

Microbial Freshwater Pollution and the Associated Risks

Vincent N. Chigor^{1*}, Chizoba A. Ozochi¹ and Veronica J. Umoh²

¹Water & Public Health Research Group, Department of Microbiology,
University of Nigeria, Nsukka, Nigeria

²Department of Biological Sciences, Akwa Ibom State University, Ikot Akpaden, Nigeria

Abstract: Microbial fresh water contamination occurs when faecal matters enter the water body. It is a global issue however; it is more severe in the developing countries due to; rapidly growing population and urbanization, land use and development, unhygienic and poor sanitation practices. Faecal matter pollution of fresh water is perhaps the most hazardous form of fresh water pollution since; it constitutes the greatest risk to the ecosystem and to public human health. Ecologically, it disrupts the nutrient load of the water body leading to eutrophication and the consequent production of toxins directly or indirectly affects man and animals especially, live of aquatic organisms. The public health risk is mainly due to the introduction of microbial pathogens whose diseases are associated with serious morbidity and mortality; and some, are capable of spreading rapidly leading to epidemics of varying proportions. In addition to causing diseases, it disseminates virulence and antibiotic resistance genes, which can be transferred to non-pathogenic and non-antibiotic resistant strains or species in the water body, resulting to diseases with less therapeutic options. The human health risk can be assessed by both the observed-adverse-effect-level approach (OAELA) and quantitative microbial risk assessment (QMRA). This paper thus, reviews risks associated with the use of microbiologically polluted freshwater and concludes that source water protection and point of use treatment measures is the ultimate means of mitigating such risks and should no longer be neglected.

Keywords: Pollution, Freshwater, Disease, Risk, Pathogen

INTRODUCTION

Water is very essential for the survival and sustenance of life yet, 844 million people worldwide still lacked even a basic drinking water service (WHO/UNICEF, 2017). As a result, 159 million people still collect drinking water directly from surface water sources, of which 58% lived in sub-Saharan Africa (WHO/UNICEF, 2017). Such water bodies are susceptible to faecal contamination of human and animal origins thereby becoming of poor microbial quality and are often contaminated by pathogens, leading to outbreaks of water-borne infections and related diseases (Chigor, *et al.*, 2013; Pandey, *et al.*, 2014; King-Abia, *et al.*, 2017). An estimated 2.3 billion people lacked even a basic sanitation service and 892 million people worldwide still practised open defecation (WHO/UNICEF, 2017). According the reports from the Nigerian Federal Ministry of Water Resources and the

United Nations Children's Fund (UNICEF), Nigeria is among the nations with the highest number of open defecation cases where 46 million estimated people are involved (FGN/UNICEF, 2017).

The total volume of water on Earth is about 1.4 billion cubic kilometres. Of this, about 97.5% of the total volume is saltwater and only about 2.5% is freshwater. Freshwater consist of surface water (0.3%), groundwater (30.1%), ice caps and glaciers (68.7%) and others (0.9%) such as; soil moisture, atmosphere, ground ice and permafrost (Igor, 1993; National Geographic, 2010). Figure 1 indicated the global freshwater content with over 68% being ice and glaciers while 30% is stored in underground aquifers. The fresh surface water (water in rivers, streams, lakes, dams, ponds and similar bodies of water) constituted only 0.3% of the world's freshwater Figure 1 (Igor, 1993).

^{1*}Corresponding Author:

Email: vincent.chigor@unn.edu.ng

Phone: +2348036922106

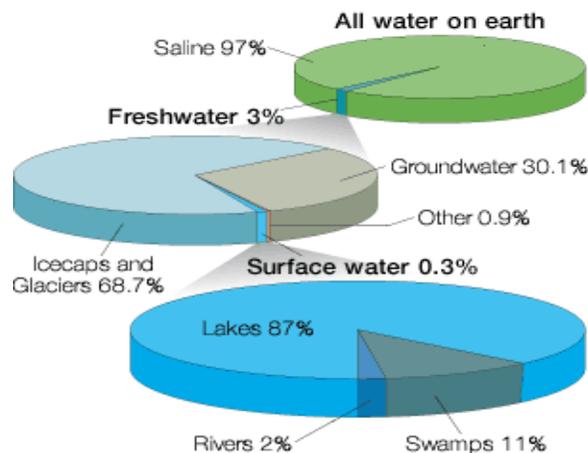


Figure 1: Distribution of earth's water. (Source: <http://ga.water.usgs.gov/edu/earthwherewater.html>)

Fresh surface waters, including dams, rivers and streams, serve for drinking, domestic, agricultural, recreational, industrial and other purposes including transportation, and hydroelectricity (Chigor *et al.*, 2012). However, these waters are vulnerable to pollution (Azizullah, *et al.*, 2011; Chigor *et al.*, 2012), and are continually being impacted on, as a result of rapid population growths, land development along river basin, agriculture, urbanization and industrialization that place increased demand on surface waters both as sources of water for different uses and as disposal channels for treated/untreated wastewaters (Suthar *et al.*, 2010; Solaraj *et al.*, 2010).

Pathogenic microorganisms (bacteria, viruses, fungi, and protozoa) introduced via faecal pollution, render water contaminated and non-potable; and could result in the transmission of water-related diseases (Delgado-Gardea *et al.*, 2016; King-Abia *et al.*, 2017). Faecal pollution also affects the ecosystem and aquatic life, in addition to causing economic losses from closure of aquatic food harvesting areas, and bathing restrictions (Pruss *et al.*, 2002; Gourmelon *et al.*, 2007). Surface water sources are vulnerable to faecal contamination, from human and animal sources. This poses grave public health risks, as cholera outbreaks and diarrhoeal diseases are frequently reported in Nigeria, and every year, an estimated 124,000 Nigerian including children under the age of 5 die because of diarrhoea, mainly due to unsafe water, sanitation and hygiene (FGN/UNICEF, 2017).

Statistics has it that about 70 million people, out of Nigeria's population of 183 million (2015 projection), lacked access to safe drinking water, and over 110 million lacked access to improved sanitation (FGN/UNICEF, 2017). Although government is charged with the duty of providing potable water to its residence, access to potable water still remains a problem in every state of the Federation; and where it exists, it is grossly inadequate to meet the needs of the ever-growing population (Idu, 2015). As a result, greater percentage resort to the use surface water while the lesser percentage digs their own wells or rely on local water sellers (Idu, 2015).

Microbial fresh water pollution refers to the degradation of water quality that is intrinsically harmful in some ways, to some degree to the health of humans, animals and the environment (ecosystems), mainly due to contamination by pathogenic microorganisms and organic matter. This review considers the problem of water pollution caused by faecal contamination and microbial contaminants in surface waters.

A Historical Perspective on Faecal Pollution

Environmental pollution began with the earliest human societies, and the stress which man's activities exerts on the environment has been multiplied by the increase in human population due to urbanization and industrialization (Chigor *et al.*, 2013; Ubani *et al.*, 2014; Parmar *et al.*, 2016). The work of John Snow (Pandey *et al.*, 2014), who proved in 1855 that the cholera outbreaks in London were spread by drinking water contaminated with sewage, was crucial in developing public awareness on the importance of controlling water pollution.

Today, the pollution of water remains a global problem that weakens one of the resource bases on which human society is built (WHO, 2015), and engages a multitude of researchers. The problem is heightened by climate change and its attendant floods and droughts (Delpla *et al.*, 2009).

Classes and Sources of Microbial Pollutants in Water

There is a broad spectrum of microbial pathogens that have been documented to be found in the water environment including bacteria, protozoa, algae, viruses and helminths (WHO, 2011; Ramírez-Castillo *et al.*, 2015). The types, numbers and distribution of these pathogens in surface waters vary across different water bodies, parts of the world and times of year. These variations depend on the incidence of disease in the contributing population, and known seasonality in human infections (Skraber *et al.*, 2004).

It is known that contaminant loads to surface water bodies start off from point or non-point sources (Parveen *et al.*, 2001; Albek, 2003). Point-source pollution originates from discrete sources whose inputs into aquatic systems can often be defined in a spatially explicit manner (Ritter *et al.*, 2002). Examples of point-source pollution include; industrial effluents (food processing plants), municipal sewage treatment plants, combined sewage-storm-water overflows, septic tank leakage (Ritter *et al.*, 2002). In Nigeria, water resources consist of surface and groundwater components that are greatly impacted by human activities. Poor environmental practices including open-defecation, animal sources, including abattoirs, as well as dumping of sewage into surface waters introduce pathogens. It is almost a norm in Nigeria to dump untreated wastes (industrial, domestic, human, and animal) into surface water bodies (Chigor *et al.* 2012; Idu, 2015). In least developed countries, 22% of health care facilities have no water service, 21% no sanitation service, and 22% no waste management service (WHO, 2019a). This adds to the microbial waste burden on freshwater sources.

Non-point-source pollution, in contrast, arises from poorly defined, diffuse sources that typically occur over broad geographical scales (Kistemann *et al.*, 2002; Ritter *et al.*, 2002), with

examples that includes; agricultural runoff (pathogens and organic matter), storm-water and urban runoff and open-grazing. Worldwide, 2.0 billion people still do not have basic sanitation facilities such as toilets or latrines, in 2017 and of these, 673 million still defecate in the open, for example in street gutters, behind bushes or into open bodies of water (WHO, 2019b).

Risks Associated with Faecal Contamination of Surface Water

Faecal pollution of water sources comes with it a lot of risks both for aquatic ecosystems and for public health (Zhukinskii, 2003). The key public health problems arising from microbial contamination of freshwater include waterborne diseases (Igbiosa and Okoh, 2009; Chigor *et al.*, 2010a, b) and the dissemination of antimicrobial resistance (Chigor *et al.*, 2013; Sidrach-Cardona, 2014). The presence of microbial pathogens in aquatic systems also represents substantial economic losses mainly related to morbidity and mortality amongst the exposed populations or due to closure of recreational beaches (Gourmelon *et al.*, 2007).

Ecological Risks

When sewage, which contains microorganisms and decomposable organic matter, pollutes water, changes in the patterns of microbial activity occur due to increase nutrient composition (Albek, 2003). Decomposition of organic matter by microbes results in eutrophication of the polluted water and depletion of dissolved oxygen. Such anaerobiosis causes the death of fish and other oxygen-dependent water animals and permits the release of hydrogen sulphide and other malodorous substances by sulphate-reducing bacteria.

Eutrophic water bodies are prone to massive phytoplankton blooms and blooms of various planktonic species are directly or indirectly hazardous to human and animal health (Hitzfeld *et al.* 2000; Hunter 2003). Since the identification of *Nodularia spumigena* bloom in Lake Alexandria, Australia, numerous poisonings have been reported (Hitzfeld *et al.*, 2000). In 1988, a bloom of small flagellate algae, *Chrysochromolina polylepsia* damaged seaweeds, invertebrates and fish along a 200 km stretch of the coasts of Denmark, Norway and Sweden (McEldowney *et al.*, 1993).

Scum of Cyanobacteria accumulating along shores of ponds and lakes present a hazard to wild and domestic animals and the death of farm animals drinking scum of cyanobacterially-contaminated ponds and poisoning of dogs swimming in cyanobacterial scum have been described (Hitzfeld *et al.*, 2000).

Public Health Risks

The Spread of antimicrobial resistance as public health risk

Resistance to antimicrobial agents began soon after the introduction antibiotics in the 1940s and has increased remarkably in the last three decades (Chigor *et al.*, 2010; CDC, 2013). The review, on trends in antimicrobial susceptibilities of Enterobacteriaceae isolated from hospitalized patients in the United States from 1998 to 2001, showed that decreased flouoroquinolone susceptibility was most pronounced for *E. coli* (Karlowsky *et al.* (2003). Other reports demonstrate, fresh water environment as a hot spot for the emergence and dissemination of antibiotic resistances (Sidrach-Cardona, 2014). Currently, microbial resistance to antibiotics spans all known classes of natural and synthetic drug agents (Zhang *et al.*, 2010), and bacterial resistance to antibiotics continues to pose a serious threat to human and animal health (Chigor *et al.*, 2010).

Literature is replete with evidences that faecal pollution and discharge of antibiotic-resistant strains of pathogens into water can result in the transfer of resistance to previously susceptible strains or species (Ash *et al.*, 2002; Blake 2003; Zhang *et al.*, 2010; Chigor *et al.*, 2010; Sidrach-Cardona, 2014). Studies demonstrated the transfer of plasmid-borne resistance in aquatic organisms like in *E. coli*, Enterobacteriaceae and *Pseudomonas aeruginosa* (Veal *et al.*, 1992). The threat due to the transmissibility of resistance genes stands multiplied considering the vast potential hosts presented by microbial population in the gut and water environments (Woegerbauer *et al.*, 2002). This risk is further amplified were a river continuum passes through different communities and possibly disseminate antibiotic resistance determinants (Leff, 1994). In a review of antibiotic resistance genes (ARGs) in water environment, Zhang *et al.* (2010) revealed that the emergence of ARGs in the water environment is becoming an increasing worldwide concern. Hundreds of various ARGs encoding resistance to a broad range of antibiotics have been found in microorganisms distributed not only in hospital wastewaters and

animal production wastewaters, but also in sewage, wastewater treatment plants, surface water, groundwater, and even in drinking water (Guyomard-Rabenirina *et al.*, 2017; Ng and Gin, 2019).

Waterborne Diseases

Human infectious diseases are among the most serious effects of faecal pollution of freshwater, especially in developing countries, where sanitation may be inadequate (WHO, 2011). Water-borne pathogens are responsible for several water-related diseases such as diarrhoea, dysentery, gastroenteritis, cholera, typhoid, polio and wound infections. Diarrhoea is usually a symptom of an infection in the intestinal tract, which is caused by variety of bacterial, viral, protozoa and parasitic organisms with more than 50% cases being bacterial intestinal infections (Cabral, 2010). Diarrhoea contributes about 4.8% to the global burden of disease and is the leading cause of death in children under 5 years of age (Pruss *et al.*, 2002; Hatami, 2013).

Globally, in 2017, at least 2 billion people used drinking water source contaminated with faeces, and contaminated water can transmit several diseases (see Table 1 to 3) that contribute significantly to the global disease burden (Pruss *et al.*, 2002; WHO, 2015). Enteric pathogens are transmitted mainly by the faecal-oral route, either directly from person-to-person or via consumption of contaminated food or water (Haramoto *et al.*, 2008). The transmission pathways are shown in Figure 2. The use of contaminated water in kitchen may also bring about the contamination of food and utensils. Poor sanitation is linked to transmission of diseases such as cholera, diarrhoea, dysentery, hepatitis A, typhoid and polio and exacerbates stunting. It is estimated to cause 432 000 diarrhoeal deaths annually and is a major factor in several neglected tropical diseases, including intestinal worms, schistosomiasis, and trachoma. Poor sanitation also contributes to malnutrition (WHO, 2019b).

Table 1: Pathogenic protozoa, algae and helminths linked to drinking water or recreational water contact.

| Organism | Disease | Transmission | Clinical features |
|--|--|--|--|
| Helminths | | | |
| <i>Schistosoma spp.</i> | Schistosomiasis | Contact with surface water infected with free swimming cercariae | Urinary and intestinal damage, bladder cancer |
| <i>Dracunculus medinensis</i> | Dracunculiasis | Drinking water | Painful ulcers on lower limbs and |
| Protozoa | | | |
| <i>Giardia duodenalis</i> | Giardiasis | Faecal oral spread through drinking water or recreational water | Diarrhoea and abdominal pain, weight loss and failure to thrive |
| <i>Cryptosporidium parvum</i> | Cryptosporidiosis | Faecal oral spread through drinking water or recreational water | Diarrhoea, often prolonged |
| <i>Cyclospora cayetanensis</i> | Cyclosporiasis | Faecal oral spread through drinking water | Diarrhoea and abdominal pain, weight loss and failure to thrive |
| <i>Entamoeba histolytica</i> | Amoebiasis | Faecal oral spread through drinking water | Diarrhoea, may be severe dysentery |
| <i>Toxoplasma gondii</i> | Toxoplasmosis | Drinking water contaminated by feline animals | Glandular fever, foetal damage in pregnant women |
| Free-living amoebae | Amoebic meningoencephalitis | Aspiration of infected surface water into nose | Fatal encephalitis |
| Algae | | | |
| Cyanobacteria <i>Pfiesteria piscicida</i> | Various Estuary-associated syndrome | Toxins in drinking water or direct Toxins in water | Dermatitis, hepatitis, respiratory Respiratory and eye irritation, deficiencies in learning and |

Source: Hunter (2003).

Table 2: Bacterial pathogens linked to drinking water or recreational water contact

| Organism | Disease | Transmission | Clinical feature |
|---|-----------------------------------|---|---|
| <i>Vibrio cholerae</i> | Cholera | Drinking water | Watery diarrhoea, may be severe |
| <i>Salmonella</i> spp. | Salmonellosis | Occasional outbreaks with drinking water | Diarrhoea, colicky abdominal pain and fever |
| <i>Salmonella typhi</i> | Typhoid | Drinking water | Fever, malaise and abdominal pain with high mortality |
| <i>Shigella</i> spp. | Shigellosis (Bacillary dysentery) | Both drinking and recreational water | Diarrhoea frequently with blood loss |
| <i>Campylobacter</i> spp. | Campylobacteriosis | Both drinking and recreational water | Diarrhoea frequently with blood loss |
| Enterotoxigenic <i>Escherichia coli</i> | | Drinking water | Watery diarrhoea |
| Enterohaemorrhagic <i>E. coli</i> | | Drinking water and recreational water contact | Bloody diarrhoea and haemolytic uraemic syndrome in children |
| <i>Yersinia</i> spp. | Yersiniosis | Drinking water | Fever, diarrhoea and abdominal pain |
| <i>Francisella tularensis</i> | Tularaemia | Drinking water | Typhoid-like or mucocutaneous with suppurative skin lesions |
| <i>Helicobacter pylori</i> | | Drinking water | Gastritis that can progress to gastric cancer |
| <i>Mycobacterium</i> spp. (Not <i>M. tuberculosis</i>) | Varies | Potable water systems in hospitals, some recreation | Varies, includes respiratory diseases, wound infections, skin disease |

Source: Hunter (2003).

Table 3: Human viruses documented to be found in the water environment.

| Genus (genome) | Popular name | Disease caused | Genus (genome) | Popular name | Disease caused |
|-----------------------------|----------------------|--|----------------------------------|-------------------|---|
| Enterovirus (ssRNA) | Poliovirus | Paralysis, meningitis, fever | Polyomavirus (dsDNA) | Polyomavirus | Progressive multifocal leucoencephalopathy, diseases of urinary tract |
| | Coxsackie A, B virus | Herpangina, meningitis, fever, respiratory disease, hand-foot-and-mouth disease, myocarditis, heart anomalies, rash, pleurodynia, diabetes | | | |
| | Echovirus | Meningitis, fever, respiratory disease, rash, gastroenteritis | | | |
| Hepatovirus (ssRNA) | Hepatitis A virus | Hepatitis | Mamastrovirus (ssRNA) | Human astrovirus | Gastroenteritis |
| Reovirus (segmented dsRNA) | Human reovirus | Unknown | Coronavirus (ssRNA) | Human coronavirus | Gastroenteritis, respiratory disease, SARS |
| Rotavirus (segmented dsRNA) | Human rotavirus | Gastroenteritis | Orthomyxovirus (segmented ssRNA) | Influenza virus | Influenza, respiratory disease |
| Norovirus (ssRNA) | Norovirus | Gastroenteritis | Parvovirus (ssDNA) | Human parvovirus | Gastroenteritis |
| Sapovirus (ssRNA) | Sapporo-like virus | Gastroenteritis | Mastadenovirus (dsDNA) | Human adenovirus | Gastroenteritis, respiratory disease, conjunctivitis |
| Hepevirus (ssRNA) | Hepatitis E virus | Hepatitis | Circovirus (ssDNA) | Torque Tenovirus | Unknown, hepatitis |

Source: Bosch *et al.* (2008).

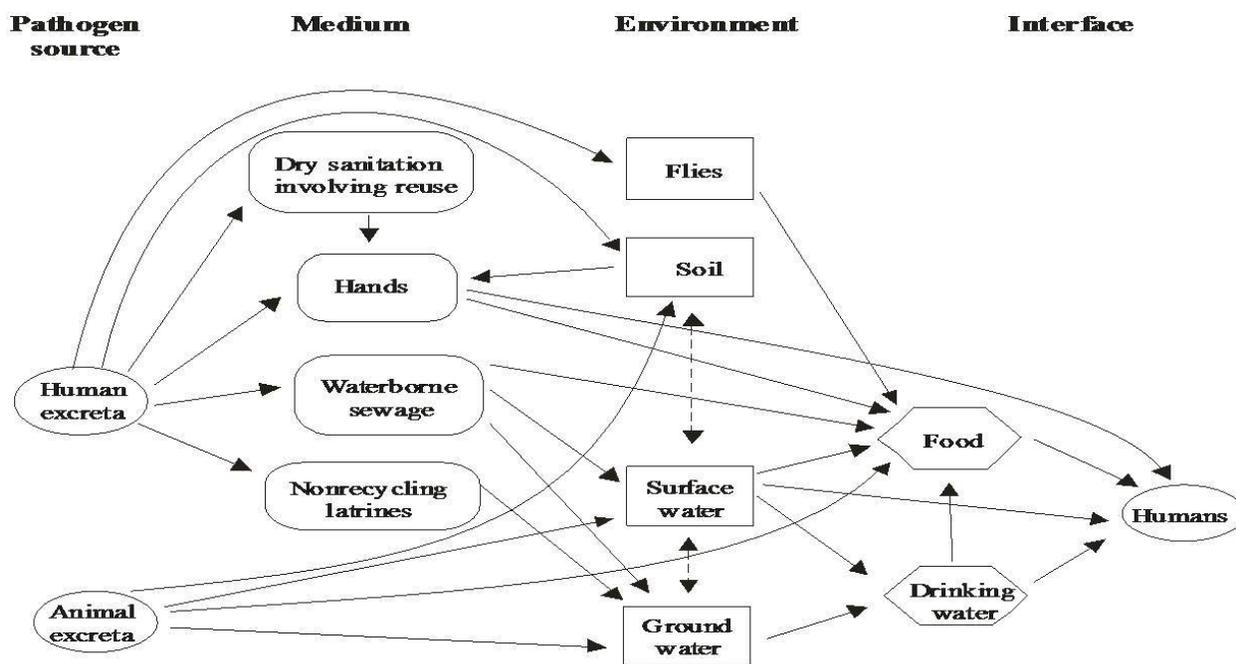


Figure 2: Transmission pathways of faecal-oral disease. (Pruss *et al.* (2002)).

Cholera, the classical waterborne disease has caused seven pandemics and still represents a serious problem, causing repeated epidemics especially in developing countries due to poor sanitation, water shortages, natural disasters (like, floods and wars) (Stewart-Tull 2001). Typhoid fever poses a serious health problem to the developing world. The annual incidence of this disease is estimated to be 20 million cases, resulting in more than 700,000 deaths (Mills-Robertson *et al.*, 2003). Most cases are the result of infection with *Salmonella typhi*, but colonization with *S. paratyphi* A, B or C, results in paratyphoid fever, a contagious condition similar to typhoid fever (WHO, 2011). Amongst other waterborne bacterial pathogens, *E. coli* O157:H7 has over the past 36 years emerged as a public health concern with worldwide distribution (Riley, *et al.*, 1983; Effler *et al.*, 2001; Chigor *et al.*, 2010). The first *E. coli* O157: H7 outbreak in Africa occurred in 1992 and was traced to river water contaminated by cattle faeces and carcasses in Swaziland and South Africa (Effler *et al.*, 2001).

According to the WHO (2011), when drinking water is contaminated with sewage, gastroenteritis and hepatitis could occur in epidemic proportions. It has been estimated that 30-90% of waterborne

disease outbreaks worldwide are caused by human enteric viruses (HEntVs) (Fong *et al.*, 2010). HEntVs have been detected in water sources globally (Bosch *et al.*, 2008; Iwai *et al.*, 2009; Fong *et al.*, 2010). HEntVs are capable of producing a wide variety of syndromes including rashes, fever, gastroenteritis, myocarditis, meningitis, respiratory disease and hepatitis (Bosch *et al.*, 2008; Buckwalter *et al.*, 2012). HEntVs include adenoviruses, rotaviruses, enteroviruses, hepatitis A virus, etc. (see, Table 3). Certain fungi are also known to cause infections in swimmers using recreational waters contaminated by faecal matter and organisms from the skin and nasopharynx. Such infections include “athlete’s foot” due to *Epidermophyton* and *Trichophyton* species (Ekowatia *et al.*, 2018). Phytoplankton blooms result in the release of cyanobacterial toxins that may present hazards for water supply safety. These toxins (microcystins, nodularins, saxitoxins, anatoxin-a, anatoxins-a(s), cyhndrospermopsin), when ingested or inhaled, are known to produce effects ranging from liver damage, including liver cancer, to neurotoxicity (Hitzfeld *et al.*, 2000; Carmichael *et al.*, 2001; Chia *et al.*, 2009).

The tragic death of 60 dialysis patients in Caruaru, Brazil in 1996 was attributed to the presence of cyanobacterial toxins in water supply used in a haemodialysis unit (Pouria *et al.*, 1998). Subsequent examination by Carmichael *et al.* (2001) of phytoplankton from the dialysis clinic's water source, analyses of the clinic's water treatment system, plus serum and liver tissue of clinic patients led to the identification of two groups of cyanobacterial toxins, the hepatotoxic cyclic peptide microcystins and the hepatotoxic alkaloid cylindrospermopsin.

Apart from the pathogen-mediated waterborne diseases discussed and/or listed above, public health concern over faecally polluted water exists regarding diseases associated with excessive levels of nitrate in aquatic systems (WHO, 2007). Nitrate itself does not pose any health threat; however, nitrate (NO_3^-) is readily reduced to nitrite (NO_2^-) by the enzyme nitrate reductase found in microorganisms (McEldowney *et al.*, 1993). Nitrite poses two distinct health risks, being potentially carcinogenic and causing methaemoglobinaemia (blue-baby syndrome).

Risk Assessment

Microbial risk assessment is a process that evaluates the likelihood of adverse human health effects following exposure to a medium in which pathogens are present (Soller and Eisenberg, 2008). The risk for human health associated with the presence of pathogens in water bodies can be evaluated using both the observed-adverse-effect-level approach (OAELA) and quantitative microbial risk assessment (QMRA). The OAELA is based on the occurrence of microbiological indicator organisms instead of actual pathogens (Steyn *et al.*, 2004), and the basic assumption in this indicator concept is that their presence indicates the presence of faecal pollution and the potential for the presence of pathogens (Savichtcheva and Okabe, 2006; Abdelzaher *et al.*, 2010). The QMRA process involves four steps: hazard identification, exposure assessment, dose-response assessment and risk characterization (Toze *et al.*, 2010). The quantitative methods to characterize human health risks associated with exposure to pathogens have been reported in the last four decades (Haas *et al.*, 1993; Ahmed *et al.*, 2010; Chigor *et al.* 2014) and guidelines have, accordingly, been established (FAO/WHO, 2003; USEPA/USDA/FSIS, 2012).

Protecting Water Sources

Source Water Protection (SWP) is recognized as the first barrier and the most effective means of reducing the risk of water contamination (Ibrahim and Patrick, 2017; Bruni, 2019). It involves protecting water sources from contamination and overuse especially, at the source. By so doing, public health risks associated with contaminated water, as well as the cost of water treatment/purification are reduced. According to UNEP (2010), three basic strategies exist for protection of surface water sources. They include preventing (waste, pollutants or untreated water from domestic, industrial or agricultural use from been discharged into the water body), treatment (of polluted water, including stormwater management before discharge into water bodies) and a mind set to restore the ecosystem.

For the protection of water sources to be achieved, a legal framework (which has to involve a protection plan, formulated responsibilities, specific protection measures and basic rules that apply to all community members and water source users) needs to be implemented (Bruni, 2019). Above all, water education and public enlightenment on the dangers of water contamination and the need for water protection will go a long way to seeing that all and sundry gets involved in this urgent and vital need to protect our ecosystem.

CONCLUSION

Freshwater sources are vulnerable to contamination. Poor environmental practices including open defecation, untreated wastewater disposal, and open grazing, with the attendant *in-situ* herd watering introduce organic matter and pathogens into the water resources; which might lead to diseases like diarrhoea, cholera, typhoid fever, to mention but a few. Disease with multidrug resistance strains reduces therapeutic options, increases hospital stay, causes more economic losses, as well as increased fatal cases. The best, safest and most assured way of reducing these risks is by protecting our water sources from pollution and employing point of use treatment measures. Protection and conservation of surface freshwater resources should no longer be neglected. It requires a clear legal framework that outlines responsibilities, specific protection measures and basic rules that apply to all community members and water source users.

REFERENCES

- Abdelzaher, A.M., Wright, M.E., Ortega, C., Solo-Gabriele, H.M., Miller, G., Newman, X., Shih, P., Bonilla, A., Bonilla, T.D., Palmer, C.J., Scott, T., Lukasik, J., Harwood, V.J., McQuaig, S., Sinigalliano, C., Gidley, M., Plano, L.R.W., Zhu, X., Wang, J.D. and Fleming, L.E. (2010). Presence of pathogens and indicator microbes at a non-point source subtropical recreational marine beach. *Applied and Environmental Microbiology*. 76: 724–732.
- Ahmed, W., Vieritz, A., Goonetilleke, A. and Gardner, T. (2010). Health risk from the use of roof-harvested rainwater in southeast Queensland, Australia, as potable or nonpotable water, determined using quantitative microbial risk assessment. *Applied and Environmental Microbiology*. 76: 7382–7391.
- Albek, E. (2003). Estimation of point and diffuse containment loads to streams by non-parametric regression analysis of monitoring data. *Water Air and Soil Pollution*. 147: 229–243.
- Ash, R.J, Mauck, B. and Morgan, M. (2002). Antibiotic resistance of gram-negative bacteria in rivers, United States. *Emerging Infectious Diseases*. 8: 713-716.
- Azizullah, A., Khattak, M.N., Richter, P. and Hader, D.P. (2011). Water pollution in Pakistan and its impact on public health: a review. *Environment International*. 37: 479-497.
- Blake, D.P., Humphry, R.W., Scott, K.P., Hillman, K., Fenlon, D.R. and Low, J.C. (2003). Influence of tetracycline exposure on tetracycline resistance and the carriage of tetracycline resistance genes within commensal *Escherichia coli* populations. *Journal of Applied Microbiology*. 94: 1087-1097.
- Bosch, A., Guix, S., Sano, D. and Pinto, R.M. (2008). New tools for the study and direct surveillance of viral pathogens in water. *Current Opinion in Biotechnology*. 19: 1–7.
- Bruni, M. (2019). Water Source Protection. Available at: <https://sswm.info/arctic-wash/module-4-technology/further-resources-water-sources/water-source-protection>
- Buckwalter, S.P., Teo, R., Espy, M.J., Sloan, L.M., Smith, T.F. and Pritt, B.S. (2012). Real-time qualitative PCR for 57 human adenovirus types from multiple specimen sources. *Journal of Clinical Microbiology*. 50 (3):766-771.
- Cabral, J.P.S. (2010). Water microbiology: bacterial pathogens and water. *International Journal of Environmental Research and Public Health*. 7: 3657-3703
- Carmichael, W.W., Azevedo, S.M.F.O., An, J.S., Molica, R.J.R., Jochimsen, E.M., Lau, S., Rinehart, K.L., Shaw, G.R. and Eaglesham, G.K. (2001). Human fatalities from cyanobacteria: chemical and biological evidence for cyanotoxins. *Environmental Health Perspectives*. 109: 663-668.
- CDC (2013). Antibiotic Resistance Threats in the United States 2013. Available online at: <http://www.cdc.gov/drugresistance/threat-report-2013/index.html>. Assessed 11/2/19.
- Chia, A. M., Abolude, D. S., Ladan, Z., Akanbi, O. and Kalaboma, A. (2009). The presence of microcystins in aquatic ecosystems in Northern Nigeria: Zaria as a case study. *Research Journal of Environmental Toxicology*. 3: 170–173.
- Chigor, V. N., Sibanda, T. and Okoh, A.I. (2013). Studies on the bacteriological qualities of the Buffalo River and three source water dams along its course in the Eastern Cape Province of South Africa. *Environmental Science and Pollution*. 20(6): 4125-4136.
- Chigor, V.N., Sibanda, T. and Okoh, A.I. (2014). Assessment of the risks for human health of adenoviruses, hepatitis A virus, rotaviruses and enteroviruses in the Buffalo River and three source water dams in the Eastern Cape. *Food and Environmental Virology*. 6(2): 87-98.
- Chigor, V.N., Umoh, V.J. and Smith, S.I. (2010b). Occurrence of *Escherichia coli* O157 in a river used for fresh produce irrigation in Nigeria. *African Journal of Biotechnology*. 9: 178-182.

- Chigor, V.N., Umoh, V.J., Okuofu, C.A., Ameh, J.B., Igbinsosa, E.O. and Okoh, A.I. (2012). Water quality assessment: Surface water sources used for drinking and irrigation in Zaria, Nigeria are a public health hazard. *Environmental Monitoring and Assessment*. 184: 3389–3400.
- Chigor, V.N., Umoh, V.J., Smith, S.I., Igbinsosa, E.O. and Okoh, A.I. (2010a). Multidrug resistance and plasmid patterns of *Escherichia coli* O157 and other *E. coli* isolated from diarrhoeal stools and surface waters from some selected sources in Zaria, Nigeria. *International Journal of Environmental Research and Public Health*. 7: 3831-3841.
- Delgado-Gardea, M.E., Tamez-Guerra, P., Gomez-Flores, R., Zavala-Díaz de la Serna, F.J., Eroza-de la Vega, G., Nevárez-Moorillón, G.V., Pérez-Recoder, M.C. Sánchez-Ramírez, B., González-Horta, M. and Infante-Ramírez, R. (2016). Multidrug-resistant bacteria isolated from surface water in Bassaseachic Falls National Park, Mexico. *International Journal of Environmental Research and Public Health*. 13: 597 – 612.
- Delpla, I., Jung, A.-V., Baures, E., Clement, M. and Thomas O. (2009). Impacts of climate change on surface water quality in relation to drinking water production. *Environment International*. 35: 1225-1233.
- Effler, P., Isaacson, M., Arntzen L., Heenan, R., Canter P., Barrett, T., Lee L., Mamba, C., Levine, W., Zaidi, A. and Griffin, P.M. (2001). Factors contributing to the emergence of *Escherichia coli* O157, H7 in Africa. *Emerging Infectious Diseases*. 7: 812-819.
- Ekowatia, Y., Ferreroa, G., Kennedy, M.D., Husmanc, A.M. and Schetsc, F.M. (2018). Potential transmission pathways of clinically relevant fungi in indoor swimming pool facilities. *International Journal of Hygiene and Environmental Health*. 221: 1107–1115.
- Federal Government of Nigeria and UNICEF (FGN/UNICEF) (2017). *Making Nigeria Open-Defecation-Free —A National Road Map*. Pp 1-72.
- Fong, T.T., Phanikumar, S.S., Xagorarakis, I. and Rose, J.B. (2010). Quantitative detection of human adenoviruses in wastewater and combined sewer overflows influencing a Michigan river. *Applied and Environmental Microbiology*. 76, 715–723.
- Food and Agriculture Organization and World Health Organization (FAO/WHO) (2003). *Hazard Characterization for Pathogens in Food and Water: Guidelines*. The Food and Agriculture Organization and the World Health Organization. Available online: <http://whqlibdoc.who.int/publications/2003/9241562374.pdf>
- Gourmelon, M., Caprais, M.P., Se'gura, R., Le Mennec, C., Lozach, S., Piriou, J.Y. and Rince, A. (2007). Evaluation of two library-independent microbial source tracking methods to identify sources of fecal contamination in French estuaries. *Applied and Environmental Microbiology*. 73: 4857–4866.
- Guyomard-Rabenirina S., Dartron C., Falord M, Sadikalay S, Ducat C, Richard V, et al. (2017). Resistance to antimicrobial drugs in different surface waters and wastewaters of Guadeloupe. *PLoS ONE*. 12(3): e0173155.
- Haas, C.N., Rose, J.B., Gerba, C. and Regli, S. (1993). Risk assessment of virus in drinking water. *Risk Analysis*. 13: 545–552.
- Haramoto, E., Katayama, H., Oguma, K. and Ohgaki, S. (2008). Application of cation-coated filters method to detection of noroviruses, enteroviruses, adenoviruses and torque teno viruses in the Tamagawa River in Japan. *Applied and Environmental Microbiology*. 71: 2403–2411.
- Hatami, H. (2013). Importance of water and water-borne diseases: on the occasion of the world water day (march 22, 2013). *International Journal of Preventive Medicine*. 4(3): 243–245.

- Hitzfeld, B.C., Hoger, S.J. and Dietrich, D.R. (2000). Cyanobacterial toxins: removal during drinking water treatment and risk assessment. *Environmental Health Perspective*. 108, 113S1-122S1.
- Hunter, P.R. (2003). Climatic change and waterborne and vector-borne disease. *Journal of Applied Microbiology*. 94: 37S-46S.
- Ibrahim, A.A. and Patrick, R.J. (2017). Source Water Protection Planning and Management in Metropolitan Canada: A Preliminary Assessment. *Water*. 9: 497 – 511.
- Idu, A.J. (2015). Threats to water resources development in Nigeria. *Journal of Geology and Geophysics*. 4(3): 1-10
- Igbinosa, E. O. and Okoh, A. I. (2009). Impact of discharge wastewater effluents on the physico-chemical qualities of a receiving watershed in a typical rural community. *International Journal of Environmental Science and Technology*. 6: 175-182.
- Igor S. (1993). World fresh water resources. In Peter H. Gleick Edited, *Water in Crisis: A Guide to the World's Fresh Water Resources*. Oxford University Press, New York. Available online at: <http://ga.water.usgs.gov/edu/earthhowmuch.html>
- Iwai, M., Hasegawa, S., Obara, M., Nakamura, K., Horimoto, E., Takizawa, T., Kurata, T., Sogen, S. and Shiraki, K. (2009). Continuous presence of noroviruses and sapoviruses in raw sewage reflects infections among inhabitants of toyama, Japan (2006 to 2008). *Applied and Environmental Microbiology*. 75: 1264–1270.
- Karlowsky, J.A., Jones, M.E., Thornsberry, C. and Friedland, I.R. (2003). Trends in antimicrobial susceptibilities among enterobacteriaceae isolated from hospitalized patients in the United States from 1998-2001. *Antimicrobial Agents and Chemotherapy*. 47: 1672-1680.
- King-Abia, A. K., Schaefer, L., Ubomba-Jaswa, E. and Le Roux, W. (2017). Abundance of pathogenic *Escherichia coli* virulence-associated genes in well and borehole water used for domestic purposes in a peri-urban community of South Africa. *International Journal of Environmental Research and Public Health*, 14: 320 – 331.
- Kistemann, T., Claßen, T., Koch, C., Dagedorf, F., Fischeder, R., Gebel, J., Vacata, V. and Exner, M. (2002). Microbial load of drinking water reservoir tributaries during extreme rainfall and runoff. *Applied and Environmental Microbiology*. 68: 2188-2187.
- Leff, L.G. (1994). Stream bacterial ecology: a neglected field? *ASM News*. 60: 135-138.
- McEldowney, S., Hardman, D.J. and Waite, S. (1993). *Pollution: Ecology and Biotreatment*. Longman Group Ltd., Essex, England, pp. 135-157.
- Mills-Robertson, F., Crupper, S.S., Addy, M.E. and Mensah, P. (2003). Antibiotic resistance and genotyping of clinical group B *Salmonella* isolated in Accra, Ghana. *Journal of Applied Microbiology*. 94: 289-294
- National Geographic (2010). *The Water Issue*, National Geographic —the Official Journal of the National Geographic Society. <https://www.nationalgeographic.com/magazine/2010/04/>
- Ng, C. and Gin, K.Y. (2019). Monitoring Antimicrobial Resistance Dissemination in Aquatic Systems. *Water*. 11: 71
- Pandey, P.K., Kass, P.H., Soupir, M.L., Biswas, S. and Singh, V.P. (2014). Contamination of water resources by pathogenic bacteria. *AMB Express*. 4: 51- 67.
- Parmar, T. K., Rawtani, D. and Agrawal Y. K. (2016). Bioindicators: the natural indicator of environmental pollution. *Frontiers in Life Science*. 9(2): 110–118.
- Parveen, S., Hodge, N.C., Stall, R.R., Farrah, S.R. and Tamplin, M.L. (2001). Phenotypic and genotypic characterization of human and non-human *Escherichia coli*. *Water Research*. 35: 379-386.
- Pouria, S., de Andrade, A., Barbosa, J., Cavalcanti, R., Barreto, V., Ward, C., Preiser, W., Poon, G., Neild, G. and Godd, G. (1998). Fatal microcystin intoxication in haemodialysis unit in Caruaru, Brazil. *Lancet*. 352: 21-26.

- Prüss, A., Kay, D., Fewtrell, L. and Bartram, J. (2002). Estimating the burden of disease from water, sanitation, and hygiene at a global level. *Environmental Health Perspectives*, 110(5): 367-542.
- Ramírez-Castillo, F.Y., Loera-Muro, A., Jacques, M., Garneau, P., Avelar-González, F.J., Harel, J. and Guerrero-Barrera, A.L. (2015). Waterborne pathogens: Detection methods and challenges. *Pathogens*. 4: 307-334.
- Riley, L.W., Remis, R.S., Helgerson, S.D., McGee, H.B. Wells, J.G., Davis, B.R., Hebert, R.J., Olcott, E.S., Johnson, L.M., Hargrett, N.T., Blake, P.A. and Cohen, M.L. (1983). Hemorrhagic Colitis Associated with a Rare *Escherichia coli* Serotype. *The New England Journal of Medicine*. 308: 681-685.
- Ritter, L., Solomon, K., Silbey, P., Hall, K., Keen, P., Mattu, G. and Linton B. (2002). Sources, pathways, and relative risks of contaminants in surface water and groundwater: a perspective prepared for the Walkerton inquiry. *Journal of Toxicology and Environmental Health*. 65: 1-142.
- Savichtcheva, O. and Okabe, S. (2006). Alternative indicators of fecal pollution: Relations with pathogens and conventional indicators, current methodologies for direct pathogen monitoring and future application perspectives. *Water Research*. 40: 2463-2476.
- Sidrach-Cardona, R., Hijosa-Valsero, M., Marti, E., Balcázar, J. L., & Becares, E. (2014). Prevalence of antibiotic-resistant fecal bacteria in a river impacted by both an antibiotic production plant and urban treated discharges. *Science of the Total Environment*. 488(1): 220–227.
- Skraber, S., Gassilloud, B. and Gantzer, C. (2004). Comparison of coliforms and coliphages as tools for assessment of viral contamination in river water. *Applied and Environmental Microbiology*. 70: 3644-3649.
- Solaraj G., Dhanakumar, S., Murthy, R.K. and Mohanraj, R. (2010). Water quality in select regions of Cauvery Delta River basin, southern India, with emphasis on monsoonal variation. *Environmental Monitoring and Assessment*. 166: 435–444.
- Soller, J.A. and Eisenberg, J.N.S. (2008). An evaluation of parsimony for microbial risk assessment models. *Environmetrics*. 19: 61-78.
- Stewart-Tull, D.E.S. (2001). Vaba, hariza, cholera, foklume or cholera: in any language, still the disease of seven pandemics. *Journal of Applied Microbiology*. 91: 580-581.
- Steyn, M., Jagals, P. and Genthe, B. (2004). Assessment of microbial infection risks posed ingestion of water during domestic water use and full-contact recreation in a mid-southern African region. *Water Science and Technology*. 50: 301-308.
- Suthar, S., Sharma, J., Chabukdhara, M. and Nema, A.K. (2010). Water quality assessment of river Hindon at Ghaziabad, India: impact of industrial and urban wastewater. *Environmental Monitoring and Assessment*. 165: 103–112.
- Toze, S., Elise Bekele, E., Page, D., Sidhu, J. and Shackleton, M. (2010). Use of static quantitative microbial risk assessment to determine pathogen risks in an unconfined carbonate aquifer used for managed aquifer recharge. *Water Research*. 44: 1038-1049.
- Ubani, O., Mba, E. and Ozougwu, M. (2014). An Assessment of the Pollution Levels of Rivers in Enugu Urban Nigeria and their Environmental Implication. *Journal of Environmental and Earth Science*. 4(3): 18-24.
- UNEP (2010): Clearing the Waters. A Focus on Water Quality Solutions. Oakland: United Nations Environment Programme (UNEP). Available online at: https://sswm.info/sites/default/files/reference_attachments/UNEP%202010%20Clearing%20the%20Waters.pdf

- United States Environmental Protection Agency and U.S. Department of Agriculture/Food Safety and Inspection Service (USEPA/USDA/FSIS) (2012). *Microbial Risk Assessment Guideline: Pathogenic Microorganisms with Focus on Food and Water*. EPA/100/J-12/001; USDA/FSIS/2012-001.
- Veal, D.A., Strokes, H.W. and Daggard, G. (1992). Genetic exchange in natural microbial communities. In: Marshal, K.C. (Ed). *Advances in Microbial Ecology* (Vol. 12). Plenum Press, New York; pp. 383-430.
- WHO (2015). Mortality and burden of disease from water and sanitation. Available online at: www.who.int/gho/phe/water_sanitation/burden_text/en/
- WHO (2019a). *Drinking water: Key Fact*. Available at: <https://www.who.int/news-room/fact-sheets/detail/drinking-water>; Accessed 20/06/2019.
- WHO (2019b). *Sanitation: Key Fact*. Available at: <https://www.who.int/en/news-room/fact-sheets/detail/sanitation>; Accessed 20/06/2019.
- Woegerbauer, M., Jenni, B., Thalhammer, F., Graninger, W. and Burgmann, H. (2002). Natural genetic transformation of clinical isolates of *Escherichia coli* in urine and water. *Applied and Environmental Microbiology*. 68: 440-443.
- World Health Organization (WHO) (2007). *Nitrate and nitrite in drinking-water*. WHO Press, 1211 Geneva, Switzerland; pp: 1-21.
- World Health Organization (WHO) (2009). *World Health Statistics 2009*; WHO Press: Geneva, Switzerland; pp. 1-149.
- World Health Organization (WHO) (2011). *Guidelines for Drinking-water Quality*. WHO Press, Geneva, Switzerland; pp. 117-153, 231-306.
- World Health Organization (WHO) and United Nations Children's Fund (UNICEF) (2017). Progress on drinking water, sanitation and hygiene: 2017 update and SDG baselines.
- Zhang, M., Zhao, H., Yang, J., Jiang, S. and Cai, B. (2010). Detection and quantification of enteroviruses in coastal seawaters from Bohai Bay, Tianjin, China. *Journal of Environmental Sciences*. 22: 150-154.
- Zhukinskii, V.N. (2003). Environmental risk and environmental damage to surface water quality: topicality, terminology, quantitative estimates. *Water Resources*. 30: 111-198.