinking water over extended periods of time to check bacterial contamination in water and antibiotic resistant pattern with time and season. In order to properly identify the sources of resistant germs, such as humans, animals, or the environment, researchers should also employ contemporary laboratory techniques. Further research is required to determine whether simple and affordable water treatment techniques can lower dangerous and drug-resistant microorganisms. Educating peoples about bacterial contamination and also how to maintain water cleanliness is also plays a vital role with can reduce Antibiotic resistant in drinking water.

This study highlights that Rural drinking water is contaminated by various antibiotic drug resistant bacteria. Multidrug-resistant bacteria in drinking water pose a major threat to public health, especially for rural communities with poor access to infrastructure for water treatment and medical care. The study's overall findings support the necessity of integrated surveillance and intervention techniques that concurrently address environmental protection, antimicrobial usage, and water safety.

Author Contributions

S. Arul Jothy: Investigation, formal analysis, writing—original draft. M. Prakash: Validation, methodology, writing—reviewing. K. Arivazhagan:—Formal analysis, writing—review and editing. S. Saranya: Investigation, writing—reviewing. S. Sivakumar: Resources, investigation writing—reviewing. Subasri Prakash: Validation, formal analysis, writing—reviewing.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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