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Guidelines for Canadian Drinking Water Quality:

Guideline Technical Document

Bacterial Waterborne Pathogens — Current and Emerging Organisms of Concern

Prepared by the
Federal-Provincial-Territorial Committee on Drinking Water
of the
Federal-Provincial-Territorial Committee on Health and the Environment

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Other Guideline Technical Documents for the Guidelines for Canadian Drinking Water Quality can be found on the Water Quality and Health Bureau web page at http://www.healthcanada.gc.ca/waterquality.

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Bacterial Waterborne Pathogens — Current and Emerging Organisms of Concern

1.0 Guideline

No maximum acceptable concentration (MAC) for current or emerging bacterial waterborne pathogens has been established. Current bacterial waterborne pathogens include those that have been previously linked to gastrointestinal illness in human populations. Emerging bacterial waterborne pathogens include, but are not limited to, Legionella, Mycobacterium avium complex, Aeromonas hydrophila*, and* Helicobacter pylori.

Note: Further information on the current and emerging bacterial waterborne pathogens is outlined beginning in section 3.0, Application of the guideline.

2.0 Executive summary for microbiological quality of drinking water

2.1 Introduction

The information contained in this Executive summary applies to the microbiological quality of drinking water as a whole. It contains background information on microorganisms, their health effects, sources of exposure, and treatment. Information specific to bacteria is included as a separate paragraph. It is recommended that this document be read in conjunction with other documents on the microbiological quality of drinking water, including the guideline technical document on turbidity.

2.2 Background

There are three main types of microorganisms that can be found in drinking water: bacteria, viruses, and protozoa. These can exist naturally or can occur as a result of contamination from human or animal waste. Some of these are capable of causing illness in humans. Surface water sources, such as lakes, rivers, and reservoirs, are more likely to contain microorganisms than groundwater sources, unless the groundwater sources are under the direct influence of surface water.

The main goal of drinking water treatment is to remove or kill these organisms to reduce the risk of illness. Although it is impossible to completely eliminate the risk of waterborne disease, adopting a multi-barrier, source-to-tap approach to safe drinking water will reduce the numbers of microorganisms in drinking water. This approach includes the protection of source water (where possible), the use of appropriate and effective treatment methods, well-maintained distribution systems, and routine verification of drinking water safety. All drinking water supplies should be disinfected, unless specifically exempted by the responsible authority. In addition, surface water sources and groundwater sources under the direct influence of surface water should be filtered. Drinking water taken from pristine surface water sources may be exempt from filtration requirements (Health Canada, 2003).

The performance of the drinking water filtration system is usually assessed by monitoring the levels of turbidity, a measure of the relative clarity of water. Turbidity is caused by matter such as clay, silt, fine organic and inorganic matter, plankton, and other microscopic organisms, which is suspended within the water. Suspended matter can protect pathogenic microorganisms from chemical and ultraviolet (UV) light disinfection.

Currently available detection methods do not allow for the routine analysis of all microorganisms that could be present in inadequately treated drinking water. Instead, microbiological quality is determined by testing drinking water for *Escherichia coli*, a bacterium that is always present in the intestines of humans and other animals and whose presence in drinking water would indicate faecal contamination of the water. The maximum acceptable concentration (MAC) of *E. coli* in drinking water is none detectable per 100 mL.

2.3 Bacteria

E. coli is a member of the total coliform group of bacteria and is the only member that is found exclusively in the faeces of humans and other animals. Its presence in water indicates not only recent faecal contamination of the water but also the possible presence of intestinal disease-causing bacteria, viruses, and protozoa. The detection of *E. coli* should lead to the immediate issue of a boil water advisory and to corrective actions being taken. Conversely, the absence of *E. coli* in drinking water generally indicates that the water is free of intestinal disease-causing bacteria. However, because *E. coli* is not as resistant to disinfection as intestinal viruses and protozoa, its absence does not necessarily indicate that intestinal viruses and protozoa are also absent. Although it is impossible to completely eliminate the risk of waterborne disease, adopting a multi-barrier approach to safe drinking water will minimize the presence of disease-causing microorganisms, reducing the levels in drinking water to none detectable or to levels that have not been associated with disease.

While *E. coli* is the only member of the total coliform group that is found exclusively in faeces, other members of the group are found naturally in water, soil, and vegetation, as well as in faeces. Total coliform bacteria are easily destroyed during disinfection. Their presence in water leaving a drinking water treatment plant indicates a serious treatment failure and should lead to the immediate issue of a boil water advisory and to corrective actions being taken. The presence of total coliform bacteria in water in the distribution system (but not in water leaving the treatment plant) indicates that the distribution system may be vulnerable to contamination or may simply be experiencing bacterial regrowth. The source of the problem should be determined and corrective actions taken.

In semi-public and private drinking water systems, such as rural schools and homes, total coliforms can provide clues to areas of system vulnerability, indicating source contamination as well as bacterial regrowth and/or inadequate treatment (if used). If they are detected in drinking water, the local authority responsible for drinking water may issue a boil water advisory and recommend corrective actions. It is important to note that decisions concerning boil water advisories should be made at the local level based upon site-specific knowledge and conditions.

The heterotrophic plate count (HPC) test is another method for monitoring the overall bacteriological quality of drinking water. HPC results are not an indicator of water safety and,

as such, should not be used as an indicator of adverse human health effects. Each system will have a certain baseline HPC level and range, depending on site-specific characteristics; increases in concentrations above baseline levels should be corrected.

There are naturally occurring waterborne bacteria, such as *Legionella* spp. and *Aeromonas hydrophila*, with the potential to cause illnesses. The absence of *E. coli* does not necessarily indicate the absence of these organisms, and for many of these pathogens, no suitable microbiological indicators are currently known. However, the use of a multiple-barrier approach, including adequate treatment and a well-maintained distribution system, can reduce these bacterial pathogens to non-detectable levels or to levels that have never been associated with human illness.

2.4 Health effects

The health effects of exposure to disease-causing bacteria, viruses, and protozoa in drinking water are varied. The most common manifestation of waterborne illness is gastrointestinal upset (nausea, vomiting, and diarrhoea), and this is usually of short duration. However, in susceptible individuals such as infants, the elderly, and immunocompromised individuals, the effects may be more severe, chronic (e.g., kidney damage), or even fatal. Bacteria (such as *Shigella* and *Campylobacter*), viruses (such as norovirus and hepatitis A virus), and protozoa (such as *Giardia* and *Cryptosporidium*) can be responsible for severe gastrointestinal illness. Other pathogens may infect the lungs, skin, eyes, central nervous system, or liver.

If the safety of drinking water is in question to the extent that it may be a threat to public health, authorities in charge of the affected water supply should have a protocol in place for issuing, and cancelling, advice to the public about boiling their water. Surveillance for possible waterborne diseases should also be carried out. If a disease outbreak is linked to a water supply, the authorities should have a plan to quickly and effectively contain the illness.

2.5 Exposure

Drinking water contaminated with human or animal faecal wastes is just one route of exposure to disease-causing microorganisms. Outbreaks caused by contaminated drinking water have occurred, but they are relatively rare compared with outbreaks caused by contaminated food. Other significant routes of exposure include contaminated recreational waters (e.g., bathing beaches and swimming pools) and objects (e.g., doorknobs) or direct contact with infected humans or domestic animals (pets or livestock). Although surface waters and groundwater under the direct influence of surface water may contain quantities of microorganisms capable of causing illness, effective drinking water treatment can produce water that is virtually free of disease-causing microorganisms.

2.6 Treatment

The multi-barrier approach is an effective way to reduce the risk of illness from pathogens in drinking water. If possible, water supply protection programs should be the first line of defence. Microbiological water quality guidelines based on indicator organisms (e.g., *E. coli*) and treatment technologies are also part of this approach. Treatment to remove or inactivate

pathogens is the best way to reduce the number of microorganisms in drinking water and should include effective filtration and disinfection and an adequate disinfection residual. Filtration systems should be designed and operated to reduce turbidity levels as low as reasonably achievable without major fluctuations.

It is important to note that all chemical disinfectants (e.g., chlorine, ozone) used in drinking water can be expected to form disinfection by-products, which may affect human health. Current scientific data show that the benefits of disinfecting drinking water (reduced rates of infectious illness) are much greater than any health risks from disinfection by-products. While every effort should be made to reduce concentrations of disinfection by-products to as low a level as reasonably achievable, any method of control used must not compromise the effectiveness of water disinfection.

3.0 Application of the guideline

Routine monitoring is not recommended for either current or emerging bacterial waterborne pathogens. *E. coli* is used to indicate the presence of the current bacterial waterborne pathogens, but it does not indicate the presence of the emerging bacterial waterborne pathogens. The use of a multiple-barrier approach, including adequate treatment, a well-maintained distribution system, and source protection (in the case of enteric bacteria), can reduce both current and emerging bacterial pathogens to non-detectable levels or to levels that have not been associated with human illness.

4.0 Introduction

Throughout history, consumption of drinking water supplies containing enteric pathogenic bacteria has been linked to illnesses in human populations. These illnesses commonly present as gastrointestinal-related symptoms, such as diarrhoea and nausea. Faecal indicators, such as *E. coli*, are the best available surrogates for predicting the presence of such organisms. In this document, these organisms have been identified as current bacterial pathogens of concern.

However, in recent decades, there has been an increasing amount of interest in naturally occurring waterborne bacteria with the potential to cause gastrointestinal and non-gastrointestinal illnesses, particularly respiratory illnesses. These organisms have been defined within this document as emerging pathogens of concern. In most cases, although *E. coli* is able to indicate the presence of enteric pathogenic bacteria, it does not correlate with the presence of these emerging organisms. In addition, there are currently no suitable microbiological indicators for many of these bacterial pathogens.

It is not necessary to establish MACs for current and emerging waterborne pathogens at this time. The use of a multiple-barrier approach, including adequate treatment, a well-maintained distribution system, and source protection, in the case of enteric bacteria, can reduce these bacterial pathogens to non-detectable levels or to levels that have not been associated with human illness.

The following bacteria, identified as either current or emerging concerns, are those commonly recognized as the etiological agents in waterborne outbreaks or those being recognized more often as causes of other serious illnesses that have the potential for waterborne transmission. The information provided in this document focuses on emerging bacteria of

concern, as there are more unknowns associated with these organisms, and their overall significance, in many cases, still needs to be established. Additionally, the bacteria identified should not be considered a complete list of bacterial pathogens that may be present and potentially responsible for isolated cases of waterborne illness. However, they do encompass the majority that have been responsible for waterborne outbreaks. Information on protozoan and viral pathogens of concern can be found, respectively, in the protozoa and enteric viruses guideline technical documents of the *Guidelines for Canadian Drinking Water Quality* (Health Canada, 2004a, 2004b).

5.0 Current bacterial pathogens of concern

5.1 *Escherichia coli* O157:H7

5.1.1 Description, sources, health effects, and exposure

Escherichia coli is a bacterium found exclusively in the digestive tract of warm-blooded animals, including humans. As such, it is used in the drinking water industry as the definitive indicator of recent faecal contamination of water. While most strains of *E. coli* are non-pathogenic, some can cause serious diarrhoeal infections in humans. The pathogenic *E. coli* are divided into six groups based on serological and virulence characteristics: enterohaemorrhagic, enterotoxigenic, enteroinvasive, enteropathogenic, enteroaggregative, and diffuse adherent (APHA *et al.*, 1998; Rice, 1999). One enterohaemorrhagic strain, *E.coli* O157:H7, has been implicated in many foodborne and a few waterborne outbreaks. It was first recognized in 1982, when it was associated with two foodborne outbreaks of bloody diarrhoea and abdominal cramps (Gugnani, 1999). The primary reservoir of this bacterium has been found to be healthy cattle (Jackson *et al.*, 1998). In foodborne transmission, outbreaks are generally through the consumption of undercooked minced beef and unpasteurized juices or milk that have been contaminated with the bacteria (Gugnani, 1999). Although *E. coli* O157:H7 is not usually a concern in treated drinking water, outbreaks involving consumption of drinking water contaminated with human sewage or cattle faeces have been documented (Swerdlow *et al.*, 1992; Bruce-Grey-Owen Sound Health Unit, 2000).

E. coli serotype O157:H7 causes abdominal pain, bloody diarrhoea, and haemolytic uraemic syndrome (HUS). This bacterium produces potent toxins (verotoxins) related to *Shigella* toxins. The incubation period is 3–4 days, and the symptoms occur for 7–10 days (Moe, 1997; Rice, 1999). It is estimated that 2–7% of *E. coli* O157:H7 infections result in HUS, in which the destruction of erythrocytes leads to acute renal failure (Moe, 1997).

Studies have shown that the dose required to produce symptoms is lower than that for most other enteric pathogenic bacteria. The probability of becoming ill depends on the number of organisms ingested, the health status of the person, and the resistance of the person to the organism or toxin (AWWA Committee Report, 1999). Children and the elderly are most susceptible to HUS complications. Evidence suggests that the incidence of *E. coli* O157:H7 infections and HUS has increased since the serotype was first recognized.

5.1.2 Treatment technology

Similar to the non-pathogenic strains of *E. coli, E. coli* O157:H7 is susceptible to disinfection (Kaneko, 1998; Rice *et al.*, 2000). Further information on treatment technology for *E.coli* can be found in the *Escherichia coli* guideline technical document of the *Guidelines for Canadian Drinking Water Quality* (Health Canada, 2006a). In addition, a multi-barrier approach based upon source protection (where possible), effective treatment, and a well-maintained distribution system will reduce the levels of *E. coli* O157:H7 in drinking water to none detectable or to levels that have never been associated with human illness.

5.1.3 Assessment

Studies have shown that the survival rate of *E. coli* O157:H7 approximates that of typical *E. coli* in the aquatic environment (AWWA Committee Report, 1999; Rice, 1999). Also, although routine examination methods for generic *E. coli* will not detect *E. coli* O157:H7, the former will always occur in greater concentration in faeces than the pathogenic strains, even during outbreaks. *E. coli* O157:H7 will also never occur in the absence of generic *E. coli*. As a result, the presence of *E. coli* can be used as an indicator of the presence of *E. coli* O157:H7.

5.2 *Salmonella* and *Shigella*

5.2.1 Description, sources, health effects, and exposure

Salmonella and *Shigella* are common etiological agents of gastrointestinal illnesses. Consequently, they are present in the faeces of colonized individuals. These organisms are also commonly present in the faeces of a variety of other animals. The presence of either of these organisms in the environment is generally the result of recent faecal contamination. Numerous outbreaks linked to contaminated drinking water have been reported (Boring *et al.*, 1971; White and Pedersen, 1976; Auger *et al.*, 1981; CDC, 1996; Angulo *et al.*, 1997; Alamanos *et al.*, 2000; R. Taylor *et al.*, 2000; Chen *et al.*, 2001). In most cases, the drinking water was not treated or was improperly treated prior to consumption.

5.2.2 Treatment technology

Salmonella and *Shigella* survival characteristics in water and their susceptibility to disinfection have been demonstrated to be similar to those of coliform bacteria (McFeters *et al.*, 1974; Mitchell and Starzyk, 1975). Further information on treatment technology for coliforms can be found in the total coliforms guideline technical document of the *Guidelines for Canadian Drinking Water Quality* (Health Canada, 2006b). In addition, a multi-barrier approach based upon source protection, effective treatment, and a well-maintained distribution system will reduce the levels of *Salmonella* and *Shigella* in drinking water to none detectable or to levels that have never been associated with human illness.

5.2.3 Assessment

The absence of *E. coli* during routine verification should be an adequate indication of the absence of *Salmonella* and *Shigella*. However, instances have been reported in which these pathogens were isolated from drinking water in the absence of coliforms (Seligmann and Reitler, 1965; Boring *et al.*, 1971). Coliform suppression by elevated HPCs and poor recovery of stressed

coliforms seem to be the most plausible explanations for these discrepancies. Total coliform and *E. coli* recoveries are not affected by elevated HPCs and environmental stress in the newer defined-substrate methods.

5.3 *Campylobacter* and *Yersinia*

5.3.1 Description, sources, health effects, and exposure

Waterborne outbreaks of gastroenteritis involving *Campylobacter jejuni* and *Yersinia enterocolitica* have been recorded on numerous occasions (Eden *et al.*, 1977; McNeil et al., 1981; Mentzing, 1981; Vogt *et al.*, 1982; Taylor *et al.*, 1983; Lafrance *et al.*, 1986; Sacks *et al.*, 1986; Thompson and Gravel, 1986). The most notable Canadian waterborne outbreak involving *Campylobacter* in recent history occurred in Walkerton, Ontario, in May 2000 (Clark *et al.*, 2003). This outbreak was linked to faecally contaminated well water that was not properly treated before consumption. Other reports of *Campylobacter* and *Yersinia* isolation from surface and well waters can be found in the literature (Caprioli *et al.*, 1978; Schiemann, 1978; Blaser *et al.*, 1980; OME, 1980; Taylor *et al.*, 1983; Weagant and Kaysner, 1983; El-Sherbeeny *et al.*, 1985). The survival characteristics of *C. jejuni* are similar to those of coliforms, but the frequency of isolation of *Y. enterocolitica* is higher in winter months, indicating that it can survive for extended periods and perhaps even multiply when water temperatures are low (Berger and Argaman, 1983).

5.3.2 Treatment technology

The findings of Wang *et al.* (1982) indicated that conventional water treatment and chlorination will probably destroy *C. jejuni* and *Y. enterocolitica* in drinking water. In addition, a multi-barrier approach based upon source protection (where possible), effective treatment, and a well-maintained distribution system will reduce the levels of *Campylobacter* and *Yersinia* in drinking water to none detectable or to levels that have never been associated with human illness.

5.3.3 Assessment

The presence of *Y. enterocolitica* has been demonstrated to be poorly correlated with levels of coliforms and HPC bacteria (Wetzler *et al.*, 1979). In addition, studies have shown no correlation between indicator organisms (e.g., *E. coli*, thermotolerant coliforms) and the presence of *Campylobacter* in raw surface water supplies (Carter *et al.*, 1987; Hörman *et al.*, 2004). Thus, coliforms may not be adequate indicators of the presence of both *C. jejuni* and *Y. enterocolitica*.

6.0 Emerging bacterial pathogens of concern

6.1 *Legionella*

6.1.1 Description

Legionellae were first recognized as human pathogens after a 1976 outbreak of pneumonia among veterans attending a convention in Philadelphia. Since that time, at least 42 distinct *Legionella* species have been identified. Approximately half of these species have been associated with disease in humans, with the majority of illnesses resulting from *Legionella*

pneumophila infection. Other than *L. pneumophila*, human illnesses are generally the result of infection with *L. micdadei*, *L. bozemanii*, *L. longbeachae*, and *L. dumoffi*, although many other species have been implicated on occasion.

6.1.2 Sources

Unlike most other common waterborne pathogens, *Legionella* species are naturally present in water environments, including surface water (Palmer *et al.*, 1993) and groundwater (Lieberman *et al.*, 1994). Their ubiquitous nature reflects their ability to survive under varied water conditions, including temperatures from 0 to 63°C and a pH range of 5.0–8.5 (Nguyen *et al.*, 1991). Their survival is, at least in part, attributed to their interactions with other members of the heterotrophic flora. For example, their ability to develop symbiotic relationships with other bacteria, such as *Flavobacterium*, *Pseudomonas*, *Alcaligenes*, and *Acinetobacter*, is thought to be important for their survival and proliferation in water (Lin *et al.*, 1998). In addition, some protozoa that are naturally occurring in water, such as *Hartmanella* sp., *Acanthamoeba castellanii*, and *Echinamoeba*, can harbour *Legionella* organisms, protecting them from environmental stresses and providing a suitable environment for their amplification (Kilvington and Price, 1990; Kramer and Ford, 1994; Fields, 1996). In general, the amount of legionellae in source waters is low compared with the concentrations that can be reached in human-made systems, as natural water conditions are not as conducive to growth.

In human-made systems, *Legionella* colonizes various locations within buildings (e.g., cooling towers, hot water tanks, shower heads, aerators) and contaminates potable water and air. Generally, the areas of a human-made system contaminated with legionellae are those where biofilm formation is most prevalent. This is because *Legionella* can thrive in biofilms. Concentrations have been found to be as much as 10 times higher in biofilms from faucets than from water collected from that faucet (Ta *et al*., 1995). There is some evidence that pipe material can also affect colonization by legionellae. For example, studies have found that copper piping may be inhibitory for *Legionella* growth (Tiefenbrunner *et al.*, 1993; Rogers *et al.*, 1994; van der Kooij *et al.*, 2002). Water temperature is an additional factor that influences colonization, with temperatures between 20°C and 50°C being hospitable for colonization, although legionellae generally only grow to high concentrations at temperatures below 42°C. Measurable inactivation of legionellae begins at temperatures greater than 50°C (WHO, 2002). It is through human-made systems that *Legionella* is most often disseminated, causing sporadic or outbreak cases of illness.

6.1.3 Health effects

There are two distinct illnesses caused by *Legionella*: Legionnaires' disease and Pontiac fever. Collectively, these illnesses are referred to as legionellosis.

Legionnaires' disease is a severe pneumonia that can be accompanied by extrapulmonary manifestations, such as renal failure, encephalopathy, and pericarditis (Oredugba *et al.*, 1980; Johnson *et al.*, 1984; Nelson *et al.*, 1985). Other common early features include confusion, disorientation, lethargy, and possible gastrointestinal symptoms, such as nausea, vomiting, and diarrhoea (U.S. EPA, 2001). The incubation period is generally 2–10 days. One problem in diagnosing Legionnaires' disease is a lack of any specific symptom that distinguishes it from other bacterial pneumonias. Early diagnosis and consequently appropriate antibiotic therapy

are important in successfully treating the disease. Overall, the mortality rate of Legionnaires' disease is approximately 15% (Oredugba *et al.*, 1980; Johnson *et al.*, 1984; Nelson *et al.*, 1985).

Pontiac fever, on the other hand, is a non-pneumonic, febrile illness with an incubation period of 24–48 hours. Unlike Legionnaires' disease, Pontiac fever has a high attack rate (Mangione *et al.*, 1985). However, this illness typically resolves without complications in 2–5 days (Glick *et al*., 1978; Fallon *et al*., 1993).

6.1.4 Exposure

Individuals considered to be at the highest risk of contracting Legionnaires' disease are those who are immunocompromised, especially transplant patients, and those with underlying lung conditions. Outside of the high-risk category, other predisposing risk factors commonly acknowledged include being male, smoking, alcoholism, being over 40 years of age, working more than 40 hours a week, and spending nights away from home. It is therefore not surprising that children and young people are rarely affected by the disease (WHO, 1990; Straus *et al.*, 1996). An additional determinant for human infection is the concentration of *Legionella* present, as a minimum infectious dose is required to cause illness. It is not known precisely what this dose is, as infection is dependent on other factors, including the virulence of the organism and, as mentioned previously, the health status of the host. There is some evidence that replication within amoebae may contribute to enhanced virulence of legionellae (Kramer and Ford, 1994). It is speculated that infectivity may also be enhanced if amoebae containing *Legionella* cells are inhaled or aspirated, as this provides a mechanism for introducing hundreds of *Legionella* cells into the respiratory tract (Rowbotham, 1986; Berk *et al.*, 1998).

Since *Legionella* is a respiratory pathogen, systems that generate aerosols, such as cooling towers, whirlpool baths, and shower heads, are the more commonly implicated sources of infection, with the hot water supply system generally being the origin of the contamination (Spitalny *et al.*, 1984; Mangione *et al.*, 1985; Fallon and Rowbotham, 1990; Jernigan *et al.*, 1996; Hershey *et al.*, 1997; Brown *et al.*, 1999; Benin *et al.*, 2002). However, the cold water supply, when held within the range of *Legionella* multiplication (25°C), has also been implicated (Hoebe *et al.*, 1998). *Legionella* contamination is particularly troublesome in hospitals, where susceptible human populations are present and can be exposed to aerosols containing hazardous concentrations of *Legionella* spp., generally *L. pneumophila* (Dufour and Jakubowski, 1982). Although more prominent in hospital settings (up to 50% of nosocomial pneumonias) (Breiman and Butler, 1998), *Legionella* spp. have been estimated to cause 1–15% of community-acquired pneumonias (Lieberman *et al.*, 1996; Breiman and Butler, 1998). Within the community, large buildings such as hotels, community centres, industrial buildings, and apartment buildings are most often implicated as sources of infection (Yu, 2002). Single-family dwellings have rarely been identified as the source of infection. However, studies have shown that contamination of domestic hot water systems in single-family homes with *Legionella* does occur (Arnow *et al.*, 1985; Lee *et al.*, 1988; Stout *et al.*, 1992b; Borella *et al.*, 2004). In a few instances, cases of Legionnaires' disease have been linked to these dwellings (Stout *et al.*, 1992a).

The challenge to preventing *Legionella*-associated illnesses is controlling their growth in these human-made environments. Once *Legionella* becomes established in a water system (i.e., in the biofilm), it is nearly impossible to eradicate it. However, it can be kept to a minimum by implementing some control procedures. This is particularly important in health care settings.

In addition to being a waterborne illness, outbreaks of Legionnaires' disease have been associated with potting soils. In these cases, the causative agents were found to be *L. longbeachae*, *L. bozemanii*, and *L. dumoffi*, as opposed to *L. pneumophila*.

6.1.5 Treatment technology

As with other bacteria, physical removal mechanisms used during drinking water treatment, such as coagulation, flocculation, sedimentation, and filtration, will reduce the number of *Legionella* present in finished water. Disinfection can further lower the number present. In comparison with indicator organisms commonly used in the drinking water industry, such as *E. coli* or total coliforms, a higher CT value (i.e., a longer contact time, a higher disinfectant concentration, or a combination of both) is necessary to achieve a comparable level of reduction in *Legionella* using chlorine, chlorine dioxide, and ozone. The one exception appears to be with the use of chloramine. Laboratory tests have shown that legionellae seem to be more susceptible to chloramination than *E. coli* (Cunliffe, 1990). As further support for this finding, it was found that hospitals with a free chlorine residual were 10 times more likely to have reported cases of Legionnaires' disease than hospitals with monochloramine residuals (Kool *et al.*, 1999). Kool *et al.* (1999) also reported that when a few selected municipalities were investigated, it was found that legionellae could be isolated from systems with a free chlorine residual, but those systems with monochloramination were negative for the bacterium. UV light is also effective for inactivating *Legionella*, at doses commonly used in drinking water treatment (WHO, 2002). In the distribution system, current recommended disinfectant residuals are sufficient to keep the concentration of *Legionella* at levels that have not been associated with disease (WHO, 2002).

6.1.6 Assessment

Unlike the case with gastrointestinal pathogens, where *E. coli* can be used to indicate their potential presence, no suitable indicators have been identified to signal increasing concentrations of *Legionella* spp. in a building's plumbing system. There is some evidence that increasing *Legionella* concentrations are accompanied by, or preceded by, an increase in other bacteria, resulting in an elevated HPC measurement (i.e., >100 CFU/mL) (WHO, 2002). Hence, elevated HPCs may indicate the presence of *Legionella*. However, the correlation between HPC and *Legionella* is not consistent. This may partially result from the accompanying chlorination of the water, since HPC bacteria are more readily killed than legionellae (Zacheus and Martikainen, 1996).

The ubiquitous nature of legionellae in water ensures that water supplies, regardless of their source, may contain *Legionella* spp. in low quantities. On a daily basis, the population at large is exposed to these low levels with no reaction or with asymptomatic production of antibodies. In Canada, *Legionella pneumophila* and other *Legionella* species have been recovered in low concentrations from the drinking water (Dutka *et al.*, 1984; Tobin *et al.*, 1986). However, no illnesses have ever been linked to these low concentrations. For these reasons, the presence of the organism is not sufficient evidence to warrant remedial action in the absence of disease cases (Dufour and Jakubowski, 1982; Tobin *et al.*, 1986).

6.2 *Mycobacterium avium* complex (Mac)

6.2.1 Description

The *Mycobacterium avium* complex (Mac) consists of 28 serovars of two distinct species: *Mycobacterium avium* and *Mycobacterium intracellulare.* Based on phenotypic and genetic characteristics, three subspecies of *M. avium*, including *M. avium* subsp. *avium*, *M. avium* subsp. *paratuberculosis*, and *M. avium* subsp. *silvaticum*, have been identified (Nichols *et al.*, 2004). . Mac organisms, along with many other environmental mycobacteria species, comprise the non-tuberculous mycobacterium (NTM) group. These organisms are designated as NTM to distinguish them from *Mycobacterium tuberculosis* and *Mycobacterium leprae*, the infectious agents of tuberculosis and leprosy. Unlike their NTM counterparts, neither of the latter organisms is present in the environment, and, consequently, they are not a concern in drinking water.

6.2.2 Sources

Mac organisms have been identified in a broad range of environmental sources, including marine waters, rivers, lakes, streams, ponds, springs, soil, piped water supplies, plants, and house dust (Ichiyama *et al.*, 1988; Covert *et al.*, 1999; Falkinham *et al.*, 2001). Falkinham *et al.* (2001) did note, however, that both *M. avium* and *M. intracellulare* were seldom recovered from well water. In addition to these sources, Wendt *et al.* (1980) reported the isolation of NTM (mostly *M. intracellulare*) from aerosol samples taken near a river. It should be noted that although water is the focus of this document, *M. avium* levels can be hundreds or thousands of times higher in soils than in treated drinking water (LeChevallier, 1999).

The ubiquitous nature of Mac organisms results from their ability to survive and grow under varied conditions. For example, Mac organisms can proliferate in water at temperatures up to 51°C (Sniadack *et al.*, 1992). In one instance, it was found that temperatures between 52°C and 57°C encouraged proliferation of *M. avium* in hospital water supplies (du Moulin *et al.*, 1988). Mac organisms have also been shown to grow in natural waters over a wide pH range (Kirschner *et al*., 1999). As with most organisms, some conditions will favour their growth. For example, humic and fulvic acids stimulate the growth of *M. avium* (Kirschner *et al.*, 1999). As well, natural water with zinc concentrations greater than 0.75 mg/L (Kirschner *et al.*, 1992) and waters with a low pH and a high organic content (Iivanainen *et al.*, 1993) are more likely to contain Mac organisms. The survival of Mac organisms can also be enhanced by their ability to invade and survive in some species of amoeba (Plum and Clark-Curtiss, 1994; Bermudez *et al.*, 1997; Cirillo *et al.*, 1997), such as *Acanthamoeba polyphaga* or *A. castellanii*, as well as to grow as free-living saprophytes on products secreted by these organisms (Steinert *et al.*, 1998).

Similar to *Legionella*, Mac organisms survive and persist in biofilms. In one study of 50 biofilm samples from water treatment plants, domestic water supply systems, and aquaria, 90% were positive for mycobacteria species, with concentrations up to 5.6×10^6 CFU/cm^2 (Schulze-Röbbecke *et al.*, 1992). Although this study did not identify the percentage of Mac organisms within the mycobacteria species isolated, a separate study found that 131 of 267 biofilm mycobacteria isolates were *M. intracellulare* (average 600 CFU/cm^2), and 4 were *M. avium* (<0.5 CFU/cm^2). This confirms that Mac organisms are present in biofilm matrices. An additional

study into several types of commonly used plumbing materials concluded that the frequency of recovery of Mac organisms from biofilm was not dependent on the material type (Falkinham *et al.*, 2001).

6.2.3 Health effects

The clinical presentation of Mac infections can include a productive cough, fatigue, fever, weight loss, and night sweats. It is also a leading cause of mycobacterial lymphadenitis in children less than 12 years of age. Current research suggests a possible role for Mac organisms in the development of Crohn's disease, an inflammatory bowel disease similar to Johne's disease in sheep, cattle, and goats. Johne's disease is caused by *M. avium* subsp. *paratuberculosis*. Strains of *M. avium* subsp. *paratuberculosis* have been isolated from some Crohn's patients. Although the evidence is still inconclusive, due mainly to difficulties in reliably detecting the pathogen, improvements in detection methodologies are providing better evidence linking the pathogen to Crohn's disease (Reynolds, 2001; Hermon-Taylor and El-Zaatari, 2004). Diagnosis of Mac infections is difficult and time-consuming. Therefore, treatment is usually initiated before confirmation is made as to the cause of the infection. The treatment regimen for Mac infections may include high doses of antimicrobials. These drugs can have a variety of side effects, including nausea, vomiting, diarrhoea, rashes, abdominal pain, hearing loss, eye inflammation, and damage to blood vessels or the liver (Reynolds, 2001).

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. Unlike *Mycobacterium tuberculosis* (the infectious agent of tuberculosis), Mac organisms have low pathogenicity, so individuals can become colonized with the organisms without any adverse health effects. Individuals who are immunocompetent without underlying disease conditions have a very low risk of becoming symptomatic with a Mac infection. Recently, reports have shown an increasing recognition of Mac in individuals, especially women, with apparently no predisposing disorders of the lungs or immune system. Although recognition of this disease in immunocompetent individuals is increasing, the risks of becoming ill are still very low. Whereas the majority of healthy individuals who contract Mac infections have localized infection, disseminated Mac infections occur in a large proportion of AIDS patients (80% of those patient that are colonized), as well as in other immunosuppressed populations, such as those with severe combined immunodeficiency syndrome, transplant recipients, and patients treated with corticosteroids or cytotoxic drugs (von Reyn *et al.*, 1993a,b). The true prevalence of Mac infections is not known, as it is not a reportable illness in Canada or the United States. It has been suggested, based on studies in Houston and Atlanta, that the rate of illness is 1 in 100 000 persons per year (Reynolds, 2001).

6.2.4 Exposure

Exposure to Mac organisms may occur through the consumption of contaminated food, the inhalation of air with contaminated soil particles, or contact with or ingestion, aspiration, or aerosolization of potable water containing the organisms. Person-to-person contact is thought to be possible but has not yet been observed (Reynolds, 2001; Le Dantec *et al.*, 2002).

With respect to water supplies, infection with *M. avium* and *M. intracellulare* has been well documented (Wendt *et al.*, 1980; Grange, 1991; von Reyn *et al*., 1993a, 1994; Glover *et al.*,

1994; Montecalvo *et al*., 1994; Kahana *et al.*, 1997; Aronson *et al.*, 1999; Mangione *et al.*, 2001) with *M. avium* being the leading cause of NTM infections. The route of exposure, in most cases, is inhalation of contaminated aerosols, particularly through contaminated hot tubs. Some research has shown that one *M. avium* strain in particular (Mav-B sequevar) is responsible for the majority of cases. This may be the result of a higher virulence of this strain or an increased prevalence of this strain in the environment (Hazra *et al.*, 2000). The proportion of infections caused by *M. avium* and *M. intracellulare* has been shown to vary between populations. In one study, AIDS patients were more often infected with *M. avium* (98% of 45 patients) than with *M. intracelluare* when compared with non-AIDS patients, in whom 60% of the infections were shown to be caused by *M. avium* and the remaining 40% were the result of *M. intracellulare* (Guthertz *et al.*, 1989). The infectious dose appears to range from 10^4 to 10^7 organisms, but this number depends on numerous factors, including, but not limited to, the virulence of the organism and the immune status of the host.

6.2.5 Treatment technology

Water treatment technologies commonly used, including chemical disinfection and physical removal methods, have been tested for their ability to inactivate or remove mycobacteria from water supplies. Of these technologies, the most effective has been physical removal using sand filtration and coagulation–sedimentation techniques . For example, it was shown, using a surface water source, that mycobacterial numbers were reduced by almost 2 log, with the majority of the 2 log removal attributed to removal by filtration (Falkinham *et al.*, 2001). The disinfection employed contributed only slightly to the overall log removal. In comparison with conventional indicators, Mac organisms are more resistant to the commonly used disinfectants . For example, the CT values necessary for inactivation using free chlorine (pH 7, 23°C) are 2–3 orders of magnitude higher for *M. avium* than for *E. coli*. Therefore, in a typical drinking water system, the chlorine dose added will unlikely be effective in controlling the Mac organisms (AWWA Committee Report, 1999). Similar results have been found with other commonly used disinfectants in the drinking water industry (Yu-Sen *et al.*, 1998; R.H. Taylor *et al.*, 2000). Non-chemical treatment methods should be effective for Mac removal and/or inactivation. Even with good removal of organisms from the source water, the number of Mac organisms may increase in the distribution system (Falkinham *et al.*, 2001). Conditions identified to encourage growth in the distribution system include old pipes, long storage times, and high assimilable organic carbon levels (Falkinham *et al.*, 2001).

6.2.6 Assessment

Unlike gastrointestinal pathogens, where *E. coli* can be used to indicate their potential presence, no suitable indicators have been identified to signal increasing concentrations of Mac organisms in water systems. For example, studies have found no relationship between the numbers of NTM recovered from reservoir water and coliform counts, HPCs, and total and free chlorine levels (Glover *et al.*, 1994; Aronson *et al.*, 1999). There is some evidence that *M. avium* presence is associated with turbidity in raw waters (Falkinham *et al.*, 2001), but further exploration of this issue is needed.

Currently, the presence of mycobacteria in water is not regulated by any countries or international organizations, including Canada. The U.S. Environmental Protection Agency (EPA)

has identified *M. avium* and *M. intracellulare* as waterborne health-related microbes that need additional research on their health effects, their occurrence in water, and their susceptibility to treatment methods (Reynolds, 2001). These organisms have also been included in a list of candidate contaminants for possible regulation by the U.S. EPA (LeChevallier, 1999). At the present time, there is not sufficient information to warrant actions based on the presence of the organisms in the absence of disease.

6.3 *Aeromonas hydrophila*

6.3.1 Description

Aeromonas hydrophila are Gram-negative, non-spore-forming, rod-shaped, facultative anaerobic bacilli belonging to the family Aeromonadaceae. Although *A. hydrophila* is the focus of this section, other aeromonads, such as *A. caviae* and *A. sobria*, have also been isolated from human faeces and from water sources (Havelaar *et al.*, 1992; Janda and Abbott, 1998; Villari *et al.*, 2003). Morphologically, aeromonads are indistinguishable from members of the Enterobacteriaceae family, such as *E. coli.* They also share many biochemical characteristics, with the differentiation being that aeromonads are oxidase positive and Enterobacteriaceae are oxidase negative.

6.3.2 Sources

Previous work has firmly established that *Aeromonas* species, including *A. hydrophila*, are ubiquitous in the environment. These organisms have been found in lakes, rivers, marine waters, sewage effluents, and drinking waters, among other places (Allen *et al.*, 1983; Nakano *et al.*, 1990; Poffe and Op de Beeck, 1991; Payment *et al.*, 1993; Ashbolt *et al.*, 1995; Bernagozzi *et al.*, 1995; Chauret *et al.*, 2001; El-Taweel and Shaban, 2001). The concentration of *Aeromonas* species varies with the environment being investigated. In clean rivers, lakes, and storage reservoirs, concentrations of *Aeromonas* spp. have been found to typically be around 10^2 CFU/mL. Groundwaters generally contain less, with fewer than 1 CFU/mL. Additionally, drinking water immediately leaving the treatment plant has been found to contain between 0 and 10^2 CFU/mL, with potentially higher concentrations in drinking water distribution systems, attributed to growth in biofilms (Payment *et al.*, 1988; U.S. EPA, 2000; Chauret *et al.*, 2001). Depending on the study, *A. hydrophila* comprised 20–60% of the aeromonads isolated (Millership *et al.*, 1986; Notermans *et al.*, 1986; Kühn *et al.*, 1997). *Aeromonas* spp. have been found to grow between 5°C and 45°C (U.S. EPA, 2000). Water temperature is a significant factor for *Aeromonas* growth (Sautour *et al.*, 2003). Coinciding with the optimal growth range of *Aeromonas*, seasonal variation has been reported for public water systems, with *Aeromonas* more often recovered during the warmer months (Gavriel *et al.*, 1998). The same trend has been observed with stool samples (Burke *et al.*, 1984; Moyer, 1987).

6.3.3 Health effects

In recent years, *A. hydrophila* has gained public health recognition as an opportunistic pathogen. It has been implicated as a potential agent of gastroenteritis, septicaemia, cellulitis, colitis, and meningitis, and is frequently isolated from wound infections sustained in aquatic environments (Krovacek *et al.*, 1992; Gavriel *et al.*, 1998). It has also recently been implicated

in respiratory infections (Janda and Abbott, 1998). Treatment for infection with *Aeromonas* is generally not necessary for gastrointestinal illness. However, for other presentations of infection, antibiotic therapy is usually implemented. Individuals at the greatest risk of infection are children, the elderly, and the immunocompromised (Merino *et al.*, 1995).

6.3.4 Exposure

The common routes of infection suggested for *Aeromonas* are the ingestion of contaminated water or food or contact of the organism with a break in the skin (Schubert, 1991). No person-to-person transmission has been reported. It should be noted that although *A. hydrophila* is water based, waterborne outbreaks have not been reported, and waterborne transmission has not been well established. For example, various studies have been unsuccessful in linking patient isolates of *A. hydrophila* with isolates recovered from the water supply (Havelaar *et al.*, 1992; Moyer *et al.*, 1992; Hänninen and Siitonen, 1995; WHO, 2002; Borchardt *et al.*, 2003). As mentioned above, the growth of *A. hydrophila* is temperature dependent. Therefore, the risk of infection is highest in the summer months, when these microorganisms are multiplying more rapidly (Holmes and Nicolls, 1995).

The dose necessary to cause infections in humans has not been established. In the limited number of studies done, the dose was quite high, and only a limited number of participants were infected (Morgan *et al.*, 1985; Janda and Abbott, 1998; WHO, 2002). The virulence of the strain is one factor that can influence the infectious dose needed. For *A. hydrophila*, the virulence of the organism is, at least in part, thought to result from the production of specific enterotoxins (Schubert, 1991). The primary toxins are haemolysins(Janda, 1991). In addition, some aeromonads produce a range of cell surface and secreted proteases that may enhance their virulence (Janda, 1991; Gosling, 1996). It has been demonstrated that a significant proportion of the *A. hydrophila* isolated from water (chlorinated and unchlorinated supplies) contained genes responsible for enterotoxigenic or cytotoxic activity (Ormen and Ostensvik, 2001). Expression of virulence factors has been shown to be influenced by environmental temperature. *A. hydrophila* isolated from the environment produced significantly less enterotoxins when grown at 37°C compared with 28°C, whereas the clinical isolates tested produced more enterotoxins at 37°C than at 28°C (Mateos *et al.*, 1993). The temperature of the human body is approximately 37°C; therefore, strains that produce virulence factors at this temperature are likely to be more important as pathogens.

6.3.5 Treatment technology

As mentioned previously, aeromonads are ubiquitous in many water environments. Consequently, they will be present in most source waters used for drinking water production. The methods currently used for treatment and disinfection are effective in minimizing the level of aeromonads in the finished drinking water. For example, it has been shown that *A. hydrophila* is generally more susceptible to chlorine and monochloramine than coliforms (Knøchel, 1991; Sisti *et al.*, 1998). Chlorine dioxide has also been shown to be an effective disinfectant (Medema *et al.*, 1991). In the distribution system, there is the potential for *Aeromonas* to regrow. Maintaining chlorine at or above 0.2 mg/L should provide adequate control of *A. hydrophila* in the water (Holmes and Nicolls, 1995). However, it is difficult to control its growth in biofilms (Gavriel *et al.*, 1998; Chauret *et al.*, 2001; WHO, 2002). The most effective approach for controlling

Aeromonas growth is to limit the *Aeromonas* spp. entering the distribution system through effective treatment and maintenance, to maintain temperatures below 14°C, to provide free chlorine residuals above 0.1–0.2 mg/L, and to limit the levels of organic carbon compounds (WHO, 2002). If there are significant increases in *Aeromonas* concentrations in a drinking water supply, this indicates a general deterioration of bacteriological quality.

6.3.6 Assessment

Some studies have been undertaken to determine if the indicators currently used in the drinking water industry, including *E. coli,* total coliforms, and HPC, can be used as surrogates for the presence of *Aeromonas*. Several studies, including a large study in England, showed no relationship between *Aeromonas* incidence and coliforms, *E. coli*, or HPCs (Holmes *et al.*, 1996; Gavriel *et al.*, 1998; Fernandez *et al.*, 2000). Although all the studies had similar findings, not all could draw definite conclusions, because of limited sample sizes, minimal occurrences of coliforms, and/or the absence of *E. coli* in the water.

When looking at the overall public health significance of *A. hydrophila* in drinking water, further epidemiological studies are needed to ascertain the relationship between *Aeromonas* illness and the presence of these organisms in drinking water (WHO, 2002). The European Community has established a drinking water standard for *A. hydrophila* of no more than 20 CFU/100 mL in water leaving the treatment plant and 200 CFU/100 mL in distribution system water (van der Kooj, 1993; Moyer, 1999). These values are based on an assessment of achievability, motivated by a precautionary approach, and not on the public health significance of their occurrence in drinking-water (WHO, 2002). Based on what is currently known, treated drinking water probably represents a very low risk. However, it is advisable to minimize the concentration of *A. hydrophila*, as well as other aeromonads, in drinking water supplies until their public health significance has been fully investigated.

6.4 *Helicobacter pylori*

6.4.1 Description

Helicobacter pylori, formerly known as *Campylobacter pylori*, was first recognized as a human pathogen in 1983 (Postius, 2001) and was subsequently identified as a human carcinogen by the International Agency for Research on Cancer (IARC, 1994).

Two morphologically distinct forms of *H. pylori*, a spiral shape and a coccoid form, have been identified (van Duynhoven and de Jonge, 2001). The spiral shape is cultured routinely from clinical samples. To date, the coccoid form has been found to be non-culturable. Transformation from the spiral-shaped bacterium grown in culture to the non-culturable coccoid form is thought to result from variations in the environment, such as oxygen stress, temperature changes, the presence of antibiotics, and other stress-inducing conditions (Engstrand, 2001). At present, it is still unclear whether the coccoid form is viable but non-culturable (VBNC), similar to VBNC states found with *Salmonella, Campylobacter*, and *Vibrio* spp. (Byrd *et al.*, 1991), and therefore able to infect humans, or if it is simply non-viable (van Duynhoven and de Jonge, 2001). Attempts to revert the coccoid form to the spiral form using nutrient supplementation (Sörberg *et*

al., 1996) have been unsuccessful. Reversion has been successful in only one report, using mice (Wang *et al.*, 1995). Attempts to use the same procedure in pigs resulted in contradictory results (Eaton *et al.*, 1995).

6.4.2 Sources

H. pylori has not yet been isolated from environmental sources, including water. However, other methods have been able to detect *H. pylori*. For example, it has been found microscopically, using a fluorescent antibody, in surface waters and shallow groundwaters (Hegarty *et al.*, 1999). Molecular methods, such as polymerase chain reaction, have also been used to detect the presence of *H. pylori* DNA in water (Enroth and Engstrand, 1995). Under laboratory conditions, *H. pylori* has been shown to survive for days, up to weeks, in sterile river water, saline solution, and distilled water at a wide variety of pH levels and in temperatures ranging from 4°C to 15°C (West *et al.*, 1992; Shahamat *et al.*, 1993). These results indicate that water may be a potential source of transmission for *H. pylori*. Currently, the only substantial reservoir of *H. pylori* has been found to be the human stomach (Dunn *et al.*, 1997). Domestic cats have been found to harbour the organisms, but studies conducted have been unsuccessful at linking pet ownership with *H. pylori* seropositivity (Webb *et al.*, 1996b; Bode *et al.*, 1998). The bacterium has also been isolated from primates, but, due to rare contact, primates are unlikely to be important reservoirs.

6.4.3 Health effects

Human infection with *H. pylori* has been linked to gastritis, duodenal ulcers, and an increased risk of gastric adenocarcinoma (Jekel, 1993; Hunter, 1997; Engstrand, 2001). These health effects reflect the ability of *H. pylori* to colonize the human stomach and establish a chronic infection associated with an inflammatory response. In addition to gastrointestinal disorders, some studies have shown an association between *H. pylori* infection and anaemia (i.e., decreased serum ferritin levels) (Milman *et al.*, 1998; Peach *et al.*, 1998; CDC, 1999), although there are also studies to the contrary (Haruma *et al.*, 1995; Perez-Perez, 1997). The prevalence of *H. pylori* infection in the world is assumed to be 50%, with higher prevalence in developing countries (90%). Both immunocompromised and immunocompetent individuals can become infected with *H. pylori*, and both groups can develop associated illnesses (Battan *et al.*, 1990; Edwards *et al.*, 1991; Vaira *et al.*, 1995). In children, *H. pylori* can cause antral gastritis and duodenal ulcer disease, although most infections in children are asymptomatic (Rowland and Drumm, 1998). It has been well established that infections with *H. pylori* are generally acquired during childhood, with a lower frequency of infection in adults (Feldman *et al.*, 1998; Allaker *et al.*, 2002). The infectious dose necessary for colonization of humans is not known. It is assumed to be low because of the high percentage of infected individuals; in human testing, however, it was shown that the minimum required dose was 3×10^5 CFU when given in combination with an acid suppressant (Morris and Nicholson, 1987). Incidences of accidental infection, such as ingestion resulting from laboratory work (Matysiak-Budnik *et al.*, 1995) and use of improperly maintained endoscopes, suggest that the dose could be much lower. Of those individuals who become infected, only a subpopulation (6–20%) will develop gastroduodenal disease (Go, 1997; Parsonnet, 1998; Patchett, 1998; Engstrand, 2001), with approximately 1% of all infections progressing ultimately to gastric cancer. Gastric cancer is the second most common cause of

cancer, and 40–50% of these cases are related to *H. pylori* (Parsonnet, 1998; Parkin *et al.*, 1999). Infection with *H. pylori* is treatable using a combination of bismuth and antibiotics or a combination of a proton-pump inhibitor and antibiotics (Scott *et al.*, 1998). This translates into a significant number of cases of disease due to *H. pylori* that are preventable.

6.4.4 Exposure

How the organism is transmitted is still not fully understood; however, the fact that it has been recovered from saliva, dental plaques, the stomach, and faecal samples strongly indicates oral–oral or faecal–oral transmission (Ferguson *et al.*, 1993; Jekel, 1993; Nguyen *et al.*, 1993; Goodman *et al.*, 1996; Dunn *et al.*, 1997; Feldman *et al.*, 1998). Associations between the seroprevalence of hepatitis A, which is known to be transmitted by the faecal–oral route, and *H. pylori* shows the potential for faecal–oral transmission (Hazell *et al.*, 1994; Rudi *et al.*, 1997). As well, consumption of uncooked vegetables irrigated with untreated sewage has been suggested as a risk factor for *H. pylori* (Hopkins *et al.*, 1993). On the other hand, there have been studies using hepatitis A showing no association with *H. pylori* infection and consequently no link to faecal–oral transmission (Webb *et al.*, 1996a; Furuta *et al.*, 1997). Additional studies examining *H. pylori* seropositivity in sewage workers (Friis *et al.*, 1996) and in travellers recently returned from areas of the world with a high prevalence of *H. pylori* (Lindkvist *et al.*, 1995) also found no connection to faecal–oral transmission. It has been suggested that the link to faecal samples is better when looking at transmission routes for children than for adults (Thomas *et al.*, 1992; Mapstone *et al.*, 1993). Studies in some developing countries found that transmission of *H. pylori* was due to environmental conditions, such as poor hygiene or the consumption of contaminated water (Klein *et al.*, 1991; Hopkins *et al.*, 1993) . Evidence that waterborne transmission may be important in areas of the world with less than adequate water quality comes from studies conducted worldwide, including in Inuit communities in Canada (Klein *et al.*, 1991; Goodman *et al.*, 1996; Hulten *et al.*, 1996; McKeown *et al.*, 1999). Epidemiological studies conducted in developed countries have found no association between environment and infection (Hultén *et al.*, 1998). In the latter studies, clustering of infections within families was prevalent, supporting the oral–oral route (Brenner *et al.*, 1999; Allaker *et al.*, 2002), with infected mothers playing a key role in transmission (Rothenbacher *et al.*, 1999). In contrast, it was found that oral–oral transmission between spouses was unlikely to be an important mode of transmission (Luman *et al.*, 2002).

Overall, the predominant transmission route for *H. pylori* seems to be situation dependent, with person-to-person transmission playing a key role in many circumstances. Water and food appear to be of lesser direct importance, but they can still play a significant role in situations with improper sanitation and lax hygiene. Further investigation into the role of water is needed.

6.4.5 Treatment technology

Some work has been carried out on the relative sensitivities of *H. pylori* and *E. coli* to currently used drinking water treatment methods. Further information on the role of *E. coli* in drinking water can be found in *The Guideline for Canadian Drinking Water Quality*: *Guideline Technical Document — E. coli* (Health Canada, 2006a). Similar to other bacteria, a proportion of the *H. pylori* present in the source water will be removed using physical methods, such as

coagulation, sedimentation, and filtration. This organism is also susceptible to disinfectants commonly used in drinking water treatment. In laboratory disinfectant testing, *E.coli* proved to be more sensitive to chlorine and ozone than *H. pylori* (Johnson *et al.*, 1997; Baker *et al.*, 2002); however, there was little difference between the effectiveness when monochloramine was used (Baker *et al.*, 2002). Although *E. coli* is easier to inactivate than *H. pylori* with some disinfectants, the CT provided by a typical water treatment plant is sufficient to inactivate *H. pylori* in the finished water (Peeters *et al.*, 1989; Johnson *et al*., 1997). However, if *H. pylori* does enter the distribution system, potentially through a break in treatment or infiltration into the system, the disinfectant residuals found in the distribution system are probably not sufficient for inactivation (Baker *et al.*, 2002).

6.4.6 Assessment

Currently, there are no regulations governing the presence of *H. pylori* in drinking water, either nationally or internationally. The U.S. EPA has included it on their list of candidate contaminants for possible regulation in drinking water. Further studies are needed to confirm that *H. pylori* are present in drinking water in a viable state and that they can be transmitted by this medium.

7.0 Conclusions and recommendations

The organisms identified as current bacterial waterborne pathogens of concern within this document are those that have a well-established history of being responsible for bacterial waterborne outbreaks, presenting as gastrointestinal illnesses. Drinking water is not tested for these organisms directly; instead, *E. coli* is used as an indicator of their presence. The guideline value of no *E. coli* in 100 mL of drinking water is set to protect human health from these organisms.

The emerging pathogenic bacteria of concern outlined here also have the potential to be spread through drinking water, but they do not correlate with the presence of *E. coli* or with other commonly used drinking water quality indicators, such as total coliforms and HPC bacteria. In most cases, there are no satisfactory microbiological indicators of their presence. Although surrogate organisms are not known, it is not practical to routinely monitor the drinking water for the pathogens themselves. The use of a multiple-barrier approach, including source water protection (where possible), adequate treatment, and a well-maintained distribution system, can reduce these pathogens to non-detectable levels or to levels that have never been associated with human illness.

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Appendix A: List of acronyms

AIDS	acquired immunodeficiency syndrome
CFU	colony-forming unit
CT	product of disinfectant concentration and contact time
DNA	deoxyribonucleic acid
HPC	heterotrophic plate count
HUS	haemolytic uraemic syndrome
Mac	*Mycobacterium avium* complex
MAC	maximum acceptable concentration
NTM	non-tuberculous mycobacteria
U.S. EPA	United States Environmental Protection Agency
UV	ultraviolet
VBNC	viable but non-culturable