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Bacterial Contamination and Antibiotic Susceptibility of Isolates from Tanker-Distributed Drinking Water in Kabul, Afghanistan

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ABSTRACT

Water quality is critical for public health, and access to safe drinking water is essential for preventing infectious diseases. In many areas of Kabul city, tanker-distributed water is an essential source, but its microbial quality remains uncertain. This cross-sectional study evaluated bacterial contamination and microbial resistance in tanker-distributed treated water in Kabul, comparing it to established standards. One hundred samples from 20 companies were collected between January and June 2024. Samples were cultured for total bacteria and coliform counts using spread plate and filtration methods. Confirmatory tests were performed on colonies. Antibiotic susceptibility was tested by disk diffusion .The results indicated that all samples positive for bacterial contamination exceeded established standards, with 45% containing more than three species. None of the samples contained coliform bacteria. Seventeen distinct bacterial species were identified, including *Acinetobacter baumannii* (21%) and *Staphylococcus aureus* (10%). Additionally, the isolates displayed antibiotic resistance, posing significant health risks. Previously, there was a lack of reliable information regarding the bacterial contamination of water distributed by tankers. The results of this study revealed that bacterial contamination in water exceeded accepted standards. Additionally, pathogenic and antibiotic-resistant microorganisms were detected. Therefore, relevant authorities must implement strict control and monitoring measures.

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INTRODUCTION

Water is essential for sustaining life, as it supports critical physiological functions such as regulating body temperature, aiding digestion, facilitating nutrient absorption, and removing waste products from the body (Popkin et al., 2010). Its importance goes beyond hydration; water is a cornerstone of good health and well-being, contributing to the proper functioning of all body systems (Jéquier & Constant, 2010). Access to clean drinking water is crucial for preventing dehydration, ensuring optimal organ function, and reducing the risk of waterborne diseases. Infection diseases like cholera, dysentery, and diarrhea, which are

transmitted through contaminated water, pose significant health threats, particularly in low-income countries with limited access to sanitation facilities (Zahid et al., 2021).

The global situation regarding access to clean water is alarming. As of 2022, approximately 6 billion people worldwide have access to safely managed drinking water, unprotected wells, or surface water, significantly increasing their risk of waterborne diseases (UNICEF, n.d.2023). In regions with inadequate water treatment infrastructure, drinking water safety cannot be ensured despite the growing demand for treated water (Daud et al., 2017). Microbial contamination, including bacteria, viruses, and fungi, often exceeds safe limits in many areas, leading to gastrointestinal diseases and other public health issues (Hamad et al., 2022). Studies have also uncovered other harmful bacteria in treated water sources, such as *Vibrio cholerae*, *Salmonella* species, and *Pseudomonas* species, contributing to the spread of waterborne diseases (Pant et al., 2016).

Contamination typically originates during the water sourcing, treatment, or distribution stages. For instance, *Escherichia coli* (E. coli) is commonly used to indicate fecal contamination in water, signaling potential health risks (Chidya et al., 2019). Microbiological parameters can be divided into fecal and non-fecal indicators. Fecal indicators, such as total coliforms, *Escherichia coli*, *fecal streptococci*, and *enterococci*, help determine the presence of fecal contamination in water. In contrast, non-fecal indicators include pathogenic microorganisms that can harm humans, such as *Pseudomonas aeruginosa*, *total staphylococci*, coagulase-producing *staphylococci*, and *Legionella* (Criteria, 1985).

The count of viable microorganisms at 37°C estimates the total microbial load present in water (Ashbolt, 2015). Therefore, measuring this parameter is vital for evaluating the microbiological integrity of water distributed by tankers and the effectiveness of its treatment processes. Total coliforms and *Escherichia coli* are key indicators of fecal contamination in water sources. The presence of these microorganisms signifies microbial pollution or a failure in water treatment systems. *Escherichia coli* is part of the fecal coliform group and naturally inhabits the human body. Due to its pathogenic nature, it should not be present in drinking water; its detection indicates fecal contamination and potential health risks (World Health Organization, 2006).

The emergence of antibiotic-resistant strains among waterborne pathogens complicates efforts to control and treat these diseases, presenting a pressing public health dilemma (Tang et al., 2023). A 2023 survey of bottled water in Kabul revealed alarming levels of bacterial contamination, with 55% of bottled water samples contaminated with harmful bacteria. Among these, 15% contained coliform bacteria, and pathogenic bacteria such as *Enterobacter cloacae, Klebsiella pneumoniae, Proteus mirabilis, Pseudomonas aeruginosa, Serratia marcescens,* and *Staphylococcus aureus* were identified (Yousufi et al., 2024).

Continuous monitoring of this parameter is crucial, as values exceeding the standard threshold indicate potential contamination and necessitate further investigation (World Health Organization, 2006). This is particularly alarming in resource-limited regions with high

infection risks. In Afghanistan, the situation is particularly dire, with approximately 80% of the population lacking access to safe drinking water (UNICEF, 2022). The absence of functional public water treatment plants or filtration systems in Afghanistan exacerbates this issue (Hamdard, 2023).

Many communities in Afghanistan depend on shallow wells or untreated surface water, increasing their exposure to different pathogens (UNICEF, 2022). In Kabul City, half of the population is dissatisfied with their home drinking water quality, and most rely on unsafe and often contaminated sources (Zahid et al., 2021). Therefore, Water is often transported via tankers, raising concerns about microbial quality since the safety of tanker-distributed water is mainly unknown. The lack of a comprehensive monitoring system for water quality in Afghanistan adds to this uncertainty, as tanker drivers and distributors may not adhere to proper hygiene standards during transportation and distribution, which could introduce contaminants. Additionally, the risk of contamination increases when water is stored in tanks that may not be adequately cleaned or maintained (Tulchinsky & Varavikova, 2014).

There is no study investigating the bacterial contamination and antibiotic susceptibility pattern in water supplied by tankers in Kabul City. Therefore, the current study aims to:

1. Evaluate the bacterial contamination levels in water distributed by tankers in Kabul City.
2. Assess the antibiotic susceptibility patterns of bacterial species isolated from the mentioned water samples.
3. Provide valuable insights into the safety of water comparing to standards.

METHODS AND MATERIALS

In this cross-sectional study, we randomly selected 100 samples from distribution tankers belonging to 20 companies in Kabul city. A survey revealed that 20 private companies transport mineral and purified water by tankers to various locations in Kabul, the capital city of Afghanistan. The water is sold to the public for one Afghani per liter. Five different tankers from each company were selected to collect samples, and one sample was taken from each tanker between January and June 2024. Each company was labeled with letters from "A" to "T." The samples were sequentially numbered from "1" to "100". The samples were collected in sterile bottles and transported to the microbiology laboratory at the Pharmacy Faculty of Kabul University within three hours of collection. The samples were kept at 1–4°C temperature to maintain microbiological integrity during transportation and testing.

We examined the samples for total plate count, total coliform count, fecal coliform count, types of bacterial contamination, and antibiotic resistance profiles of the isolates. Each sample was cultured using both spreading and filtration techniques.

In the spread plate technique, we inoculated 0.1 ml of each water sample onto three types of agar media: Nutrient Agar, Mannitol Salt Agar, and MacConkey Agar, all sourced from Oxoid, England. Nutrient Agar is commonly used to cultivate a wide range of organisms.

Mannitol Salt Agar is selective for *Staphylococcus* species, and MacConkey Agar targets *Gram-negative bacteria*, particularly *Enterobacteriaceae* such as *Escherichia coli*.

Using the spread plate technique, we employed the filtration method for samples that did not show growth. Each sample (100 ml) was diluted to 1:100 and 1:1000 with sterile distilled water and then filtered through a 0.45 µm cellulose nitrate membrane filter from Sartorius Company. All inoculated plates were incubated at 37°C for 18 to 24 hours under aerobic conditions. Colonies on each plate were counted and represented as colony-forming units per milliliter (CFU/ml).

After incubation, we examined the colony morphology, focusing on characteristics such as size, pigmentation, shape, margin, opacity, and elevation. Following the morphological examination, we assessed the microscopic characteristics using Gram staining to identify the bacteria's shape, size, and arrangement. We conducted a catalase test for Gram-positive cocci to differentiate between *Staphylococcus* and *Streptococcus* and a coagulase test to distinguish *Staphylococcus aureus* from other coagulase-negative *staphylococci*. For *Gram*-negative bacilli, we performed an oxidase test to differentiate between *Enterobacteriaceae* and other *Gram*-negative bacilli, followed by further biochemical analysis using the Analytical Profile Index 20E.

Antibiotic susceptibility testing was conducted using the Kirby-Bauer disk diffusion method, measuring the inhibition zones to assess susceptibility to various antibiotics. The results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines, explicitly following the CLSI-2020 recommendations, which provide standardized criteria for evaluating antibiotic resistance (Cockerill, 2013).

The antibiotic susceptibility tests were performed on Mueller-Hinton agar (Oxoid, England). Commonly used antibiotics, including amoxicillin (AML, 30 µg), amoxicillin-clavulanic acid (AMC, 30 µg), erythromycin (E, 15 µg), gentamicin (CN, 10 µg), trimethoprim-sulfamethoxazole (SXT, 1.25/23.75 µg), tobramycin (TOB, 10 µg), ciprofloxacin (CIP, 5 µg), levofloxacin (LV, 5 µg), imipenem (IMI, 10 µg), ceftazidime (CAZ, 30 µg), amikacin (AMI, 30 µg), ceftriaxone (CRO, 30 µg), chloramphenicol (C, 10 µg), vancomycin (VA, 30 µg), and kanamycin (KAN, 30 µg), were tested in this study, all antibiotic discs obtained from Oxoid Company.

The bacterial suspension for antimicrobial susceptibility testing (AST) was prepared in 5 mL of normal saline, and its turbidity was adjusted to match the 0.5 McFarland standard, ensuring an approximate bacterial concentration of 1×10^6 colony-forming units (CFU) per mL. Antibiotic discs were applied 15 minutes after inoculating Mueller-Hinton agar with each isolate, followed by incubation at 35–37°C for 18–24 hours. A sliding metal caliper measured the inhibition zone diameter around each disc. To ensure accuracy, all antibiotic susceptibility tests were conducted in triplicate.

RESULTS

Laboratory analysis of bacterial contamination revealed that all 100 tanker water samples were contaminated with bacteria. Furthermore, pathogenic bacteria were found in 15 out of 20 companies (75%). Total bacterial counts for the 20 companies (100%) in the samples ranged from 12,400 to 2,546,000 colony-forming units (CFU)/mL, with a mean ± standard deviation of 423,880 ± 10,089. Furthermore, total coliform counts for the 20 companies (100%) ranged from 1,000 to 22,654 CFU/100 mL, with a mean ± standard deviation of 56.33 ± 66.55. Fecal coliform counts for all 20 companies were zero. Additionally, in 45% of the samples, three or more than three different pathogenic organisms were isolated. *Acinetobacter baumannii* was detected from 11 distinct companies (55%), while *Staphylococcus aureus*, a known pathogen, was found in 10% of the samples or from eight companies (Table 1).

Table 1: *Analysis of total plate count, total coliform count, and fecal coliform count (count/100 mL), along with the organisms isolated from samples of 20 different companies*

S.N	Company code	No of Samples	Total Plate Count (Mean±SD)	Total Coliform Count (mean±SD)	Fecal Coliform Count (mean±SD)	Pathogen Organisms (S) Isolated
1	A	5	432600±5116566	22654±4336.19	0	*Acinetobacter baumanii, Enterobacter Cloacea, Staphylococcus Aureus*
2	B	5	387732±718399	6699±835.01	0	*Pseudomonas Aeruginosa, Enterobacter Cloacea, Staphylococcus Aureus*
3	C	5	410666±715569	1000±141.8	0	*Acinetobacter baumanii, Staphylococcus Aureus*
4	D	5	39200±37698	2000±376.81	0	*Acinetobacter baumanii,*
5	E	5	77600±96844	1500±968.2	0	*Acinetobacter baumanii*
6	F	5	55800±82147	2000±1581.71	0	*Staphylococcus Aureus*
7	G	5	113000±96581	2500±616.67	0	Gram-positive bacilli
8	H	5	43800±87482	1500±856.3	0	Gram-positive bacilli
9	I	5	6600±7829	2000±230.17 3	0	Gram-positive bacilli
10	J	5	3400±3361	2000±336.547	0	Gram-positive bacilli
11	K	5	15200±19892	2000±211.1	0	Gram-positive bacilli
12	L	5	16000±11379	1000±113.81	0	*Acinetobacter baumanii, Enterobacter Cloacea*
13	M	5	210400±441496	3000±934.447	0	*Acinetobacter baumanii*
14	N	5	2115200±4409178	3000±446	0	*Acinetobacter baumanii*
15	O	5	2546000±423880	2000±1032.796	0	*Acinetobacter baumanii, Enterobacter Cloacea*
16	P	5	12400±10089	2000±894.4272	0	*Acinetobacter baumanii, Staphylococcus Aureus*
17	Q	5	1013000±2228854	5300±237.3 2	0	*Acinetobacter baumanii*
18	R	5	465800±501392	19000±3305.99	0	*Acinetobacter baumanii, Staphylococcus Aureus*
19	S	5	189400±206755	17300±16399.7	0	*Acinetobacter baumanii, Staphylococcus Aureus*
20	T	5	823000±1286813	5000±2738.613	0	*Staphylococcus Aureus*

The laboratory results analysis indicated that seventeen distinct bacterial species were isolated from 100 samples. Among them, *Staphylococcus aureus*, a well-known pathogen, was found in 10% of the samples. Although *Acinetobacter baumannii,* recognized as a significant hospital-acquired opportunistic pathogen, was detected in 21% of the samples. *Pseudomonas oryzihabitans*, a non-pathogenic organism, was identified in 20% of the samples. In contrast, only 1% of the samples were contaminated with the opportunistic pathogen *Pseudomonas aeruginosa* (Table 2).

Table 2*: Pathogenic bacteria isolated from drinking water samples collected from distribution tankers in Kabul city*

S.N	Isolated Organism	Percentage
1	Acinetobacter baumanii	21 %
2	Pseudomonas oryzihabitans	20%
3	Staphylococcus. aureus	10%
4	Erwinia spp	9 %
5	Chromobacterium violaceum	6 %
6	Klebsiella oxytoca	6 %
7	Pantoea, Erwinia	6 %
8	Providencia alcalifaciens	6 %
9	Acinetobacter calcoaceticus	5 %
10	Brucella anthropic	5 %
11	Providencia stuartii	5 %
12	Enterobacter cloacae	4 %
13	Mannheimia haemolytica	4 %
14	Pasteurella pneumotropica	4 %
15	Pseudomonas luteola	4 %
16	Raoultella planticola	4 %
17	Pseudomonas aeruginosa	1 %

The World Health Organization sets the standard for total plate count, total coliform count, and fetal coliform count in drinking water at a level of one colony-forming unit (CFU) per 100 ml. In contrast, the European Parliament and the Council of the European Union specify that the Total Plate Count should be less than 20 CFU per ml. In comparison, the Total Coliform Count and Fecal Coliform Count should be fewer than 1 CFU per 250 ml.

Table 3: *Proportion of contamination range in drinking water samples from distribution tankers in Kabul city, based on Total Plate Count (TPC), Total Coliform Count (TCC), and Fecal Coliform Count (FCC), compared to the standards of the World Health Organization (WHO) and EPCEU*

Range per 100ml	WHOa/100mL	EPCEUb	Contaminated Tanker Water brands N (%)	Range per 100ml	Mean± SD
Total Plate Count	< 1 CFU / 100ML	<20 FU/mL	20 (100%)	12400 ±2546000	10089±423880
Total Coliform Count	< 1 CFU / 100ML	<1 CFU/250mL	20 (100%)	1000±22654	113±433
Faecal	< 1 CFU / 100ML	<1 CFU/250mL	0 (00 %)	00	00

Coliform Count				

a. World Health Organization b. European Parliament & Council of the European Union, 2009

Based on laboratory findings, we observed that the Total Plate Count, Total Coliform Count, and overall bacterial levels in the water samples from all companies exceeded the standard limits. However, Escherichia coli, a common indicator of fecal contamination, was not detected Table 3 above.

Based on the results of antibiotic susceptibility testing performed on the isolated pathogens, all strains of *Staphylococcus aureus* were found resistant to ceftazidime. Additionally, 9 out of 10 strains (90%) were resistant to amoxicillin. However, the strains exhibited varying susceptibility to different groups of antibiotics, exhibiting resistance to 13 antibiotics, while they were sensitive to 2 antibiotics, with none showing resistance to vancomycin or imipenem. Despite the common public belief that this water is safe and properly filtered, it may pose a significant health risk to consumers, especially those with weakened immune systems (Table 4).

Table 4: *Antibiotic susceptibility test of Staphylococcus aureus isolated from water sample*

Tested Antibiotic		Sensitive N (%)	Intermediate N (%)	Resistant N (%)
Penicillins	Amoxicillin + Clavulanic acid	4 (40)	2 (20)	4 (40)
	Amoxicillin	1(1)	0 (0)	9 (90)
Macrolides	Erythromycin	2 (20)	1 (10)	7 (70)
3rd generation of Cephalosporins	Ceftriaxone	1 (10)	4 (40)	5 (50)
	Ceftazidime	0 (0)	0 (0)	10 (100)
Quinolones	Levofloxacin	7 (70)	1 (10)	2 (20)
	Ciprofloxacin	7 (70)	0 (0)	3 (30)
Sulphonamides	Cotri-moxazole	5 (50)	0 (0)	5 (50)
Aminoglycosides	Gentamicin	8 (80)	0 (0)	2 (20)
	Amikacin	9 (90)	0 (0)	1 (10)
	Kanamycin	8 (80)	0 (0)	2 (20)
	Tobramycin	6 (60)	0 (0)	4 (40)
Carbapenems	Imipenem	9 (90)	1 (10)	0 (0)
Polypeptides	Vancomycin	10 (100)	0 (0)	0 (0)
Divers	Chloramphenicol	3 (30)	3 (30)	4 (40)

The antibiotic susceptibility testing conducted on 10 different bacterial strains revealed diverse resistance patterns. *Pseudomonas aeruginosa* was resistant to seven antibiotics but sensitive to six, while three distinct strains of *Enterobacter cloacae* exhibited varying levels of antibiotic resistance. *Enterobacter sakazakii* resisted seven antibiotics while remaining sensitive to eight, and Klebsiella oxytoca was resistant to six antibiotics but was sensitive to nine. *Acinetobacter baumannii* was resistant to six antibiotics and sensitive to seven. Among the isolated organisms, *Chromobacterium violaceum* exhibited resistance to at least 10 out of

the 15 tested antibiotics. Interestingly, *Pseudomonas luteola* demonstrated sensitivity to all 15 antibiotics tested (Table 5).

Table 5: *Antibiotic susceptibility pattern of only 10 bacterial pathogens isolated from tanker-distributed drinking water*

Pathogens	Antibiotics															
	VA	AMX	AMC	E	TOB	CIP	LEV	CN	SXT	CRO	IMI	CAZ	AK	C	K	No of R
Enterobacter Sakazakii	R	S	S	R	S	R	R	S	R	R	S	R	S	S	S	7
Chromo bacterium Violaceum	R	R	R	R	R	S	S	R	S	S	R	R	R	I	R	10
Enterobacter Cloacae	R	R	I	R	S	S	S	S	S	I	S	I	S	I	S	3
Enterobacter Cloacea	R	R	R	R	R	S	S	R	S	S	S	R	I	R	I	8
Enterobacter Cloacea	R	R	R	R	S	S	S	S	S	I	S	I	S	I	R	5
Enterobacter Cloacea	R	R	R	R	S	S	S	S	S	I	S	R	S	S	S	5
Klebsiella Oxytoca	R	R	I	R	S	R	S	S	S	I	S	R	S	R	I	6
Pseudomonas Luteola	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	0
Acinetobacter Baumannii	R	R	R	I	S	I	S	S	S	R	S	R	S	R	S	6
Pseudomonas Aeruginosa	I	R	R	I	S	R	R	S	S	R	S	R	S	R	S	7

VA, vancomycin, AMX, amoxicillin; AMC, amoxicillin+ clavulanic acid; E, erythromycin, ; TOB, Tobramycin, CIP, Ciprofloxacin; LEV, Levofloxacin CN, Gentamicin; SXT, Sulfamethoxazole + Trimethoprim; CRO, Ceftriaxone; IPM, Imipenem; CAZ, Ceftazidime; AK, Amikacin; C, Chloramphenicol; K, Kanamycin; S, Sensitive; and R, Resistant

DISCUSSION

Safe and adequate water is crucial for sustainable development, impacting public health, food security, and poverty reduction (Mock et al., 2017). In many developing countries, inadequate water infrastructure increases the risk of waterborne diseases (Ferreira et al., 2021). Therefore, regular water quality monitoring is essential to ensure safety and prevent outbreaks. Additionally, with growing droughts and water shortages, the need for desalination and mobile water tanks is becoming increasingly important (Hochstrat et al., 2010).

Water contamination, especially from pathogenic organisms, is a leading cause of gastrointestinal and infectious diseases. Fecal coliforms are commonly recognized as the primary indicators of water contamination and potential pathogenic microorganisms (Babaei et al., 2014). According to the World Health Organization (WHO), assessing microbial quality—including monitoring total coliforms and thermotolerant coliforms—should be prioritized in water quality control programs (WHO, 2017). Coliform bacteria, particularly thermotolerant coliforms, indicate fecal contamination and pose a significant risk to public health (Gil et al., 2014). In a study by Babaei et al. (2014), positive results for thermotolerant coliform contamination coincided with zero residual chlorine, highlighting the failure of chlorine disinfection under adverse environmental conditions. Exposure of water tanks to

unfavorable conditions, such as sunlight and heat, can lead to the dissipation of residual chlorine, increasing the risk of microbial contamination (Moghadam et al., 2020).

Studies conducted in different regions reveal varying levels of microbial contamination in drinking water. In Qom City, Iran, 13% of drinking water tanks tested positive for thermotolerant coliform contamination, highlighting the vulnerability of mobile water distribution systems when hygiene practices are inadequate(Noori Sepehr et al., 2021). In Bolivia, polyethylene tanks exhibited significantly higher *Escherichia coli* counts than fiber cement and fiberglass tanks, with water temperatures reaching 34°C in black polyethylene tanks, compared to 20°C and 23°C in fiberglass and fiber cement tanks, respectively (Schafer & Mihelcic, 2012). Mobile water tanks are economically viable in arid and semi-arid regions due to their mobility and lower initial investment costs than permanent infrastructure (Constantine et al., 2017).

Studies conducted in various countries worldwide indicate that bacterial contamination in drinking water is generally higher. In a study conducted in Iran to assess the presence of bacterial indicators of fecal contamination, 121 wells were monitored. Only 17 wells showed no indication of fecal bacterial contamination. At the same time, the remaining samples were contaminated with at least one of the following bacteria: *Escherichia coli, Shigella sp., Citrobacter sp., Klebsiella-Enterobacter group, Clostridium perfringens, or Streptococcus faecalis* (Shariatpanahi & Anderson, 1987). Compared to our study, water tankers in Kabul are more contaminated as a water source. A study conducted in Delhi, India, analyzed 36 samples from four zones across the country. The study revealed contamination with *Escherichia coli* (61%), *Salmonella* (25%), *Staphylococcus aureus* (14%), and *Pseudomonas aeruginosa* (53%). Overall, the contamination level in treated water was 53% (Chauhan et al., 2017). Although still lower than the contamination levels in treated water from tankers in our study, a 100% positive rate for thermotolerant coliforms was observed, suggesting widespread microbial contamination. Comparatively, a study by Mumtaz and their colleagues (2011) in Lahore, Pakistan, reported lower median levels of coliforms, fecal coliforms, and *Escherichia coli* in drinking water samples. While these studies highlight the presence of bacterial contaminants, the contamination level in Kabul's tanker-distributed water appears to be significantly higher.

A key finding of this study is the absence of fecal coliforms, which differs from previous research by Babaei et al. (2013) and Noori et al. (2021), where fecal coliforms were detected in water samples. This discrepancy may be attributed to environmental conditions, water sources, and handling practices.

Antibiotic resistance refers to the ability of certain microorganisms to withstand the effects of antibiotic drugs. Under such conditions, microorganisms previously sensitive to a specific drug are no longer affected by it, and the antibiotic can no longer eliminate or inhibit their growth (Uddin et al., 2021). In recent years, the widespread use of antibiotics for treating bacterial infections in humans and animals and their application as growth promoters in agriculture has led to an increase in antibiotic-resistant bacterial strains across

various environments (Ma et al., 2021). This issue has posed significant challenges to the treatment of infections. The overuse and irrational prescription of antibiotics are the main factors contributing to the rise in bacterial resistance(Kilari & Oroszi, 2024).

Several reports have highlighted the presence of antibiotic-resistant bacteria in aquatic environments. For example, studies have shown that vancomycin-resistant enterococci (VRE) have been detected in the feces of individuals with no history of hospitalization or antibiotic consumption (Manaia et al., 2018). Moreover, VRE has also been found in livestock feces, animal products, sewage, and surface waters (Ma et al., 2021). Besides therapeutic applications, antibiotics are frequently used to promote the growth of livestock and poultry. A substantial portion of these antibiotics is excreted unchanged into the environment, leading to concerns about the potential impact of antibiotic residues on aquatic ecosystems (Mohammadi Kouchesfahani et al., 2015).

The presence of antibiotic-resistant bacteria and antibiotic-resistance genes (ARGs) in drinking water sources is a serious concern (Sanganyado & Gwenzi, 2019). These factors can persist in nature and facilitate the spread of resistance genes, ultimately increasing the prevalence of pathogenic strains. The excessive use of beta-lactam antibiotics, such as penicillins, cephalosporins, and carbapenems—commonly prescribed to treat Pseudomonas aeruginosa infections—has resulted in increased resistance in this bacterium (Glen & Lamont, 2021).

Recent studies have indicated that antibiotic resistance genes (ARGs) exist in drinking water sources (Jia et al., 2015). These enzymes can hydrolyze beta-lactam antibiotics and are predominantly found in *Pseudomonas* spaces and *Acinetobacter* bacteria (Walsh, 2005). Drinking water sources, especially those contaminated with urban, hospital, or agricultural wastewater, can harbor ARGs and diverse pathogenic bacteria. Some bacteria can survive and multiply in aquatic environments due to disinfectant resistance.

Studies have demonstrated that chlorination for drinking water disinfection may contribute to the proliferation of antibiotic-resistant bacteria in water systems (Cabral, 2010). Our findings indicate that resistant microorganisms against different antibiotics in water tankers pose a significant public health threat. Research has shown that antibiotic resistance persists during water treatment and even after distribution through water supply networks.

Treatment procedures may sometimes enhance the survival of resistant bacteria, and water distribution systems can serve as a reservoir for spreading antibiotic resistance to opportunistic pathogens (Baquero et al., 2008). Therefore, secondary contamination's role in reducing water quality from tanks is very evident. Water supply companies should enforce strict cleaning protocols, ensure regular disinfection of tanks, and train personnel on hygiene standards during water transportation and distribution. Given the current situation, considering the region's climate and frequent droughts, desalination devices and mobile tanks remain a practical solution for water supply.

Implementing residual chlorine monitoring throughout the distribution process is vital to prevent microbial contamination (U.S. Environmental Protection Agency, 2007). Our study emphasizes the urgent need for improved hygiene practices in water distribution systems that rely on tankers around Kabul city.

CONCLUSION

The findings of the evaluation of bacterial contamination in treated drinking water distributed by tankers in Kabul City indicate that the microbial quality of tanker water does not meet World Health Organization standards. All tanker water samples showed bacterial levels far above acceptable limits. Additionally, two brands of distributed tankers were contaminated with multiple pathogens, indicating that the water quality is substandard. Pathogenic and opportunistic organisms and several antibiotic-resistant pathogens, such as Staphylococcus aureus and *Acinetobacter baumannii,* were detected in water samples from various distributors in Kabul City. Interestingly, we did not find *Escherichia coli* or fecal coliform factors, indicating that the contamination of the water tanker was not due to fecal contamination. This situation suggests that several factors, including the water collection containers, tank washing procedures, contamination of outlet taps, contact with dust, distributor hygiene, temperature, water storage duration, and environmental sanitation, influence microbial quality. These variables should be considered in future research. Therefore, appropriate planning, site selection, and continuous monitoring are essential to ensure the safety and quality of drinking water. In addition to periodic evaluations and regular monitoring of these stations, it is crucial to provide distributors with the necessary training on maintenance and hygiene compliance. Future research should also focus on investigating specific pathogens and patterns of antimicrobial resistance in water distribution systems to assess public health risks better.

Conflict of Interest: The author(s) claimed no conflict of interest.

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