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## Chapter 2

# Ubiquitous waterborne pathogens

D.N. Magana-Arachchi<sup>1</sup>, R.P. Wanigatunge<sup>2</sup>

<sup>1</sup>*Molecular Microbiology & Human Diseases Unit, National Institute of Fundamental Studies, Kandy, Sri Lanka;* <sup>2</sup>*Department of Plant and Molecular Biology, University of Kelaniya, Kelaniya, Sri Lanka*

### 1. Introduction

In July 2010, the United Nations General Assembly (UNGA) univocally recognized the human right to water and sanitation and acknowledged that clean drinking water and sanitation are essential to the realization of all human rights (UNGA, 2010). However, due to inadequacy, unsafe, inaccessibility, and unaffordability of water, most of the people globally are deprived of this universal right. According to the Joint Monitoring Program (JMP) report, some 3 in 10 people worldwide, or 2.1 billion, lack access to safe, readily available water at home and 6 in 10, or 4.5 billion, lack safely managed sanitation (WHO and UNICEF, 2017). Due to the global efforts, billions of people have gained access to basic drinking water and sanitation services since 2000, but people in many countries are still lacking clean water and proper sanitation in their homes, healthcare facilities, and schools. Hence health of all these people is at a risk, affecting mainly the infants and young children. Water, sanitation, and hygiene were responsible for 829,000 deaths from diarrheal disease in 2016. It is estimated that every year, 361,000 children under 5 years of age die because of diarrhea. In addition, poor sanitation and contaminated water are also linked to transmission of waterborne diseases such as cholera, dysentery, hepatitis A, and typhoid (WHO and UNICEF, 2017).

In September 2015, Member States of the United Nations adopted the 2030 Agenda for Sustainable Development (UNSD, 2015) and Goal 6 of Sustainable Development Goals is to “*Ensure availability and sustainable management of water and sanitation for all.*” Targets were set by considering the freshwater cycle as a whole. Member States try to achieve these targets by improving the standard of water, sanitation, and hygiene (WASH) services; increasing treatment, recycling, and reuse of wastewater; improving efficiency and ensuring sustainable withdrawals; and protecting water-related ecosystems

as part of an integrated approach to water resources management. They also address the means of implementation for achieving these development outcomes (WHO and UNICEF, 2017).

A pathogen means an agent that causes disease to a host, and waterborne pathogens are the causative agents (usually living organisms) for diseases that are being transmitted through water. Water pollution can occur due to chemical and/or biological contaminants. These waterborne pathogens thrive in polluted waters, especially contaminated with human feces or/and urine. People could get exposed to these microorganisms while drinking water, by eating food prepared with contaminated water, bathing, during recreational activities, or even sometimes in healthcare facilities during dialysis. This exposure could be limited to an individual or it can be a community outbreak. The morbidity and mortality caused by contaminated water are enormous and it could only be controlled by providing microbiologically safe and toxin-free water for drinking, cooking, and other recreational activities.

Surface waters in most countries are polluted with pathogens and this is widely recorded in the developing world. Consumption of these waters leads to waterborne disease outbreaks (WBDOs) (Patel et al., 2016). A recent study from China has shown that potentially pathogenic bacteria were ubiquitous across all of the 16 urban sampled surface waters, and Proteobacteria and Bacteroidetes were the most commonly detected phyla accounting for 21.9%–78.5% and 19.1%–74.7% of sequences, respectively (Jin et al., 2018). Intermittent water supply (IWS) is being practiced throughout low- to middle-income countries. A study was conducted by Bivins et al. (2017) with existing data using reference pathogens *Campylobacter*, *Cryptosporidium*, and rotavirus (RV) as conservative risk proxies for infections via bacteria, protozoa, and viruses, respectively. Their findings indicated that the median daily risk of infection is 1 in 23,500 for *Campylobacter*, 1 in 5,050,000 for *Cryptosporidium*, and 1 in 118,000 for RV. Based on these risks, IWS may account for 17.2 million infections causing 4.52 million cases of diarrhea, 109,000 diarrheal disability-adjusted life years (DALYs), and 1560 deaths each year. The WHO health-based normative guideline for drinking water is  $10^{-6}$  DALYs per person per year and it is likely that the value of diarrheal disease associated with IWS will be surpassing the WHO value.

When ensuring clean water for drinking and other activities, proper management guidelines are needed to be followed. Preparation of these guidelines is not an easy task and it needs thorough understanding about the pathogenic nature of the organisms considering their shape, size, composition, and structure, their survival and behavior, and how they transmit in different waterbodies. Many countries use indicator organisms to assess the microbiological quality of drinking water. Most widely used bacteria are the enteric bacterial coliforms belonging to the family Enterobacteriaceae. In addition to being able to identify the microbial contamination of drinking water with human waste, these organisms are capable of identifying the fecal

contaminations in waters used for recreational activities as well as in shellfish production. The presence of these pathogenic organisms in waterbodies is being monitored regularly in most developed countries as new tools are available to them due to the advances made in medical and scientific research. Modern technologies have also been incorporated into the water treatment plants for the effective removal or deactivation of these waterborne pathogens, thereby minimizing the outbreaks and the risk due to exposure.

In this chapter we will be focusing on the ubiquitous waterborne pathogens which cause deadly diseases and outbreaks affecting young and old globally. Etiological agents for substantial amount of waterborne diseases are “classical” waterborne pathogens. However, fresh organisms and new strains from already known pathogens are being identified and that present important additional challenges to both the water and public health sectors. Hence we will outline the potential waterborne pathogens including *Helicobacter pylori*, *Tsukamurella*, *Cystoisospora belli*, and *Microsporidia* and also *Bacillus* species and toxic cyanobacteria that needed to be paid attention to supply clean water, prevent mishaps, and protect and improve public health. Listed pathogens for this chapter were selected from the WHO Guidelines for drinking water quality, fourth edition (2011) and from Global Waterborne Pathogen Project (GWPP) (Rusinol and Girones, 2017). Readers could gain extra knowledge on these organisms by referring to the original articles which are being included in the references. Furthermore, descriptive diagrams of these organisms can be found in the book chapter by Bridle (2013).

## 2. Waterborne pathogens

This first section is based on ubiquitous waterborne pathogens including bacteria, viruses, protozoa, and helminths, which will be discussed in chronological order, and the causative diseases and mode of transmission are summarized schematically in Fig. 2.1 for the readers’ benefit.

### 2.1 Waterborne bacteria

Bacterial pathogens are classical etiological agents of waterborne diseases globally. These organisms can occur ubiquitously in many aquatic habitats and humid soils. They are an important part of the biocenosis in various substrates or water systems, especially in their preferred habitats, the biofilms. According to WHO, from the mortality of water-associated diseases, more than 50% are due to microbial intestinal infections. There are limitations in many of the established methods used in water quality assessments, and new approaches to health-related monitoring are being introduced by WHO that can overcome many of the weaknesses in current methods and provide additional tools for reducing disease risks (WHO, 2003).

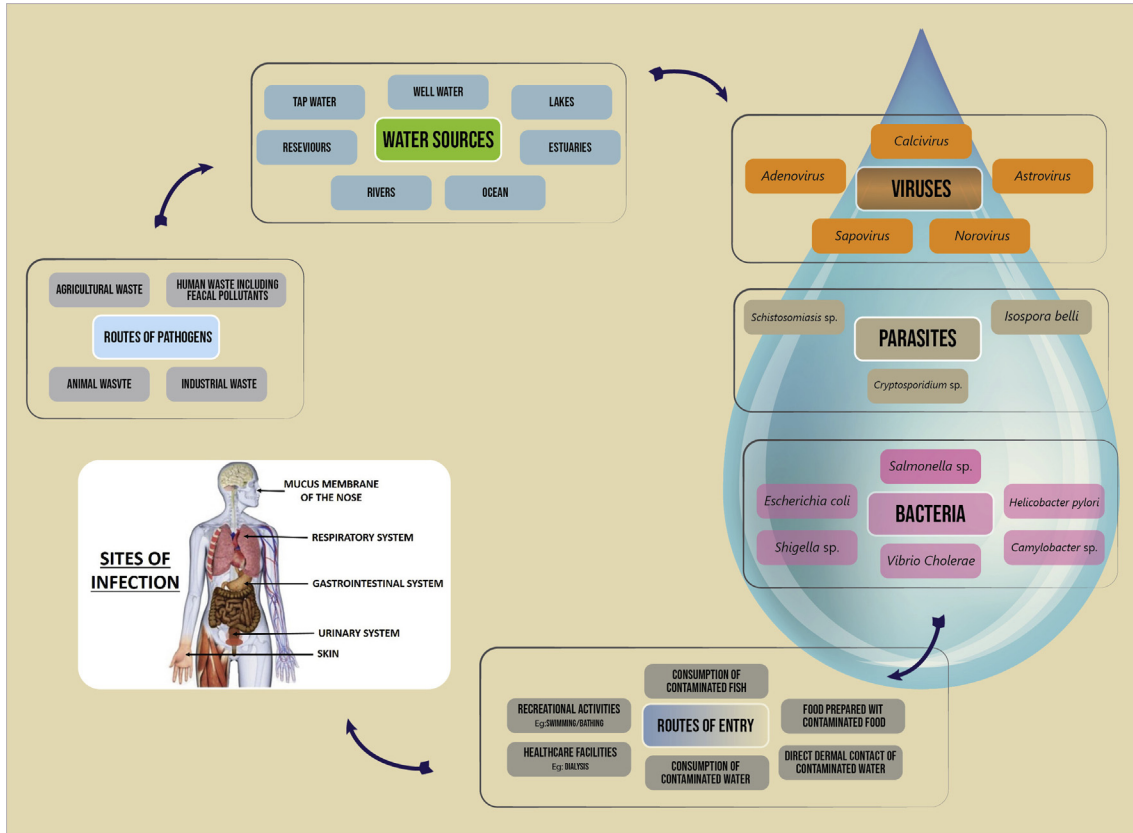


FIGURE 2.1 Generalized overview of ubiquitous waterborne pathogens, route of transmission, and sites of infection.

### 2.1.1 The genus *Vibrio*

Vibrios are small, curved-shaped or rods, facultative anaerobes with a single polar flagellum, belonging to family Vibrionaceae of order Vibrionales that are non-spore-forming and Gram-negative with a size of approximately  $1.5\text{--}3.0\ \mu\text{m} \times 0.5\ \mu\text{m}$ . Cells of *Vibrio cholerae*, *Vibrio parahaemolyticus*, and *Vibrio vulnificus* possess pili (fimbriae) structures comprising of protein TcpA. This TcpA formation is co-regulated with cholera toxin expression and is a key determinant of *in vivo* colonization.

These are primarily aquatic bacteria, common in marine and estuarine environments, living free or on the surfaces and in the intestinal contents of marine animals. Around 12 *Vibrio* species can infect humans. *V. cholerae* is, by far, the most important among them. *Vibrio fluvialis*, *Grimontia hollisae* (formerly *Vibrio hollisae*), and *Vibrio mimicus* can cause diarrhea or infections of the gastrointestinal tract. *Vibrio furnissii* has been isolated from a few individuals with diarrhea, but there is no evidence that it can actually cause this pathology.

Cholera is a well-known disease since 19<sup>th</sup> century and it is topping the list of microbial waterborne diseases. *V. cholerae* is a very diverse bacterial species. It has more than 200 serovarieties, characterized by the structure of the lipopolysaccharide (O antigens). Only serovarieties O1 and O139 are involved in true cholera (Weintraub, 2003). Some other serovarieties can cause gastroenteritis. The serovariety O1 is subdivided into classical and El Tor biotypes based on their biochemical properties and phage susceptibilities. Only toxigenic strains have the CTX $\Phi$  segment (7–9.7 kb) of the chromosome and this carries at least six genes which have the potential to encode cholera toxin. During chromosome replication, the CTX $\Phi$  fragment is able to make an autonomous copy creating an independent plasmid. The plasmid produces virus-like particles, the CTX $\Phi$  bacteriophages, which in turn infect non-toxigenic strains (Cabral, 2010). Epidemic and pandemic strains of *V. cholerae* contain another chromosomal segment designated as Vibrio Pathogenicity Island (VPI). VPI is 39.5 kb in size and contains two ToxR-regulated genes: a regulator of virulence genes (ToxT) and a gene cluster containing colonization factors, including the toxin co-regulated pili. Pathogen can be transmitted by the contaminated water or food via the fecal–oral route. *V. cholerae* O1 or O139 strains are common in estuaries being isolated from estuarine animals, such as birds, frogs, fishes, and shellfish, and are able to survive and multiply on the surface of phytoplankton and zooplankton cells.

### 2.1.2 The genus *Salmonella*

Salmonellae are rod-shaped, motile by peritrichous flagella, belonging to family Enterobacteriaceae of order Enterobacteriales that are non-spore-forming, Gram-negative bacteria with a size of a rod being  $0.7\text{--}1.5\ \mu\text{m}$  by

2.2–5.0  $\mu\text{m}$  producing colonies approximately 2–4 mm in diameter. *Salmonellae* have several endotoxins: antigens O, H, and Vi.

*Salmonella enterica* subsp. *enteric* serovar Enteritidis is the most frequently isolated serovar from humans all over the world. However, other serovars can be predominant and each outbreak had been associated with a different serotype: Mbandaka, Livingstone, and Typhi Vi+. The major habitat of *Salmonella* is the intestinal tract of humans and animals and is frequently found in environmental samples because they are excreted by humans as well as animals. Municipal sewage, agricultural waste, and storm water runoff are the main sources of these pathogens in natural waters and they do not multiply much in natural environments but can survive several weeks in water and soil when environmental factors are favorable. Paratyphi or non-Typhi serovars of *Salmonellae* are more common in the environment. From environmental sources, 73% of the isolates were from tap water in which commonly observed organisms being serovars: Corvallis, Enteritidis, and Anatum (Aissa et al., 2007). A study reported a total of 19 *Salmonella* serotypes in a comparative study carried out in rivers Aliakmon and Axios, in northern Greece (Arvanitidou et al., 2005).

### 2.1.3 The genus *Shigella*

*Shigellae* are rod-shaped and nonmotile, belonging to family Enterobacteriaceae of order Enterobacteriales that are non-spore-forming, Gram-negative with a size of a cell being 0.4–0.6  $\mu\text{m}$  by 1.0–3.0  $\mu\text{m}$  long. There are four serogroups in *Shigella*: *Shigella dysenteriae* (serogroup A) with 1–15 serotypes, *Shigella flexneri* (serogroup B) serotypes 1–8 with 9 subtypes, *Shigella boydii* (serogroup C) with serotypes 1–19, and *Shigella sonnei* (serogroup D) with one serotype. The four serogroups differ in their epidemiology and outbreaks have been attributed to the community water supplies which were not properly chlorinated.

*Shigella* has a complex antigenic pattern and the serogrouping is based on their somatic O antigens. *Shigella* emerged from *Escherichia coli* during evolution. The acquisition and evolution of the pathogenicity island, which encodes all of the genes required for cell invasion and phagolysosomal lysis, permitted a major alteration in pathogenesis. *Shigella* is the causative agent for the disease shigellosis or bacillary dysentery, naturally spread by fecal-contaminated drinking water or food or by direct contact with an infected person and considered as a disease affecting the under developed displaced people who are lacking the basic hygienic facilities.

### 2.1.4 The genus *Escherichia*

Bacteria in genus *Escherichia* are rod-shaped, non-spore-forming, Gram-negative bacteria belonging to family Enterobacteriaceae of order Enterobacteriales. Commonly found *E. coli* have a size of 2.0–0.5  $\mu\text{m}$  in

diameter. *E. coli* is a natural and essential part of the bacterial flora in the gut of humans and animals. Most *E. coli* strains inhabiting colon are nonpathogenic, but certain serotypes have a role in intestinal and extraintestinal diseases, such as urinary tract infections.

There are six different groups of *E. coli* strains isolated from intestinal diseases based on epidemiological evidence, phenotypic traits, clinical features of the disease, and specific virulence factors. Among them, enterotoxigenic *E. coli* O148, enterohemorrhagic *E. coli* O157, and enteroinvasive *E. coli* O124 serotypes are major disease-causing organisms and can be transmitted through contaminated water.

Enterotoxigenic *E. coli* (ETEC) serotypes can cause infantile gastroenteritis. Disease is caused due to consumption of ETEC-contaminated food or water and is characterized by profuse watery diarrhea continuing for several days leading to dehydration and malnutrition in young children. ETEC serotype 148 is one of the causative agents of “travelers’ diarrhea” that affects individuals who are involved in global traveling.

Shiga toxin-producing *E. coli* O157:H7 is considered as food and waterborne pathogen that causes diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome (HUS) in humans in both sporadic cases and outbreaks (Wasey and Salen, 2019). The incubation period is 3–4 days, and the symptoms last for 7–10 days. HUS associated with Shiga toxin-producing *E. coli* O157:H7 cause acute renal failure mostly in children. These bacteria are naturally not a concern in treated drinking water, but outbreaks related to consumption of contaminated water or use of surface water for recreational activities have been documented (Bruneau et al., 2004). Enterohemorrhagic *E. coli* have also been isolated from ponds, streams, wells, and water troughs, and they can survive for months in manure and water-trough sediments. Personal contacts are an important mode of transmission and disease spread through the oral–fecal route.

Enteroinvasive *E. coli* act as same as *Shigella*. They are capable of invading and multiplying in the intestinal epithelial cells of the distal large bowel in humans. The illness is characterized by abdominal cramps, diarrhea, vomiting, fever, chills, a generalized malaise, and the appearance of blood and mucus in the stools of infected individuals. *E. coli* O124 had been isolated from cases of gastroenteritis, enterocolitis, and dysentery. Food prepared by using water contaminated with human waste could cause the disease in humans.

### 2.1.5 The genus *Burkholderia*

Bacteria in the genus *Burkholderia* are straight or slightly curved, rod-shaped, non-spore-forming and Gram-negative, and motile due to a single or multiple polar flagella except in one species, belonging to family Burkholderiaceae of order Burkholderiales. The genus comprises of 60 species of obligatory



aerobes that are ubiquitous in nature and are waterborne pathogens. Clinically relevant species include *Burkholderia cepacia* complex species, *Burkholderia pseudomallei*, *Burkholderia mallei*, *Burkholderia gladioli*. *B. pseudomallei* is with a diameter of 0.8  $\mu\text{m}$ , and a length of 1.5  $\mu\text{m}$  can be present in soil or water whether it is surface or ground. Melioidosis is a life-threatening disease caused by *B. pseudomallei* and is endemic to southeast Asians and to northern Australians and randomly affects people living close to the equator. It is more common during the monsoon season than in dry months and literature confirms that it became more prevalent after 2004 Tsunami (Currie et al., 2008).

Melioidosis has been reported from Thailand and the disease is highly endemic to the northeast. Most infected community is agricultural farmers with repeated environmental exposure (Limmathurotsakul et al., 2013). Water supply-related melioidosis has also been documented and the disease could be acute or chronic. Signs and symptoms may include pain in the chest, bones, or joints; cough; skin infections, lung nodules, and pneumonia, which is a life-threatening infection that is estimated to account for nearly 89,000 deaths per year worldwide (Wiersinga et al., 2018). Melioidosis is an emerging disease in Sri Lanka (Corea et al., 2012).

### 2.1.6 The genus *Campylobacter*

The bacteria in genus *Campylobacter* are Gram-negative, 0.5–8  $\mu\text{m}$  long, and 0.2–0.5  $\mu\text{m}$  wide with characteristically curved, spiral, or S-shaped cells belonging to the family Campylobacteraceae in order Campylobacterales. This genus consists of 29 species and 12 subspecies. The most important *Campylobacter* species in human gastroenteritis is *Campylobacter jejuni* followed by *Campylobacter coli*, *Campylobacter lari*, and *Campylobacter fetus*. *Campylobacter enteritis* was the causative agent for 8.5% of the total burden of diarrheal disease, standing fourth after RV, cryptosporidiosis, and *E. coli* diarrhea (combined enterotoxigenic and enteropathogenic *E. coli* infections) (Murray et al., 2012).

Disparities have been observed between developed and developing countries in the epidemiology and demography of *Campylobacter* infections. In developing countries, symptomatic disease is most commonly seen only during the first 2 years of life, and symptomatic illness in adults is scarce because of the endemic nature. In developed world, the most common symptoms include an acute, self-limiting gastroenteritis, with an incubation period of 2–5 days, whereas in developing nations, watery diarrhea is mostly observed. This is considered also as a zoonotic disease and wide variety of animals, especially poultry, wild birds, cattle, and sheep carry high numbers of *C. jejuni* and *C. coli* as commensals in their intestines. Fecal contamination of food, recreational water, and drinking water contributes to human infections and the fecal material of infected persons spread the organisms back to environment through sewage plants and toilets.

### 2.1.7 The genus *Francisella*

The genus *Francisella* is 0.7–1.7  $\mu\text{m}$  in size, nonmotile, Gram-negative, strictly aerobic, and facultative intracellular coccobacilli species. The type species of the genus is the *Francisella tularensis*, which contains four subspecies, i.e., *tularensis*, *holarctica*, *mediasiatica*, and *novicida*. *F. tularensis* is a highly infectious bacterium causing disease in mammals including humans and a potential bioterror weapon (Colquhoun et al., 2014). Tularemia is a zoonotic infection caused by *F. tularensis* mainly transmitted to humans through arthropod bites, direct contact with infected animals, and inhalation or ingestion of contaminated water. The organism can persist in water or mud at least for 1 year and that indicates the environment may be important reservoirs for this pathogen. Recent and historical outbreaks indicate that environmental exposure to the organism is a significant source of morbidity.

### 2.1.8 The genus *Legionella*

Legionellae are rod-shaped, Gram-negative bacteria being the only genus in family Legionellaceae. The genus includes 52 validated species with 71 serotypes out of which 24 *Legionella* species are described as occasional human pathogens. *Legionella pneumophila* cause Legionnaires' disease, which is a severe type of pneumonia occurring worldwide. The transmission can occur via inhalation of contaminated aerosols generated by cooling towers, bath tubs, whirlpools, ornamental fountains, and showers. In nature, *Legionella* live in freshwater and rarely cause illness. Outbreaks of Legionnaires' disease are often associated with man-made water settings, with large or complex water systems. Most outbreaks have been due to *L. pneumophila*, serogroup 1, and although this may be due to increased virulence, it may simply reflect the greater prevalence of this particular organism (Yu et al., 2002). Biofilms and free-living amoebae are considered to serve as main environmental reservoirs for *L. pneumophila* and represent a potential source of drinking water contamination, resulting in a potential health risk for humans.

### 2.1.9 *Mycobacterium avium* complex

The genus *Mycobacterium* belongs to family Mycobacteriaceae of order Actinomycetales. The *Mycobacterium avium* complex (MAC) consists of 28 serovars of two distinct species: *Mycobacterium avium* and *Mycobacterium intracellulare*. MAC has been recovered from drinking water systems both before and after treatment, hot water heaters, freshwater, brackish, sea water, and wastewater, occasionally being high in numbers, and the infection to humans occurs through the inhalation of aerosolized droplets containing *M. avium* cells.

The organisms of MAC have the ability to survive and grow under diverse and extreme conditions. Hence mycobacteria are highly resistant to chlorine and other chemical disinfectants as such standard drinking water treatments

will not completely eliminate MAC organisms but can minimize the risk. The symptoms encountered with MAC infections result from colonization of either the respiratory or the gastrointestinal tract, with possible dissemination to other locations in the body.

## 2.2 Waterborne viruses

Diarrheal disease and WBDs from drinking, recreational, and groundwaters are often caused by waterborne viruses, which tend to be more persistent in the environment than bacteria (Gibson, 2014). WHO has classified adenovirus (AdV), astrovirus (AstV), hepatitis A and E viruses, RV, norovirus, and other caliciviruses and enteroviruses, including coxsackieviruses and polioviruses as water-transmitted viral pathogens having a moderate to high health significance (WHO, 2011). Also, polyomaviruses and cytomegalovirus that are excreted through urine can potentially be spread through water. Influenza and coronaviruses have been proposed as organisms that can be transmitted through drinking water, but evidences are lacking. These viruses are mostly associated with gastroenteritis, which can cause diarrhea as well as other symptoms including abdominal cramping, vomiting, and fever. Some of these same viruses could also cause more severe illnesses including encephalitis, meningitis, myocarditis (enteroviruses), cancer (polyomavirus), and hepatitis (hepatitis A and E viruses) (WHO, 2011).

### 2.2.1 Adenoviruses

AdVs, belonging to the family Adenoviridae, genus *Mastadenovirus*, have over 51 serotypes differentiated to six subgroups (A to F), which are the causative agents of many human diseases. They are 80–90 nm in size containing double-stranded linear DNA and a nonenveloped icosahedral shell that has slender projections from each of its 12 vertices. They can infect many organs in the body including the eye, upper respiratory tract, lower respiratory tract, gastrointestinal tract (gastroenteritis and intussusception), urinary bladder, central nervous system, and genitalia. The enteric adenoviruses types 31, 40, 41, and subgenus F are responsible for the majority of adenovirus-mediated cases of gastroenteritis. Pathogenicity of the virus varies with the species and serotype, and organ specificity and disease patterns appear to be serotype-dependent.

Human adenoviruses are transmitted by the fecal–oral route and through inhalation of water droplets. They are listed as pathogens of childhood gastroenteritis as most affected are being children of under 5 years of age. AdV resistance to purification and disinfection processes (i.e., UV inactivation) and the virus's ability to survive in the environment have increased the importance of monitoring AdVs in water (Jiang, 2006). These adenoviruses are being documented everywhere in the world, without any seasonal

variability and could be found in drinking water if not properly treated, in raw sewage, polluted waters such as rivers and dams, swimming pools, and even in shellfish.

### 2.2.2 Astroviruses

AstVs are nonenveloped, icosahedral viruses belonging to family Astroviridae. They are 28–41 nm in size, containing positive-sense, single-stranded RNA, genome of approximately 7 kb in size. They have been classified into two genera: *Mamastrovirus* and *Avastrovirus*. Genera *Mamastrovirus* and *Avastrovirus* cause infection to mammals and avian, respectively. Three divergent groups of human astroviruses (HAstVs) have been identified and according to research, the classic AstV group contains eight serotypes accounting for less than 10% of all acute nonbacterial gastroenteritis in children worldwide without any geographical boundaries. Children get infected in the first few years of life regardless of their level of hygiene, quality of water, food or sanitation, or type of behavior. Although children are vulnerable, there are reports of disease in normal healthy adults (Pager and Steele, 2002) and also immunocompromised individuals (González et al., 1998). This infection induces mild, watery diarrhea that lasts 2–3 days, associated with vomiting, fever, anorexia, and abdominal pain. In comparison to RV or calicivirus infection, infections due to AstVs have a longer incubation period.

These viruses can be transmitted by the contaminated water via the fecal–oral route, and higher incidence has been recorded in cold months. In temperate regions, most AstV infections are during winter, whereas in tropics, infections occur during rainy months. These viruses are being detected both in surface and groundwaters which are being used as drinking water sources, freshwater, and marine waters as well as in wastewater effluents. Moreover, waterborne transmission of HAstVs has been suggested as a risk of digestive morbidity for the general population (Gofti-Laroche et al., 2003). Chlorine and other disinfectants are effective for the inactivation of these viruses in water.

### 2.2.3 Caliciviruses

Caliciviruses are nonenveloped, 27–40 nm single-stranded RNA viruses in the family Caliciviridae. They are an important group of human viruses capable of causing gastrointestinal disease in humans that may be found in waters intended by humans for drinking, recreation, and shellfish growing. The International Committee on Taxonomy of Viruses changed the calicivirus nomenclature and classified into four genera: *Vesivirus*, *Lagovirus*, *Norovirus*, and *Sapovirus*. Sapoviruses (SaVs) and noroviruses (NoVs) are included in the latest US Drinking Water Contaminant Candidate List (CCL) (Rusinol and Girones, 2017). They get spread by the fecal–oral route and are found in contaminated surface and groundwaters. The presence of caliciviruses in

groundwaters is an important consideration, as a number of outbreaks have been linked to these drinking water sources (often from shallow wells and springs) (Schaub and Oshiro, 2000).

#### 2.2.4 *Noroviruses*

Noroviruses (NoVs) (formerly Norwalk virus) were first identified following an outbreak of enteric illness among children and adults in the town of Norwalk, Ohio (Adler and Zickl, 1969). They are a group of nonenveloped, single-stranded RNA viruses with an icosahedral symmetry classified into the genus *Norovirus* of the family *Caliciviridae* with a size of 27–32 nm. Most norovirus genomes contain three open reading frames (ORFs). They have rough, non-distinct borders and lack the calyx appearance. Noroviruses are divided into five genogroups (GI to GV), three of which (GI, GII, and GIV) cause human disease. This virus is extremely infectious and humans are the only known reservoir for human norovirus. NoVs cause acute onset of projectile vomiting and diarrhea, sometimes with low-grade fever, headache, and malaise. Symptoms are usually self-limited, lasting for 24–72 h. The incubation period is usually 24–48 h, but onset of symptoms as soon as 10 h after exposure has been reported. Disease outbreaks have been associated with consumption of these viruses in drinking water and also in contaminated shellfish (Maunula et al., 2005; Boxman et al., 2006).

#### 2.2.5 *Sapoviruses*

Sapovirus (SaV) is one of the etiological agents of human gastroenteritis, is named after the Japanese city Sapporo, where it was first discovered (Chiba et al., 1979). SaV is an RNA virus with a nonsegmented, positive-sense, single-stranded RNA molecule of approximately 7.3–7.5 kb, belonging to the family *Caliciviridae*. Genome organization of SaVs differs to NoV and contains only two ORFs instead of three. SaVs have a nonenveloped viral capsid with icosahedral symmetry and display a characteristic surface that has cup-shaped depressions on the surface, formed by the 32 cups or “calices,” which is a typical calicivirus morphology. SaVs show a high level of diversity in their genomes and are currently divided into at least five genetically distinct genogroups. Infections in humans are caused by viruses of genogroup GI, GII, GIV, and GV, and at present human SaV genogroups are classified into 16 genotypes. The disease outbreaks are reported in all age groups including the elderly people (Lee et al., 2012). SaVs are transmitted from person to person via fecal–oral routes and through contaminated foods and water.

#### 2.2.6 *Enteroviruses*

The waterborne polioviruses, coxsackieviruses, echoviruses, hepatoviruses, and certain unclassified enteroviruses together as a group named as enteroviruses are belonging to the family *Picornaviridae*. They are small in size,

22–30 nm in diameter, and nonenveloped, and the virions are relatively simple, consisting of a protein capsid surrounding a single-stranded, positive-sense RNA genome and it is assumed that only reservoir for enteroviruses are humans. They are present mainly in sewage contaminated with human feces but can be found in groundwaters, coastal river and marine waters, sewage treatment plants and from solid waste landfills, and insufficiently treated drinking water.

These have been identified as sensitive to formaldehyde, hydroxylamine, UV, ionizing irradiations, and also to ozone but cannot be inactivated with changing pH or with usual chlorination. It is assumed that infections from enteroviruses are associated with poverty and poor hygienic conditions.

### 2.2.7 Hepatovirus A

*Hepatovirus A* (HAV) is a nonenveloped virus with an icosahedral capsid of about 27–32 nm, single-stranded having an RNA genome of approximately 7.5 kb and belongs to the family Picornaviridae. HAV is the causative agent of type A viral hepatitis and only one serotype has been reported (Cristina and Costa-Mattioli, 2007). Virus transmission occurs through the fecal–oral route by direct contact with an infected person or exposure to contaminated water or consumption of contaminated food.

The incidence of HAV shows distinct patterns of geographic distribution and being related to standards of hygiene and sanitation, demographic factors and socioeconomic conditions of the population. Most of the infections occur in Africa and Asia, followed by Central and South America, Eastern Europe are considered as areas of intermediate endemicity. Children are more vulnerable to disease in highly endemic areas while adolescents and adults are susceptible to infection in intermediate endemic areas (WHO, 2012).

### 2.2.8 Hepatovirus E

*Hepatovirus E* (HEV) is a nonenveloped, positive-sense, single-stranded RNA genome of 7.2 kb in length and belongs to the family Hepeviridae. Family Hepeviridae contains two genera: *Orthohepevirus* and *Piscihepevirus*. Four main genotypes of HEV (HEV-1, HEV-2, HEV-3, and HEV-4) belonging to the *Orthohepevirus A* species are able to infect humans. HEV is primarily transmitted by fecal–oral routes through contaminated foods and water in endemic areas. Also, zoonotic and person-to-person transmission is possible. HEV causes acute hepatitis E in human and an infection is considered to be endemic in many developing countries in Africa and Asia. HEV genotypes 1 and 2 cause epidemic and endemic diseases in developing countries, mainly through contaminated drinking water, while genotypes 3 and 4 cause autochthonous infections mainly in developed countries through a unique zoonotic foodborne transmission (Khuroo et al., 2016).

### 2.2.9 Rotaviruses

RVs are nonenveloped, double-stranded RNA viruses, belonging to the family Reoviridae. RV is composed of the outer capsid, inner capsid, and core, and genome is composed of 11 segments of double-stranded RNA, which code for six structural and five nonstructural proteins. RV is mainly classified into seven groups (A–G) based on the antigenicity of the inner capsid protein VP6 and genomic characteristics. Among them, rotavirus group A (RVA) strains with distinct G-genotype and P-genotype are the major etiological agents in humans worldwide. Infection with RVA is the most common cause of diarrheal disease among infants and young children and one of the common causes of death in children under 5 years of age (Walker et al., 2013). Virus transmission occurs through the fecal–oral route by direct contact with an infected person and possibly by the respiratory route. RV causes an estimated 2 million hospitalizations and 450,000 deaths among children annually, and the majority of deaths are reported from developing countries in Asia and Africa (Wang et al., 2014; Liu et al., 2015). The WHO has recommended that the use of RV vaccines in routine immunization programs worldwide to reduce the burden of disease (WHO, 2009).

## 2.3 Waterborne protozoa

Protozoan parasites were the most frequently identified etiologic agents in WBDOs in 1990s. Further from 1978 through 1991, *Giardia lamblia* was the most commonly identified pathogen, while in 1992, the numbers of outbreaks reported for giardiasis and cryptosporidiosis were matching. *Naegleria fowleri*, *Acanthamoeba* spp., and *Entamoeba histolytica* are also considered as etiologic agents in WBDOs. Since the potential threat of infection via the waterborne route is being recognized for many of these protozoans, it is crucial that the water industry pays its attention to finding ways to detect these emerging and well-recognized protozoan pathogens in water (Marshall et al., 1997).

### 2.3.1 The genus *Cryptosporidium*

Cryptosporidia are zoonotic protozoan parasites with worldwide distribution, consisting of 27 species and more than 60 genotypes. Among *Cryptosporidium* species identified, *Cryptosporidium hominis* and *Cryptosporidium parvum* are the major disease-causing organisms in human. They cause cryptosporidiosis which is a gastrointestinal illness that can last for several days to several weeks. This infection is commonly found in children, immunocompromised individuals, and workers who are frequently exposed to wastewater. The major routes of transmission are not only water and food but also person-to-person contact and respiratory transmission is possible.

### 2.3.2 The genus *Giardia*

*Giardia* are flagellated protozoan parasites belonging to the phylum Metamonada that cause giardiasis, a diarrheal disease in humans and other mammals throughout the world. Since 1920, six *Giardia* species have been described; *Giardia duodenalis* (syn. *Giardia intestinalis* and *G. lamblia*) is the major disease-causing organisms in human. Risk from *Giardia* can be through occupational, accidental, or recreational exposure to surface waters. [Brodsky et al. \(1974\)](#) reported that water contaminated with *G. lamblia* cysts causes travel-related giardiasis in tourists in certain areas of the world. *Giardia* species have two major stages in their life cycle, i.e., rapidly multiplying trophozoites and cysts. Cysts are excreted with feces and survive in a variety of environmental conditions. They can be transmitted through contaminated water, food, or direct fecal–oral route.

### 2.3.3 *Entamoeba histolytica*

*E. histolytica* belongs to the family Entamoebidae, an invasive, pathogenic protozoan causing amebiasis while other two species *Entamoeba dispar* and *Entamoeba moshkovskii* are nonpathogenic. Life cycle of this *E. histolytica* includes trophozoite, precyst, cyst, metacyst, and metacystic trophozoite stages. Mature cysts have four nuclei and average 20  $\mu\text{m}$  in diameter, while the motile form trophozoite has a size range of 10–60  $\mu\text{m}$ . The cyst form is the infective form for humans, which can survive in water and food. Infections due to *E. histolytica* have been recorded globally and it is suggested that from the infected persons around 10% show clinical symptoms. According to literature except for the two parasites, plasmodia and schistosomes, most deaths have been assigned to *E. histolytica* than any other parasite. In developed countries, risk groups include travelers, immigrants, migrant workers, and immunocompromised individuals. Transmission of this protozoan by water is common in developing countries, where much of the water supply for drinking is untreated and fecally contaminated ([Marshall et al., 1997](#)).

## 2.4 Waterborne helminths

The helminths, generally known as parasitic worms, are invertebrates with elongated, flat, or round bodies which belong to Kingdom Animalia. The major parasitic helminths include in the phylum Nematoda (roundworms) and the phylum Platyhelminthes (trematodes). Helminth parasites infect a large number of people and animals worldwide, mainly in developing countries due to lack of water, sanitation, and hygiene facilities. *Dracunculus medinensis* (Guinea worm) and *Fasciola* spp. (*Fasciola hepatica* and *Fasciola gigantica*) (liver flukes) are the major helminths which can be transmitted through drinking water.



### 2.4.1 The genus *Dracunculus*

The genus *Dracunculus* belongs to the phylum Nematoda and family Dracunculidae, which is parasite of mammals and reptiles. There are 14 valid species in this genus but *D. medinensis* has been well-studied because of human infections. Dracunculiasis or Guinea-worm disease (GWD) is an avoidable waterborne disease caused by the parasite *D. medinensis* which affect the populations in rural parts of South Asia and Africa. Reported cases worldwide annually have declined from an estimated 3.5 million cases in 1986 to only 28 cases in 2018 (WHO, 2019). GWD is now restricted to some communities in remote parts of Africa. Humans get exposed to the disease through consumption of drinking water containing *Cyclops* spp. carrying infectious *D. medinensis* larvae. After ingestion, larvae are released, penetrate the intestinal and peritoneal walls, and inhabit the subcutaneous tissues.

### 2.4.2 The genus *Fasciola*

The genus *Fasciola* belongs to the phylum Platyhelminthes and family Fasciolidae, which causes fasciolosis in human and ruminants. The main pathogenic species are *F. hepatica* (temperate fluke) and *F. gigantica* (tropical fluke). It is estimated that more than 17 million people are infected worldwide and about 180 million people living in endemic areas are at risk to infection (Cwiklinski et al., 2016). Human infection generally occurs through consumption of aquatic vegetables such as watercress, drinking water contaminated with encysted cercariae, or washing utensils with contaminated water.

The above-discussed and the most important waterborne pathogens belonging to the four categories bacteria, viruses, protozoa, and helminths, their diseases, and mode of transmission are summarized in Table 2.1.

## 3. Potential waterborne pathogens

In 1997, WHO defined emerging pathogens as those that have appeared in a human population for the first time or have occurred previously but are increasing in incidence or expanding into geographical areas where they have not previously been reported. Reemerging pathogens are those whose occurrence is increasing as a result of long-term changes in their underlying epidemiology (WHO, 2003). By these criteria, 175 species of infectious agent from 96 different genera were classified as emerging pathogens in 1970s and from this group, 75% were zoonotic species. However, currently several of this microorganism from environmental sources, including water, have been confirmed as pathogens, including *Cryptosporidium*, *Legionella*, *E. coli* O157, RV, hepatitis E virus, and norovirus. *H. pylori* is an example of a recently emerged pathogen that may be transmitted through water (WHO, 2003).

**TABLE 2.1** The waterborne pathogens.

Pathogen	Disease	Mode of transmission
<b>Bacteria</b>		
<i>Vibrio cholera</i> , serovarieties O1 and O139	Cholera, gastroenteritis	Fecal–oral route
<i>Salmonella</i> sp.	Salmonellosis, gastroenteritis	Fecal–oral route
<i>Shigella</i> sp.	Shigellosis	Fecal–oral route
<i>Escherichia coli</i> , serotype O157:H7	Diarrhea, hemorrhagic colitis, hemolytic uremic syndrome	Fecal–oral route
<i>Burkholderia pseudomallei</i>	Melioidosis	Direct contact with contaminated soil and surface waters
<i>Campylobacter</i> sp.	Diarrhea, gastroenteritis	Consumption of contaminated food
<i>Francisella tularensis</i>	Tularemia	Arthropod bites, direct contact with infected animals, and inhalation or ingestion of contaminated water
<i>Legionella pneumophila</i>	Acute respiratory illness, pneumonia (legionellosis)	Inhalation of contaminated aerosols
<i>Mycobacterium avium</i> complex (MAC)	Pulmonary disease, skin infection	Inhalation of contaminated aerosols
<b>Viruses</b>		
Adenovirus	Gastroenteritis, respiratory, ocular, and urinary tract infections	Inhalation of contaminated aerosols, fecal–oral route
Astrovirus	Gastroenteritis, respiratory infections	Fecal–oral route
Norovirus	Gastroenteritis, diarrhea	Fecal–oral route
Sapoviruses	Acute viral gastroenteritis	Fecal–oral route
Hepatitis A and E viruses	Hepatitis	Fecal–oral route
Rotavirus	Diarrhea, gastroenteritis	Fecal–oral route

Continued

TABLE 2.1 The waterborne pathogens.—cont'd

Pathogen	Disease	Mode of transmission
<b>Protozoa</b>		
<i>Cryptosporidium</i> sp.	Cryptosporidiosis	Fecal–oral route
<i>Giardia intestinalis</i>	Giardiasis	Fecal–oral route
<i>Entamoeba histolytica</i>	Amebiasis	Fecal–oral transmission
<i>Toxoplasma gondii</i>	Toxoplasmosis	Ingestion of water contaminated with oocysts
<b>Helminths</b>		
<i>Dracunculus medinensis</i>	Dracunculiasis	Consumption of contaminated water
<i>Fasciola hepatica</i> , <i>Fasciola gigantica</i>	Fascioliasis	Consumption of aquatic plants with metacercariae

### 3.1 Potential waterborne bacteria

#### 3.1.1 *Helicobacter pylori*

Bacteria of genus *Helicobacter* are Gram-negative, curved, or spiral-shaped belonging to the family Helicobacteraceae and class Epsilonproteobacteria. *H. pylori* is a helix-shaped bacterium, 3  $\mu\text{m}$  long with a diameter about 0.5  $\mu\text{m}$ . Genus *Helicobacter* contains more than 40 described species and 4 *Candidatus* species, a designation of provisional status by International Committee on Systematic Bacteriology for incompletely described prokaryotes, and is divided according to their major colonization sites as gastric or lower intestinal tract–associated bacterial species. It is a genetically diverse gastric pathogen, carrying a range of antibiotic resistance patterns, and varies in geographic occurrence.

These are considered as major etiologic agent for gastritis and are also connected to pathogenesis of peptic and duodenal ulcer disease and gastric carcinoma. But most individuals remain asymptomatic. Approximately 70%–90% of persons in developing countries and 25%–50% of those in developed countries are colonized by *H. pylori* and it is transmitted mainly by fecal–oral or oral–oral routes, with water and food as the sources (Doyle, 2012). Epidemiological studies have associated the *H. pylori* infection with lack of access to potable drinking water and proper sanitation *H. pylori* in drinking water biofilms, change their morphology, and persist for more than 1 month, with densities exceeding  $10^6$  cells/cm<sup>2</sup> (Giao et al., 2008).

### 3.1.2 *Aeromonas hydrophila*

*Aeromonas* are straight, coccobacillary to bacillary, belonging to family Aeromonadaceae of order Aeromonadales who are non-spore-forming, facultative anaerobic, Gram-negative bacteria with cells having a size of  $0.3\text{--}1.0 \times 1.0\text{--}3.5 \mu\text{m}$ . Although *Aeromonas hydrophila* is usually the dominant species, other aeromonads, such as *Aeromonas caviae* and *Aeromonas sobria*, have also been isolated from human feces and water sources.

*A. hydrophila* has been recognized as an opportunistic pathogen being identified as a potential agent of gastroenteritis, septicemia, meningitis, and in wound infections. It plays a significant role in intestinal disorders in children under 5 years old, the elderly, and immunosuppressed people. Ubiquitous in nature, it is frequently isolated from food, drinking water, and aquatic environments. In surface waters, mainly rivers and lakes, concentrations of *Aeromonas* spp. are high but groundwaters generally contain lesser numbers. Drinking water immediately leaving the treatment plant could contain between 0 and  $10^2$  CFU/mL and these waters can display higher *Aeromonas* concentrations, due to the growth in biofilms (Chauret et al., 2001). *A. hydrophila* is resistant to standard chlorine treatments and it is assumed that they survive by being within the biofilms. The common routes of infection are the ingestion of contaminated water or food or through skin. No person-to-person transmission has been reported.

### 3.1.3 The genus *Leptospira*

The genus *Leptospira* belongs to family Leptospiraceae of the phylum Spirochaete and currently contains 20 species including 9 pathogenic, 6 saprophytic, and 5 being intermediate. They are thin, tightly coiled, motile spirochetes, generally 6–20  $\mu\text{m}$  in length, but during culturing they may produce much longer cells. The surface structure of the *Leptospira* shows both Gram-negative and Gram-positive characteristics. The disease leptospirosis is one of the most widespread zoonotic diseases, infecting both human and animals caused by the *Leptospira*. The major route of exposure to the pathogen is indirect contact with contaminated water or moist soil. In developing countries from tropics, leptospirosis is an occupational infection, most affected being the people who are engaged in farming, sharecropping, and in animal husbandry (Levett, 2001). Furthermore, there is a significant risk of exposure during recreational activities. Leptospirosis is essentially waterborne infection, as several outbreaks of disease have been recorded during rainy season. Both pathogenic and saprophytic strains of leptospirosis have been isolated from water sources including rivers and lakes as they are able to survive in moist soil and freshwater for long periods of time (Pal and Hadush, 2017).

### 3.1.4 The genus *Tsukamurella*

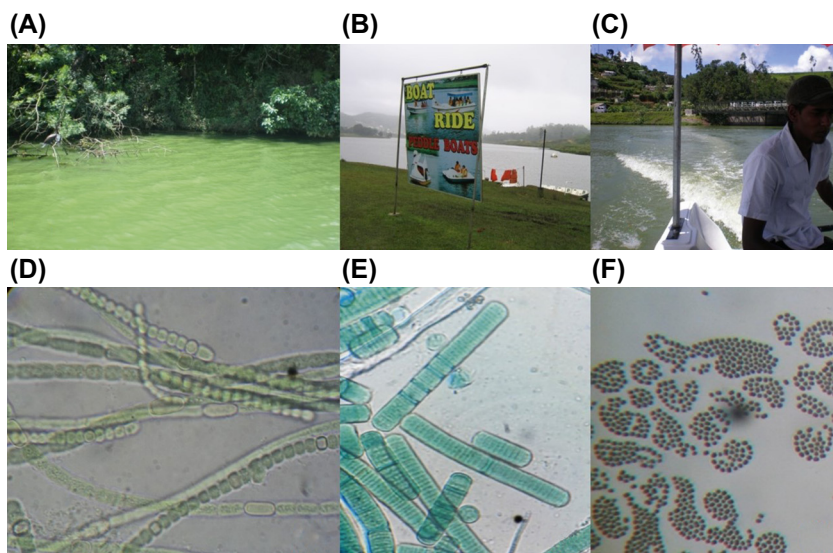
Bacteria belonging to genus *Tsukamurella* of order Actinomycetales are Gram-positive, nonmotile, obligate aerobic, irregular, and rod-shaped. The genus includes 11 species and out of which 9 *Tsukamurella* species have been isolated from human infections. Most of *Tsukamurella* species exist as environmental saprophytes present in soil, arthropods, water, sludge foam, and sponges. Some species have been detected in drinking water supplies, but there is no evidence of correlation between the presence of organisms and the disease. They are opportunistic pathogens and can transmit through clinical instruments such as catheters or lesions. *Tsukamurella* cause various infections in humans, including pulmonary and cutaneous infections and meningitis and most vulnerable are immunocompromised individuals.

### 3.1.5 The genus *Bacillus*

Bacteria belonging to genus *Bacillus* of phylum Firmicutes are rod-shaped, Gram-positive, strictly aerobic, or facultatively anaerobic and are capable of endospore formation. *Bacillus* species are commonly found in soil and water. They have been detected in drinking water supplies even after disinfection processes, but waterborne transmission is not yet confirmed. Only few *Bacillus* species are pathogenic to human. With *Bacillus cereus* causing bacteremia in immunocompromised patients, *B. anthracis* causes anthrax in humans and animals. In a study conducted by [Taylor et al. \(2005\)](#), strains of *Bacillus megaterium*, *Bacillus firmus*, *Bacillus simplex*, and *B. cereus* were found to produce heat-stable toxins, with varying levels of toxicity.

### 3.1.6 Cyanobacteria and cyanotoxins

Cyanobacteria are a phylum with an estimated 150 genera of cyanobacteria containing approximately 2000 species, of which around 46 have been reported as being toxigenic. They are oxygenic, photosynthetic, Gram-negative bacteria that inhabit a large variety of terrestrial and aquatic habitats, showing a wide diversity in morphology and their average cell size ranges from 0.5 to 60  $\mu\text{m}$ . In 1998, cyanobacteria were included as a microbial contaminant to CCL because of their potential for transmission through drinking water. Furthermore, microcystin-LR, cylindrospermopsin, and anatoxin-a produced by several species of cyanobacteria are also included in the CCL. These cyanotoxins have been reported from water reservoirs around the world which had caused acute and chronic illnesses in animals and humans ([Liyanage et al., 2016](#)). Exposure to cyanotoxins can be through contaminated drinking water, ingestion and dermal skin contact during recreational activities ([Fig. 2.2](#)), inhalation of aerosols, medical treatments (dialysis), or through algal food supplements.



**FIGURE 2.2** A lake in a developing country where people are engaged in recreational activities. (A) Lake Gregory, Sri Lanka; (B) recreational activity area; (C) people engaged in boat riding; potential toxic cyanobacteria; (D) *Anabaena* sp.; (E) *Oscillatoria* sp.; (F) *Microcystis* sp. (Magana-Arachchi et al., 2011).

### 3.2 Potential waterborne viruses

In 2017, GWPP reported 10 emerging viruses with potential for waterborne transmission including genera *Alphatorquevirus*, *Cyclovirus*, *Erythroparvovirus*, *Bocaparvovirus*, *Protoparvovirus*, *Alphapapillomavirus*, *Betapapillomavirus*, *Picobirnavirus*, *Betapolyomavirus*, and *Alphapolyomavirus* (Rusinol and Girones, 2017) (Table 2.2).

### 3.3 Potential waterborne protozoa

#### 3.3.1 Microsporidia

*Microsporidia* belonging to the phylum Microspora include over 140 genera and 1200 species that are parasitic in all major animal groups. They are obligate intracellular, spore-forming protists. The spore is the only stage that can survive outside the host cell in their life cycle and it contains a characteristic coiled polar filament for injecting the sporoplasm into a host cell to initiate infection. After infection, a complex process of multiplication takes place within an infected cell and new spores are produced and released to feces, urine, respiratory secretions, or other body fluids, depending on the type of species and the site of infection. Among 14 human pathogenic *Microsporidia* species, two species, *Enterocytozoon bieneusi* and *Encephalitozoon*

**TABLE 2.2** The potential waterborne pathogens.

Pathogen	Disease	Mode of transmission
<b>Bacteria</b>		
<i>Helicobacter pylori</i>	Gastritis, peptic and duodenal ulcer disease, and gastric carcinoma	Oral–oral or fecal–oral transmission
<i>Aeromonas hydrophila</i>	Gastroenteritis, septicemia, meningitis, and wound infections, intestinal disorders in children	Ingestion of contaminated water or food, through skin
<i>Leptospira</i> sp.	Leptospirosis	Through water contaminated by urine from infected animals
<i>Tsukamurella</i> sp.	Pulmonary and cutaneous infections, meningitis	Through clinical instruments such as catheters or lesions
<i>Bacillus</i> sp.	Diarrhea	Through drinking water
Cyanobacteria and cyanotoxins	Gastrointestinal symptoms, skin rashes, kidney disease	Through drinking water, bathing in contaminated water
<b>Viruses<sup>a</sup></b>		
<i>Alphatorquevirus</i>	Asymptomatic. May be associated with hepatitis, pulmonary diseases, hematologic disorders, myopathy, and lupus	Fecal–oral route
<i>Cyclovirus</i>	Systemic infections may play a role in development of paraplegia	Fecal–oral and foodborne transmission
<i>Erythroparvovirus</i>	Fifth disease in children, arthropathy, hepatitis	Respiratory route
<i>Bocaparvovirus</i>	Gastroenteritis, related to respiratory infections	Respiratory and fecal–oral routes
<i>Protoparvovirus</i>	Gastroenteritis	Respiratory and fecal–oral routes
<i>Alphapapillomavirus</i>	Cervix, penis, anus, and vulva cancers	Direct skin-to-skin or skin-to-mucosa contact
<i>Betapapillomavirus</i>	Related to genital warts	Direct skin-to-skin or skin-to-mucosa contact
<i>Picobirnavirus</i>	May be implicated in gastroenteritis	Fecal–oral route
<i>Betapolyomavirus</i>	Progressive multifocal encephalopathy	Fecal–oral route

**TABLE 2.2** The potential waterborne pathogens.—cont'd

Pathogen	Disease	Mode of transmission
<i>Alphapolyomavirus</i>	Associated to Merkel cell carcinoma	Fecal–oral route
<b>Protozoa</b>		
<i>Microsporidia</i>	Microsporidiosis	Fecal–oral transmission
<i>Cyclospora cayetanensis</i>	Diarrheal illness, gastroenteritis	Fecal–oral transmission
<i>Cystoisospora belli</i>	Cystoisosporiasis	Fecal–oral transmission
<b>Helminths</b>		
<i>Schistosoma</i> sp.	Schistosomiasis, liver and kidney damage	Penetrate the skin during contact with infested water

<sup>a</sup>Adapted from *Table 2.2* in summary of excreted and waterborne viruses (Rusinol and Girones, 2017).

*intestinalis*, are the most prevalent species which associated with gastrointestinal disease in humans. Person-to-person contact and ingestion of spores in water and food contaminated with human feces or urine are considered as important routes of exposure. A study by Dowd et al. (1998) showed that 7 out of 14 water concentrates tested were contaminated with *E. intestinalis*, *E. bienensei*, and *Vittaforma corneae* which represent human pathogenic microsporidia species. Their study is the first species level confirmation of human pathogenic microsporidia in water, indicating that these human pathogenic microsporidia possibly be waterborne pathogens. Microsporidiosis is an emerging disease in immunosuppressed persons with AIDS, but microsporidia have the ability to cause disease even in immunologically normal hosts.

### 3.3.2 *Cystoisospora belli*

*Cystoisospora* (formerly *Isoospora*) are coccidian parasites, belonging to the phylum Apicomplexa, found mainly in tropical and subtropical areas. Many *Cystoisospora* species can infect animals, but human is the only known host for *C. belli* (Lindsay et al., 1997). *C. belli* infects the epithelial cells of the small intestine of human, and immunocompromised individuals are more susceptible to the infection. The immature form of the parasite is known as oocysts; they are passed out with feces and then mature outside the body in 2–3 days, depending on environmental conditions. It can be transmitted



through contaminated water and food. However, direct person-to-person transmission is unlikely. The improved practice of personal hygiene and sanitation may help in preventing transmission of disease.

### 3.3.3 *Cyclospora cayetanensis*

*Cyclospora cayetanensis* belongs to the family Eimeriidae, 7.5–10 µm in diameter, cyst-forming, and unsporulated when passed in feces. It is an apicomplexa coccidia closely related to *Eimeria* species, recognized as an emerging protist that causes diarrheal illness and significantly contributes to the burden of gastroenteritis worldwide.

## 3.4 Potential waterborne helminths

### 3.4.1 *The genus Schistosoma*

Schistosomes are trematode parasites which cause schistosomiasis (or bilharzia) in human. The main human pathogenic species are *Schistosoma mansoni*, *Schistosoma japonicum*, and *Schistosoma haematobium*. Schistosomiasis is a waterborne disease mostly seen in the tropics and subtropics. The humans get exposed when their skin comes into contact with infested freshwater, into which the cercariae of the parasite are released by freshwater snails. It is understood that for each of the human schistosomes, the presence of a specific genus of snail is necessary for transmission to occur. This disease has been considered as a disease due to poverty, and controlling of this disease has been a problem because of the lack of clean water available to people living in the developing countries.

The most important potential waterborne pathogens as described by WHO belonging to the four categories bacteria, viruses, protozoa, and helminths, their diseases, and mode of transmission are summarized in [Table 2.2](#).

## 4. Summary

This chapter provides a general description on current waterborne pathogens as well as emerging and potential pathogens which could be categorized into bacteria, viruses, protozoans, and helminths. Most of these microorganisms are ubiquitous in waters regardless of ground, surface, fresh, or marine. People utilize these waters for drinking, cooking, and other domestic actions, bathing, medically, and also for recreations. The water sources become polluted due to the mixing of fecal matter from human and animal and also waste generated by other direct and indirect anthropogenic activities. As a result, waters become reservoirs for the pathogens making it unsafe for human consumption causing many waterborne diseases. In addition, with the increase in global population, changes in climatic patterns, and the presence of antibiotic resistant bacteria in waste waters, it is predicted that there will be a rise in waterborne diseases

especially diarrhea and cholera. Therefore, still the global populations infants, young, or old are at a risk from waterborne diseases and outbreaks whether the countries are developed or developing or in tropics or temperate in geographical distribution. Hence to minimize the adverse effects from these waterborne pathogens and to improve the water quality, regular monitoring of water sources is essential with advanced but cost-effective detection techniques, precise disinfectant procedures with proper management.

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