



Review article

Occurrences and implications of pathogenic and antibiotic-resistant bacteria in different stages of drinking water treatment plants and distribution systems

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ABSTRACT

Different stages of drinking water treatment plants (DWTPs) play specific roles in diverse contaminants' removal present in natural water sources. Although the stages are recorded to promote adequate treatment of water, the occurrence of pathogenic bacteria (PB) and antibiotic-resistant bacteria (ARB) in the treated water and the changes in their diversity and abundance as it passed down to the end users through the drinking water distribution systems (DWDSs), is a great concern, especially to human health. This could imply that the different stages and the distribution system provide a good microenvironment for their growth. Hence, it becomes pertinent to constantly monitor and document the diversity of PB and ARB present at each stage of the treatment and distribution system. This review aimed at documenting the occurrence of PB and ARB at different stages of treatment and distribution systems as well as the implication of their occurrence globally. An exhaustive literature search from Web of Science, Science-Direct database, Google Scholar, Academic Research Databases like the National Center for Biotechnology Information, Scopus, and SpringerLink was done. The obtained information showed that the different treatment stages and distribution systems influence the PB and ARB that proliferate. To minimize the human health risks associated with the occurrence of these PB, the present review, suggests the development of advanced technologies that can promote quick monitoring of PB/ARB at each treatment stage and distribution system as well as reduction of the cost of environmental analysis to promote better microbial analysis.

1. Introduction

For the reduction of human health risks associated with exposure to contaminated and untreated drinking water, a reliable supply of safe drinking water is needed. The supply of safe drinking water depends on the effectiveness of different stages of drinking water treatment plants (DWTPs) and adequately maintained drinking water distribution systems (DWDSs) [1,2]. Consumption of drinking water contaminated with micropollutants, and microorganisms is a serious human health risk that any country cannot permit [1,2]. Satterthwaite [3] stated that research by the WHO indicates that about 80% of diseases globally are linked to the consumption and use

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of contaminated drinking water. Although organic pollutants create serious human health challenges in drinking water, contamination of drinking water by microbes especially PB as well as both non-pathogenic and pathogenic antibiotic-resistant bacteria (ARB) is of more concern as most water-associated health problems are connected to their proliferation, especially in the final treated water that gets to the end users [4–6].

Studies have shown incidences of pathogenic bacterial communities in drinking water with an implication of increased human exposure and considerable health risk [7,8]. In addition, due to increased anthropogenic activities and incessant intake of antibiotics, many PB have acquired antibiotic-resistant genes (ARGs) and become pathogenic ARB. According to Sevillano et al. [9], antimicrobial resistance by PB is common in both treated and untreated drinking water which creates a great concern about the microbial reduction/eradication role of the different drinking water treatment processes especially for the treated water. Given the occurrence of these PB and ARB in the drinking water system, the need for constant monitoring of the changes in their abundance and diversity at the different drinking water treatment processes and along the distribution system becomes pertinent.

Sedimentation and filtration processes/stages have been used in many DWTPs for the purification of drinking water to remove solid particles as well as microorganisms. However, studies have shown the need for the improvement of these stages to control the proliferation of PB as well as pathogenic and non-pathogenic ARB [10]. A more advanced barrier to PB and ARB proliferation in the DWTPs is the disinfection stage. This stage is exceptional in the reduction of the abundance of PB and their spread to the DWDSs [8]. Chlorine is an oxidant that is widely used in the disinfection stage. Other disinfectants used include chloroamine, ozone, and UV light [11,12]. To ensure the maintenance of the microbiological safety of the final treated water, a constant concentration of residual chlorine is maintained as the water moves down the pipeline in the distribution system [13–15].

Despite the positive impact of the disinfection stage in the eradication of PB and ARB, the detection of PB and pathogenic ARB belonging to the genera *Acinetobacter*, *Burkholderia* and *Pseudomonas* in the final treated water and along the distribution system pose great concerns [16–18]. In addition, the leaching of Phthalate esters (PAEs) from the plastic pipes in the distribution system promotes biofilm formation and development of chlorine-resistant microbes which could be pathogenic [19,20]. This calls on the need to validate the effectiveness of the different stages of DWTPs and access the inherent conditions within the DWDSs that promote the proliferation of PB and ARB as well as decade-per-decade evaluation of the progressive improvement of the different stages of the treatment concerning the diverse adopted modifications plans and technologies.

In this review, a publication search on Web of Science, Science-Direct database, Google Scholar, and Academic Research Databases such as National Center for Biotechnology Information (NCBI), Scopus, and SpringerLink was performed between February 2023 and September 2023 on PB and ARB in the different stages of DWTPs and different components of DWDSs such as pipelines and tap water. The following term combinations were used in this research: “PB” and “ARB” or “drinking water treatment plants” or “drinking water distribution systems” or “human health risk associated with PB and ARB in drinking water” and “pathogenic ARB” or “PB and ARB in different stages of drinking water treatment plants” and “contributing factor to the growth of PB in drinking water treatment plants” or “contributing factor to the growth of PB in drinking water distribution systems”. The literature search was not limited by publication year or publication language. After an exhaustive search, 208 publications were selected and scholars whose previous works were relevant to the scope of the study utilized were cited. Furthermore, the authors identified numerous gaps with recommendations highlighted in the conclusion of the review.

2. Spatial changes in pathogenic bacterial communities from natural water sources through the different stages of drinking water treatment plants to distribution system

DWTPs stand as an intermediary between the natural water sources and the end user’s consumption of potable water that aligns with public health regulations. The treatment processes of DWTPs alter the physicochemical and biological profiles of natural water sources positively to ensure the good health of the populace [21,22]. Hence, adequate performance of all the processes involved in the DWTPs is vital to ensure the treated water safety, and maintenance of the microbial load and diversity within the stipulated standard because of the direct linkage between the treatment processes and the occurrence and distribution of pathogens that are of public health concerns [23].

2.1. Natural water sources

The natural water which serves as the source of water for the DWTPs is the receiving end of most human settlement activity as well as other anthropogenic activities due to increased population and high levels of urbanization and industrialization [24,25]. Deterioration of water quality in most countries has been linked to the increase in industrial processes, domestic sewage discharge, agricultural chemicals, and eroded soil [26,27]. This is due to the proximity between the industries, domestic houses, agricultural farmlands as well as wastewater treatment plants (WWTPs) and natural water sources like rivers resulting in the direct discharge of their waste or final effluents in the case of WWTPs into the natural water sources [28,29]. This discharge contributes to the increase in the load and diversity of PB present in the natural water source.

Agricultural practices such as manure application contribute to the load and diversity of PB in natural water sources [30–32]. Thurston-Enriquez et al. [33] evaluated the movement of pathogens from agricultural fields to natural waters as well as the concentration of human health-related pathogenic microbes in the runoff from the plots treated with manure. They observed that heavy precipitation events producing runoffs from the manure-treated plots caused large microbial loads that are capable of impacting water bodies within the watershed. The enrichment of surface water with nutrients is particularly high in the region of the world where industrial activities and agricultural practices as well as local and international trading are intense [34,35]. This nutrient enrichment

causes harmful algal blooms in surface water sources leading to the degradation of the structure and functioning of surface water ecosystems as well as promoting the growth of microorganisms including PB that are detrimental to human health [36–40]. In addition, the proliferation of these microorganisms results in an increased oxygen consumption creating a state of hypoxia in the surface water ecosystem which is also a great ecological concern. About 27 % of rivers, 25 % of lakes, 37 % of transitional waters, and 46 % of coastal water bodies of the European Union are impacted by nutrient pollution with the likelihood of extending to 413,000 km of the EU27, the United Kingdom, Norway, and Switzerland stream network [41–43].

Environmental factors that include pollutants and hydrological conditions affect the surface water ecosystems leading to the alteration of the microbial compositions and the emergence of pathogenic microbes of high human health risks [44–47]. In surface waters like rivers, due to the sensitivity of the microbial communities to the changes in the environment, the microbial communities show high possibility of changing with temporo-spatial variations in the environmental conditions [48]. Some studies have indicated a greater impact of seasonal differences (temperatures and water levels among seasons) in the selection of bacteria that proliferate in the

Table 1

Occurrence of pathogenic bacteria in natural water sources, different stages of drinking water treatment plant, and distribution systems.

Raw Water, Stages of Treatment and Distribution	Country	Pathogenic Bacteria (Genera/Species) Detected	References
surface raw water	Belgium	<i>Pseudomonas aeruginosa</i>	[54]
	China	<i>Aeromonas veronii</i> , <i>Rhodococcus erythropolis</i> , <i>Pseudomonas fluorescens</i> and <i>Aeromonas hydrophila</i> ; <i>Legionella</i> spp., <i>Mycobacterium</i> spp., <i>Mycobacterium avium</i> , <i>Pseudomonas aeruginosa</i> ; <i>Pseudomonas</i> , <i>Acinetobacter</i> , <i>Citrobacter</i> , <i>Mycobacterium</i> , <i>Salmonella</i> ,	[7,57,60,61]
	Brazil	<i>hydrophila</i> ; <i>Legionella</i> spp., <i>Mycobacterium</i> spp., <i>Mycobacterium avium</i> , <i>Pseudomonas aeruginosa</i> ; <i>Pseudomonas</i> , <i>Acinetobacter</i> , <i>Citrobacter</i> , <i>Mycobacterium</i> , <i>Salmonella</i> ,	[62,63]
	Barcelona	<i>hydrophila</i> ; <i>Legionella</i> , <i>Streptococcus</i> , <i>Enterococcus</i> ; <i>Escherichia coli</i> , <i>Salmonella</i> spp.,	[23]
	USA	<i>Staphylococcus</i> , <i>Legionella</i> , <i>Streptococcus</i> , <i>Enterococcus</i> ; <i>Escherichia coli</i> , <i>Salmonella</i> spp.,	[64]
	South	<i>Shigella</i>	[65–67]
	Africa	<i>Escherichia coli</i> O157:H7, <i>Shigella flexneri</i> , and <i>Shigella boydii</i> ; <i>Staphylococcus aureus</i>	[68]
	Nigeria	<i>Clostridium perfringens</i> and <i>Escherichia coli</i>	[69]
	Kenya	<i>Staphylococcus aureus</i>	[70]
	Norway	<i>Aeromonas</i> and <i>Pseudomonas</i> species; <i>Staphylococcus aureus</i> ; <i>Shigella</i> spp.	[39]
	Nepal	<i>Escherichia coli</i> , <i>Staphylococcus aureus</i> , <i>Klebsiella</i> spp., and <i>Shigella</i> spp.	[71–73]
	India	<i>Escherichia coli</i>	[74]
	Russia	<i>Escherichia coli</i>	[75]
	Burkina	<i>Escherichia coli</i>	[76]
	Faso	<i>Escherichia coli</i> ; <i>Klebsiella</i> spp.; <i>Salmonella</i> spp.	[77]
	Uganda	<i>Klebsiella</i> spp.	[78]
	Haiti	<i>Vibrio cholerae</i>	[79]
	Canada	<i>Vibrio cholerae</i>	[80]
	Netherlands	<i>Vibrio cholerae</i>	[81]
	Sedimentation	Czech	<i>Salmonella</i> spp.
Republic		<i>Salmonella</i> spp.	
Filtration	France	<i>Salmonella</i> spp. <i>Shigella</i> spp.	
	China	<i>Aeromonas veronii</i> , <i>Rhodococcus erythropolis</i> , <i>Pseudomonas fluorescens</i> and <i>Aeromonas hydrophila</i> ; <i>Legionella</i> spp., <i>Mycobacterium</i> spp., <i>Mycobacterium avium</i> , <i>Pseudomonas aeruginosa</i>	[7,57]
Disinfection	China	<i>Aeromonas veronii</i> , <i>Rhodococcus erythropolis</i> , <i>Pseudomonas fluorescens</i> and <i>Aeromonas hydrophila</i> ; <i>Legionella</i> spp., <i>Mycobacterium</i> spp., <i>Mycobacterium avium</i> , <i>Pseudomonas aeruginosa</i> ; <i>Aeromonas hydrophila</i> , <i>Aeromonas veronii</i> , <i>Brucella suis</i> , <i>Pseudomonas aeruginosa</i> ; <i>Citrobacter</i> , <i>Rhodoplanes</i> , <i>Pseudomonas</i> , and <i>Acinetobacter</i>	[7,10,57,60]
	USA	<i>Mycobacterium</i> spp. and <i>Legionella</i> spp.; <i>Pseudomonas</i> , <i>Acidovorax</i> , <i>Sphingomonas</i> , <i>Pleomonas</i> , and <i>Undibacterium</i> ; <i>Pseudomonas fluorescens</i> , <i>Rhodococcus erythropolis</i> , <i>Rhodococcus fascians</i> , and <i>Bacillus thuringiensis</i> ; <i>Aeromonas hydrophila</i> , <i>Bordetella pertussis</i> , <i>Brucella suis</i> , <i>Enterobacter aerogenes</i> , <i>Pseudomonas aeruginosa</i> , <i>Shigella sonnei</i> , <i>Staphylococcus saprophyticus</i> , and <i>Streptococcus pneumoniae</i> , <i>Pseudomonas</i> , <i>Acinetobacter</i> , <i>Citrobacter</i> , <i>Mycobacterium</i> , <i>Salmonella</i> , <i>Staphylococcus</i> , <i>Legionella</i> , <i>Streptococcus</i> , <i>Enterococcus</i> , <i>Mycobacterium</i> spp. and <i>Blastococcus</i> spp.	[10,57,82,83, 60]
Final treated water	South	<i>Mycobacterium mucogenicum</i> , <i>Mycobacterium phocaicum</i> , <i>Mycobacterium triplex</i> , <i>Mycobacterium fortuitum</i> , and <i>Mycobacterium lentiflavum</i>	[84]
	Africa	<i>Aeromonas</i> and <i>Pseudomonas</i> spp.	[85]
Distribution system	South	<i>Escherichia coli</i> , <i>Vibrio cholerae</i> , and <i>Shigella</i> spp.	[86]
	Africa		
	China	<i>Legionella</i> spp., <i>Mycobacterium</i> spp., <i>Mycobacterium avium</i> , <i>Pseudomonas aeruginosa</i> ;	[7,10,57,87]
	Hungary	<i>Pseudomonas fluorescens</i> , <i>Mycobacterium gordonae</i> , <i>Mycobacterium mucogenicum</i> , <i>Mycobacterium smegmatis</i> , <i>Mycobacterium fortuitum</i> and <i>Mycobacterium chelonae</i> ; <i>Burkholderia mallei</i> , <i>Mycobacterium tuberculosis</i> , <i>Klebsiella pneumoniae</i> , <i>Acinetobacter calcoaceticus</i> , <i>Escherichia coli</i> , and <i>Pseudomonas aeruginosa</i> ; <i>Leptospira interrogans</i> and <i>Pseudomonas aeruginosa</i>	[88]
Distribution system	South	<i>Legionella</i> spp., <i>Pseudomonas aeruginosa</i> , <i>Escherichia albertii</i> , <i>Acinetobacter lwoffii</i> , and <i>Corynebacterium tuberculostearicum</i>	[65,85,86, 89]
	Africa	<i>Legionella</i> spp., <i>Pseudomonas aeruginosa</i> , <i>Escherichia albertii</i> , <i>Acinetobacter lwoffii</i> , and <i>Corynebacterium tuberculostearicum</i>	
		<i>Escherichia coli</i> , <i>Vibrio cholerae</i> , and <i>Shigella</i> spp.; <i>Aeromonas</i> and <i>Pseudomonas</i> spp.; <i>Aeromonas</i> and <i>Pseudomonas</i> spp.; <i>Escherichia coli</i> , <i>Salmonella typhimurium</i> , <i>Shigella dysenteriae</i> , <i>Vibrio cholerae</i>	

rivers than spatial differences [49,50].

According to Wang et al. [48], urban rivers' ecosystems are spatially heterogeneous and majorly impacted by terrestrial environments. Among the terrestrial environmental factors, human activities contribute to diverse point source and non-point source pollution such as the release of sediment pollutants and surface runoff caused by rainfall events [51,52]. Hou et al. [53] investigated the infectious risk of the Qiu Jiang River in Shanghai, China and observed that the concentrations of K^+ , and NH_4^+-N as impacted by pollution influenced the growth of the bacteria with high infectious risk of intestinal and lung infectious diseases due to the presence of opportunistic pathogens such as *Enterobacter cloacae complex* and *Klebsiella pneumoniae*. In Belgium, the biodiversity of *Pseudomonas aeruginosa*, a human pathogenic bacterium, was evaluated for a river bimonthly for a year at seven sites evenly dispersed with a positive relationship being observed between the extent of pollution and the prevalence of *P. aeruginosa* [54]. The river was further identified to be laden with a diverse *P. aeruginosa* population with nearly all known clonal complexes [55,56]. These findings implied that river water is a reservoir and source of potentially pathogenic *P. aeruginosa* strains that can affect human health negatively if not properly removed by DWTPs. This assumption could be justified by the presence of the strains of *P. aeruginosa* in the different stages of DWTPs as shown in Table 1. In China, Jiang et al. [57] observed the abundance of *Aeromonas veronal*, *Rhodococcus erythropolis*, *Pseudomonas fluorescens* and *Aeromonas hydrophile* in surface water. Studies have shown that there are distinct variations in the bacterial composition and population between tap water and natural water sources because of the impact of the different treatment stages in DWTPs as well as pipeline transportation of treated water [58,59].

2.2. Coagulation-flocculation, sedimentation, and filtration stages

In relationship to treatment and treatment objectives at each stage, pathogenic populations from the raw water undergo significant changes. Jiang et al. [57] metagenomically assessed the variations in the bacterial communities and potentially PB in DWTP in China. Their result showed clear variation in the bacterial composition and PB in the natural water source and DWTP. The authors observed a decrease in the abundance of *Aeromonas veronal*, *Rhodococcus erythropolis*, *Pseudomonas fluorescens* and *Aeromonas hydrophile* after the sedimentation and filtration stages. This implied that these stages play a crucial role in the reduction of the diversity of the PB, but the limitation is the inability of these stages to completely eradicate the PB. This limitation is justified by the abundant proliferation of *Pseudomonas* in filtered water obtained from DWTP [10]. In addition, the increase in the abundance of *Legionella* spp., *Mycobacterium* spp., *M. avium*, *P. aeruginosa* after filtration provides another justification to the limitation of these stages of DWTPs [7].

2.3. Disinfection stage

The stage serves as a solid barrier to the growth of potentially PB and ensures the microbiological safety of drinking water [59]. With disinfectant added, and a constant concentration of the residual chlorine maintained, treated water is expected to remain sterile [14,15,90]. However, variations in the abundance of PB have been reported after the use of different disinfectants. Genus *Deliveroo*, *Optus*, and *Gp6* decreased after chlorination whereas genus *Sphenodons* and *Aciduria* increased [82]. Phylum *Chlorolipid* almost disappeared after disinfection by sodium hypochlorite [91]. Genus *Nitrosomonas* and *Gallionella* increased after chloramination [92]. Genus *Legionella*, *Escherichia*, *Coxiella*, *Yersinia*, *Sphenodons*, and *Mycobacterium* increased during monochloramine treatment [93]. This implied that the oxidants used, select for some PB (*Legionella*, *Escherichia*, *Coxiella*, *Yersinia*, and *Mycobacterium*) which could withstand their oxidation property.

Furthermore, more studies have shown that chlorine disinfection may select for some chlorine-resistant opportunistic pathogens like *Mycobacteria* spp. and *Pseudomonas* spp [94,95]. In agreement with Ma et al. [83], opportunistic pathogens like *Mycobacterium* spp. and *Legionella* spp. increased in their relative abundance after the application of $NaClO$ during the disinfection stage and was passed down to the distribution system. *Pseudomonas aeruginosa* has been reported as the most prevalent *Pseudomonas* spp. in post-chlorination drinking water [82,96]. Recently, *Pseudomonas fluorescens* was discovered as the most dominant *Pseudomonas* sp. in the post-chlorination samples [57]. This could be attributed to them belonging to the same genera and to possess same ability to withstand the toxicity of chlorine and proliferate. *P. fluorescens* could be referred to as an emerging opportunistic pathogenic bacterium in DWTP, hence there is need for more research on the factors that enhance its proliferation as well as its pathogenicity and virulence potential. Opportunistic pathogens tend to survive in distribution systems after drinking water treatment because some develop adaptive features and mechanisms that include slow growth and decay rates, oligotrophy, formation of protective biofilms, and resistance to disinfection and heat [97–99].

2.4. Distribution system

A clear variation in the opportunistic PB in DWTPs and DWDSs was observed by Huang et al. [7]. The authors observed that *Legionella* spp., *Mycobacterium* spp., *M. avium*, *P. aeruginosa* were abundant in the natural water source, sedimentation stage, and filtration stage but significantly removed in the disinfected water. Strikingly, they re-emerged in the distribution system and appeared in the tap water [7]. Although the reason behind this was not stated in the study, it can be suggested that there could be some inherent factors such as a decline in residual chlorine concentration within the distribution system that selects those pathogens which are resistant to chlorine or other disinfectants. Jiang et al. [57] observed increased proliferation of *Pseudomonas fluorescens*, *Mycobacterium gordonae*, *Mycobacterium mucogenicum*, *Mycobacterium smegmatis*, *Mycobacterium fortuitum* and *Mycobacterium chelonae* in the drinking water distribution system in three water sampling points located 10 km, 30 km, and 40 km away from the waterworks respectively. The similarity in the pathogen's composition could be attributed to their proximity to the waterworks. Table 1 provides more data on the

PB occurrences in the natural water sources, different stages of treatment plants and the distribution systems. Furthermore, percentage occurrence of the PB genera based on studies from 2013 to 2023 on the different treatment stages in DWTPs and distribution system is summarised in Fig. 1. This provides an overview of the differential selection of PB genera by the different treatment stages (Fig. 1).

3. Dynamics of antibiotic-resistant bacteria from natural water sources through the different stages of drinking water treatment plants to distribution system

Microorganisms are faced with diverse challenges in their environment including chemical pollutants, competition for food against other macro-and-microorganisms, attacks from other organisms, etc. In the quest to survive, the microorganisms tend to find coping mechanisms such as the secretion of chemical antimicrobial substances called antibiotics whose identification dates to the time of Alexander Fleming in 1928 [100–102]. Despite the usefulness of these antibiotics, their abuse in the health and agricultural industries has led to the discharge of large amounts of antibiotics through human and livestock faeces into the environment. The antibiotic molecules persist in the discharged environment and promote the emergence of both pathogenic and non-pathogenic ARB through the acquisition of antibiotic-resistant genes (ARGs) which are distributed from one environment to another environment including natural water sources [103–105].

3.1. Natural water sources

Natural water which serves as a source of water for the DWTPs is faced with the challenge of increased ARB due to the direct discharge of domestic, industrial, and agricultural wastewater laden with antibiotics and the release of treated water from the WWTPs which contain some residues of antibiotics and ARGs that was not properly removed through the treatment processes [106,107]. This affects the natural water ecosystem and diversity of microorganisms including the pathogenic and non-pathogenic ARB. In south-east Louisiana, the USA, Bergeron et al. [108] reported the abundance of *E. coli*, *Enterobacter cloacae*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* (pathogenic ARB) in the natural water source. After some months, the ARGs analysis was done to see the release of ARGs into the water, *sulI* and *tetA* resistance genes were dominant in the natural water source [109]. This implied that the PB acquired the ARGs from the natural water or released them into the water. This creates a critical challenge for the DWTPs whose function is to ensure the safety of the drinking water through total removal of the ARBs and associated ARGs.

3.2. Coagulation-flocculation, sedimentation, and filtration stages

Coagulation and sedimentation comprise the major factors that contribute to the efficiency of water treatment. However, in recent years, there has been a paucity of studies on the effect and mechanism of removing the ARGs and ARB by coagulation and sedimentation in DWTPs as well as identification of the diversity of ARBs present during and after these treatment processes which may be one of the directions of development in the field. Based on the ability of coagulation and sedimentation processes to remove PB, it is believed that the process can also influence the removal of ARGs and ARB. Most work done has been focusing on the impact of the

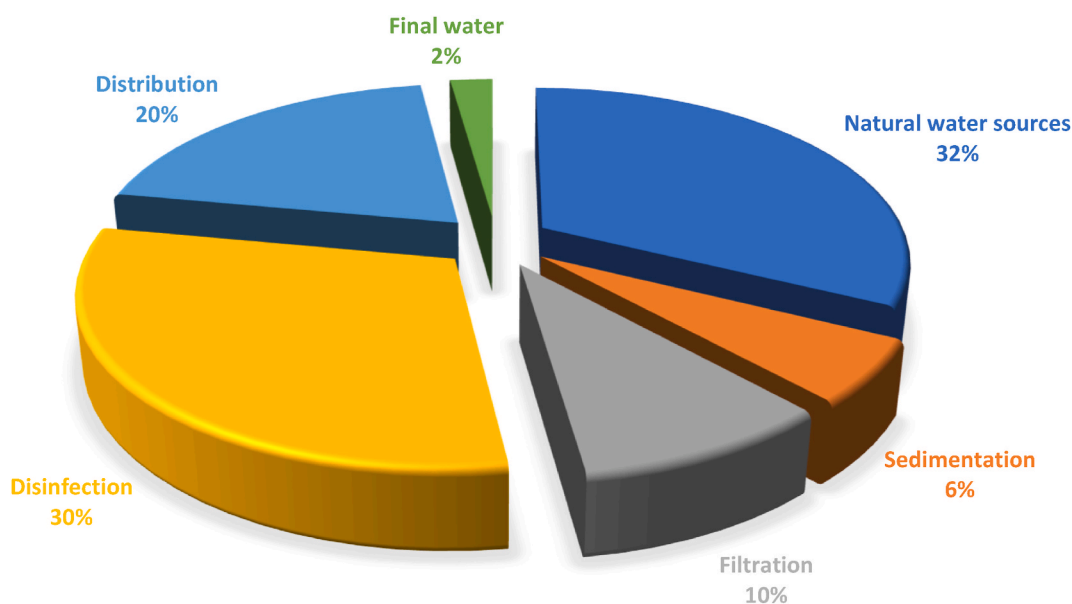


Fig. 1. Percentage occurrence of the pathogenic bacteria genera across the different stages of drinking water treatment plants and distribution system based on the collated information from studies between 2013 and 2023 (a decade).

filtration process and the use of different filtration materials in the removal of ARGs in DWTPs [110–112]. Su et al. [112] observed increased proliferation of *Pseudomonas* alongside the increase in the dissemination of ARGs in the filtration stage of drinking water treatment and suggests that *Pseudomonas* could be a facilitator in the ARGs increase and abundance of pathogenic ARB in the stage of treatment. Ke et al. [113] further observed a high relative abundance of the genera *Mycobacteria* and *Sphingopyxis* after activated carbon filtration. The presence of these pathogenic ARBs during and after the filtration stages indicates the need for future studies to be geared towards advance optimization of the process and the materials employed.

3.3. Disinfection stage

Variations in the ARBs diversity and abundance in this stage are inevitable because of the difference in the type of oxidants (disinfectant) employed by the different DWTPs globally [9,95,114]. The bactericidal action of these oxidants could create an environment for the release of ARGs from lysed bacterial cells possessing the genes which could be transferred horizontally within different species or vertically from the same species leading to the increase in the diversity of ARB. This is supported by some studies where the authors observed that disinfectant selects and enriches ARB [115–118]. Recently, Ke et al. [113] also observed increased proliferation

Table 2
Antibiotic-resistant bacteria in the different stages of drinking water treatment plant and distribution systems.

Raw Water, Stages of Treatment and Distribution	Country	Antibiotic-Resistant Bacteria (Genera/Species) Detected	References
Surface raw water	USA	<i>Escherichia coli</i> , <i>Enterobacter cloacae</i> , <i>Klebsiella pneumoniae</i> , and <i>Pseudomonas aeruginosa</i>	[108]
	China	<i>Escherichia</i> spp., <i>Enterobacter</i> spp., <i>Klebsiella</i> spp., and <i>Acinetobacter</i> spp.; <i>Mycobacterium</i> ,	[11,94]
	Nigeria	<i>Synechococcus</i> , <i>Planctomycetaceae</i> , <i>Actinobacteria</i> , and <i>Rhodobacter</i>	[131]
	India	<i>Escherichia coli</i> , <i>Enterobacter aerogenes</i> and <i>Klebsiella pneumoniae</i>	[132]
	USA	<i>Escherichia coli</i> , total coliform, and fecal coliform	[133]
	Chile	<i>Escherichia coli</i> , <i>Citrobacter freundii</i> , and <i>Enterobacter cloacae</i>	[134]
	USA	<i>Aeromonas</i> spp.	[135]
	Nigeria	<i>Enterococcus</i> spp., <i>Escherichia coli</i> , and fecal coliforms.	[136]
	Guinea-	<i>Escherichia coli</i> , <i>Salmonella typhi</i> , <i>Shigella</i> spp.	[137]
	Bissau	Fecal coliforms and fecal enterococci	[138]
	Nigeria	<i>Bacillus</i> , <i>Micrococcus</i> , <i>Pseudomonas</i> , <i>Streptococcus</i> , <i>Proteus</i> , and <i>Staphylococcus</i> spp.	[139]
	South Africa	Faecal coliforms, faecal <i>Streptococci</i> and <i>Escherichia coli</i> .	[140]
	Iran	<i>Enterococcus faecium</i>	[141]
	Cameroon	<i>Vibrio cholerae</i>	[142]
	France	<i>Escherichia coli</i> and <i>Pseudomonas</i> spp.	
Filtration Sludge	China	<i>Pseudomonas</i> spp.	[112]
	Norway	<i>Achromobacter</i> , <i>Arcicella</i> , <i>Chitinophaga</i> , <i>Chryseobacterium</i> , <i>Comamonas</i> , <i>Ferruginibacter</i> , <i>Flaviumibacter</i> , <i>Flavobacterium</i> , <i>Granulicella</i> , <i>Heliomonas</i> , <i>Herbaspirillum</i> , <i>Micrococcus</i> , <i>Mucilagibacter</i> , <i>Mycobacterium</i> , <i>Pannonibacter</i> , <i>Parasediminibacterium</i> , <i>Pedobacter</i> , <i>Phreatobacter</i> , <i>Polaromonas</i> , <i>Reyranella</i> .	[120]
Disinfection stage	Lebanon	<i>Aeromonas</i> spp.	[143]
	Portugal	<i>Sphingomonadaceae</i> , <i>Klebsiella</i> , <i>Raoultella</i> .	[144]
	China	<i>Enterobacter</i> , and <i>Citrobacter</i>	[11,145],
	Poland	<i>Pseudomonas</i> , <i>Massilia</i> , <i>Acinetobacter</i> , <i>Sphingomonas</i> , <i>Methylobacterium</i> , and <i>Brevundimonas</i> ; <i>Bacillus</i> spp., <i>Sinorhizobium</i> spp., <i>Bradyrhizobiaceae</i> spp., <i>Comamonadaceae</i> spp., <i>Enterobacter hormaechei</i> , <i>Sphingomonas</i> spp., <i>Enterobacter</i> spp., and <i>Ensifer</i> spp.; <i>Escherichia</i> , <i>Acinetobacter</i> , <i>Aeromonas</i> , <i>Pseudomonas</i> , <i>Bacteroides</i>	[2,146]
Distribution system	USA	<i>Mycobacterium frederiksbergense</i> , <i>Brevundimonas mediterranea</i> , and <i>Bacillus zhangzhouensis</i> .	
	USA	<i>Pseudomonas stutzeri</i> and <i>Pseudomonas diminuta</i>	[148]
	Nigeria	<i>Escherichia coli</i> , <i>Enterobacter aerogenes</i> and <i>Klebsiella pneumoniae</i>	[131]
	India	<i>Escherichia coli</i> , total coliform, and fecal coliform	[132]
	Scotland	<i>Paenibacillus</i> , <i>Burkholderia</i> , <i>Escherichia</i> , <i>Sphingomonas</i> , and <i>Dermacoccus</i> ;	[126,127]
	Poland	<i>Brevundimonas</i> spp. and <i>Pseudomonas</i> spp.	[149]
	Argentina	<i>Pseudomonas</i> and <i>Citrobacter</i>	[150]
	India	<i>Klebsiella oxytoca</i> , <i>Enterobacter aerogenes</i> , and <i>Enterobacter cloacae</i>	[151]
	Brazil	Thermotolerant <i>Escherichia coli</i>	[152]
	Canada	<i>Aeromonas</i> spp.	[153]
	Fiji	<i>Escherichia coli</i>	[154]
	Portugal	Heterotrophic and fecal coliform bacteria	[144]
	India	<i>Sphingomonas</i> and <i>Sphingobium</i>	[155]
	Kuwait	<i>Escherichia coli</i>	[156]
	Bangladesh	<i>Cupriavidus</i> , <i>Pseudomonas</i> , <i>Bacillus</i> , and <i>Paenibacillus</i>	[157]
	Tanzania	<i>Escherichia coli</i>	[158]
	India	<i>Escherichia coli</i>	[159]
	Nigeria	<i>Escherichia coli</i>	[160]
	Iran	<i>Bacilli</i> , α - <i>Proteobacteria</i> , β - <i>Proteobacteria</i> , γ - <i>Proteobacteria</i> , <i>Flavobacteriia</i> , and <i>Actinobacteria</i> spp.	[161]
	Cameroon	<i>Helicobacter pylori</i>	[141]
France	<i>Vibrio cholerae</i> O1	[142]	
		<i>Escherichia coli</i> and <i>Pseudomonas</i> spp.	

of the genera *Sphingomonas*, *Limnohabitans*, *Polynucleobacter*, *Candidatus*, *Brevundimonas*, and *Sphingobium* in the disinfection stage.

3.4. Produced sludge

Produced sludge is a by-product of the water treatment process and can be taken as a simple type of waste that can be considered as an extra revenue source in the case of other beneficial applications [119]. To save the cost of disposal, the reuse of produced sludge is an end-point solution that is believed to be a sustainable and favoured disposal option. Given this reuse option, it becomes pertinent to evaluate the microbial composition of the sludge to identify PB and ARB that are of economic interest to ensure the health of our crops and human who depends on the yield from the plants. Ullmann et al. [120] examined the ARB in sludge samples from Norwegian drinking water treatment plants. The authors identified 20 bacterial genera that were resistant to the aminoglycoside such as *Achromobacter*, *Arcicella*, *Chitinophaga*, *Chryseobacterium*, *Comamonas*, *Ferruginibacter*, *Flaviumibacter*, *Flavobacterium*, *Granulicella*, *Helimonas*, *Herbaspirillum*, *Micrococcus*, *Mucilaginibacter*, *Mycobacterium*, *Pannonibacter*, *Parasediminibacterium*, *Pedobacter*, *Phreatobacter*, *Polaromonas*, and *Reyranella*. *Mycobacterium* spp. are known for their pathogenic nature and the release of the sludge to an environment needs extra caution due to the spread of this pathogen. Other recent studies have focused on the identification of ARB from sludge in wastewater treatment plants [121–124]. However, limited studies have been done on the ARB abundance in the sludge produced in DWTPs. Hence, more studies are required to provide more insight into the changes in the abundance of ARB in drinking water treatment sludges.

3.5. Distribution system

The storage spaces, pipelines, and drinking water receiving portals called the DWDSs [125]. Treated water from the DWTPs gets to the end users through the DWDSs. This entails that the components of the DWDSs must be constantly maintained to ensure the microbiological safety of the water consumed by the end users. However, improperly treated water from the DWTPs that comprise ARGs, organic materials, and low concentrations of residual chlorine creates an environment that supports the growth of pathogenic ARB in the distribution system. Pathogenic ARB has become a global health concern. In Glasgow, Scotland, the genera such as *Paenibacillus*, *Burkholderia*, *Escherichia*, *Sphingomonas*, and *Dermaococcus* were identified as ARB in tap water [126,127]. The possession of ARGs by the PB *Burkholderia* spp. and *Escherichia* spp. creates more health-challenging situations as they could serve as a potential source for the transmission of these ARGs to other PB [128]. Recently, the genera *Mycobacteria*, *Pseudomonas* and *Sphingomonas* were dominantly identified in the DWDSs in China with variations in seasons [113]. *Pseudomonas* is cosmopolitan with the ability to persist in drinking water because they tend to resist oligotrophic environment and residue disinfectant in DWDSs through the formation of biofilm [117,129]. The genera *Sphingopyxis* was reported to possess sulfonamide ARG and was predominant in the DWDSs pipe biofilms which suggests the genera as a disseminator of sulfonamide ARG within the DWDSs pipeline [130]. Other studies that identified ARB in natural water sources, different stages of DWTPs and DWDSs in many countries are presented in Table 2.

4. Implication of the pathogenic and antibiotic-resistant bacterial community in the different stages of DWTPs and DWDSs

Bacterial diversities and communities in DWTPs reflect on the quality of water as well as public health. Leakage and regrowth of PB

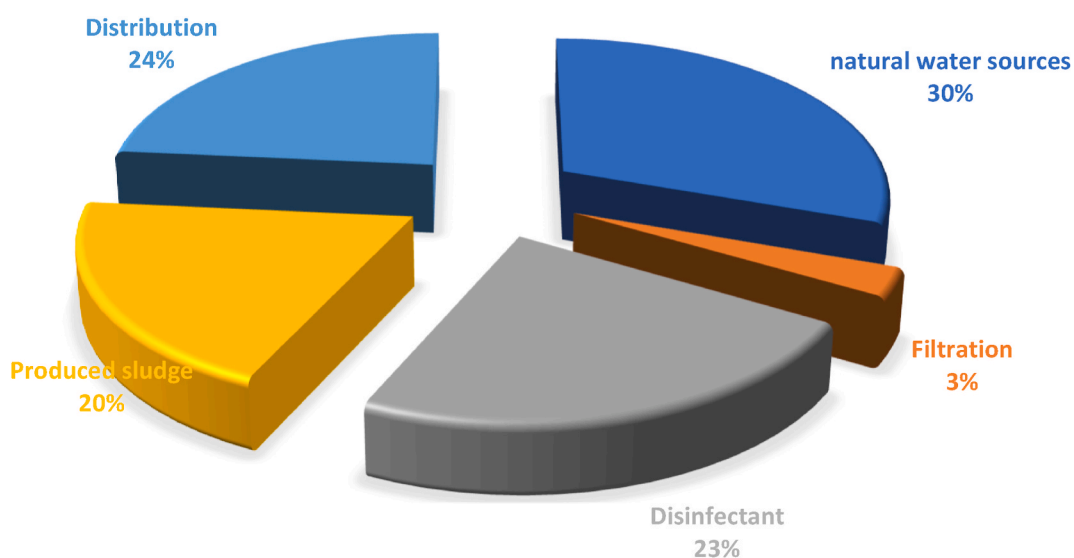


Fig. 2. Percentage occurrence of antibiotic resistant bacterial genera based on collated studies done between 2013 and 2023 (a decade) on natural water sources, drinking water treatment stages and distribution system.

and ARB in the different stages of DWTPs and DWDSs contribute to the deterioration of water quality and consequent health problems [84,162]. Tables 1 and 2 provided a summary of studies done that enlisted the PB and ARB present in each stage of DWTPs and the DWDSs respectively. Furthermore, the percentage occurrence of the pathogenic bacterial genera and antibiotic-resistant bacterial genera for the different stages of DWTPs and distribution system based on the previous studies done between 2013 and 2023 (a decade) are presented in Figs. 1 and 2 respectively.

Flocculation ensures a proper mixture of coagulants and feed water to form flocs. The formed flocs could contain some PB and ARB removed from the feed water. This makes unveiling the diversity of bacteria present in this stage of drinking water important as it can infer the type of coagulants that can be used. However, there is a paucity of studies on the occurrence of PB and ARB in this stage of drinking water treatment (Tables 1 and 2, Figs. 1 and 2). Most of the work done in this stage to identify PB present were in wastewater treatment plant [163–165]. This implies that studies are needed in this stage of drinking water treatment. The sedimentation stage provides the means to separate the suspended flocs through gravitation principles known as conventional gravity sedimentation. In Table 1, few studies have focused on the bacterial community's identification in the sedimentation stage. Furthermore, in the percentage occurrence of PB obtained from studies done in the present decade (2013–2023), only 6% of the pathogenic bacterial genera have been identified in the sedimentation stage. This low percentage occurrence could be attributed to fewer studies done at this sedimentation stage or the impact of the treatment stage on the removal of PB. Record for ARB in the stage was scarce in the literature as shown in Table 2 and Fig. 2. Adequate sedimentation process helps in the removal of accumulated flocs which contain both PB and ARB and prevent the formation of unconsolidated particles. Hence, proper documentation of the PB and ARB in this stage will provide insight into the effectiveness of this stage in the removal of these PB and possibly indicate the best optimization method that can be adopted to ensure a better treatment stage. A similar trend was also observed in the filtration stages and treated water (Tables 1 and 2, Figs. 1 and 2). This implied that more studies are needed in the filtration stages to ensure better optimization of the process and treated water to promote continuous monitoring of water that leaves the DWTPs and gets to the end users through the DWDSs.

More attention has been paid to the PB and ARB in natural water, water after disinfection, and tap water which is the terminal of the distribution system and the route through which treated drinking water gets to the end users (Tables 1 and 2). This is also evident in Figs. 1 and 2 where the percentage occurrence of the pathogenic bacterial genera and ARB genera were high in natural water sources, disinfection stage and distribution systems. The high percentage occurrence of the pathogenic bacterial genera and ARB genera of disinfection stage and distribution systems could be attributed to the applied disinfectants such as chlorine and the residual chlorine present in the distribution system as well as other inherent factors within the treatment plants and distribution system that could promote the growth of these bacteria. The increase abundance of genus *Sphenodons*, *Aciduria*, *Nitrosomonas*, *Gallionella*, *Legionella*, *Escherichia*, *Coxiella*, *Yersinia*, *Sphenodons*, and *Mycobacterium* after the application of different disinfectant and along the distribution system provide a support and justification to the above-mentioned assumption [82,91–93]. Chlorination is known for its potential in the killing and inhibition of drinking water microbiomes [113,118,166,167]. However, the application of chlorine is reported to select the bacteria that are resistant to chlorine toxicity. Some of these chlorine-resistant bacteria are pathogenic and tends to absorb ARGs released from other bacteria whose cell membrane are being disrupted by the chlorine to become pathogenic ARB [168,169].

In summary, the presence of PB and ARB in each stage of the drinking water treatment from diverse DWTPs across the globe is an indication of the global need for optimized drinking water treatment stages that will take into consideration the underlying factors that promote the proliferation of these bacteria and ensure the production of quality water and microbiological safety of the water.

5. Contributing factors to the spread of pathogenic and antibiotic-resistant bacteria along the distribution system

5.1. Chlorination

Chlorination has been widely applied in DWTPs to kill diverse bacteria and other microorganisms present in the treated water. Its application and other forms of disinfectants are intended for the complete removal of PB and opportunistic microbial species [170, 171]. Chlorine application causes the release of ARGs creating an environment for horizontal gene transfer where the ARGs could be transferred into pathogenic and non-pathogenic bacterial communities that are resistant to the toxicity of the chlorine and other applied disinfectants through increased cell permeability [172]. Hence, the application of chlorine has the potential to increase the relative abundance of ARB in the treated water [126]. Shi et al. [94] observed an abundance of potential plasmids and mobile genetic elements such as insertion sequences in water treated with chlorine. Hence, chlorination enhances ARG enrichment in the environment. In support of this, other studies have shown that chlorination promotes ARG release and may not be efficient in demobilizing mobile genetic elements and the associated ARGs leading to the abundance of ARB in the final treated water [173–175].

The formation of disinfectant by-products (DBPs) due to the interaction between the disinfectant organic materials in the source water is another challenging problem emanating from the use of chlorine and chlorine additives which could cause the spread of PB and ARB in the distribution system. Dibromoacetic acid, dichloroacetonitrile, potassium bromates, and 3-chloro-4-(dichloromethyl)-5-hydroxy-2(5H)-furanone were identified by Lv et al. [176] as disinfectant by-products that co-select antibiotic resistance in bacteria. The authors further indicated that the mutagenic activities of the disinfection by-products induced antibiotic resistance in the opportunistic pathogen *P. aeruginosa* PAO1. In consonant with the above statement, Mantilla-Calderson et al. [177] discovered an increase in the antibiotic resistant transformation rate of eDNA in *Acinetobacter baylyi* ADP1 as impacted by the DBPs selective action through conserved cellular functions and pathways.

Another impact of chlorination is the release of virulence protein from the less chlorine-resistant bacteria that are pathogenic. Finlay and McFadden [178] explained virulence proteins as a vital set of proteins that enhances the invasion of the host immune mechanisms by the PB and the pathogenic ARB to cause disease in the host. Huang et al. [10] observed an increase in the relative

abundance of the virulence proteins such as flagellar motor switch protein, Clp protease and inner membrane protein in chlorinated water. According to Brown et al. [179], the flagellar motor switch controls the swimming behaviour of and flagellar rotation of PB. This accounts for the increased spread of PB along the distribution system coupled with other facilitating factors in the distribution system. A recent study conducted by Olowe et al. [180] on the impact of chlorine on the virulence factors of Carbapenems-Resistant *Enterobacteriaceae* observed the abundance of OXA gene and plasmid in the chlorinated water which poses a serious human health risk. Further, Zhang et al. [124] showed that an increased virulence factor in the chlorinated water resulted in the co-occurrence of 243 subtypes of ARGs in the water. In this context and looking at the negative health impacts of the spread of PB and ARB in the distribution systems associated with chlorination and other disinfectants, one could ask: *Are there chemicals that are safe for human consumption and are bactericidal or bacteriostatic in nature as well as having the potential to inactivate permanently the ARGs and other virulence proteins/factors which can be applied individually or in combination with other chemicals to deal with this situation?* Khadayeir et al. [181] evaluated the effect of exposing α -Fe₂O₃ thin film to plasma on its structure, self-cleaning, and antibacterial characteristics. The authors observed increased antibacterial activities of α -Fe₂O₃ modified by plasma application. The application of α -Fe₂O₃ thin film in this stage of water treatment is recommended as a promising tool due to its antibacterial properties. However, more study is needed to examine if its application will promote the inactivation of ARGs and other virulence proteins/factors as well as reduce the formation of DBPs. Furthermore, human health impact of α -Fe₂O₃ needs further studies to ensure its safe application in the drinking water systems.

5.2. Suspended particles

Suspended particles serve as another conveying vehicle for these PB and ARB in the drinking water distribution system. Their presence in drinking water affects the quality because of water discoloration and changes in the taste of the water they cause. In addition to this problem caused by suspended particles, Fang et al. [182] indicated that the suspended particles tend to serve as an anchorage for the attachment of bacteria and promote their growth during water treatment and distribution. In DWDSs, the main sources of suspended particles could be traced to detachment from biofilm, precipitation and flocculation, sediment resuspension, corrosion, and bio-aggregation [183]. Pathogenic bacteria that attach to the suspended particles create a serious human health challenge as the possibility of them reaching drinking water taps through the distribution channels is high due to their ability to use the substances in the suspended particles as sources of energy and increase their diversity, abundance, and richness better than the free-living bacteria [184–186]. This implies that there is high probability of increased genetic materials coding for antibiotic resistance in the bacteria attached to the suspended particles due to the high proximity of the cells leading to the formation of ARB via vertical and horizontal gene transfer [187]. In the study by Wang et al. [188], the introduction of antibiotics such as sulfadiazine, ciprofloxacin, and sulfadiazine/ciprofloxacin promoted the abundance of ARGs (mexA and int1) in bacteria attached to the suspended particles after chlorination. The authors further observed an increase in the extracellular polymeric substances (EPSs) in the presence of antibiotics. The EPS is a substance that provides a protective barrier for bacteria against disinfectants. It enhances the aggregation of microbes and promotes their attachment to suspended particles [189,190]. The apprehension of the impact of EPSs on the increase in the adsorption of pathogenic ARB to the suspended particles as influenced by the antibiotics present in the distribution system provides enlightenment on the risk of human exposure due to the increased mobility of the pathogens to the end users. Hence, the need to provide a lasting solution to the formation of these suspended particles remain high. Nescerecka et al. [191] reported the abundance of opportunistic PB in the EPS package. Some studies have also shown that opportunistic PB possess a stronger ability to produce EPS, resist disinfectant, survive oligotrophic environmental conditions and affect the health safety of the water users [192, 83]. In this context, constant monitoring of the drinking water treatment and distribution systems to track the changes in the structure and diversity of the PB and ARB becomes pertinent.

5.3. Loose deposits (unconsolidated sediments)

Unconsolidated sediments that were not taken out after chlorination form loose deposits and could find their way into the DWDSs where they can settle in the pipes and be transported across the DWDSs through resuspension, re-sedimentation, and bed transportation [193]. Upon the settlement of these loose deposits, they tend to interact with organic matter as well as inorganic nutrients and EPSs available in the DWDSs creating an environment suitable for the attachment and growth of pathogenic bacteria and ARB [193,194]. Comparison of the bacterial community's diversity in piping biofilm, suspended particles, bulk water, and loose deposits, it was found that loose deposits possess the most diverse bacterial communities [193]. This accounts for the postulation of El-Chakora et al. [195] that loose deposits promote the proliferation of about 80% of the total bacteria in DWDSs. Zhuang et al. [196] assessed the human risk associated with loose deposits in the DWDSs and observed that loose deposits play a critical role in the discoloration of water and show high cytotoxicity to the liver at a concentration >10 mg/L.

5.4. Biofilm formation

A residual chlorine level that is safe for human consumption is required to be maintained in DWDSs after chlorination to ensure that the microbiological safety and the quality of the water are maintained. The reduction in the residual chlorine and improvement of the oligotrophic microenvironment in the pipeline results in the regrowth of bacteria especially the PB and ARB [108]. Prolonged chlorine applications as well as the presence of antibiotics trigger adaptive response of the bacteria leading to the formation of biofilms which serve as antibiotic-resistant reservoirs [197]. The predicted function of biofilm in a DWDSs in altering the microbial structure and functional profiles indicated that many of the microbes within the biofilm were linked to human infectious diseases [198]. Chen et al.

[199] investigated the prevalence of ARGs in drinking water and biofilms and correlated them with the microbial community and opportunistic pathogens. The authors observed a strong correlation between opportunistic bacteria and the relative abundance of ARGs. Chen et al. [200] metagenomic results showed an abundance of ARGs in biofilms in the DWDSs under starvation treatment which promoted the growth of chemolithotrophs within the biofilms. Biofilms create a microenvironment for the proliferation of ARB and promote the exchange of ARGs vertically and horizontally [199]. Biofilm formed in the pipeline can cause the regrowth of PB and ARB and the extent of the regrowth is also dependent on the factors such as temperature, residence time and materials of the pipeline.

5.5. Pipe materials

The drinking water distribution channel comprises pipes made from different materials. The most widely used pipes are the plastic ones that are made of high-density polyethylene (HDPE) and polyvinyl chloride (PVC) due to affordability and flexibility [201]. In China, pipes made of PVC and polyethylene (PE) are mostly used especially in rural areas [202]. Phthalate esters (PAEs) known as plasticizers are among the major constituents of these plastic pipes and they are not bound chemically to the polymers that make up the plastic pipes hence, they can leach from the pipes and be discharged into the environment [19]. These plasticizers enhance the formation of biofilms and promote chlorine-resistant microbes which could be pathogenic [19]. Perfluoroalkyl substances (PFAS) such as perfluorooctane sulfonic acid (PFOS) and perfluorooctanoic acid (PFOA) are classes of synthetic organic compounds that have been detected in drinking water. They have been reported to increase the potential for bacterial infections in humans through the promotion of a pathogenic bacterial community along the distribution channel [203]. Yin et al. [87] evaluated the effect of the co-occurrence of phthalate esters and perfluoroalkyl substances on bacterial communities and PB growth in rural drinking water distribution systems. Their results showed that the co-occurrence of PAEs and PFAS promoted the growth of potential human PB such as *Burkholderia mallei*, *Mycobacterium tuberculosis*, *Klebsiella pneumoniae*, *Acinetobacter calcoaceticus*, *Escherichia coli*, and *Pseudomonas aeruginosa*. In the fabric industries, Za'im et al. [204] synthesized a new hydrophobic hexyltrimethoxysilane (HTMS) coating for polyester fabric through a one-step water-based sol-gel method under acidic condition. This HTMS coating developed provide a hydrophobic surface to the polyester fabric and prevents attachment of water molecules on the surfaces of the fabric. A similar technology is needed in the water distribution pipes productions as the formation of biofilms is initiated by the droplets of water on the walls of the pipeline followed by the accumulation of the loosed particles, PB, and ARB. The formation of a hydrophobic surface on the walls of the distribution pipelines coupled with good chlorine-residue status could be a direction worthy of study in the future to ensure the safety of our drinking water that gets to the end users.

5.6. Age of water

The age of water is the length of time the water stays in distribution system. The age of water is believed to have a direct effect on the chemistry of the water which can lead to the proliferation of PB and ARB [166]. A high relative abundance of *Mycobacterium* and *P. aeruginosa* was observed with increased age of water in the distribution system due to a decline in residual chlorine [98]. It is worth noting that water age, disinfectant used, loose deposits, suspended particles, and pipe material may not act independently. There is a possibility of synergism between the factors capable of creating a microhabitat within the distribution system that selects the bacteria

Table 3

A summary list of some pathogenic antibiotic-resistant bacteria (ARB) identified in drinking water and associated diseases.

Pathogenic ARB	Diseases
<i>Aeromonas hydrophila</i>	Septicemia
<i>Aeromonas veronii</i>	Gastroenteritis
<i>Bordetella pertussis</i>	Whooping cough
<i>Brucella suis</i>	Brucellosis
<i>Enterobacter aerogenes</i>	Opportunistic infections
<i>Leptospira interrogans</i>	Leptospirosis
<i>Pseudomonas aeruginosa</i>	Pseudomonas infection
<i>Shigella sonnei</i>	Bacillary dysentery/Shigellosis
<i>Staphylococcus saprophyticus</i>	Cystitis in women
<i>Streptococcus pneumoniae</i>	Acute bacterial pneumonia and meningitis in adults. Otitis media and sinusitis in children
<i>Legionella</i> spp.	Legionnaires' disease
<i>Rhodococcus erythropolis</i>	bloodstream infection
<i>Mycobacterium</i> spp	chronic pulmonary disease
<i>Escherichia coli</i>	cholecystitis, bacteremia, cholangitis, urinary tract infection (UTI), traveler's diarrhea, pneumonia, and neonatal meningitis.
<i>Shigella flexneri</i>	gastrointestinal infections (food poisoning)/Shigellosis
<i>Citrobacter</i> spp.	Citrobacter Bacterial Pneumonia, Lung Abscess, and Empyema
<i>Rhodoplanes</i> spp.	chronic rhinitis, local skin abscess, and ulcer
<i>Acinetobacter</i> spp.	blood infections, urinary tract infections, pneumonia, an infection of the lungs, infections in wounds
<i>Acidovorax</i> spp.	bloodstream infection (BSI) and implanted port- or catheter-related infections
<i>Sphingomonas</i> spp.	sepsis, meningitis, endocarditis, visceral abscesses, enteritis, osteoarticular, urinary, skin, or soft tissue infections.
<i>Burkholderia mallei</i>	Glanders
<i>Klebsiella pneumoniae</i>	pneumonia, meningitis, and liver abscess
<i>Corynebacterium tuberculostrepticum</i>	bacteremia, endocarditis, valvular damage, meningitis, vaginitis and infections of the urinary tract, the respiratory tract, wounds, skin, and eye

especially pathogenic and ARB that proliferate in the environment.

6. Health risk associated with the pathogenic and antibiotic-resistant bacteria in the drinking water treatment plants and distribution

Tap water is one of the direct routes to human exposure to PB and pathogenic ARB through consumption, skin exposure or inhalation of aerosols [205]. Eissa et al. [206] observed the proliferation of heterotrophic bacteria in water obtained from various distribution systems that supplies water to selected healthcare facilities. Some of these heterotrophic bacteria could be pathogenic. The implication of this is that drinking water laden with PB is a serious health risk to humans, most especially, to immunocompromised or immunodeficiency individuals [207]. The treatment processes in the drinking water treatment and other factors within the distribution channel tend to alter the structure of survived PB leading to the change in the functional profile relating to their pathogenicity and virulence creating a more difficult situation for the community and the health of the people when consumed.

Antibiotic resistance is among the inherent challenges in the DWTPs and distribution system. The acquisition of antibiotic resistance by any PB may result in disease outbreaks and transmission of infections that are cost-intensive to control leading to long illness, hospitalization, and even death [103,208]. The human health risk associated with antibiotic resistance and pathogenic ARB is more predominant in developing countries than developed ones because of poor health facilities, inadequate drinking water treatment facilities, poor distribution systems and the incessant outbreak of diseases that necessitate constant use of antibiotics [187]. The constant use of antibiotics promotes the development of ARB with a greater implication on the health of humans as more pressure is on the DWTPs to provide remediation to the problem. Hence, there is a need to keep surveillance on the development of antibiotic resistance in drinking water. Table 3 provides a summary of the diseases associated with some pathogenic-ARB in drinking water.

7. Concluding remarks and recommendations

The current review examined the selective impact of the different stages of drinking water treatment and distribution systems on the occurrence of PB and ARB. Theoretically, the treatment stages are designed to perform specific functions towards the reduction of the PB and ARB alongside other contaminants that cause deterioration of treated water. This entails good design plan in the establishment of the different stages of DWTPs and the provision of proper management/maintenance procedures, monitoring, and policies to ensure the effectiveness of the stages. Based on the collated information from previous and recent studies, the presence of the PB and ARB indicates that the different treatment stages select the PB and ARB that proliferate and are passed down to the end users. This defeats the main objectives of their development and design. This could be attributed to raw water quality, capacity of the plant, treatment processes employed, condition of the plant, operational aspects, maintenance, and quality assurance/monitoring. Hence, the main contribution of the present study is creating more awareness of the stages of treatment that promote the proliferation of PB and ARB as well as provoke more multidisciplinary research to proffer a solution to the epidemiological, microbiological, engineering, societal, and chemical aspects of PB and ARB in the drinking water systems.

Furthermore, most of the data obtained were done in developed countries which implied that limited data exist in the subject in developing countries where drinking water sources are usually partially treated surface water. This becomes a strong limitation to the evaluation of the impact of the different stages of DWTPs and DWDSs on the PB and ARB in these developing countries. In addition, informed decision on the actual technological optimization of the different stages of treatment due to this limitation could be impaired. Thus, more studies are recommended in developing regions, particularly in Africa, where antibiotics are incessantly used due to the constant outbreak of infectious microbial diseases. With respect to the bacterial genera (PB and ARB), the disinfection stage and distribution system show more selection of genera in the present decade. This creates a serious health risk to humans upon consumption of the treated water. Although some evidence shows the linkage between pathogenic ARB and human health risks, several knowledge gaps still exist, and future research should be directed towards optimization of each stage of the drinking water treatment system and developing a good water distribution pipeline system that will not interact and promote the growth of pathogenic ARB in the distribution system. In addition, future studies should be directed towards the development of advanced molecular epidemiology techniques that will ensure prompt outbreak analysis and quick detection of the various PB. To promote more studies in the identification of the occurrence of these PB in developing countries, there is a need for minimized sampling and analysis techniques' cost to encourage frequent and regular monitoring.

Data availability statement

Has data associated with your study been deposited into a publicly available repository?

No.

Please select why?

The data presented in this study are available in the article.

Additional information

No additional information is available for this article.

CRediT authorship contribution statement

Chimdi M. Kalu: Writing – original draft, Conceptualization. **Khuthadzo L. Mudau:** Validation, Conceptualization. **Vhangwele Masindi:** Writing – review & editing. **Grace N. Ijoma:** Writing – review & editing. **Memory Tekere:** Writing – review & editing, Supervision, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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