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# Contamination of water resources by pathogenic bacteria

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## Abstract

Water-borne pathogen contamination in water resources and related diseases are a major water quality concern throughout the world. Increasing interest in controlling water-borne pathogens in water resources evidenced by a large number of recent publications clearly attests to the need for studies that synthesize 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. Providing a broader perceptive of pathogen contamination in freshwater (rivers, lakes, reservoirs, groundwater) and saline water (estuaries and coastal waters) resources, this review paper attempts to develop the first comprehensive single source of existing information on pathogen contamination in multiple types of water resources. In addition, a comprehensive discussion describes the challenges associated with using indicator organisms. Potential impacts of water resources development on pathogen contamination as well as challenges that lie ahead for addressing pathogen contamination are also discussed.

**Keywords:** Pathogens; Contamination; Water resources; Watershed; Pathogens transport

## Introduction

Water-borne pathogen contamination in ambient water bodies and related diseases are a major water quality concern throughout the world. Pathogen contamination is a serious issue for almost all types of ambient water bodies, making its recognition and understanding essential (U.S. EPA 2012a). The United Nations identified improving water quality as one of the eight Millennium Development Goals (MDGs). Its target is to reduce the number of people without access to safe water by 50% by 2015 (WHO 2011). Because of the overwhelming scientific evidence for climate change (IPCC 2007), it is also important to understand how perturbations in weather patterns can potentially impact pathogen levels in water resources. To meet future demands of water for food, energy, and ecosystems, increasing water storage structures (i.e., dams) must be a component of long-range planning (World Bank 2010). However, such new structures can potentially degrade water quality and exacerbate public health risk.

While several review papers 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), there is a manifest need for additional transdisciplinary studies that assimilate knowledge gained from multi-research endeavors studying pathogen contamination, and provide a comprehensive synopsis in order to comprehend the entirety of the problem. Therefore, the goal of this review is to present a broad research scope assessment of pathogen contamination of water resources and the associated challenges it presents. We synthesize the potential health risks imposed by pathogens in water resources by providing existing knowledge that covers surface water, groundwater, fresh water, and saline water. Further, the impact of water resources development on pathogen contamination, future challenges, and recommendations are summarized. In addition, we provide a brief discussion describing water-borne pathogen footprints and potential challenges associated with the use of indicator organisms for assessing water quality.

### Health risk

Water-borne diseases (i.e., diarrhea, gastrointestinal illness) caused by various bacteria, viruses, and protozoa have been

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the causes of many outbreaks (Craun et al. 2006). In developing countries, such as those in Africa, water-borne diseases infect millions (Fenwick 2006). According to World Health Organization (WHO), each year 3.4 million people, mostly children, die from water-related diseases (WHO 2014). According to United Nations Children's Fund (UNICEF) assessment, 4000 children die each day as a result of contaminated water (UNICEF 2014). WHO (2010) reports that over 2.6 billion people lack access to clean water, which is responsible for about 2.2 million deaths annually, of which 1.4 million are in children. Improving water quality can reduce the global disease burden by approximately 4% (WHO 2010).

Although water-associated diseases in developing countries are prevalent, they are also a serious challenge in developed countries. A study by Arnone and Walling (2007), who compiled data of outbreaks in the U.S. (1986 – 2000), reported 5,905 cases and 95 outbreaks associated with recreational water. Gastrointestinal Illness (GI) caused by variety of different microbes and germs, which causes symptoms, such as diarrhea, nausea, vomiting, fever, abdominal pain, was responsible for about 29.53% cases. More than 27% of cases were caused by *Shigella spp*. In addition, 10.99%, 10.08%, and 6.59% of the cases were caused by *Cryptosporidium parvum*, Adenovirus 3, and Leptospira, respectively. Nearly 23% and 21% of the outbreaks were caused by GI and *Shigella spp*, respectively. In addition, 16.84%, 12.63%, and 7.37% of the outbreaks were caused by *Naegleria fowleri*, *E. coli* 0157:H7, and *Schistosoma spp*., respectively. Besides acute gastroenteritis, major etiological agents such as *Giarida*, *Cryptosporadium*, *E. coli* 0157:H7, *V. cholera*, and *Salmonella* were the agents responsible for many outbreaks (Craun et al. 2006). During the same period 437,082 cases and 48 outbreaks were caused by contaminated drinking water, of which about 95.89% of the cases were caused by *Cryptosporidium parvum*. Nearly 42% and 31% of the outbreaks were caused by *Giardia lamblia* and GI, respectively. Reporting statistics on water-borne outbreaks in the U.S., Craun et al. (2006) found that at least 1870 outbreaks (23 per year) occurred between 1920 and 2002. These reported outbreaks and their reported incidence of illnesses are likely to be an underestimation of actual numbers because of non-reported cases and missing exposure information. To protect public health, the U.S. EPA's National Primary Drinking Water Regulations (NPDWRs) contain standards describing the Maximum Contaminant Level (MCL) – the highest level of a contaminate allowable in drinking water. The U.S. EPA has defined the MCL of various microorganisms, such as *Cryptosporidium*, *Giardia lamblia*, *Legionella*, and Total Coliforms (including fecal coliform and *E. coli*), and viruses (U.S. EPA 2012b). The Maximum Contaminant Level Goal (MCLG) – the level of a

contaminant in drinking water below which there is no known risk to public health, has also been proposed by the U.S. EPA. The MCLC levels for *Cryptosporidium*, *Giardia lamblia*, *Legionella*, and Total Coliforms are zero. The EPA requires 99% removal of *Cryptosporidium* in drinking water, and the removal percentages of *Giardia lamblia* and viruses are 99.9 and 99.99%, respectively. Although there is no limit for *Legionella*, EPA believes that if *Giardia lamblia* and viruses are removed/inactivated, then drinking water likely to be free of *Legionella*. The U.S. EPA requires routine sampling of drinking water for testing total coliform and *E. coli*, and if a routine sample is positive, then repeat samples are required. If, in any repeat sample, total coliform or *E. coli* is detected then the drinking water has an acute MCL violation. For a drinking water system that collects fewer than 40 routine samples per month, no more than one sample can be total coliform-positive per month. For a system that collects more than 40 routine samples, no more than 5% of samples total coliform-positive in a month is allowed (U.S. EPA 2012b).

Each year approximately 42,000 cases of salmonellosis are reported in the U.S. (CDC 2014). Schistosomiasis is not reported in the U.S. because it is not endemic; however, 200 million people are infected worldwide. In 2011, about 1,060 cases of Guinea worm disease, caused by the parasite *Dracunculus medinensis*, were reported in many remote parts of Africa that do not have safe drinking water. Malaria, a protozoal disease of the Genus Plasmodium transmitted by mosquitos breeding in contaminated water, affects 300–500 million people, and causes over one million deaths each year (more than 90% of deaths in Africa). Overall the morbidity and mortality caused by contaminated water are enormous and need to be controlled by improving the security of safe water (i.e., recreational as well as drinking water) in both developing and developed countries.

## Historical perspective of water-borne diseases

Water contamination has a long presence in human history, with descriptions in the Sushruta Samshita about water-borne diseases resembling cholera in an Indian text written in Sanskrit as early as 500–400 B.C. (Colwell 1996). Although cholera infections have not been reported in recent years in developed countries mainly due to improved sanitation, millions of people each year continue to get infected by *Vibrio cholera* in developing countries (Nelson et al. 2009). The World Health Organization reports about 3–5 million cholera cases and 10,000 – 120,000 deaths, mainly in developing countries, due to cholera every year. Over time, cholera has caused millions of deaths in developing as well as developed countries (Colwell 1996; Okun 1996). For instance, a major outbreak of cholera was reported in

London in 1849. Dr. John Snow, a physician to Queen Victoria, showed a relationship between people infected by cholera and contaminated water (Snow 1854; Colwell 1996). Jordan et al. (1904), Ruediger (1911), Simons et al. (1922), and Rudolfs et al. (1950) provide excellent reviews on incidents during the early 19th century. Colwell (1996) reported that in the mid and late 18th century, cholera infected millions of people all over the world. The worst outbreak in recent memory occurred in Haiti following the devastating earthquake affecting the capital and surrounding regions, with almost a half a million cases, killing thousands of people (CDC 2011).

### Water-borne pathogen footprints and challenges

Indicator organisms are commonly used to assess the levels of pathogens in water resources; i.e., water-borne pathogen footprints of water resources. Monitoring the levels of indicator organisms (such as fecal coliforms, *E. coli*) (Figure 1) is a common approach for quantifying the potential pathogen loads in ambient water bodies. For decades, public health officials/scientists have evaluated water quality by enumerating fecal coliforms and *E. coli* levels in rivers, lakes, estuaries, and coastal waters (Malakoff 2002; Pandey et al. 2012a; Pandey et al. 2012b; Pandey and Soupir 2013). There is, however, much debate regarding current indicator organisms and their ability to represent the potential presence of pathogenic bacteria. In addition, identifying the source of pathogens (e.g., human waste, animal waste, wildlife excreta, and waterfowl droppings) (Figure 2) is challenging (Malakoff 2002; Dickerson et al. 2007). There is potential to use a relatively new approach such as microbial source tracking (MST) to trace the origin of fecal coliform (Scott et al. 2002; Grave et al. 2007; Dickerson et al. 2007; Ibekwe et al. 2011; Ma et al. 2014). In the past, the MST method was exploited by antibiotic resistance analysis to assess the impact of cattle on water quality on a watershed scale (Grave et al. 2007). The authors suggested that host-origin libraries, based on a phenotypic method, are useful for tracking the pathogen sources. Many MST methods, however, rely on the assumption that some strains of bacteria are found only within a single kind or group of animals. This assumption can be debatable when it comes to the common fecal bacteria *E. coli* (Malakoff 2002). Therefore, caution is needed while using *E. coli* for source tracking (Gordon 2001). Further, the cost to develop libraries, implement extensive sampling programs needed for verifying the MST method, and calculate uncertainties associated with the method are legitimate issues, which requires attention before exploiting the MST method at watershed scale.

Currently, public health officials/scientists rely on exposure limits for assessing pathogen levels in water resources, which have been established to protect human
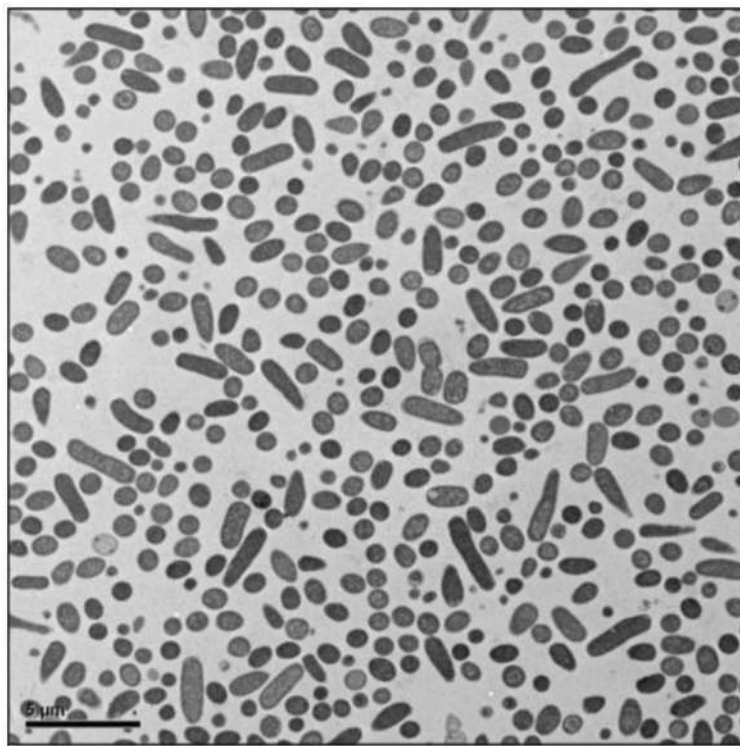


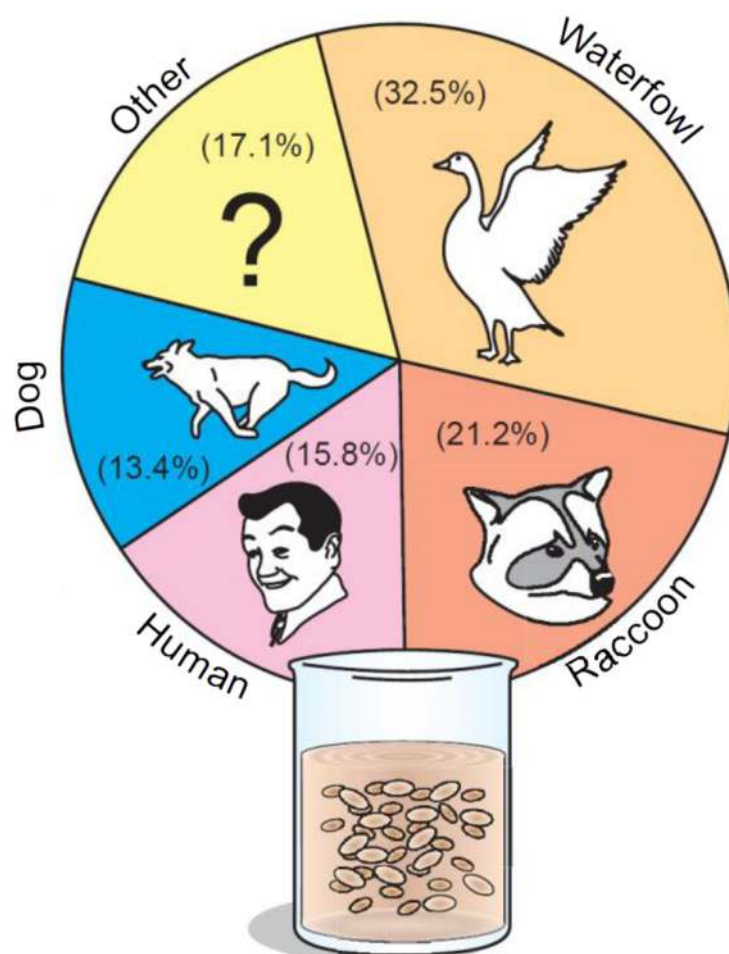**Figure 1 Transmission electron micrograph of *E. coli* (0157:H7; ATCC: 35150).**

**Figure 2 Challenges in identifying enteric pathogen sources (source: Malakoff, 2002).**

health. The EPA defines acceptable recreational limits as those that will result in eight or fewer swimming-related gastrointestinal (GI) illnesses out of every 1,000 swimmers (U.S. EPA 1986). The current U.S. EPA fresh water quality criteria for *E. coli* is a geometric mean not exceeding 126 CFU/100 ml, or no samples exceeding a single sample maximum of 235 CFU/100 ml (U.S. EPA 2001). Criteria were developed based on the U.S. EPA measurements of total and Highly Credible Gastrointestinal Illnesses (HCGI), which correlated with *E. coli* densities (r = 0.804) in fresh recreational waters (Dufour 1984). Multiple studies have identified trends between indicator organisms in water and GI illness in humans, including vomiting, diarrhea, and fever (Cabelli 1983; Wade et al. 2006). Recent work by Edge et al. (2010) detected water-borne *E. coli* in 80% of water samples with *E. coli* levels of less than 100 CFU/100 ml. Another study by Wade et al. (2006) reported significant positive trends between increased GI illness and indicator organisms at the Lake Michigan beach, and a positive trend with indicators such as *E. coli* at a Lake Erie beach. Recently, the use of indicator

organisms (e.g., fecal coliforms, *E. coli*) for assessing pathogen levels has been debated more often than ever; however, the use of indicator organisms is likely to continue for assessing pathogen levels in water resources potentially because of the lack of an alternative reliable solution.

**Pathogen contamination in water resources**
The U.S. EPA, which monitors water quality of various ambient water bodies, estimated that pathogens impair more than 480,000 km of rivers and shorelines and 2 million ha of lakes in the U.S. (U.S. Environmental Protection Agency 2010a). According to EPA estimates, pathogens are the leading cause of impairment for 303 (d) listed waters (i.e., list of impaired and threatened waters that the Clean Water Act requires all states to submit for EPA approval) (Figure 3) (U.S. EPA 2014a, 2014b, 2014c). A total of 71,917 causes of impairment have been reported, and the top five causes of impairment are shown in Figure 3. Pathogen contamination clearly dominates the causes of impairment (U.S. EPA 2014a, 2014b, 2014c).
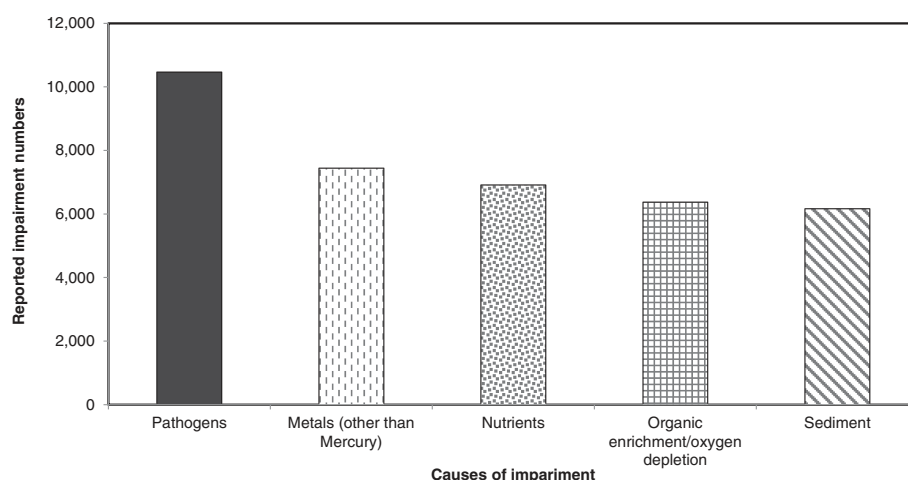
**Figure 3 Causes of impairment in the U.S. (data source: U.S. EPA (2014a, 2014b, 2014c)).**

Studies by Diffey (1991), Brookes et al. (2004), Jamieson et al. (2004), Gerba and Smith (2005), Gerba and McLeod (1976), Hipsey et al. (2008), Pachepsky and Shelton (2011) reviewed the current studies of water-borne pathogen transport, with particular reference to freshwater and estuarine sediments. In addition, many current reviews focus on specific aspects of water resources, for instance, John and Rose (2005) focused on groundwater, Brookes et al. (2004) focused on reservoirs and lakes, Jamieson et al. (2004) focused on agricultural watersheds, and Kay et al. (2007) reviewed catchment microbial dynamics. The review study presented here uses a relatively broader approach for understanding how water-borne pathogens can potentially impact public health and various ambient water bodies. In addition, existing challenges, while assessing pathogen levels in water resources are discussed.

**Coastal and estuarine environments**
In the U.S., elevated pathogen levels are a leading cause of impairments of coastal environments (U.S. EPA 2014a, 2014b, 2014c). Urban runoff and sewers have been identified as the primary source of coastal water impairments. Rippey (1994) reported about 400 outbreaks and 14,000 cases caused by pathogen contaminated coastal water since the late 1800s in the U.S. Impairments of coastal environments have major economic impacts on the U.S. For example, losses caused by pathogen contamination in Massachusetts are more than $75 million each year (Weiskel et al. 1996). The studies, which elaborate various pathogens in coastal environment and their survival mechanism, are summarized in Table 1.

The sources of coastal water contamination are: point discharges of treated and untreated sewage from shoreline outfalls, and non-point discharges. The non-point sources, such as runoff from naturally vegetated areas, discharge pathogens into coastal waters. Besides runoff from vegetated areas, the storm water runoff from urban, commercial, and industrial lands also discharges pathogens into coastal waters. In addition, other sources, such as malfunctioning or poorly sited septic systems, can also introduce significant amounts of pathogens (Sayler et al. 1975; Howe et al. 2002). Weiskel et al. (1996) reported that direct deposition of waterfowl feces was a considerable source of pathogens. Fayer and Trout (2005) summarized the transport of various pathogens, such as *Giardia*, *Toxoplasma*, and *Cryptosporidium* (zoonotic parasites) in the coastal environment. Moreover, the presence of sediment in seawater can also increase the survival chance of fecal coliforms, such as *E. coli* (Gerba nd McLeod 1976; Goyal et al. 1977). Solo-Gabriele et al. (2000) showed that the location and timing of storms of the coastal area in tropical and subtropical environments are also important factors that can potentially influence coastal water quality.

Previous studies have shown that the direct discharge of storm water runoff into coastal waters through storm drain systems can cause pathogen contamination, even where separate storm and sanitary sewer systems are in place. For instance, Weiskel et al. (1996) found that about 16% of the total fecal coliform inputs were caused by storm water entering Buttermilk Bay in Massachusetts. In addition, coastal rivers draining largely undeveloped watersheds with extensive riparian wetlands can be a natural source of fecal pathogens to coastal waters (Viau et al. 2011; Staley et al. 2014; Roberts et al. 2013; Liang et al. 2013; Wilkes et al. 2014). On-site septic systems can also contribute significant amounts of fecal pathogens to coastal waters in low-lying fine-grained geological settings where saturated soils enhance pathogen growth. Weiskel et al. (1996) reported that shoreline wrack deposits could act as a reservoir

**Table 1 Studies describing pathogen contamination in saline water (coastal and estuary environments)**

| Author(s) year | Organisms | Results | Study remarks |
|---|---|---|---|
| **Coastal water** | | | |
| Gerba and McLeod (1976) | *E. coli*, fecal coliform | Longer survival in the sediment presence in seawater | Sediment influence on pathogen survival |
| Goyal et al. (1977) | Total coliform, fecal coliform | Sediments of shallow canal can act as a reservoir | Pathogens distribution in water and sediment |
| Kapuscinski and Mitchell (1983) | *E. coli*, bacteriophages | *E. coli* survives longer than bacteriophages | Survival of pathogens in sunlight |
| Rao et al. (1984) | Enteroviruses (Polio and Rota) | Abundance viruses were attached with sediment | Viruses distribution in water and sediment |
| Weiskel et al. (1996) | Fecal coliform | Waterfowl major source of fecal coliform inputs | Pathogen source and transport pathways |
| Sinton et al. (1999) | Bacteria and Fecal bacteriophages | Somatic coliphages shown prolonged survival | Sunlight influence on sewage-polluted seawater |
| Solo-Gabriele et al. (2000) | *E. coli* | Riverbanks as the primary pathogen source | Sources of pathogens on subtropical environment |
| Nasser et al. (2003) | *Cryptosporidium*, viruses, *E. coli* | *E. coli* die-off was faster than other pathogens | Comparative survival of various pathogens |
| Schriewer et al. (2010) | *Bacteroidales,* fecal indicator, protozoa, bacteria | *Bacteroidales* have shown higher predictive skill than fecal indicators | *Bacteroidales* as a predictor of pathogens in coastal water |
| **Estuaries** | | | |
| Ketchum et al. (1952) | Coliform, zooplankton | Sactericidal and predation caused coliform die-off | Processes responsible for pathogens decrease |
| Smith et al. (1978) | Echovirus 1, coxsackieviruses | Sediment prolonged viruses survival | Persistence of pathogen viruses |
| Rhodes and Kator (1990) | *E. coli* | Mortality rises in sunlight | Indigenous microbiota and sunlight influence |
| White et al. (1998) | *Perkinsus marinus* | Use of Kriging analysis for disease prevalence | Use of GIS in pathogen distribution analysis |
| Lipp et al. (2001) | *Vibrio vulnificus* | Salinity controls the distribution of pathogens | Distribution of human pathogens |
| Desmarais et al. (2002) | *E. coli, C. perfringens* | Pathogens re-grown with tides and sterile sediment | Influence of soil on fecal indicator in tidally influenced environment |
| Frias-Lopez et al. (2002) | *Clostridium, Campylobacter, Arobacter* | Pathogen partitioning was found in surface and overlying water | Bacterial communities partitioning between sea water, dead coral surface |
| Chandran and Hatha (2005) | *E. coli, Salmonella* | *E. coli* shows better survival capacity than *Salmonella* | Relative survival in microcosm studies |
| Baker-Austin et al. (2009) | *Vibrio vulnificus* | Prevalence of antibiotic resistance in a human pathogen | Multi-site analysis shows widespread antibiotic resistance in pathogens |

of fecal bacteria, and the removal of wrack deposits from inter-tidal zones can improve the water quality of adjacent coastal waters.

Similar to the coastal environment, increasing water-borne pathogen levels in estuaries are a serious threat to public health. Human activities can impact estuary pathogen levels when they are adjacent to populated areas, and often provide a means of transportation and substantial recreation (Schriewer et al. 2010; Pachepsky and Shelton 2011). The most common pathogens, previously identified in estuaries by Rhodes and Kator (1990), were *Vibrio cholerae, Giardia, Cryptosporidium, Salmonella*, and *Campylobacter* spp. As shown in Table 1, the presence of various pathogens (e.g., *E. coli, C. perfringens,*

*Clostridium, Salmonella*) has been reported in many previous studies. Municipal point sources are the primary cause of pathogen contamination in estuaries. Urban water disposed through combined sewer outflows is the cause of approximately 12% of estuary impairments in the U.S. (Arnone and Walling 2007). Pathogens, including *Vibrio vulnificus* which carries the highest fatality rate of any food-borne pathogen in the U.S., were detected in the Gulf of Mexico Estuary (Lipp et al. 2001; Baker-Austin et al. 2009). Several studies discovered that bed sediment plays a vital role (i.e., with the release of particle-attached pathogens from bed sediment to a water column through a resuspension process) for the persistence and transport of pathogens in the estuaries (Smith et al. 1978; Desmarais

et al. 2002). Previous studies have shown that pathogen growth and decay are influenced by environmental conditions. For instance, a study by Chandran and Hatha (2005) revealed that sunlight is a major factor that influences survival of pathogens like *E. coli* and *S. typhimurium* in the estuarine water.

### Groundwater

Groundwater is heavily used all over the world as the primary source of domestic drinking water supplies, and contaminated groundwater certainly enhances risk to public health. Nationally, 40% of the U.S. domestic water supply originates from groundwater, and over 40 million people use groundwater as their drinking water via private wells (Alley et al. 1999). Groundwater pathogen contamination has led to numerous disease outbreaks in the U.S.; for example, at least 46 outbreaks of disease occurred between 1992 and 1999, resulting in 2,739 cases of illness and several deaths (John and Rose 2005). These are reported cases; due to underdiagnosis and underreporting, the actual morbidity is almost certainly higher.

Several studies have shown that microbial pathogens, such as *Salmonella*, *E. coli*, *S. faecalis*, and enteroviruses are relatively stable in groundwater (Bittion et al. 1983; Schijven and Hassanizadeh 2000; Pang et al. 2004) (Table 2). Controlling groundwater pathogen contamination has recently been emphasized in many countries, as pathogens can survive up to 400 days depending on the soil temperature (Nevecherya et al. 2005; Filip and Demnerova 2009). For example, identifying sources of groundwater pathogen contamination has received significant attention in France (Grisey et al. 2010). Many studies reported that health risks caused by chlorine-resistant protozoans, such as *Cryptosporidium* spp. (Ferguson et al. 2003; Kay et al. 2007; Kay et al. 2008), are considerable. One of the major concerns is that wetlands without lining might cause pathogen contamination of groundwater (Kay et al. 2007). Similar concerns have been expressed in the United Kingdom by water regulators. The European Union (EU) has also emphasized protecting groundwater from pathogen contamination. Pathogen-contaminated groundwater can cause pollution in coastal environments. 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). The risk of contaminating groundwater particularly increases in areas where shallow aquifers exist. In these situations it is more likely that contaminated surface water or water from septic tanks can reach groundwater (Weiskel et al. 1996). Precipitation events are likely to increase groundwater pathogen contamination because of contaminated ground water recharge.

Pathogen contamination (e.g., bacteria, protozoa, and viruses) poses a serious risk in water resources. The transport of pathogens from surface water to groundwater increases the vulnerability of groundwater (Jin and Flury 2002). These authors reported that 70% of the water-borne microbial illness outbreaks in the United States have been associated with ground water. Pathogens such as viruses are much smaller than bacteria and protozoa, and many can potentially reach groundwater through porous soil matrices. Jin and Flury (2002) reviewed the fate and transport of viruses in porous media to understand mechanisms and modeling of virus sorption, and concluded that factors such as solution chemistry, virus properties, soil properties, temperature, and association with solid particle influences virus survival, transport, and sorption in porous media. Pang (2009) studied microbial removal rates in subsurface media, and reported that soil types considerably influence microbial removal rates. For instance, volcanic soils, pumice sand, fine sand, and highly weathered aquifer rocks showed high removal rates. The author found that microbial removal rates were inversely correlated with infiltration rates and transport velocity.

Considerable work recently has been done towards understanding pathogen transport in the vadose zone (Wang et al. 2014a; 2014b; Unc and Goss 2004; Darnault et al. 2004). Groundwater can be contaminated by seepage and percolation of contaminated water from the vadose zone (Darnault et al. 2004). The macropores of agricultural land are also known to play a considerable role in polluting groundwater, particularly from fields where manure is applied (Jamieson et al. 2002). Unc and Goss (2004) evaluated the influence of manure on the transport of bacteria from land receiving manure to water resources. These authors reported that manure application in the land influences pathogen transport in the vadose zone. The presence of straw and coarse organic matter influences the persistence of bacteria, and manure application changes the physical configuration of soil, the soil chemistry, and the properties of the microbial cells, which control the survival and persistence of bacteria in soils. Another recent study by Wang et al. (2014) assessed the transport of *E. coli* in soils with preferential flow. The authors reported that a decrease in macropore length resulted in a decreased apparent saturated hydraulic conductivity of the macropore and an increase in the mass transfer. Wang et al. (2014a; 2014b) concluded that macropore length has a considerable influence on preferential transport of *E. coli*.

### Reservoirs and lakes

Previous studies have shown the presence of many pathogens in lakes and reservoirs (Table 2), and that these pathogens can pose risks to human health. In many countries surface reservoirs serve as the main source

**Table 2 Pathogen contamination in freshwater environment (ground water, rivers and lakes and reservoirs)**

| Author(s) year | Organisms | Results | Study remarks |
|---|---|---|---|
| **Groundwater** | | | |
| Bitton et al. (1983) | *Salmonella, E. coli, S. faecalis,* enteroviruses | *S. faecalis* decay rate was similar to viruses | Survival of pathogens in groundwater |
| Schijven and Hassanizadeh (2000) | Viruses | Viruses attachment with soil was influenced by pH, and favorable sites | Soil passage impacts on virus removal at field-scale |
| Pang et al. (2004) | *E. coli* and F-RNA phages | Pathogens were sorbed in aquifer material | Transport of *E. coli* and F-RNA phages |
| Nevecherya et al. (2005) | *Salmonella*, viruses, *E. coli*, shigellos | Mathematical model was derived for temperature depends inactivation rate | Pathogenic bacteria and viruses survival in groundwater |
| Filip and Demnerova (2009) | *Bacillus megaterium* and *Staphylococcus* | Pathogens survived 10 to 100 days | Pathogens survival in groundwater; FT-IR characterization |
| Grisey et al. (2010) | Total coliforms, *E. coli, Enterococci, Pseudomonas aeruginosa, Salmonella* and *Staphylococcus aureus* | Bacterial density monitoring coupled with artificial trace experiments proved useful in locating pathogens sources | Pathogens survival in groundwater and landfill leachate |
| **Rivers** | | | |
| Chin (2010) | Fecal coliform | Summer and rainfall raises pathogens | Urban areas impacts on stream pathogens |
| Smith et al. (1973) | *Salmonella*, fecal coliforms, streptococci | *Salmonella* decline was close to fecal coliform | Usefulness of indicators organisms |
| Burton et al. (1987) | *Pseudomonas aeruginosa, Salmonella newport, E. coli* | Clay in sediments improves *E. coli* survival | Survival of pathogens in fresh water sediments |
| Smith et al. (1987) | *E. coli*, Fecal bacteria | U.S. rivers shows decline in fecal indicator | Water quality assessment from 1974 to 1981 |
| Terzieva and McFeters (1991) | *E. coli, Campylobacter jejuni, Yersinia enterocolitica* | Temperate zone surface water serve as a rersistent verhicle in transimsision of bacteria between animals and humans | Survival and injury study of bacteria in agricultural surface water |
| Terzieva and McFeters (1991) | *Yersinia enterocolitica* and *E. coli* | Experimental design and environmental play major role in pathogens survival | Survival in stream water, comparison between field and lab studies |
| Fraser et al. (1998) | Fecal coliform | Model predicted pathogens | Modelling non-point source pollution |
| **Lakes and reservoirs** | | | |
| Beaver and Crisman (1989) | Ciliates | Grazing habits of ciliates are discussed | Predators roles in fresh water |
| Rubentschik et al. (1936) | *Serratia marcescens* | Adsorption of bacteria could be questionable | Adsorption of bacteria in salt lakes |
| Mac Kenzie et al. (1994) | *Cryptosporidium* | *C. oocysts* study passes through the filtration system of water supply | Contaminated water from Milwaukee lake caused outbreak |
| Wcislo and Chrost (2000) | *E. coli* | Predators controlled pathogen levels | Survival of pathogens in man-made reservoir |
| Kistemann et al. (2002) | *E. coli*, coliform, fecal streptococcal, and *Clostridium perfringens* | Most of the pathogens increases during extreme runoff events | Microbial load in drinking water reservoir during rainfall events |
| Howe et al. (2002) | *Cryptosporidium oocysts* | Animal feces was a major source of pathogens | Water supply's oocysts caused outbreak in northern England |
| Ishii et al. (2006) | *E. coli* | *E. coli* survived longer in soil | Presence and growth of *E. coli* in Lake superior watershed |

of drinking water, and these surface water bodies are often vulnerable to pathogen contamination (Kistemann et al. 2002). In the developed world, although there is increased awareness of water treatment for pathogen contamination and water quality, outbreaks of water-borne disease via public water supplies continue to be reported (Gibson et al. 1998; Howe et al. 2002; Brookes et al. 2004).

In the past, more than 403,000 residents of the greater Milwaukee, Wisconsin area experienced gastrointestinal illnesses due to infection with the parasite *Cryptosporidium*

*parvum* following contamination of the city's water supply, which was associated with inadequate filtration of contaminated water from Lake Michigan (Mac Kenzie et al. 1994; Cicirello et al. 1997). In the 1990s, *Cryptosporidiosis* became the most common cause of outbreaks associated with public drinking water supplies in the United Kingdom (Howe et al. 2002). In developing countries, diseases such as diarrhea and cholera are the leading cause of morbidity (Nelson et al. 2009). Overall, diarrhea associated with drinking contaminated water is responsible for 2 to 2.5 million deaths annually (Fenwick 2006). In lakes and reservoirs, increased pathogens are often associated with storm events, and the stream inflow is considered to be the major source of pathogens during storm events. Elevated flows in rivers most likely agitate bed sediment, which causes enhancement of pathogen levels of the water column (Jamieson et al. 2005a; Jamieson et al. 2005b; Pandey and Soupir 2013; Bai and Lung 2005). During the rainy season, the influx of contaminated water from rivers to lakes and reservoirs can substantially increase pathogen levels (Kistemann et al. 2002). The quantity of pathogen influxes from tributaries of lakes and reservoirs during the rainy season is of particular importance in determining pathogen transport and distribution (Brookes et al. 2004).

### Rivers

Pathogen contamination is a major cause of stream impairments. The sources of impairment and health risks induced by water-borne pathogens are extensively reported (Table 2). In the U.S. pathogen contamination is the leading cause of stream water pollution. The EPA's National Water Quality Inventory Report suggests that about 53% of the assessed rivers are impaired, and a majority of them are contaminated by pathogens (U.S. EPA 2012a). The cost to implement the total maximum daily load (TMDL) plans to improve stream water is estimated as $0.9 to $4.3 billion per year (U.S. EPA 2010b).

Pathogen influxes into rivers from agricultural lands (Figure 4) are the main cause of stream impairments (Chin 2010; U.S. EPA 2012a). A weak understanding of pathogen transport from agricultural lands to rivers is considered to be a major challenge in implementing and deriving suitable land management practices capable of improving stream water quality. For instance, despite common knowledge that agricultural land's non-point source pollution is a leading cause of stream impairment, it is difficult to identify points of origin of pathogens and the pathways by which they enter streams. As an example, pathogens are likely to enter rivers from many potential sources, including lateral inputs from pastures and riparian zones, influx of pathogen-contaminated groundwater, direct deposit of fecal matter from livestock and wildlife, discharge of contaminated sanitary sewer flows, and wastewater treatment plant effluents. In rainy events,

pathogens in rivers are influenced by fresh input from watersheds as well as sub-surface flow. In addition, the resuspension of legacy pathogens from bed sediments can considerably increase pathogen levels (Cho et al. 2010; Droppo et al. 2009; Jamieson et al. 2005b; Kiefer et al. 2012; Nagels et al. 2002; Muirhead et al. 2004; Kim et al. 2010; Smith et al. 2008).

Controlling pathogen contamination from livestock/wildlife to streams is challenging (Terzieva and McFeters 1991). For example, it is doubtful that pathogen contamination can be prevented by fencing off riparian buffers, and even if buffers are useful in controlling stream water pathogens, it is not certain what their width must be (Nagels et al. 2002). There are review studies that elaborate on stream water pathogen contamination (Fraser et al. 1998; Jamieson et al. 2004; Pachepsky et al. 2006).

Many studies have emphasized the use of mathematical models to understand pathogen transport from agricultural land to rivers (Kim et al. 2010; Muirhead et al. 2004; Jamieson et al. 2005a; Jamieson et al. 2005b). Previous studies (Gerba and Smith 2005; Pandey et al. 2012b; Pandey and Soupir 2013; Pachepsky and Shelton 2011; Martinez et al. 2014) have emphasized the need to improve existing models for calculating the fate and transport of pathogens at the watershed scale. Currently, empirical as well as mechanistic models are being used to calculate microbial fate and transport (Muirhead and Monaghan 2012). Numerous studies are available for exploiting watershed scale models such as WATFLOOD (Dorner et al. 2006), the Soil and Water Assessment Tool (SWAT) (Neitsch et al. 2005), the Spatially Explicit Deliver Model (SEDMOD) (Fraser 1999), and KINEROS/STWIR (Guber et al. 2011) for predicting pathogen transport. Though numerous watershed scale models are available, which can be exploited for calculating pathogen transport at watershed scale, considerable difficulties exist while using the models (Pandey et al. 2012b; Pandey and Soupir 2013). For instance, correctly identifying the model input parameter values is a daunting task. Recently, considerable emphasis has been given to understand the sensitivity of the input parameters to the model output (Martinez et al. 2014; Parajuli et al. 2009).

When implementing watershed scale models for predicting pathogen transport, difficulties related to the selection of model input parameters are common (Martinez et al. 2014). A study by Parajuli et al. (2009) evaluated the sensitivity of fecal coliform bacteria loads modeled with SWAT, and the authors reported that many of the parameters (e.g., bacterial die-off rates, the temperature adjustment factor) were insensitive to the model output. Similarly, Coffey et al. (2010) reported that initial concentration of *E. coli* and the bacterial partition coefficient parameters of the SWAT model were overly

**Figure 4 Simplified path of animal waste pathogen transport from agricultural land to rivers.**

sensitive in affecting the model's output. Another recent study by Martinez et al. (2014) evaluated the KINEROS/STWIF model input parameter sensitivities to the output. These authors reported that environmental controls such as soil saturation, rainfall duration, and rainfall intensity had the most sensitivity, while parameters such as soil and manure properties were the least sensitive in affecting model output. Many previous studies (Pandey and Soupir 2012a, 2012b; Kim et al. 2010; Martinez et al. 2014; Parajuli et al. 2009) reported that identification and selection of model input parameters are major challenges when implementing the model for predicting fate and transport of pathogens at the watershed scale.

**Blooming of cyanobacteria**

While water-borne pathogens are a serious concern, excessive algal bloom (Figure 5) in water resources can potentially limit their uses for recreation activities as well as for drinking water. Cyanobacteria (blue-green algae) have unique roles in oxygenation of the atmosphere (Hofer 2013); however, their excessive growth or dense algal bloom in water resources diminishes the quality and

quantity of light in the water column (U.S. EPA 2014b). When blooms are excessive, the risk of toxin contamination (released by harmful algal bloom (HABs)) is likely to be elevated. The HAB includes many types of algal taxa such as dinoflagellates, diatoms, and cyanobacteria. Eutrophication caused by excessive algal bloom can cause fish kills and reduce the diversity of aquatic life (U.S. EPA 2014b). In hypoxic water, dissolved oxygen levels can be less than 2 – 3 ppm (U.S. EPA 2014c). For example, in the hypoxic zone in the northern Gulf of Mexico, an area along the Louisiana-Texas coast, less than 2 ppm of dissolved oxygen concentration has been reported. This is believed to be caused by excess nutrients delivered from the Mississippi River, in combination with seasonal stratification of Gulf waters (U.S.G.S., 2014). The largest U.S. hypoxic zone, which occurred in 2002 in the Gulf of Mexico, was about 13,518 square kilometers (U.S. G.S. 2012).

Freshwater cyanobacterial blooms produce highly potent cyanotoxins and cyanobacterial HABs, which can affect the liver, nervous system, and skin (U.S. EPA 2014b). Cyanobacterial blooms can be potentially detrimental to

**Figure 5** Algal bloom in Squaw Creek, Iowa, U.S.

human and animal health, aquatic habitats, and aquaculture industries (Kaloudis et al. 2013; Carmichael 2001; Falconer 2005; Codd et al. 1999). Previous studies (Mackintosh et al. 1990; Yoshizawa et al. 1990) have shown that microcystins (i.e., cynotoxins) are hepatotoxic and act as tumor promoters through the inhibition of protein phosphatases, which play a key role in cellular regulation. Eutrophic water conditions combined with warm surface water temperatures (15 – 30°C) can potentially enhance cyanobacterial blooms in water (Oikonomou et al. 2012; Vareli et al. 2009). Currently more than 400 hypoxic zones exist in the world affecting 245,000 square kilometers (Diaz and Rosenberg 2008). These dead zones in coastal waters have spread exponentially since the 1960s and have considerably impacted ecosystems. The increase in these dead zones is likely to be influenced by climate change. Various factors such as how climate change affects water-column stratification and how nutrient runoff affects organic matter production will determine further expansion of the dead zones (Diaz and Rosenberg 2008). For instance, climate predictions of the Mississippi River basin indicate a 20% increase in river discharge, which will enhance nutrient loading and result in expansion of the oxygen depleted area (IPCC 2007). Considering the importance of fresh water, estuarine, and marine environment to public health and aquatic life, identifying approaches capable of controlling excessive algal blooms is required before these dead zones spread globally.

**Impact of water resources development**
Water resources development involves altering the natural flow path of rivers and lakes, as well as designing irrigation schemes and dams. These activities have been alleged to be responsible for causing new diseases and enhancing health risks (Fenwick 2006; Steinmann et al. 2006).

The influence of water resources development in spreading diseases, such as schistosomiasis, a parasitic disease which is ranked second only to malaria with regard to the number of people infected, has been reported extensively; one estimate says that about 103 million out of 779 million infected people live in close proximity to large reservoirs and irrigation schemes (Steinmann et al. 2006).

Designing dams and irrigation schemes in tropical and subtropical climate zones has often resulted in disease outbreaks caused by water-borne pathogens. Consider, for example, the Sennar Dam on the Blue Nile River and Sudan's Gezira Scheme, the world's largest irrigation project. Because of the dam's commercial success, irrigation in the region has doubled from the 1940s and 1950s. After the 1950s, infections from malaria and schistosomiasis increased significantly, becoming the subject of the first integrated disease-control program, the Blue Nile Health Project, implemented from 1978 to 1990. The project failed to have any impact in controlling the prevalence of schistosomiasis (Eltoum et al. 1993; Fenwick 2006; Steinmann et al. 2006). Another example is China's Three Gorges Dam, built across the Yangtze River and completed in 2009, which created a 50,700 $km^2$ reservoir and submerged more than 220 counties. Hotez et al. (1997) reported that the reservoir would produce environmental changes that could lead to the transmission of schistosomiasis in the area served by the dam. A recent study by Schrader et al. (2013) found major high risk areas for schistosomiasis occurrence in the large lakes and flood plain regions of the Yangtze River. Another study by Gray et al. (2012) reported that the Three Gorges Dam will likely to impact the transmission of schistosomiasis in China.

In the U.S., because of increasing concern for produce safety, pathogen-free irrigation water is attracting considerable attention (Martinez et al. 2014). Painter et al. (2013) reported that produce accounted for nearly half of food-borne illnesses in the U.S. between 1998 and

2008. Growing concern about the safety of food and water will likely help in developing improved strategies while planning and designing large dams for irrigation purposes.

### Challenges and recommendations

Infectious diseases caused by pathogens are the third leading cause of death in the United States, and the leading cause in the world (Binder et al. 1999). The past two decades have seen the emergence of many new pathogenic infectious diseases (Daszak et al. 2000). Many of these are caused by anthropogenic changes, such as water resources development, climate warming, and interactions between humans and animals, both domestic and wild (Krause 1994; Epstein 2001; Woolhouse 2002; Fenwick 2006; Schriewer et al. 2010).

Multidisciplinary knowledge about how ambient water bodies, wildlife, domestic animals, and human populations interact with and impact each other are crucial in dealing with future challenges. Generally, domestic animals, wildlife, and humans are considered to be major sources of water-borne pathogens; however, finding the specific culprit—the primary pathogen source—is challenging (Malakoff 2002). A watershed, for example, can have many pathogen sources, such as agricultural land, riparian areas, agricultural feeding operations, livestock, wildlife, and humans.

Developing models that are reliable in predicting pathogen survival and transport at the watershed scale can be helpful in implementing/evaluating the strategies for mitigating ambient water body pathogen levels. Evaluating the impacts of various environmental factors on pathogen survival in water resources is crucial. Various publications (i.e., Dorner et al. 2006; Kim et al. 2010; Rehmann and Soupir 2009; Droppo et al., 2011; Cho et al. 2010; Pandey et al. 2012b; Pandey and Soupir 2013) are available describing models capable of predicting pathogen contamination levels in ambient water bodies; however, further work is required to improve model predictions. The evaluation of predictions by existing models clearly demonstrates the need for improvement. Many pathogen transport models use only temperature-induced mortality and growth, and do not include interactions among other environmental factors (e.g., pH, nutrients, DO, solar radiation); future inclusion of these environmental factors will likely improve the model predictions.

Typically most studies have relied on *E. coli* and other indicator bacteria to indicate pathogen levels in water. Although widely used in monitoring contamination levels, *E. coli* alone can lead to mercurial and misleading information (Gordon 2001). Schriewer et al. (2010) suggested that with improved pathogen detection technology (i.e., PCR-based detection) an indicator organism, such as *E. coli*, can be sufficiently accurate in most cases. Overall, improving technology to identify causative agents more accurately, creating standard epidemiological data for diseased populations, and enhancing the knowledge of disease dynamics can improve the understanding of risks caused by interactions among various populations (Harvell et al. 1999; Daszak et al. 2000; Harvell et al. 2002).

In the past, a number of studies on pathogen contamination have been conducted on a scale where the conditions of ambient water bodies were simulated in laboratories. These studies are helpful in understanding pathogen behavior only up to a point. For enhancing the understanding of pathogen interactions in the environment, more emphasis should be given to field-scale studies.

### Conclusions

This review examines studies from various disciplines to understand pathogen contamination in ambient water bodies. The worldwide prevalence of pathogen contamination is a serious concern, and enhancing the understanding of major pathogen sources and their significant impacts on water resources is crucial. A considerable number of studies on pathogen contamination have been conducted on a laboratory-scale; more emphasis should be given to field-scale studies for enhancing the understanding of pathogen interactions in the environment. Developing new models, and improving existing modeling approaches commonly used for predicting water-borne pathogen levels will likely to help in assessing pathogen contamination at watershed-scale. Considering the limited ability of existing models to predict pathogen contamination, improvement and development of new models are needed so that pathogen levels can be predicted more accurately. Integrating knowledge from multiple fields (e.g., hydrology, microbiology, and ecology) would increase the understanding of pollution levels and potential causes of pollution, and can also help devise long-term strategies to improve water quality.

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