

REVIEW

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How flooding, antimicrobial resistance and groundwater impact drinking water safety

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Abstract

Climate change is leading to increased flooding events globally, which poses a significant threat to drinking water safety. This review explores the current literature available on flooding, antimicrobial resistance and groundwater as a source of drinking water. Highlighted within the review is the incorrect assumption that a country's economic status does guarantee access to water, sanitation and hygiene (WASH) facilities. While high-income countries are better equipped to deal with flooding events, there are areas within these countries where people lack access to basic WASH facilities. It's largely accepted that floodwaters contain contaminants which are harmful to animal, environmental and human health, but recommendations regarding floodwater surveillance appear limited in the current literature. Despite evidence that waterborne disease incidence and antimicrobial resistance are increasing post major flooding events, the risk that floodwaters pose to public health is largely unquantified at present. The introduction of monitoring of floodwaters could be a potential solution for revealing disease outbreaks and patterns during times of flooding emergencies. Groundwater, which is increasingly used as a source of drinking water, is also impacted by flooding and therefore brings into question the safety of this source of water for consumption. In Europe, currently, microbiological testing of private drinking water sources does not include all sources of water for consumption. Based on emerging evidence of antimicrobial-resistant bacteria from such water sources, it's advised that these regulations be reviewed and all water sources be included in drinking water legislation. Additionally, routine microbiological testing of drinking water remains limited to faecal indicator bacteria and total coliforms, despite the evidence of pathogenic and antimicrobial-resistant bacteria. We recommend review and expansion of the current guidelines in order to safeguard public health.

Keywords Climate change, Antimicrobial resistance, Drinking water, One health, Bacteria, Groundwater

1 Introduction

The Earth's surface consists of approximately 70% water, of which approximately 3% is fresh water. The availability of high-quality, safe and sanitary water is paramount to health. Access to safe drinking water (DW) is of utmost importance for sustainable



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development, socio-economic growth, and overall health and well-being in both the short and long-term. Groundwater (GW) accounts for approximately 99% of Earth's liquid fresh water supply, making it an extremely precious natural resource [1]. Groundwater refers to water which is located below the earth's surface, for example, wells, springs, and aquifers, while surface water (SW) refers to water that is above the surface of the earth, including streams, rivers and lakes [2]. Groundwater has a vital role in human and animal survival as a source of DW. Approximately 50% of the global urban population avail of GW for their daily water needs, while the majority of rural populations depend on GW for DW purposes, with reliance on GW increasing in developing economies as people seek access to water supplies [1]. The increasing demand for GW is largely attributed to many factors, with key reasons including population growth, urbanisation, increasing agriculture and industry usage, in addition to climate change (CC) [3, 4]. Climate change is impacting the hydrological cycle through altered precipitation, temperature variations, and extreme weather events, which directly impact the availability, distribution and quality of SW, leading to its depletion. Much research to date has focused on the impacts of climate on SW [5], with research expanding into the area of GW, as its usage increases.

In Europe, CC has and will continue to result in increased temperatures, increased rain and river flows leading to flooding, decreased snow and ice formation [6, 7]. In July 2021, 212 deaths and over 800 injuries were attributed to severe flooding in Belgium, Germany, Luxembourg, the Netherlands and to a lesser extent, Austria, France, Italy, Poland, Romania and Switzerland following extensive rainfall [8, 9]. In late 2024, unprecedented flooding in Valencia, Spain, led to 223 fatalities as well as the displacement of approximately 15,000 individuals [10]. In addition to death and displacement, public health authorities reported an increase in waterborne diseases (WBDs), including respiratory and gastrointestinal infections of approximately 20%, as water supplies were contaminated and sanitation systems affected [10]. Water-borne diseases are defined as illnesses which are established following the ingestion of, or contact with, water which has been contaminated with microorganisms such as bacteria [11]. Waterborne diseases include gastrointestinal diseases caused by bacteria (*Escherichia coli*, *Salmonella enterica*), viruses (norovirus, rotavirus) and parasites (*Cryptosporidium* species (sp.)), which can have short, medium and long-term impacts on the population, environment, food and water safety [8, 12]. Floodwaters frequently carry harmful microorganisms due to heavy rain overwhelming sewage and waste facilities, or inducing run-off from industrial or agricultural waste, for example, which can then enter GW sources, contaminating the water supply and the GW ecosystem.

Treatment of WBDs with antimicrobials reduces the risk of death and further transmission of infections. However, with increasing levels of antimicrobial resistance (AMR), the treatment of outbreaks is becoming more difficult. In 2019, an estimated five million human deaths were associated with bacterial AMR, of which the 'priority pathogens' *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa* were amongst the most frequent pathogens responsible for these deaths [13, 14].

With approximately 50% of the global urban population and the majority of rural populations depending on GW for their water needs, including DW [1], water safety and quality are important public health priorities. Global research has identified the presence

of antimicrobial-resistant bacteria (ARBs) in drinking water [15–23]. Of these studies, five also explicitly included samples from GW sources, where they identified ARBs [15, 16, 20–22], but despite this evidence, drinking water safety testing remains limited to traditional faecal indicator bacteria and does not consider antimicrobial resistance genes (ARGs) or ARBs [15].

Biofilms are aggregated communities of microorganisms encased within a self-made extracellular polysaccharide (EPS) matrix. Biofilms are present globally in many environments and are identified most frequently in water systems [24]. They provide a protective habitat for microorganisms. Within water systems, biofilms can negatively impact water quality through the introduction of polluting microorganisms [25, 26]. Within biofilms, bacterial cell proximity creates optimum conditions for horizontal gene transfer (HGT). Horizontal gene transfer is an evolutionary mechanism by which microorganisms, including bacteria, disseminate genetic material between cells, frequently containing ARGs. This process is an adaptive and survival stress response of microorganisms to their environment [27]. Biofilms are associated with increased levels of HGT when compared to bacteria in a planktonic state [28].

The purpose of this review is to explore the relationships between flooding, bacterial AMR, WBD and GW. This literature review investigates the intersection of water, sanitation and hygiene (WASH) in high-income countries (HICs), floodwater contamination testing, waterborne diseases (WBD), and antimicrobial resistance (AMR), and their potential impacts on groundwater quality when used as a private drinking water source (PDWS). This review seeks to explore the literature on how water, sanitation and hygiene floodwater testing, WBD and AMR, may impact GW as a private drinking water source (PDWS). Through reviewing the current available literature, knowledge gaps have been identified, and recommendations to expand knowledge and data, bridging these gaps, have been proposed.

For this review, NCBI PubMed and Science Direct platforms were used to search the following terms: “antimicrobial resistance”, “AMR”, “climate change”, “bacteria”, “biofilm”, “drinking water”, “flooding”, “groundwater”, “high-income countries”, and “waterborne disease”. Additionally, through the literature identified via these terms, we also explored the literature cited by these papers. Trustworthy health organisations and authoritative websites were also utilised to look for materials using the same search terms. Where possible, literature published from the last 13 years (2013–2026) was utilised.

1.1 Waterborne disease and WASH

Annually, an estimated 1 million individuals die due to diarrhoeal disease as a result of unsafe water, sanitation and hygiene (WASH) facilities [29]. While the incidence of WBDs globally has been declining in recent years, particularly as a result of the introduction of WASH programmes, CC events impacting temperature, precipitation, flooding and drought pose a major risk to this continued reduction [30]. Climate change may influence WBD burden by directly impacting pathogen growth, survival and dissemination [30]. Floods are one of the most common natural disasters globally, imposing major global health and security threats [31]. Bacterial agents frequently linked to WBD outbreaks post flooding include *Campylobacter* sp., *E. coli*, *Legionella* sp., *Mycobacteria* sp., *Salmonella* sp., *Shigella* sp., and *Pseudomonas* sp. [32, 33].

Waterborne diseases are more commonly associated with low-middle income countries (LMICs), as infrastructure for flood protection is limited, there are issues with access to healthcare, and slower socio-economic development has meant that, in general, water quality is already unsafe [34]. In HICs, less consideration is given to WBD prevalence due to an assumption that it is not a major issue and doesn't pose a significant risk to public health, as witnessed in LMICs [35]. An introductory piece by Underhill, Sylvester and Meehan has gathered evidence from within the Special Collection "Uncovering WASH Inequalities in High Income Countries: Re-Imagining Equitable Services" to support the proposal that WASH problems are not only confined to the boundaries of LMICs but are often found siloed within HICs [36]—where issues such as WASH are compartmentalised and confined to certain groups or populations within HICs. These issues are then addressed in isolation without coordination or input from all relevant stakeholders.

Currently, research communities are attempting to bring global attention to this issue, making inequities visible, regardless of socio-economic background [32]. Some examples of silos in HICs include the United States, where over 2 million individuals do not have access to WASH services including, basic running water, indoor plumbing or waste sanitation facilities [37]. These individuals include those in Black, Indigenous, and other racial minority communities, as well as those who are lower-income and those in rural areas [37]. In Ireland, annually, there are increasing numbers of private group water schemes that are not meeting the national regulatory standards for *E. coli* contamination [38]. In 2022, there was 96.5% *E.coli* compliance, 94.1% in 2023 and 93.7% in 2024, with some group schemes having repeated failures to meet *E.coli* regulatory standards in drinking water [38]. In the European Region in 2022, 93% of the population had access to safely managed drinking water, while 7% (~ 16 million people) did not have access to safely managed drinking water [39]. To further highlight the risk faced by the public in what is largely considered to be an area of high socio-economic status, approximately 29 million people living in the European Region have limited access to WASH facilities [39].

1.2 Waterborne disease and floodwater

Flooding is one of the most common natural disasters globally [31]. Consideration should be given to the risk that floodwater poses to the health of animals, humans and the environment. Floodwater can become contaminated with chemicals, heavy metals, toxins, waste and microorganisms as it flows over land, picking up agricultural run-off, and inundating waste systems. Human pathogens and ARB have been detected in floodwater [40, 41]. However, there is a significant lack of guidelines or statutory requirements to test floodwater for microbial contamination. While reviewing the literature, only one guideline regarding the testing of floodwaters was identified, which was published by Public Health England in 2014 [42]. Public Health England advises against routine microbiological testing of floodwater on the grounds that it would probably detect disease-causing microorganisms. While the presence of such pathogens is acknowledged, the absence of testing prevents accurate risk assessment, leaving potential threats to human and environmental health largely unquantified and highlighting a critical knowledge gap. Floodwater surveillance could protect public health by revealing disease patterns and predicting outbreaks. The data would characterise antimicrobial resistance profiles (*i.e.*, indicate which antimicrobials a bacterial isolate is resistant or susceptible

to) in bacterial isolates, supporting clinical treatment decisions, tracking emerging environmental resistance trends, and strengthening infection control measures through evidence-based risk assessment after environmental health incidents.

While it is recognised that it is not currently feasible to screen all bacteria present in floodwaters, screening for the presence of known pathogens, for example, faecal coliforms, *enterococcus* sp. or pathogens listed on the World Health Organisation Priority Pathogen List [43], may be an initial starting point. Furthermore, it's important to highlight that while AMR and infectious disease outbreaks occur frequently together, consideration should be given to pathogens considered to be non-pathogenic, as they too have the potential to be resistant to antimicrobials. This is particularly relevant to consider when investigating AMR using a One Health approach, and CC. In these instances, microbes which were once not considered a threat may pose a threat to environmental or public health or may act as vehicles for the dissemination of AMR.

Given the time- and labour-intensive manner of screening bacterial presence in floodwater, perhaps a more suitable option is the use of DNA-based analysis such as shotgun metagenomics. Metagenomics is the DNA sequencing of the entire microbial community. Using this method, scientists can gather evidence of all microorganisms present, community diversity, and microbial function, giving a deeper dataset than isolation of individual species. A study published in 2019 [44] investigated the bacterial profile and resistome of flooded sediment samples in Kerala, India. Using metagenomics resulted in the detection of 103 AMR genes unique to the flooded soil or sediment samples when compared to the publicly available data of mangrove ecosystems within the same geographical location [44]. These unique genes were associated with resistance to twelve classes of antimicrobials, including aminoglycosides, beta-lactams, tetracyclines, fluoroquinolones, macrolides, phenicols and sulfonamides. In vitro evaluation of AMR of pathogenic bacterial species identified the predominance of AMR phenotypes in *P. aeruginosa*, *E. coli*, *Acinetobacter baumannii*, *K. pneumoniae*, *Shigella flexneri*, *Vibrio cholerae*, *E. faecalis*, and *S. aureus* [44]. Among the flooded samples, 38% of the resistance genes detected are known to be potentially plasmid-encoded [44], which could be attributed to HGT, but more research is needed to determine AMR mechanisms during flooding.

A more recent study by Rahman et al. [45] also implemented metagenomic analysis to investigate floodwater in Bangladesh during the peak flooding season. The study further demonstrated the use of DNA-based analysis as a potential method for the detection of pathogens and their related AMR-profiles [45]. Through metagenomic analysis, geographical patterns of pathogens in floodwater were detected, including the World Health Organisation Priority Pathogens; *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* [45]. This identification of pathogen patterns across locations may be valuable knowledge in guiding clinical assessment and treatment of affected individuals who present for medical care following flooding-related incidents. Studies such as these provide evidence to support the use of DNA-based technologies to survey and determine the risk flooding and floodwaters pose through the identification of microorganisms, as well as determining gene presence for AMR.

1.3 Groundwater

Groundwater is vulnerable to flooding, and it is also subject to the pressures of climate change-associated flooding. Floodwaters which have been contaminated on the Earth's surface can seep into GW sources, carrying with them pollutants and microbial contamination. Private drinking water sources, which are largely supplied from GW, may present the greatest health risk, as there is often no statutory regulation or analysis to ensure these sources are monitored for contamination—microbial or chemical. In Europe, PDWS which serve less than 50 people or $< 10 \text{ m}^3$ per day are exempt from the EU Directive 2020/2184 on the quality of water intended for human consumption [46], and water quality and safety are solely the responsibility of the PDWS owner [47, 48].

Antimicrobial-resistant, clinically relevant pathogens have been isolated from private drinking water (PDW) in Ireland and Canada, including *E. coli*, *Enterococcus* sp., *Enterobacter* sp., *Acinetobacter* sp., and *Pseudomonas* sp. [15–17, 22]. A study of 353,388 Canadian PDW samples found 4.5% of samples were contaminated with *E. coli*, of which 10.5% had AMR and 3.7% were multi-drug resistant (MDR) [22]. Furthermore, in Ireland, MDR bacteria were also detected among PDW samples, including *E. coli*, *Enterococcus* sp., *Enterobacter* sp., *Stenotrophomonas* sp., and *Serratia* sp. [15]. The findings of these studies from HICs reflect that DW from GW can be a risk to public health.

In Europe, current DW microbiological testing includes faecal indicator bacteria (*E. coli* and *Enterococci*), including coliforms [46]. However, the results of the aforementioned studies highlight the need for broadening these test parameters as well as the need to introduce mandatory testing of all PDWS, regardless of how many people it serves daily. Consideration of AMR profiles associated with bacteria present in DW should also be considered, as it has been noted that Enterobacterales, excluding *E. coli*, were antimicrobial resistant [15, 17], suggesting that, while *E. coli* is an important pathogen, other bacterial species could also pose serious health risks in PDWS.

The water environment, including GW, is a suitable location for biofilm formation [49–51]. Despite available knowledge pertaining to the presence of biofilms in GW, there is limited literature available on GW biofilms and AMR. One such study found in relation to GW biofilms and AMR explores biofilm microbial communities affected by stormwater recharge of GW aquifers [52]. Sidhu et al. [52] used a high-throughput gene array for ARGs and virulence genes (VGs) in three boreholes over three months and discovered clinically relevant bacterial species. *Escherichia*, *Citrobacter*, *Enterobacter*, *Klebsiella* and *Pseudomonas* species, among others, were ubiquitously found across test site biofilms carrying ARGs and VGs isolated from biofilms [48]. While variation in abundance and type was noted across the three study sites, ARGs and VGs remained largely similar at each site over the three month period, suggestive that biofilm communities can persist for extended periods of time in the aquatic environment [52]. The authors of this study cannot exclusively state that the AMR bacteria identified are responsible for the dissemination of resistance within biofilms [52]. This is an important factor to consider when contemplating the potential pathways for AMR dissemination in the aquatic environment, as presence doesn't equate to dissemination and therefore further investigation is warranted [52]. This paper also highlights the need for further exploration into hydrological events, such as recharge mechanisms altered by CC, which will impact the quality of water sources. Additional biofilm studies from GW will provide valuable insights into the environmental health of GW sources, provide evidence of the AMR

profiles that lie beneath the Earth's surface, as well as providing valuable information to aid in the understanding of microbial ecology from natural resources, which directly contribute to public health.

2 Areas that require action and recommendations

This review has highlighted four main areas which require action:

1. *Access to WASH facilities in HICs*: Evidence provided within this review has highlighted that a country's socio-economic status does not equate to equitable access to safe and sanitary water. There are areas which exist, and there are still large cohorts and communities that are without adequate and safe WASH facilities. To ensure equitable access to WASH facilities for all individuals, collaboration is needed from all relevant stakeholders to identify and address problems which currently exist. Once identified, the assessment of areas and their respective communities should be carried out to clearly identify the issue with access to safe and sanitary water. Based on root cause identification, goals can be designed and implemented, ensuring that all relevant stakeholders are involved in the decision-making process. Review of the changes is required to ensure continued success and implementation of the changes. This will reduce inequity, public health burdens, improve transparency and health outcomes.
2. *Floodwater surveillance*: Evidence exists that pathogens and ARBs exist within floodwaters, yet there is a clear lack of floodwater surveillance globally. While it is not feasible to survey all floods, areas which are more prone to extensive flooding should be prioritised. In terms of microbiological screening of floodwaters, screening for known waterborne pathogens should take precedence. Based on knowledge of AMR presence in floodwater, screening for the World Health Organisation list of current Priority Pathogens [43] may also help guide clinical treatments for those impacted by floodwaters. Floodwater surveillance data could be utilised to develop floodwater surveillance models that could be used in pathogen prediction or early warning systems of subsequent flooding events.
3. *Mandating testing of all water sources for human consumption*: All humans need access to water for consumption, and ensuring the water is of high quality and safe to drink is paramount for public health. Rather than excluding cohorts of PDWS, an inclusive approach would ensure all water sources are tested. To ensure all water for human consumption is tested regularly, each country or regulatory region could consider how it manages and regulates water for human consumption. In the event of flooding impacting DW sources, it may be recommended or mandatory for sources to be tested to ensure water remains safe for consumption. Records of all water sources for consumption would need to be updated and regularly maintained, in turn allowing for local/national water governing bodies to set up schemes or systems for ensuring all water supplies are regularly tested. Additionally, regular water testing would generate data which could, if permission were granted, be used in research for surveillance of bacteria.
4. *Review and expand current standard microbiological testing of drinking water*: Based on emerging evidence of pathogens and AMR in drinking water, it's recommended that the current microbial testing standards be reviewed. In addition to the current analysis of bacteria, we suggest that testing should include the World Health Organisation Priority Pathogens [43] and possibly extend testing to include other

markers of AMR. Testing of the expanded microorganisms would be most effective in DW that currently doesn't receive any treatment prior to consumption.

3 Conclusion

In conclusion, the unknown risks associated with flooding, waterborne disease, AMR and GW need to be assessed as they are closely linked to public health. This review highlights four key areas for prioritisation.

Author contributions

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Data availability

No datasets were generated or analysed during the current study.

Declarations

Ethics approval and Consent to participate

Not applicable.

Consent for publication

The authors confirm that the manuscript has been read and approved by all named authors for publication.

Competing interests

The authors declare that they have no conflict of interest, including competing financial interests or personal relationships that could have influenced this paper.

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