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A review on ingestion of water supplies by pathogenic bacteria

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Abstract

The pollution of water resources with water-borne pathogens and illnesses that may be contracted as a result is a serious problem about water quality all over the globe. Evidenced by a large number of recent publications, the growing interest in controlling water-borne pathogens in water resources clearly attests to the need for studies that synthesise knowledge from multiple fields covering comparative aspects of pathogen contamination, and unify them in a single place in order to present and address the problem as a whole. This review paper attempts to develop the first comprehensive single source of existing information on pathogen contamination in multiple types of water resources, with the goal of providing a broader perspective of pathogen contamination in freshwater (rivers, lakes, reservoirs, groundwater) and saline water (estuaries and coastal waters) resources. Specifically, the paper focuses on freshwater and saline water resources. In addition, a detailed discussion outlines the difficulties that might arise when utilising indicator organisms. The potential effects of water resources development on the presence of pathogen contamination and the difficulties that still need to be overcome in the fight against pathogen contamination are both highlighted in this article.

Keywords: Pathogens, contamination, water resources, watershed, pathogens transport

1. Introduction

A significant worry about water quality all around the globe is the presence of water-borne pathogens in ambient water bodies and the illnesses that may be contracted as a result. Because contamination with pathogens is a severe problem in practically all kinds of ambient water bodies, awareness of the problem and a knowledge of it are both crucial (U.S. EPA 2012a). One of the eight goals set for the Millennium Development Plan by the United Nations is to improve the quality of the world's water supplies (MDGs). Its goal is to bring the percentage of people who do not have access to clean water down by fifty percent by the year 2015. (WHO 2011). It is essential to have a solid understanding of how changes in weather patterns might possibly have an effect on the amount of pathogens found in water resources in light of the overwhelming scientific data that points to climate change (IPCC 2007). Long-term planning must include the construction of additional water storage facilities (i.e. dams) in order to fulfil the anticipated need for water in the production of food, the generation of electricity, and the maintenance of ecosystems (World Bank 2010). However, these new buildings have the potential to diminish the quality of the water and to worsen the threat to public health.

There are several review papers that are currently available (Bradford *et al.* 2013; Pachepsky and Shelton 2011; Pang 2009; Jin and Flury 2002; John and Rose 2005; Jamieson *et al.* 2004; Jamieson *et al.* 2002; Arnone and Walling 2007; Kay *et al.* 2007) ^[8, 50, 2, 1], but there is a manifest need for additional transdisciplinary studies that assimilate knowledge gained from multiple research endeavours studying pathogen contamination and provide a comprehensive synopsis. As a result, the objective of this review is to provide a comprehensive analysis of the study spectrum of pathogen contamination of water resources and the accompanying issues that it brings. We provide a synopsis of the possible health hazards imposed on humans by pathogens in water resources by giving information that spans surface water, groundwater, fresh water, and salt water. This allows us to evaluate the potential impact that pathogens have on human health. In addition, a summary of the influence that the development of water resources has had on the contamination of pathogens, as well as future difficulties and suggestions, is included. In addition to this, we provide a concise discussion that details the water-borne pathogen footprints and possible issues related with the use of indicator organisms for the purpose of determining the quality of the water.

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2. Health Risk

Numerous epidemics have been attributed to diseases that are transmitted by water, such as diarrhoea and gastrointestinal illnesses caused by a variety of bacteria, viruses, and protozoa (Craun *et al.* 2006) ^[20]. Millions of people are affected by illnesses that are transmitted via water in impoverished nations like those in Africa (Fenwick 2006). According to the World Health Organization (WHO), water-related illnesses claim the lives of 3.4 million people every year, the majority of whom are children (WHO 2014). According to an estimate provided by the United Nations Children's Fund (UNICEF), the use of tainted water causes the deaths of four thousand children every single day (UNICEF 2014). According to the World Health Organization (2010), over 2.6 billion people do not have access to clean water. This lack of access results in around 2.2 million fatalities per year, of which 1.4 million are in children. The burden of illness throughout the globe might be reduced by around 4 percent if water quality were improved (WHO 2010).

Although water-related disorders are more common in underdeveloped nations, industrialised countries face a significant obstacle in the form of this global health problem as well. Arnone and Walling (2007) ^[2] conducted a research in which they collated data on outbreaks that occurred in the United States between the years 1986 and 2000. They found that recreational water was connected with 5,905 cases and 95 outbreaks. About 29.53 percent of cases were caused by gastrointestinal illness (GI), which is an illness that may be caused by a wide range of microorganisms and germs and that can result in symptoms such as diarrhoea, nausea, vomiting, fever, and abdominal discomfort. The *Shigella* spp. bacteria were responsible for more than 27 percent of the cases. In addition, *Cryptosporidium parvum* was responsible for 10.99 percent of the cases, while Adenovirus 3 was responsible for 10.08 percent, and *Leptospira* was responsible for 6.59 percent of the cases. GI was responsible with over 23 percent of the outbreaks, while *Shigella* spp was responsible for nearly 21 percent of the outbreaks. In addition, *Naegleria fowleri* was responsible for 16.84 percent of the outbreaks, while *E. coli* 0157:H7 was responsible for 12.63 percent, and *Schistosoma* spp. was responsible for 7.37 percent of the outbreaks. In addition to severe gastroenteritis, other significant etiological agents responsible for numerous outbreaks include *Giardia*, *Cryptosporidium*, *E. coli* 0157:H7, *V. cholera*, and *Salmonella* (Craun *et al.* 2006) ^[20]. During the same time period, polluted drinking water was the source of 437,082 cases and 48 outbreaks. Approximately 95.89 percent of the cases were caused by *Cryptosporidium parvum*. *Giardia lamblia* was responsible for around 42 percent of the outbreaks, whereas GI was responsible for approximately 31 percent of the outbreaks. According to data on water-borne outbreaks in the United States that were reported by Craun *et al.* (2006) ^[20], at least 1870 outbreaks occurred in the United States between the years 1920 and 2002, which is an average of 23 outbreaks per year. As a result of unreported cases and a lack of information about exposure, it is very probable that the reported outbreaks and the reported frequency of diseases represent an underestimate of the true number of cases and illnesses. The National Primary Drinking Water Regulations (NPDWRs) of the United States Environmental Protection Agency (EPA) contain standards that describe the Maximum Contaminant Level

(MCL), which is the highest level of a contaminate that is permissible in drinking water. These standards are intended to protect public health. The Maximum Contaminant Level (MCL) for a variety of bacteria and viruses, including *Cryptosporidium*, *Giardia lamblia*, *Legionella*, and Total Coliforms (including faecal coliform and *E. coli*), has been established by the United States Environmental Protection Agency (EPA) (U.S. EPA 2012b). The Maximum Contaminant Threshold Goal (MCLG) has also been suggested by the United States Environmental Protection Agency (EPA). This is the level of a contaminant in drinking water below which there is no known harm to human health. The Minimum Contaminant Lethal Concentration (MCLC) values for *Cryptosporidium*, *Giardia lamblia*, *Legionella*, and Total Coliforms are all at zero. The Environmental Protection Agency (EPA) mandates that *Cryptosporidium* be removed from drinking water at a rate of 99 percent, whereas the rates of removal for *Giardia lamblia* and viruses are 99.9 and 99.99 percent, respectively. Even though there is no set limit for *Legionella*, the Environmental Protection Agency (EPA) thinks that drinking water will likely be free of *Legionella* if *Giardia lamblia* and viruses are eliminated or rendered inactive first. The Environmental Protection Agency (EPA) in the United States mandates that regular samples of drinking water be taken in order to test for total coliform and *E. coli*; in the event that a routine sample returns positive results, further samples must be taken. A severe violation of the MCL has occurred in the drinking water supply if any sample taken more than once reveals the presence of total coliform or *E. coli*. If a drinking water system collects less than forty routine tests per month, the maximum number of positive total coliform samples that may be found in a given month is one. It is permissible to have no more than 5 percent of all samples tested positive for coliform bacteria in a given month for a system that gathers more than 40 regular samples (U.S. EPA 2012b). In the United States, there are roughly 42,000 new cases of salmonellosis recorded each year (CDC 2014) ^[14]. Schistosomiasis is not a problem in the United States since it is not an endemic disease; nonetheless, there are about 200 million individuals affected across the globe. In 2011, around 1,060 instances of Guinea worm illness, which is caused by the parasite *Dracunculus medinensis* and was recorded in many isolated areas of Africa that do not have access to clean drinking water, were reported. Malaria, which is caused by a protozoal illness of the genus *Plasmodium* and is spread by mosquitoes that spawn in water that is polluted, affects 300–500 million people and is responsible for the deaths of over one million people every year (more than 90 percent of deaths in Africa). In general, the illness and death rates caused by polluted water are quite high, and they need to be brought under control by increasing the availability of clean water (this includes recreational water as well as drinking water) in both developing nations and developed ones.

3. Historical perspective of water-borne diseases

As early as 500–400 B.C., an Indian literature written in Sanskrit has descriptions of water-borne illnesses that are similar to cholera. These diseases are mentioned in the *Sushruta Samshita*, which was published in India (Colwell 1996) ^[20]. *Vibrio cholera* continues to infect millions of people each year in impoverished nations, despite the fact that cholera cases have not been recorded in affluent

countries in recent years, mostly as a result of improvements in sanitation (Nelson *et al.* 2009) [29]. Every year, cholera is responsible for around 3–5 million cases and 10,000–120,000 fatalities, the majority of which occur in underdeveloped nations. These statistics are reported by the World Health Organization. Over the course of history, cholera has been responsible for the deaths of millions of people in both underdeveloped nations and industrialised ones (Colwell 1996; Okun 1996) [20]. For instance, in the year 1849, London was said to have seen a significant epidemic of cholera. Dr. John Snow, who served as a physician to Queen Victoria, established a connection between the spread of cholera and the use of water that was tainted (Snow 1854; Colwell 1996) [20]. Excellent assessments on events that occurred in the early 19th century may be found in the works of Jordan *et al.* (1904), Ruediger (1911), Simons *et al.* (1922), and Rudolfs *et al.* (1950). According to Colwell (1996) [20], the cholera was responsible for the deaths of millions of people all across the globe in the middle and late 18th century. Following the disastrous earthquake that struck the capital and surrounding parts of Haiti, the country had the greatest epidemic in recent memory. There were approximately half a million cases, and thousands of people lost their lives as a result of the outbreak (CDC 2011) [13].

4. Water-borne pathogen footprints and challenges

It is standard practise to utilise indicator species in order to evaluate the prevalence of water-borne pathogens in water resources, often known as the water-borne pathogen footprints of water resources. A popular strategy for measuring the possible pathogen burdens in ambient water bodies is to monitor the amounts of indicator organisms (such as faecal coliforms, *E. coli*) as shown in Figure 1. In rivers, lakes, estuaries, and coastal waterways, public health authorities and scientists have been counting the number of faecal coliforms and *E. coli* bacteria for many decades now in order to assess the water's quality (Malakoff 2002; Pandey *et al.* 2012a; Pandey *et al.* 2012b; Pandey and Soupir 2013). However, there is a great deal of controversy around the indicator species that are currently in use and their capacity to accurately indicate the possible presence of dangerous bacteria. In addition, it might be difficult to determine the origin of infections (for example, human waste, animal waste, the excrement of wild animals, and the droppings of waterfowl) (Figure 2). (Malakoff 2002; Dickerson *et al.* 2007) [26]. There is a possibility that microbial source tracing (MST), a method that is considered to be relatively new, might be used to trace the origin of faecal coliform (Scott *et al.* 2002; Grave *et al.* 2007; Dickerson *et al.* 2007; Ibekwe *et al.* 2011; Ma *et al.* 2014) [47, 26, 1]. In the past, antibiotic resistance testing used the MST approach to evaluate cattle's effect on water quality on a watershed scale. This was done using a scale that was equivalent to a watershed (Grave *et al.* 2007) [47]. The authors proposed that host-origin libraries, which are determined using a phenotypic technique, are an effective means of tracing the origins of the pathogens. A large number of MST approaches, on the other hand, are predicated on the hypothesis that some bacterial strains are confined to a specific animal species or group of animals. When it comes to the most frequent kind of faecal bacteria, *E. coli*, this notion is open to some debate (Malakoff 2002). Because of this, one must use extreme care when employing

E. coli for source tracing (Gordon 2001) [45]. In addition, the cost of developing libraries, implementing extensive sampling programmes that are required for verifying the MST method, and calculating uncertainties associated with the method are all legitimate concerns that need to be addressed before the MST method can be utilized on a watershed scale.

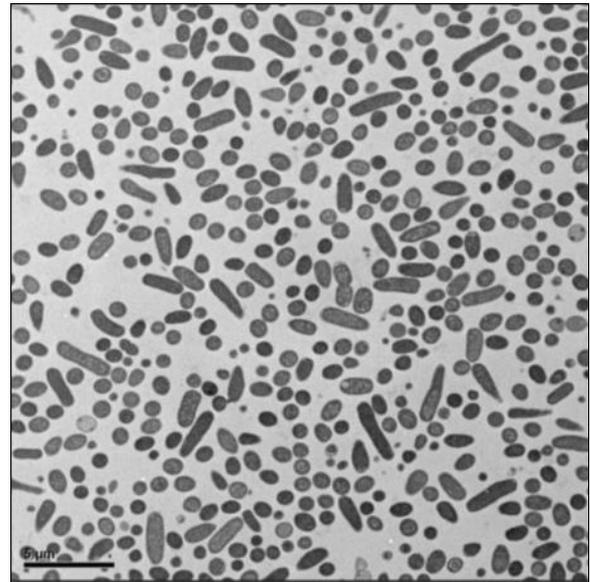


Fig 1: Transmission electron micrograph of *E. coli*

5. Pathogen contamination in water resources

It is estimated by the United States Environmental Protection Agency (EPA), which is responsible for monitoring the water quality of a variety of ambient water bodies, that pathogens pollute more than 480,000 kilometres (km) of rivers and shorelines as well as 2 million hectares (ha) of lakes in the United States (U.S. Environmental Protection Agency 2010a). Estimates provided by the EPA indicate that pathogens are the primary factor responsible for the impairment of waterways that are included on the 303(d) list (i.e., the list of impaired and endangered waters that the Clean Water Act requires each state to submit for EPA approval) (Figure 3). (U.S. EPA 2014a, 2014b, 2014c). Figure 3 presents the top five causes of impairment, which have been reported out of a total of 71,917 causes of impairment that have been reported. The contamination with pathogens is, without a doubt, the most common cause of impairment (U.S. EPA 2014a, 2014b, 2014c).

Recent research on water-borne pathogen transport has been reviewed by Diffey (1991) [27], Brookes *et al.* (2004) [9], Jamieson *et al.* (2004), Gerba and Smith (2005) [43], Gerba and McLeod (1976) [42], Hipsey *et al.* (2008), and Pachepsky and Shelton (2011) [50]. These reviews focused on freshwater and estuarine sediments in particular. In addition, many recent reviews concentrate on particular facets of water resources. For example, John and Rose (2005) reviewed groundwater; Brookes *et al.* (2004) [9] reviewed reservoirs and lakes; Jamieson *et al.* (2004) reviewed agricultural watersheds; and Kay *et al.* (2007) reviewed catchment microbial dynamics. All of these reviews can be found in the current literature. For the purpose of understanding how water-borne diseases might possibly damage public health and a variety of ambient water bodies, the review research that is given here takes an approach that is considerably more comprehensive. In addition, the

difficulties that currently exist when evaluating the presence of pathogens in water supplies are explored.

6. Ground water

Groundwater is the principal source of household drinking water supplies in many parts of the globe, and the presence of contaminants in groundwater unquestionably raises the danger to the general population's health. Groundwater contributes to the production of forty percent of the United States' domestic water supply, and more than forty million Americans get their drinking water from private wells that tap into groundwater sources (Alley *et al.* 1999) ^[1]. The pollution of groundwater by pathogens has caused a large number of disease outbreaks in the United States; for instance, at least 46 outbreaks of disease occurred in the United States between the years 1992 and 1999, which resulted in 2,739 instances of sickness and many fatalities (John and Rose 2005). These are the cases that have been reported; the actual morbidity is almost certainly going to be higher due to underdiagnosis and underreporting.

In groundwater, microbial pathogens including *Salmonella*, *E. coli*, *S. faecalis*, and enteroviruses have been proven to be rather stable in many investigations (Bittion *et al.* 1983; Schijven and Hassanizadeh 2000; Pang *et al.* 2004). Controlling the contamination of groundwater by pathogens has been a priority in many nations in recent years due to the fact that germs may live for up to 400 days, depending on the temperature of the soil (Nevecherya *et al.* 2005; Filip and Demnerova 2009) ^[39]. For instance, France has placed a large emphasis on locating the origins of pathogen contamination in groundwater in recent years (Grisey *et al.* 2010) ^[49]. According to the findings of a number of research (Ferguson *et al.* 2003; Kay *et al.* 2007; Kay *et al.* 2008) ^[38], the dangers to human health posed by chlorine-resistant protozoans, such as *Cryptosporidium* spp., are significant. The potential for pathogen contamination of groundwater by wetlands that do not have lining is one of the most significant issues (Kay *et al.* 2007). Water officials in the United Kingdom have voiced worries that are similar to those in the United States. The European Union (EU) has also placed an emphasis on the need of preventing the pollution of groundwater by pathogens. Groundwater that is infected with pathogens has the potential to pollute coastal habitats. For example, a study of Buttermilk Bay has shown that groundwater is capable of transporting a large quantity of pathogens from surface to sub-surface water either by direct discharge or by discharge to rivers flowing into the bay (Moog 1987; Weiskel *et al.* 1996). In regions where shallow aquifers are present, there is an especially elevated potential for the contamination of groundwater. In these kinds of circumstances, the possibility of polluted surface water or water from septic tanks seeping into the groundwater is increased (Weiskel *et al.* 1996). Due to the fact that precipitation events allow polluted ground water to be recharged, the likelihood of groundwater pathogen contamination being increased is high.

7. Conclusion

This review takes a look at research from a variety of fields to get a better understanding of the presence of pathogens in ambient water bodies. The widespread occurrence of pathogen contamination is a major cause for worry, and it is essential that we get a better knowledge of the key pathogen sources as well as the considerable consequences these

sources have on water resources. There have been a significant number of studies on the contamination caused by pathogens that have been carried out in a laboratory setting; however, field-scale research should be given more priority in order to improve our understanding of the ways in which pathogens interact with their surroundings. It is anticipated that the assessment of pathogen contamination on a watershed scale will be aided by the creation of new models, as well as the improvement of current modelling tools that are often employed for forecasting levels of water-borne pathogens. Because the currently available models only have a limited capacity to forecast pathogen contamination, there is a pressing need for both the improvement and creation of new models in order to achieve a greater degree of precision in the prediction of pathogen levels. The integration of knowledge from a variety of disciplines, such as hydrology, microbiology, and ecology, would lead to a greater understanding of the levels of pollution as well as the potential causes of pollution, and it would also help in the development of long-term strategies for improving water quality.

References

1. Alley WM, Reilly TE, Franke OL. Sustainability of Groundwater Resources. U. S. Geological Survey (U.S.GS), 1999.
2. Denver, CO Arnone RD, Walling JP. Waterborne pathogens in urban watersheds. *J Water Health.* 2007;5(1):149-162.
3. Bai S, Lung WS. Modeling sediment impact on the transport of fecal bacteria. *Water Res.* 2005;39:5232-5240.
4. Baker-Austin C, McArthur J, Lindell A, Wright M, Tuckfield R, Gooch J, *et al.* Multi-site analysis reveals widespread antibiotic resistance in the marine pathogen: *Vibrio vulnificus*. *MicrobEcol.* 2009;57(1):151-159.
5. Beaver JR, Crisman TL. The role of ciliated protozoa in pelagic freshwater ecosystems. *Microb Ecol.* 1989;17(2):111-136.
6. Binder S, Levitt AM, Sacks JJ, Hughes JM. Emerging infectious diseases: public health issues for the 21st Century. *Science.* 1999;284(5418):1311-1313.
7. Bitton G, Farrah SR, Ruskin RH, Butner J, Chou YJ. Survival of pathogenic and indicator organisms. *Groundwater.* 1983;21(4):405-410.
8. Bradford SA, Morales VL, Zhang W, Harvey RW, Packman AI, Mohanram A, *et al.* Transport and fate of microbial pathogens in agricultural settings. *Crit Rev Env Sci Tec.* 2013;43:775-893.
9. Brookes JD, Antenucci J, Hipsey M, Burch MD, Ashbolt NJ, Ferguson C. Fate and transport of pathogens in lakes and reservoirs. *Environ Int.* 2004;30(5):741-759.
10. Burton GA, Gunnison D, Lanza GR. Survival of pathogenic bacteria in various freshwater sediments. *Appl Environ Microbiol.* 1987;53(4):633-638.
11. Cabelli VJ. Public health and water quality significance of viral diseases transmitted by drinking water and recreational water. *Water Sci Technol.* 1983;15(5):1-15.
12. Carmichael WW. Health effects of toxin-producing cyanobacteria: the Cyano HABs. *Hum Ecol Risk Assess.* 2001;7:1393-1407.
13. Centers for Disease Control and Prevention (CDC). Cholera in Haiti: One Year Later, 2011.

- http://www.cdc.gov/haiticholera/haiti_cholera.htm
(accessed on 5/23/2014)
14. Centers for Disease Control and Prevention (CDC) Salmonella, 2014. <http://www.cdc.gov/salmonella/general/> (accessed on 4/28/2014)
 - Chandran A, Mohamed Hatha AAM. Relative survival of *Escherichia coli* and *Salmonella typhimurium* in a tropical estuary. *Water Res.* 2005;39(7):1397-1403.
 15. Chin DA. Linking pathogen sources to water quality in small urban streams. *J Environ Eng.* 2010;136(2):249-253.
 16. Cho KH, Pachepsky YA, Kim JH, Guber AK, Shelton DR, Rowland R. Release of *Escherichia coli* from the bottom sediment in a first-order creek: Experiment and reach-specific modeling. *J Hydrol.* 2010;391(3-4):322-332.
 17. Cicirello HG, Kehl KS, Addiss DG, Chusid MJ, Glass RI, Davis JP, *et al.* Cryptosporidiosis in children during a massive waterborne outbreak in Milwaukee, Wisconsin: clinical, laboratory and epidemiologic findings. *Epidemiol Infect.* 1997;119(1):53-60.
 18. Codd G, Bell S, Kaya K, Ward C, Beattie K, Metcalf J. Cyanobacterial toxins, exposure routes and human health. *Eur J Phycol.* 1999;34:405-415.
 19. Coffey R, Cummins EO, Flaherty V, Cormican M. Pathogen sources estimation and scenario analysis using the Soil and Water Assessment Tool (SWAT). *Hum Ecol Risk Assess.* 2010;16(4):913-933.
 20. Colwell RR. Global climate and infectious disease: The Cholera Paradigm. *Science.* 1996;274(5295):2025-2031.
 21. Craun GF, Fraun MF, Calderon RL, Beach MJ. Waterborne outbreaks reported in the United States. *J Water Health.* 2006;4:19-30.
 22. Darnault CJD, Steenhuis TS, Garnier P, Kim YJ, Jenkins MB, Ghiorse WC, *et al.* Preferential flow and transport of *Cryptosporidium parvum* oocysts through the vadose zone: Experiments and modeling. *Vadose Zone J.* 2004;3(2):262-270.
 23. Daszak P, Cunningham AA, Hyatt AD. Emerging infectious diseases of wildlife – threats to biodiversity and human health. *Science.* 2000;287:443-449.
 24. Desmarais TR, Solo-Gabriele HM, Palmer CJ. Influence of soil on fecal indicator organisms in a tidally influenced subtropical environment. *Appl Environ Microbiol.* 2002;68(3):1165-1172.
 25. Diaz RJ, Rosenberg R. Spreading dead zones and consequences for marine ecosystems. *Science.* 2008;321:926-929.
 26. Dickerson JW, Crozier JB, Hagedorn G, Hassall A. Assessment of 16 s-23srDNA intergenic spacer regions in *Eterococcus* spp. for microbial source tracking. *J Environ Qual.* 2007;36:1661-1669.
 27. Diffey BL. Solar ultraviolet-radiation effects on biological-systems. *Phys Med Biol.* 1991;36(3):299-328.
 28. Dorner SM, Anderson WB, Slawson RM, Kouwen N, Huck PM. Hydrologic modeling of pathogen fate and transport. *Environ Sci Technol.* 2006;40(15):4746-4753.
 29. Droppo IG, Liss SN, Williams D, Nelson T, Jaskot C, Trapp B. Dynamic existence of waterborne pathogens within river sediment compartments: Implications for water quality regulatory affairs. *Environ Sci Technol.* 2009;43(6):1737-1743.
 30. Droppo IG, Krishnappan BG, Liss SN, Marvin C, Biberhofer. Modeling sediment-microbial dynamics in the South Nation River, Ontario, Canada: Towards the prediction of aquatic and human health risk. *Water Res.* 2011;45:3797-3809.
 31. Dufour A. Health Effects Criteria for Fresh Recreational Waters. Toxicology and Microbiology Division, U.S. Environmental Protection Agency Report EPA. 1984;600-1-84-2004.
 32. Cincinnati, OH Edge TA, Hill S, Seto P, Marsalek J. Library-dependent and library independent microbial source tracking to identify spatial variation in faecal contamination sources along a Lake Ontario beach (Ontario, Canada). *Water Sci Technol.* 2010;62:719-727.
 33. Eltoum IA, Sulaiman SM, Elturabi H, Mahgoub E, Homeida MMA. Infection with *Schistosoma-Mansoni* in 2 different endemic areas – a comparative population – based study in Elzidab and Gezira-Managil irrigation schemes, Sudan. *J Trop Med Hyg.* 1993;96(2):100-106.
 34. Epstein PR. Climate change and emerging infectious diseases. *Microbes Infect.* 2001;3(9):747-754.
 35. Falconer IR. Is there a human health hazard from microcystins in the drinking water supply? *Acta Hydrochim Hydrobiol.* 2005;33:64-71.
 36. Fayer R, Trout JM. Zoonotic protists in the marine environment. In: Belkin S and Colwell RR (ed) *Oceans and Health: Pathogens in the Marine Environment.* Springer, New York, U.S, 2005, 143-163.
 37. Fenwick A. Waterborne Infectious Diseases-Could they be consigned to History? *Science.* 2006;313:1077-1081.
 38. Ferguson C, Husman AMD, Altavilla N, Deere D, Ashbolt N. Fate and transport of surface water pathogens in watersheds. *Crit Rev Environ Sci Technol.* 2003;33(3):299-361.
 39. Filip Z, Demnerova K. Survival in groundwater and FT-IR characterization of some pathogenic and indicator bacteria. In: Jones JAA, Vardanian TG, Hakopian C (ed) *Threats to Global Water Security.* Springer, Dordrecht, The Netherlands, 2009, 117-122.
 40. Fraser RH. SEDMOD: A GIS-based delivery model for diffuse source pollutants. PhD dissertation, School of Forestry and Environmental Studies, Yale University
 - Fraser RH, Barten PK, Pinney DAK (1998) Predicting stream pathogen loading from livestock using a geographical information system-based delivery model. *J Environ Qual.* 1999;27(4):935-945.
 41. Frias-Lopez J, Zerkle AL, Bonheyo GT, Fouke BW. Partitioning of bacterial communities between seawater and healthy, black band diseased, and dead coral surfaces. *Appl Environ Microbiol.* 2002;68(5):2214-2228.
 42. Gerba CP, McLeod JS. Effect of sediments on the survival of *Escherichia coli* in marine waters. *Appl Environ Microbiol.* 1976;32(1):114-120.
 43. Gerba CP, Smith J. Sources of pathogenic microorganisms and their fate during land application of wastes. *J Environ Qual.* 2005;34:42-48.
 44. Gibson CJ, Haas CN, Rose JB. Risk assessment of waterborne protozoa: current status and future trends. *Parasitology.* 1998;117:S205-S212.
 45. Gordon DM. Geographical structure and host specificity in bacteria and the implications for tracing

- the source of coliform contamination. *Microbiology* 2001;147(5):1079-1085.
46. Goyal SM, Gerba CP, Melnick JL. Occurrence and distribution of bacterial indicators and pathogens in canal communities along Texas Coast. *Appl Environ Microbiol.* 1977;34(2):139-149.
 47. Grave AK, Hagedorn C, Brooks A, Hagedorn RL, Martin E. Microbial source tracking in a rural watershed dominated by cattle. *Water Res.* 2007;41:3729-3739.
 48. Gray DJ, Thrift AP, Williams GM, Zheng F, Li Y-S, Guo J, et al. Five-year longitudinal assessment of the downstream impact on schistosomiasis transmission following closure of the Three Gorges Dam. *PLoS Negl Trop Dis.* 2012;6(4):e1588. DOI:10.1371/journal.pntd.0001588
 49. Grisey E, Belle E, Dat J, Mudry J, Aleya L. Survival of pathogenic and indicator organisms in groundwater and landfill leachate through coupling bacterial enumeration with tracer tests. *Desalination.* 2010;261(1-2):162-168.
 50. Guber AK, Pachepsky YA, Yakirevich AM, Shelton DR, Sadeghi AM, Goodrich DC, et al. Uncertainty in modelling of faecal coliform overland transport associated with manure application in Maryland. *Hydrological Process.* 2011;25(15):2393-2404.