Volume 3 Datasheets – Micro-organisms

Part 1.1: Bacteria

2019

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# Acinetobacter

### Maximum Acceptable Value

No MAV has been set for Acinetobacter in New Zealand drinking-water, or in the WHO Guidelines for Drinking-water Quality.

### Sources to drinking-water

Acinetobacters are ubiquitous, free-living saprophytes. They are widely distributed in nature, and have been isolated from soil, seawater, freshwater, estuaries, sewage, contaminated food and mucosal and outer surfaces of animals and humans. They can survive on dry surfaces much longer than many other bacteria.

A bacteriological survey was conducted of untreated, individual groundwater supplies in Preston County, West Virginia. Nearly 60 percent of the water supplies contained total coliforms in excess of the USEPA maximum contaminant level of 1 CFU/100 mL. Approximately one-third of the water systems contained fecal coliforms and/or fecal streptococci. *Acinetobacter* spp. were detected in 38 percent of the groundwater supplies at an arithmetic mean density of 8 CFU/100 mL and were present in 16 percent of the water supplies in the absence of total coliforms, posing some concern about the usefulness of total coliforms as indicators of the presence of this opportunistic pathogen (Bifulco et al 1989).

WHO (2017) reports that they have been isolated from 97 percent of natural surface water samples in numbers of up to 100 per mL. The organisms have been found to represent 1.0–5.5 percent of the HPC flora in drinking-water samples and have been isolated from 5–92 percent of distribution water samples.

### Health considerations

While *Acinetobacter* spp. are often detected in treated drinking-water supplies, an association between the presence of *Acinetobacter* spp. in drinking-water and clinical disease has not been confirmed. There is no evidence of gastrointestinal infection through ingestion of *Acinetobacter* spp. in drinking-water among the general population. However, transmission of non-gastrointestinal infections by drinking-water may be possible in susceptible individuals, particularly in settings such as health care facilities and hospitals. WHO (2017) state that WSPs should be developed for buildings, including hospitals and other health care facilities. These plans need to take account of particular sensitivities of occupants.

Acinetobacters are increasingly being associated with nosocomial infections. These include septicaemia, urinary tract infections, eye infections, meningitis, skin and wound infections, brain abscesses, lung abscesses, pneumonia and endocarditis. Acinetobacter baumanniiis often referred to as ‘[Iraqibacter](http://www.cdc.gov/mmwr/preview/mmwrhtml/mm5345a1.htm)‘ because infections caused by the bacterium were particularly prominent in military patients in Iraq and Kuwait.

### New Zealand significance

*Acinetobacter* are referred to in MoH (2007).

### Method of identification and detection

*Acinetobacter* is a bacterial genus whose members are typically Gram-negative coccobacilli, although variable Gram-staining may be evident in pure culture due to difficulties in de-staining of crystal violet. They are strictly aerobic, short and plump rod-shaped bacteria, often capsulated and non-motile.

There are 34 species of *Acinetobacter*, most of which are actually innately resistant to antibiotics.

Established selective and differential media, such as Sellers agar, Herellea agar and MacConkey agar, have also been used for the isolation of *Acinetobacter* (AWWA 1999). In the case of potable water samples, Eosin-Methylene Blue Agar can differentiate *Acinetobacter* from other heterotrophic organisms (AWWA 1999 via Percival 2014).

### Treatment of drinking-water

Acinetobacters are inactivated by chlorine, and by UV disinfection at traditional dosage. The encapsulated form may require higher C.t values. However, *E. coli* (or, alternatively, thermotolerant coliforms) cannot be used as an index for the presence/absence of *Acinetobacter* spp.

### Derivation of Maximum Acceptable Value

No MAV has been set for *Acetinobacter* in drinking-water.

### Bibliography

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# Actinomycetes

### Maximum Acceptable Value

No MAV has been set for actinomycetes in New Zealand drinking-water, or in the WHO Guidelines for Drinking-water Quality.

Organisms referred to in this datasheet include: *Actinomyces*, *Mycobacterium*, *Corynebacterium*, *Streptomyces*, *Nocardia*, *Saccropolyspora*, and *Tsukamurella*.

Note: some pesticides derived from actinomycetes have datasheets. These are: abamectin, avermectin, dihydrostreptomycin sulphate, spinosad, and streptomycin.

### Sources to drinking-water

The actinomycetes (a general descriptive term) were thought to be fungi for many years because they have filamentous forms which appear to branch. Some species form aerial mycelia in culture. Also, the clinical manifestations of infection are similar to those of a systemic fungal infection.

Actinomycetes are a collection of nine different groups of bacteria, including many familiar and important bacteria such as *Mycobacterium* (the causal agents of tuberculosis and leprosy, see *Mycobacterium* datasheet), *Corynebacterium* (a common commensal on human skin), and *Streptomyces* (the source of many antibiotics as well as the pleasant odour of freshly turned soil). *Streptomyces* is the largest [genus](http://en.wikipedia.org/wiki/Genus) (over 500 species) of [Actinobacteria](http://en.wikipedia.org/wiki/Actinobacteria) and the type genus of the family [Streptomycetaceae](http://en.wikipedia.org/wiki/Streptomycetaceae).

*Streptomyces lydicus* strain WYEC 108 is approved in the US as a biological fungicide for the control of root rot and damping-off fungi (see PMEP). It is also approved for use in New Zealand, appearing on the NZFSA’s complete database of Agricultural Compounds and Veterinary Medicines (ACVM) as at 2009 (see [https://eatsafe.nzfsa.govt.nz/web/public/acvm-register and select entire register](http://www.nzfsa.govt.nz/acvm/registers-lists/acvm-register/index.htm)).

The actinomycetes are Gram-positive, rod shaped or filamentous bacteria. Those that are rod shaped may form long, branching, chains of cells. Many actinomycetes form true filaments that branch and form colonies that look like fungi, although the diameter of the filaments is much smaller than that of the fungi. Filamentous forms produce spores that may be single, in short chains, or in very long chains that may form beautiful spirals.

There are both anaerobic and aerobic actinomycetes. The truly filamentous forms are predominantly aerobic.

*Actinomyces* is an important anaerobic genus. Members of the genus *Actinomyces* are most often found in the mouth and gastrointestinal tract of humans and other animals. *Actinomyces* may cause a range of diseases in humans. *Actinomyces* is also found in the soil.

*Nocardia* and *Streptomyces* are aerobic; both are found in soil and water, and have the ability to use a wide range of organic material as a source of energy. The streptomycetes are particularly important in degradation of dead plant materials in soil, and are often found in composts. A few species of *Nocardia* cause disease in humans. Streptomycetes do not produce disease in humans or animals and are best known for producing many clinically useful antibiotics, including streptomycin, tetracycline, and cephalosporin.

Various members of the genus *Streptomyces* often comprise the most frequently isolated actinomycetes from drinking-water.

The 2004 WHO Guidelines (section 10.1.1) state that actinomycetes and fungi can be abundant in surface water sources. They also can grow as biofilm on unsuitable materials in the water supply distribution systems, such as rubber. They can give rise to geosmin, 2-methyl isoborneol (MIB) and other substances, resulting in objectionable tastes and odours in the drinking-water, often described as earthy or musty, like soil, potatoes or fungi. Datasheets appear for many of these taste and odour chemicals.

Actinomycetes are a complex group of bacteria present in a wide variety of environments, either as dormant spores or actively growing. Some actinomycetes (usually the vegetative form) produce two potent terpenoids (geosmin and 2‑methylisoborneol) and pyrazines, common causes of drinking-water off flavours, and have frequently been implicated in taste and odour episodes. However, isolation from a water source is not evidence that actinomycetes caused a taste and odour event. Dormant spores of actinomycetes may be isolated from aquatic environments in high concentrations, despite production in the terrestrial environment. Similarly, odorous compounds produced by actinomycetes may be produced terrestrially and washed into aquatic environments, with or without the actinomycetes that produced them. Actinomycetes may exist as actively growing mycelium in small, specialised habitats within an aquatic system, but their odorous compounds may influence a wider area. Zaitlin and Watson (2006) elucidate the types and activities of actinomycetes that may be found in, or interact with, drinking water supplies.

### Health considerations

The WHO Guidelines include a datasheet for the actinomycete *Tsukamurella* (belongs to the family Nocardiaceae). WHO calls *Tsukamurella* a ‘potentially emerging pathogen’. *Tsukamurella* spp. exist primarily as environmental saprophytes in soil, water and foam (thick stable scum on aeration vessels and sedimentation tanks) of activated sludge. *Tsukamurella* are represented in HPC populations in drinking-water. *Tsukamurella* spp. cause disease mainly in immunocompromised individuals. Infections with these micro-organisms have been associated with chronic lung diseases, immune suppression (leukaemia, tumours, HIV/AIDS infection) and post-operative wound infections. *Tsukamurella* were reported in four cases of catheter-related bacteraemia and in individual cases including chronic lung infection, necrotising tenosynovitis with subcutaneous abscesses, cutaneous and bone infections, meningitis and peritonitis. *Tsukamurella* organisms have been detected in drinking-water supplies, but the significance is unclear. There is no evidence of a link between organisms in water and illness. As *Tsukamurella* is an environmental organism, *E. coli* (or, alternatively, thermotolerant coliforms) is not a suitable index for this organism. There is now a datasheet for *Tsukamurella* in this volume.

### Treatment of drinking-water

The main concern related to actinomycetes relates to taste and odour problems. Taste and odour and its control is discussed in Chapter 18: Aesthetic Considerations.

### Method of identification and detection

See APHA (2005), EA (UK) (2004) and Zaitlin and Watson (2006).

### Derivation of Maximum Acceptable Value

No MAV has been set for actinomycetes in drinking-water.

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# *Aeromonas*

### Maximum Acceptable Value

No MAV has been set for *Aeromonas* in New Zealand drinking-water. Microbial agents (including *Aeromonas*) are included in the [plan of work of the rolling revision](http://www.who.int/entity/water_sanitation_health/gdwqrevision/en/index.html) of the WHO Guidelines for Drinking-water Quality.

The absence of *E. coli*, faecal coliforms and coliforms does not indicate the absence of *Aeromonas*.

Water must be tested directly for *Aeromonas* if there is reason to suspect it could be present.

In response to suggestions that *Aeromonas* be regulated, DWI (2002) states there are a number of documented instances of the isolation of *Aeromonas spp*. from water but no evidence of outbreaks of gastroenteritis. High infective dose in conjunction with the possibility that ‘environmental’ strains isolated could be non-toxigenic may be an explanation. Given this fact they have been given the status of medium priority. Supply of water contaminated with aeromonads to the food industry or to hospitals may be undesirable. It would seem advisable to determine whether aeromonads isolated from distribution systems are toxigenic. Where routine monitoring detects the growth of large numbers of aeromonads in the distribution system, isolates could be checked for enterotoxin production in tissue culture. Alternatively, an assay for a simple virulence marker could be developed.

### Sources to drinking-water

Aeromonads are distributed widely in freshwater and are part of the natural aquatic and soil ecosystem; concentrations increase with increased nutrient concentrations in water (Rippey and Cabelli 1980; van der Kooig and Hijnen 1988) with a strong association between *Aeromonas* concentration and pollution (Wada 1984). They occur in water, soil, and foods, particularly those coming into contact with water during processing, and refrigerated foods, such as seafood and dairy products. They may be found in source waters and may colonise distribution systems. They will grow in the presence of low chlorine levels, especially when the water temperature is higher during summer. They tend to be associated with surface waters.

*Aeromonas* spp. have been detected in many treated drinking-water supplies, mainly as a result of growth in distribution systems. The factors that affect the occurrence of *Aeromonas* spp. in water distribution systems are not fully understood, but organic content, temperature, the residence time of water in the distribution network and the presence of residual chlorine have been shown to influence population sizes. The presence of *Aeromonas* in a water supply generally indicates a dirty system.

In a 16-month study of the presence of *A. hydrophila* in Indiana drinking water, 7.7 percent of the biofilm samples were positive for this organism, indicating its potential for regrowth and ability to contaminate distribution systems (in DWI 2008).

*Aeromonas* species are not normally found in human faeces in high numbers; however, a small percentage of the population can carry the bacteria in their intestinal tracts without showing symptoms of disease. The prevalence of *Aeromonas* in human faecal samples worldwide has been roughly estimated to be 0–4 percent for asymptomatic persons and as high as 11 percent for persons with diarrhoeal illness (reported in Health Canada 2013).

A rapid decline in viability of *A. hydrophila* has been observed at low temperature (5°C), whereas at 20°C (the temperature resembling water in distribution systems during the summer), *A. hydrophila* displayed a greater resistance to chlorine (from 0.20–0.25 mg/L concentration). They can grow under both aerobic and anaerobic conditions.

### Health considerations

*Aeromonas* spp. are Gram-negative, non-spore-forming, rod-shaped, facultative anaerobic bacilli belonging to the family Vibrionaceae. They bear many similarities to the Enterobacteriaceae. Many have been isolated from faeces. They are divided into two groups: the psychrophilic and mesophilic aeromonads. The mesophilic aeromonads are considered of potential human health significance and include *A. hydrophila*, *A. caviae*, *A. veronii* subsp. *sobria*, *A. jandaei*, *A. veronii* subsp. *veronii* and *A. schubertii*.

Mesophilic aeromonads have long been known to be pathogenic for cold-blooded animals such as fish and amphibians. The significance of *Aeromonas* as a cause of gastroenteritis remains controversial. In humans, three types of infections are described: systemic infections, usually in people who are seriously immunocompromised; wound infections (mainly surface contact); and diarrhoea. They have given rise to serious cases of septicaemia, often in people with underlying disease; and they have been linked with gastroenteritis in children, although no causative role has been established, and their significance as an enteropathogenic organism is not clear. Despite the demonstration of strong toxin production by *Aeromonas* strains *in vitro*, it has not been possible to induce diarrhoea in test animals or human volunteers. Despite frequent isolation of *Aeromonas* spp. from drinking-water, the body of evidence does not provide significant support for waterborne transmission. Aeromonads typically found in drinking-water do not belong to the same deoxyribonucleic acid (DNA) homology groups as those associated with cases of gastroenteritis. The presence of *Aeromonas* spp. in drinking-water supplies is generally considered a nuisance.

More recently (see DWI 2008), it has been found that *Aeromonas hydrophila* is an emerging opportunistic human pathogen that causes both gastrointestinal and non-intestinal diseases in children and adults. These bacteria are isolated from freshwater, salt water, and a variety of foods and produce an impressive array of virulence factors. The organism is becoming increasingly resistant to chlorination in water and to multiple antibiotics. As a result, the USEPA placed this organism on the “Contaminant Candidate List”, and monitoring of US water supplies for the presence of *Aeromonas* species began in 2002.

### New Zealand significance

*Aeromonas* spp. have been isolated from several drinking-waters in New Zealand but the relationship between the isolates and clinical disease is not clear as there have been no documented local cases of waterborne *Aeromonas* infection. *Aeromonas* was isolated from 1.6 percent of faecal specimens in a New Zealand study (Wright 1996), which is comparable with overseas literature. There is little information about the distribution of *Aeromonas* in New Zealand waters, although it is likely to be widespread in distribution systems with no or low disinfectant residual.

### Treatment of drinking-water

Free available chlorine residuals of 0.2 to 0.5 mg/L are generally sufficient to control *Aeromonas* in distribution systems although the tolerance to chlorine inactivation is varied. However, the organisms have been detected in the distribution systems of chlorinated drinking water supplies worldwide.

### Method of identification and detection

There is no New Zealand standard method for enumerating aeromonads in water, although several methods have been developed (Holmes and Sartory 1993). A membrane filtration method is currently being evaluated as a joint SA/SNZ standard method using MIX agar. See also APHA (2005), Method 9260 L. Since that was written CRC (2009) stated “Aeromonads were enumerated by direct plating and membrane filtration according to the Australian/New Zealand Standard™ (AS/NZS 4276.18:2001) Method 18: *Aeromonas* by membrane filtration including selected speciation with slight modifications. Appropriate biofilm and water sample volumes were prepared and membrane-filtered on to 47 mm (0.45 μm) nitrocellulose filters (Millipore Australia Pty Ltd, Sydney, Australia) which were placed on mAeromonas Agar Base (CM833, Oxoid Australia Pty Ltd, Adelaide, Australia) supplemented with 5 mg/L ampicillin. Presumptive aeromonads were confirmed to genus level.

### Derivation of Maximum Acceptable Value

No MAV has been set for *Aeromonas* in drinking-water because of difficulties in determining the pathogenicity of an isolate and its relevance to human health.

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# *Bacillus thuringiensis israelensis*

### Maximum Acceptable Value

No MAV has been set for *Bacillus thuringiensis israelensis* in New Zealand drinking-water. WHO (2017) states that it is not considered appropriate to set guideline values for pesticides used for vector control in drinking-water.

Note that *Bacillus thuringiensis sp* are used as pesticides, but have been included in the bacteria section of the datasheets. Also known as BTI or B.t. *Bacillus thuringiensis var kurstaki* has a CAS No. 68038-71-1.

Some *Bacillus subtilis* strains have also been approved for use in the US (see PMEP) as a biopesticide or a biocontrol agent, and *Bacillus subtilis* strain QST 713 appears on the NZFSA’s complete database of Agricultural Compounds and Veterinary Medicines (ACVM) as at 2009 (see [https://eatsafe.nzfsa.govt.nz/web/public/acvm-register and select entire register](http://www.nzfsa.govt.nz/acvm/registers-lists/acvm-register/index.htm)).

### Sources to drinking-water

B.t can be used in or near drinking-water sources, and even in drinking-water. It can be effective for up to 48 hours in water. Afterwards, it gradually settles out or adheres to suspended organic matter. Rapid sedimentation in all but the fastest flowing streams is regarded as an important limitation on the efficacy of such applications. However, special BTI formulations have been developed to prolong the residence time of BTI at the surface or in the water column, where target insects feed. *Bacillus thuringiensis var aizawai* and *Bacillus thuringiensis var kurstaki* appear on ERMA’s Full List of ACVM approved veterinary medicines and pesticides, as at 2009.

*Bacillus thuringiensis* is a naturally occurring facultative anaerobic, Gram-positive bacterium that produces endotoxins that are selectively toxic to many moth and butterfly larvae (caterpillars). The insects stop feeding and die within 2–3 days of ingestion. Subspecies differ in their reaction with different insects, eg, *Bacillus thuringiensis var israelensis* is particularly useful for dealing with mosquitoes, black flies and midges.

Sunlight is the primary cause of inactivation of B.t spores in the environment. Susceptibility of B.t to solar radiation is enhanced under humid conditions. B.t is moderately persistent in soil.

B.t spores are released into the soil from decomposing dead insects after they have been killed by it. Its half-life in suitable conditions is about four months. Microbial pesticides such as B.t are classified as immobile because they do not move, or leach to, groundwater (EXTOXNET 1996).

No studies on the route and rate of degradation in soil, mobility in soil and degradation in water and water sediment of *Bacillus thuringiensis* subsp. *kurstaki strains* PB54, ABTS-351, SA-11, SA-12 and EG-2348 crystalline proteins are available (EFSA 2002).

### Health considerations

BTI is a biopesticide used for several purposes including application to drinking-water containers in order to control the breeding of vectors that may cause a variety of diseases. The WHO Guidelines for Drinking-water Quality Final Task Force meeting (Geneva 2003) recommended that a background document be prepared on BTI. This was produced in 2009.

Eighteen human volunteers ingested B.t daily for five days, and five of them inhaled as well, without detection of any adverse effects.

A US Forest Service review of the literature indicates that mice, hogs, rats, cattle, dogs, guinea pigs, and rabbits exposed to B.t by routes similar to those that humans would experience in the environment showed no significant effects (in EXTOXNET 1992).

See Green Party of Aotearoa (1994) for further discussion on health effects, most of which discuss direct contact or inhalation.

No complaints were made by eight men after they were exposed for seven months to fermentation broth, moist bacterial cakes, waste materials, and final powder created during the commercial production of B.t. Dietary administration of B.t for 13 weeks to rats at dosages of 8,400 mg/kg/day did not produce toxic effects (EXTOXNET 1996).

### New Zealand significance

BTI has been used in New Zealand to control midges in oxidation ponds.

### Treatment of drinking-water

BTI is recommended under WHOPES for use in vector control, including against container-breeding mosquitoes, and can be used in drinking-water that will receive little or no further treatment for control of *Aedes aegypti*. It is essential that BTI for larvicidal use be prepared under carefully controlled conditions and properly assayed before use for evidence of potency, for excessive levels of expressed BTI constituents or metabolites that are toxic and for contamination by other undesirable microbes. BTI itself is not considered to pose a hazard to humans through drinking-water. Therefore, it is not considered necessary or appropriate to establish a health-based value for its use for controlling vector larvae in drinking-water. However, it is vital that authorities can be assured that BTI has been prepared to the highest quality and hygienic standards under appropriate conditions that will meet the WHOPES specifications. (WHO 2017).

### Method of identification and detection

B.t spore counts do not accurately reflect the insecticidal activity of a B.t strain or B.t product. The potency (international toxic units [ITU]/mg) of each B.t product is bioassayed using an international standard that uses a specific test insect.

### Derivation of Maximum Acceptable Value

No MAV. BTI itself is not considered to pose a hazard to humans through drinking-water. Therefore, it is not considered necessary or appropriate to establish a guideline for its use for controlling vector larvae in drinking-water. However, it is vital that authorities can be assured that BTI has been prepared to the highest quality and hygienic standards under appropriate conditions that will meet the WHOPES specifications. It is important that the possible risks are set against the risks from vector-borne diseases such as dengue fever (WHO 2009).

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# Bifidobacteria

### Maximum Acceptable Value

No MAV has been set for bifidobacteria in New Zealand drinking-water.

The WHO *Guidelines for Drinking-water Quality* do not mention bifidobacteria.

### Sources to drinking-water

*Bifidobacterium* is a [genus](http://en.wikipedia.org/wiki/Genus) of [Gram-positive](http://en.wikipedia.org/wiki/Gram-positive), non-motile, often branched [anaerobic](http://en.wikipedia.org/wiki/Anaerobic_organism) bacteria. Bifidobacteria are important species of the intestinal tract and they are associated with a healthy status in humans. These micro-organisms have been found to be dominant in the large intestine, especially in the proximal colon. Breast-fed babies have the highest concentrations of bifidobacteria (being up to 80 percent of the cultivable faecal bacteria), with levels declining in the body over time, to less than 25 percent. Apart from age, the proportion may depend on diet, the health of the individual and the species growing in the intestine. Geographical differences occur too, where some parts of Asia have shown bifidobacteria numbers to be higher than *E. coli*. Bifidobacteria are almost exclusively faecal in origin, with some species (mainly sorbitol-fermenting) virtually restricted to humans. Bifidobacteria may reach 109 to 1010 per gram of faeces (Gilpin 2006).

### Health considerations

Bifidobacteria (sometimes called the friendly bacteria) are considered to exert a range of biological activities related to host health. Bifidobacteria have been taken as supplements (directly, or in foods such as yoghurt) because of their reported ability to generate probiotic effects. One aspect is the inhibitory effect of these bacteria on other species, possibly excluding long-term colonisation by invasive pathogens. As probiotic agents, bifidobacteria have been studied for their efficacy in the prevention and treatment of a broad spectrum of animal and/or human gastrointestinal disorders, such as colonic transit disorders, intestinal infections, and colonic adenomas and cancer. Some claims may be more justified than others. Some species are more effective than others; research continues.

### Treatment of drinking-water

Not relevant.

### Method of identification and detection

Despite the first isolation of bifidobacteria in the late 1800s, and very high numbers in human faeces (11 percent of culturable bacteria), their oxygen sensitivity, as with most other strict anaerobes, has limited their role as useful faecal indicators in waters (WHO 2001). Bifidobacteria die off more quickly than *E. coli* so may not be as effective for monitoring water used for drinking; they are also easily inactivated by disinfectants. Research continues (Ottoson 2009).

### Derivation of Maximum Acceptable Value

No MAV.

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# *Burkholderia pseudomallei*

### Maximum Acceptable Value

No MAV has been set for *Burkholderia pseudomallei* in New Zealand drinking-water.

### Sources to drinking-water

*Burkholderia pseudomallei* is a Gram-negative bacillus commonly found in soil and muddy water, predominantly in tropical regions such as northern and western Australia and southeast Asia (CRC 2009). The organism (which has also been called *Pseudomonas pseudomallei*) is acid tolerant and survives in water for prolonged periods in the absence of nutrients. Like *Legionella* and atypical mycobacteria, *Burkholderia pseudomallei* can grow in water and soil.

### Health considerations

*Burkholderia pseudomallei* can cause the disease melioidosis, which is endemic in northern Australia and other tropical regions. The most common clinical manifestation is pneumonia, which may be fatal. In some of these areas, melioidosis is the most common cause of community-acquired pneumonia. Cases appear throughout the year but peak during the rainy season. Many patients present with milder forms of pneumonia, which respond well to appropriate antibiotics, but some may present with a severe septicaemic pneumonia. Other symptoms include skin abscesses or ulcers, abscesses in internal organs and unusual neurological illnesses, such as brainstem encephalitis and acute paraplegia. Although melioidosis can occur in healthy children and adults, it occurs mainly in people whose defence mechanisms against infection are impaired by underlying conditions or poor general health associated with poor nutrition or living conditions.

Most infections appear to be through contact of skin cuts or abrasions with contaminated water. In south-east Asia, rice paddies represent a significant source of infection. Infection may also occur via other routes, particularly through inhalation or ingestion. The relative importance of these routes of infection is not known.

In two Australian outbreaks of melioidosis, indistinguishable isolates of *B. pseudomallei* were cultured from cases and the drinking-water supply. The detection of the organisms in one drinking-water supply followed replacement of water pipes and chlorination failure, whereas the second supply was unchlorinated. CRC (2009) reports that despite its apparent ubiquity there have been few outbreaks. A single outbreak in a northern Australian community in 1990 occurred as a direct result of failure in the drinking water treatment plant’s chlorination system. There were 41 human cases of culture-confirmed melioidosis in northern Australia in 2001 and 43 in 2002, with a mortality ratio of around 20 percent.

### New Zealand significance

Remote.

### Treatment of drinking-water

*Burkholderia pseudomallei* has low resistance to chlorine. CRC (2009) reports that free chlorine effected a one to two-log reduction of sessile *Burkholderia pseudomallei* at 1 mg/L after 10 minutes, increasing to greater than three logs at 2 mg/L. In other systems, chlorine at 1 mg/L has been shown to effect a four-log inactivation of planktonic *B. pseudomallei* after 30 minutes, providing a more than 10-fold greater reduction than either monochloramine or UV.

### Method of identification and detection

See Inglis et al (2005) and CRC (2009).

HPC and the disinfectant residual as measures of water treatment effectiveness and application of appropriate mains repair procedures could be used to indicate protection against *B. pseudomallei.* Because of the environmental occurrence of *B. pseudomallei*, *E. coli* (or, alternatively, thermotolerant coliforms) is not a suitable index for the presence/absence of this organism.

### Derivation of Maximum Acceptable Value

No MAV.

The number of organisms in drinking-water that would constitute a significant risk of infection is not known.

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# *Campylobacter*

### Maximum Acceptable Value

*E. coli* (or alternatively faecal coliforms) and coliforms can be used to indicate the possible presence of pathogenic campylobacter. If sought explicitly, *Campylobacter* spp. should not be detected in drinking-water samples.

### Sources to drinking-water

Campylobacters enter waterways from wild and domestic animal (especially poultry) and wildfowl faeces, and sewage effluent. Other feral animals and domestic animals, such as pigs, cattle, dogs and cats are also reservoirs of thermophilic campylobacters. The faeces of infected animals may be important reservoirs. Studies have shown that raw sewage frequently contains concentrations of up to 100,000 cfu thermophilic *Campylobacter* per 100 mL. *Campylobacter* counts in heavily contaminated sewage can be reduced by wastewater treatment processes. Thermophilic *Campylobacter* have been found in crude sludge but were not detectable in digested conditioned sludge or filter effluent. Their occurrence in surface waters is influenced by rainfall, water temperature, and the presence of cattle and wildfowl. Inactivation rates in natural waters increase as water temperature and sunshine hours increase.

Cattle excrete large numbers of *Campylobacter jejuni* into the environment and multi-locus sequencing typing (MLST) analysis of available isolates has revealed that cattle-related isolates contribute to human cases. Recent studies suggest that frequent emptying and cleaning of cattle drinking water troughs is likely to reduce the shedding of *Campylobacter*, which is an organism that survives well in water, and thus, the contamination of the environment. Initial risk factor studies suggest that drinking water hygiene may also play some role in transmission within poultry flocks however more research is needed to conclusively support this finding (DEFRA 2010).

Following the Havelock North outbreak an ESR presentation stated:

* Scientists believe that the *Campylobacter* strains that caused the Havelock North outbreak were extremely virulent.
* It is possible that people only needed to ingest 10 *Campylobacter* cells to become infected.
* Sheep defecate 865 g of faeces per day.
* There are 3.3 million *Campylobacter* per g of sheep faeces.
* To contaminate Havelock North’s water supply for one day only 70 g of faeces would need to have entered the drinking water reticulation system.
* Havelock North residents would only have needed to drink 300 mL of water per day to become ill.

*Campylobacter*, like other bacterial pathogens, survives well at low temperatures, and can survive for several weeks in cold groundwater or unchlorinated tap water. Numbers decline slowly at normal freezing temperatures after an initial reduction; freezing therefore does not instantly inactivate the organism in food.

Campylobacters are isolated commonly from surface waters when they are surveyed, with the highest concentrations occurring in autumn and the lowest in summer, although in New Zealand occurrence is influenced greatly by intensive animal husbandry (Bolton et al 1987; Carter et al 1987; Martikainen et al 1990; Till and McBride 2004).

A large New Zealand study (Savill et al 2001) found *Campylobacter* was especially prevalent in river water (60 percent positive) and shallow groundwater (75 percent positive) samples. Drinking water (29.2 percent positive) and roof water (37.5 percent positive) also contained *Campylobacter*, but the numbers detected were very low (maximum 0.3 and 0.56 MPN per 100 mL, respectively).

NEPC (2008) reports that 7000 *Campylobacter* per litre (95 percentile) have been measured in Australian sewage. They calculated the minimum log reduction required for production of drinking water from sewage was 8.1-log.

In 2015 six monthly samples were collected from the Avon and Heathcote Rivers in Christchurch, at nine sites; *Campylobacter* were found in all but one of the river water samples, and at concentrations of up to 240 MPN per 100 mL during base flow and up to 460 MPN per 100 mL following rainfall. Speciation and genotyping of *Campylobacter* isolates suggested that base flow isolates were consistent with a wildfowl source. Following rainfall, wildfowl genotypes were still present, but supplemented by isolates more likely to come from ruminant or poultry sources. As *Campylobacter* isolates from ruminant and poultry sources are frequently found among human clinical cases, based just on *Campylobacter* genotyping, these isolates could also be from human sewage (ESR 2015).

Environmental models, aided by further strain typing of isolates from river water during flood flows, confirm that *Campylobacter* concentrations during low flow periods are usually low and are dominated by wild bird species. However during flood periods concentrations become much higher, are dominated by ruminant species, and this is the result of local runoff from farmed areas (McBride *et al* 2011).

The presence of thermophilic *Campylobacter* from piped water supplies, whether treated or untreated, suggests a serious fault in the design or management of the system.

*Campylobacter* HN16 (the Havelock North outbreak strain) was found to survive at least 16 days in anoxic groundwater, significantly longer than in oxic groundwater, and longer than the type strain NCTC11351. After seven days the outbreak strain showed very little die off in oxic and anoxic water while the type strain showed a 2 log die off (Weaver et al 2018).

### Health considerations

*Campylobacter* is themost common cause of bacterial gastroenteritis in the developed world (Skirrow 1991), and approximately 5–14 percent of all diarrhoea worldwide is thought to be caused by *Campylobacter* (WHO 2001). *Campylobacter jejuni* is the most frequently isolated species from patients with acute diarrhoeal disease, whereas *C. coli*, *C. laridis* and *C. fetus* have also been isolated in a small proportion of cases. Two closely related genera, *Helicobacter* and *Archobacter*, include species previously classified as *Campylobacter* spp.

An important feature of *C. jejuni* is its relatively high infectivity compared with other bacterial pathogens. As few as 1,000 organisms can cause infection. Most symptomatic infections occur in infancy and early childhood. The incubation period is usually 2–4 days. Clinical symptoms of *C. jejuni* infection are characterised by abdominal pain, diarrhoea (with or without blood or faecal leukocytes), vomiting, chills and fever. The infection is self-limited and resolves in 3–7 days. Relapses may occur in 5–10 percent of untreated patients.

Thermophilic *Campylobacter* are transmitted by the oral route and cause gastrointestinal illness. *Campylobacter jejuni* is the most common species isolated from human faeces as a cause of gastroenteritis (Griffiths and Park 1990; Mishu Allos and Blaser 1995). However, a range of other *Campylobacter spp.* (*C. fetus, C. coli, C. upsaliensis, C. laridis, C. sputorum* and *C. hypointestalis*) have been implicated in gastroenteritis and a range of other ailments including fever, septic abortion, bacteraemia, meningitis, absecces, pocitis and Miller-Fisger or Guillain-Barré syndrome (Mishu Allos and Blaser 1995; Salloway et al1996).

Campylobacter infection can result in long-term consequences (sequelae). Some people (2.4–2.6 percent of cases) develop arthritis. Others may develop a rare disease called Guillain-Barré syndrome (GBS) that affects the nerves of the body beginning several weeks after the diarrheal illness. This occurs when a person’s immune system is triggered to attack the body’s own nerves resulting in paralysis that lasts several weeks and usually requires intensive care. It is estimated that approximately one in every 1,000 reported campylobacterillnesses leads to GBS. Campylobacter, along with all other forms of acute gastrointestinal illness, is also understood to contribute to irritable bowel syndrome (around 0.04 percent of cases). In people with compromised immune systems, campylobacter occasionally spreads to the bloodstream and causes a serious life-threatening infection (Cressey and Lake 2007 and 2008).

Several waterborne outbreaks caused by *Campylobacter* have been reported worldwide in the past decade, including New Zealand. The numbers of people involved ranged from a few to several thousands. Unchlorinated or poorly treated contaminated drinking water obtained from rural catchments and faecal contamination of water storage reservoirs caused by wild birds and cattle were found to be the main sources. Communities are at risk of outbreaks of campylobacteriosis from the consumption of unchlorinated or inadequately chlorinated surface waters.

For *Campylobacter* NEPC (2008) equated a DALY per case of 0.046. Based on DALYs per case, the impacts of the three pathogens studied was *Campylobacter*>rotavirus>*Cryptosporidium*.

WHO (2013) reported on:

* progress made in the past 10 years in understanding and controlling campylobacteriosis, taking note of successful approaches and lessons learned, and identifying challenges in controlling *Campylobacter* from farm to table and in reducing the human health burden and attributable health consequences
* cross-cutting areas, such as food- and waterborne campylobacteriosis and antimicrobial resistance, taking into account the context of both high-income countries and low- and middle-income countries
* how WHO, FAO and OIE could take action to reduce *Campylobacter* in the food chain and the burden of foodborne campylobacteriosis.

WHO (2013) includes the statement:

“Although there has been scientific progress in fundamental and applied knowledge, there have been few successful large-scale implementations of measures to prevent disease in humans (except for New Zealand ...”.

Their Chapter 6 is titled “Lessons Learned: New Zealand”.

### New Zealand significance

In New Zealand *Campylobacter* is the main component of the reported disease burden, where reported campylobacteriosis is markedly greater than in comparable countries of similar socioeconomic status. In New Zealand, campylobacters are more important than *Salmonella* as causes of acute gastroenteritis. In fact, campylobacteriosis is New Zealand’s most frequently reported zoonosis. Its reported rate peaked in 2006 at 383 cases of illness per 100,000 people per annum, four-fold higher than the combined reported rates for the other three major notifiable zoonoses (cryptosporidiosis, giardiasis, and salmonellosis). Despite recent reductions, the reported rate remains high compared to other developed countries.

Contaminated water supplies have been implicated in outbreaks of campylobacteriosis in New Zealand (Briesman 1994). Consumption of untreated water was identified as a risk factor in a study of campylobacteriosis overseas (Adack et al 1995) and consumption of rainwater or water from a rural source was identified as risk factors in New Zealand (Adack et al 1995; Eberhart–Philips et al1995). New Zealand outbreaks of campylobacteriosis have occurred where drinking-water was implicated. An outbreak in Christchurch involving 44 cases occurred in 1990 where there was strong epidemiological evidence of a waterborne source (Stehr-Green et al1991). During 1996, a *Campylobacter* outbreak occurred in the Ashburton district, again with strong epidemiological evidence of a waterborne source and a large rural epidemiological study demonstrated an association between water supplies and campylobacteriosis (Holmes 1996; Savill *et al* 2002). On 12 September 2016, the Government announced that an Inquiry into the Havelock North water supply contamination incident would be held. The Inquiry follows the widespread outbreak of gastroenteritis in Havelock North in August 2016, with more than 5,000 people falling ill, following the confirmation of the presence of *E. coli* in the water supply. Testing through the health system led the Hastings District Council and the Hawke’s Bay District Health Board staff to suspect that *Campylobacter* was the primary infectious agent; the HN16 strain was identified. See <https://www.dia.govt.nz/Government-Inquiry-into-Havelock-North-Drinking-Water> for submissions, evidence and court transcripts. There had been a similar but smaller outbreak in 1998.

Results of a nationwide survey of 10 pathogens and indicators undertaken at 25 freshwater sites in New Zealand over a 15-month period found *Campylobacter* were detected in 60 percent of all samples, with 6 percent of all samples exceeding the upper detection limit of 110 per 100 mL. The samples with highest levels of *Campylobacter* were mainly found in catchments impacted by sheep farming, and mainly in late summer-early autumn. *C. jejuni* was found in 48 percent of the positive samples and was the most frequent thermotolerant species identified (Till et al 2008). The high degree of correlation between *E. coli* concentration and *Campylobacter* was used to formulate the acceptable limits used in the New Zealand Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas. The critical value for *E. coli* as an indicator of substantially increased risk of *Campylobacter* infection was found to be in the range of 200–500 *E. coli* per 100 mL. The correlation between turbidity and *Campylobacter* numbers may make this a useful parameter for monitoring and management programs also.

In 2012 there were 7,031 notified cases – a rate of 158.6 per 100,000 population, and comprising 34.7 percent of all notifications in that year. About one quarter of people with a notification of campylobacteriosis in 2012 and who reported exposure to campylobacteriosis risk factors consumed untreated water (ESR 2012).

Traditionally, campylobacteriosis is thought of as being associated with consumption of poorly prepared chicken. However, human campylobacteriosis cases in the Manawatu attributed to cattle and sheep in 2008 exceeded those attributed to poultry. However, poultry is still a significant part (as much as one half) of the overall attribution and so further risk management may prove beneficial in terms of burden reduction. The exploration of available data (by this project) to populate an exposure model for drinking water has revealed a shortage of information on key inputs, particularly:

* populations served by unregistered water supplies
* water sources and treatment status of such unregistered supplies
* frequency of exposure to drinking water outside of the normal home supply (eg, exposures for urban populations during camping trips, farm visits, etc) (McBride et al 2011).

The Canterbury town of Darfield (population 1,790) experienced an outbreak of campylobacteriosis in August 2012 where it is estimated that 413 people became ill due to faulty chlorination of the water supply. Heavy rains, contamination of water with animal effluent from nearby paddocks and failures in the treatment of drinking water led to pathogens being distributed through the town’s water supply. Although legislation for water safety plans based on a multi-barrier approach was in place, at the time of the outbreak it was not a requirement for the Darfield water supply. (Bartholomew et al 2014).

MPI (2014) reviewed New Zealand studies on the attribution of human campylobacteriosis to various sources.

In New Zealand, campylobacteriosis is an infectious disease notifiable to the Medical Officer of Health; see Chapter 1: Introduction, Section 1.1.3 for New Zealand statistics.

The Massey University Protozoa Research Unit is conducting a study for the Ministry of Health; 660 samples in 8.25 years have been collected from September 2009 to March 2018. Their quarterly results of groundwater and surface water samples includes testing for *Campylobacter*. Only four of 160 bore (shallow, non-secure) samples were positive. *Campylobacter* were found in 58 percent of the 139 lowland river samples, but in only about 15 percent of samples collected from intermediate rivers and bush catchments.

ESR (2015) surveyed the quality of the Avon and Heathcote Rivers. *Campylobacter* were found in all but one of the river water samples taken, and at concentrations of up to 240 MPN per 100 mL during base flow and up to 460 MPN per 100 mL following rainfall. *E. coli* numbers were about 50 to 2000 times higher. Speciation and genotyping of *Campylobacter* isolates suggested that base flow isolates were consistent with a wildfowl source. Following rainfall, wildfowl genotypes were still present, but supplemented by isolates more likely to come from ruminant or poultry sources. As *Campylobacter* isolates from ruminant and poultry sources are frequently found among human clinical cases, based just on *Campylobacter* genotyping, these isolates could also be from human sewage.

### Treatment of drinking-water

Provided the water has low turbidity, standard disinfection procedures are sufficient to prevent the spread of campylobacters in distribution systems. Disinfection experiments have shown that *Campylobacter* are as or more sensitive than *E. coli* to chlorine (Sobsey 1989), chloramines (Balser et al 1986) and ozone (Gradil et al 1995), hence it is regarded that water treatment capable of inactivating *E. coli* is sufficient to remove *Campylobacter*. However, as *Campylobacter* may transform to a viable but non-culturable form (VNC) in water, their resistance may be underestimated by conventional techniques (Martin and Harakeh 1990) presenting a potential for VNC forms to be present in drinking-water in the absence of the faecal indicator bacteria *E. coli*.

Campylobacters are easily killed by boiling.

Health Canada (2018) estimates the log reduction achieved by coagulation/ sedimentation is 1.55, with another 0.87 from rapid granular filtration = 2.42 log removal. Chlorine and ozone can achieve >8-log inactivation.

### Method of identification and detection

*Campylobacter* spp. are gram-negative, slender, comma-shaped rods. They are micro-aerophilic (require decreased oxygen: 3 to 6 percent for growth) and capnophilic (require an increased carbon dioxide level). They also appear S‑shaped and gull-winged when in pairs. The organisms show a characteristic corkscrew-like motion that can be seen easily by phase contrast microscopy.

No endorsed New Zealand standard method is available for detection of *Campylobacter* in waters. However, methods for detection are available (APHA Method 9260 G, 2005) and (Isolation of Thermotolerant Campylobacter – Review and Methods for New Zealand Laboratories 2003). It is being generally accepted that under adverse conditions *Campylobacter* undergoes a transition to a viable non-culturable “VNC” state.

A large study of 42 New Zealand river water samples compared the use of conventional culture and PCR methods for the detection of *Campylobacter* in MPN enrichment tubes. It was found that all samples positive by culture were also positive by PCR. Thirty‐seven percent more MPN tubes were positive by PCR compared with culture (Savill et al 2001).

### Derivation of Maximum Acceptable Value

*Campylobacter* in drinking-water can cause acute gastroenteritis. No MAV has been set, but if looked for expressly *Campylobacter* should be absent from drinking-water supplies.

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# *Clostridium*

### Maximum Acceptable Value

There is no MAV in the DWSNZ, and the WHO Guidelines do not include a guideline value for *Clostridium* sp.

The EU’s drinking water standards, Council Directive 98/83/EC on the quality of water intended for human consumption adopted by the Council, on 3 November 1998 established a parameter value of 0 per 100 mL for *Clostridium perfringens* (including spores). In response, DWI (2002) stated: *Clostridium perfringens* (including spores) is included in the indicator parameters for the current Directive. There appears to be a belief in the Commission and some member states that this parameter is a suitable surrogate for *Cryptosporidium* and if this belief persists, there could be a proposal to make it a mandatory standard. There is, however evidence from studies in the UK that demonstrate that such a correlation does not occur.

The presence or absence of faecal indicator bacteria is a commonly used operational monitoring parameter. However, there are pathogens that are more resistant to chlorine disinfection than the most commonly used indicator – *E. coli* or thermotolerant coliforms. Therefore, the presence of more resistant faecal indicator bacteria (eg, intestinal enterococci, *Clostridium perfringens* spores or coliphages) as an operational monitoring parameter may be more appropriate in certain circumstances.

Protozoa and some enteroviruses are more resistant to many disinfectants, including chlorine, and may remain viable (and pathogenic) in drinking-water following disinfection. Other organisms may be more appropriate indicators of persistent microbial hazards, and their selection as additional indicators should be evaluated in relation to local circumstances and scientific understanding. Therefore, verification may require analysis of a range of organisms, such as intestinal enterococci, spores of *Clostridium perfringens*, and bacteriophages.

In view of the exceptional resistance of *C. perfringens* spores to disinfection processes and other unfavourable environmental conditions, *C. perfringens* has been proposed as an index of enteric viruses and protozoa in treated drinking-water supplies. In addition, *C. perfringens* can serve as an index of faecal pollution that took place previously and hence indicate sources liable to intermittent contamination. *Clostridium perfringens* is not recommended for routine monitoring, as the exceptionally long survival times of its spores are likely to far exceed those of enteric pathogens, including viruses and protozoa.

### Sources to drinking-water

*Clostridium perfringens* and its spores are virtually always present in sewage. The organism does not multiply in water environments. *Clostridium perfringens* is present more often and in higher numbers in the faeces of some animals, such as dogs, than in the faeces of humans and less often in the faeces of many other warm-blooded animals. The numbers excreted in faeces are normally substantially lower than those of *E. coli*. Spores of *C. perfringens* are resilient and are widely distributed in soil, dust and vegetation.

### Health considerations

*Clostridium spp*. are Gram-positive, obligatory anaerobic, sulphite-reducing bacilli. They produce spores that are exceptionally resistant to unfavourable conditions in water environments, including UV irradiation, temperature and pH extremes, and disinfection processes, such as chlorination. The characteristic species of the genus, *C. perfringens* (faecally specific) is a member of the normal intestinal flora of 13–35 percent of humans and other warm blooded animals. Other species are not exclusively of faecal origin.

*C. perfringens* has been found in raw sewage at 100,000 to 1,000,000 cells per litre. It is one of the most resistant micro-organisms in water, with a half-life of 60 to >300 days (time for a 50 percent reduction in concentration).

Another species, *Clostridium botulinum*, as the name suggest, causes botulism; it is found in soil and anaerobic water/sediments. Birds, particularly mallard ducks, can develop botulism at oxidation ponds, more often during warm dry summers; deaths can be in the thousands. For humans most transmission is foodborne; person-to-person transmission does not occur. Illness due to foodborne botulism has not been reported in New Zealand since 1985 (MPI 2012).

### New Zealand significance

There is no record of *Clostridia* having been tested for in New Zealand drinking-water. Monitoring results for drinking water in Ireland were reported in EMAG (2003).

Results of a nationwide survey of 10 pathogens and indicators undertaken at 25 freshwater sites in New Zealand over a 15-month period found *Clostridium perfringens* spores were detected in 58 percent of all samples (Till et al 2008).

### Treatment of drinking-water

*Clostridium perfringens* is fairly resistant to lower doses of chlorine, so it has been suggested as an alternative indicator organism for protozoa; spores of *Clostridium perfringens* showed the strongest correlation (r = 0.76) with *Cryptosporidium* in a study on the River Meuse (WHO 2003). Finding *Clostridia* in water leaving the treatment plant generally indicates that there is a fault in the chemical or physical treatment that requires investigation and appropriate remedial action. *Clostridium perfringens* can be used to detect faecal contamination of groundwater after the more traditional indicator organisms such as *E. coli* have died.

### Method of identification and detection

Vegetative cells and spores of *C. perfringens* are usually detected by membrane filtration techniques in which membranes are incubated on selective media under strict anaerobic conditions. These detection techniques are not as simple and inexpensive as those for other indicators, such as *E. coli* and intestinal enterococci. See ISO (1986) and APHA (2005).

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# Coliforms and faecal coliforms

### Maximum Acceptable Value

If faecal coliforms or total or presumptive coliforms are tested in place of *Escherichia coli*, they should not be detected in any 100 mL sample of drinking-water. If detected, immediate action should be taken (see Drinking-water Standards for New Zealand).

The direct effect on the community of non-compliance with the Maximum Acceptable Value (MAV) will depend on whether any pathogens are also present, the number of pathogens present, their virulence, and the presence of susceptible persons in the community served.

### Sources to drinking-water

Total coliforms comprise a group of bacteria many of which are inhabitants of the gastrointestinal tract of mammals and birds (the warm-blooded animals). Some species however may also be or are more commonly found in the environment. The coliform bacteria that are most often found in association with animal waste are called faecal coliforms and are characterised by the ability to grow at elevated temperatures of  
44–44.5°C, ie, they are thermotolerant. An alternative name that is now favoured is thermotolerant coliforms (Koster et al 2003), Payment et al 2003). Amongst the faecal coliforms, *E. coli* is the most likely to be associated with faecal contamination of a water supply. Although *E. coli* is the most important thermotolerant (or faecal) coliform, some types of *Citrobacter*, *Klebsiella* and *Enterobacter* are also thermotolerant.

The total coliform group includes both faecal and environmental species. Total coliforms include organisms that can survive and grow in water. Hence, they are not useful as an indicator of faecal pathogens, but they can be used to assess the cleanliness and integrity of distribution systems and the potential presence of biofilms, as well as whether groundwater has been affected from surface activities.

The DWSNZ state that “Bore water is considered secure when it can be demonstrated that contamination by pathogenic organisms is unlikely because the bore water is not directly affected by surface or climate influences ...”. If total coliforms are found in bore water the question arises: “Where have they come from?” They can only have come from the surface. They may have detached from biofilm growing on the casing or fittings, but they still originated from the surface or water just below the surface. See Chapter 3 of the Guidelines for discussion on disinfection of bores.

Coliform bacteria will be found frequently in untreated water and may be of environmental or faecal origin depending on the source of the water. Faecal coliforms however are much more likely to indicate that the contamination is faecal in origin. For example, shallow groundwater may contain quite high numbers of “37°C coliforms” that live in the soil, but no “44.5°C faecal coliforms”.

Presumptive or total coliforms have been found to grow in New Zealand distribution systems (eg, as a biofilm) in the summer in the absence of a residual of FAC; indeed, the test can be used for that purpose or for measuring the efficacy of the various stages of water treatment (see also the datasheet for heterotrophic bacteria).

Several coliform species may proliferate to high numbers in water sources, especially where there are high organic loads, eg, agricultural and industrial discharges, and all species may colonise reticulation systems. Faecal coliforms and *E. coli* are less likely than total or presumptive coliforms to proliferate when organic pollution has occurred, and are thus preferred indicators for water supplies.

An indication of the time of contamination can be assessed by using the atypical coliforms to total coliforms (AC/TC) ratio which compares the background microflora found in the water with the high numbers of total coliforms (TC) identified in fresh faecal runoff/discharge into the water. Fresh faecal material in the water generates a low AC/TC ratio. After discharge into water, the total coliforms progressively die-off and their numbers are lower in comparison to the river microflora suggesting an aged faecal event with a correspondingly higher AC/TC ratio (ESR 2015).

### Health considerations

Coliforms, faecal coliforms or *E. coli* are not generally pathogenic but are used to indicate the possible presence of pathogens and/or the cleanliness of the water supply.

Some species of *E. coli* do however have pathogenic characteristics. See *E. coli* datasheet.

### New Zealand significance

Monitoring total coliforms in the water leaving the WTP can be used to confirm the efficacy of the disinfection process.

*E. coli* is the indicator of choice in the DWSNZ 2005 and subsequent editions. Testing for faecal coliforms (or *E. coli* or total or presumptive coliforms) is used as an indicator of the safety and acceptability of water for drinking, ie, bacterial compliance with the DWSNZ.

### Treatment of drinking-water

Treatment by chlorination or other acceptable form of disinfection (including UV irradiation) is effective in inactivating these micro-organisms in water, provided the turbidity is low. Subject to various criteria defined in the DWSNZ, free available chlorine (FAC) monitoring can be used in place of coliform testing for bacterial compliance.

### Method of identification and detection

Coliforms are gram-negative, non-sporing, rod-shaped bacteria, capable of aerobic and facultative anaerobic growth in the presence of bile-salts or other surface active agents with similar growth-inhibiting properties, which are able to ferment lactose with the production of acid and gas within 48 hours at 35°C to 37°C. As part of lactose fermentation, total coliforms produce the enzyme β-galactosidase. They are also oxidase-negative.

Many years ago an indication of sub-groups was obtained by use of the IMViC test (indole, methyl red, Voges-Proskauer, citrate test). Commercial products such as API 20E have been available for many years; using biochemical reactions to identify Enterobacteriaceae down to the genus and species level. DNA and other molecular studies are revising the understanding of the composition of this group of bacteria.

In recent years, matrix-assisted laser desorption/ionisation with time of flight mass spectrometry (MALDI-TOF MS) has emerged as a promising technique for the rapid and reliable identification of microorganisms, particularly bacteria. MALDI-TOF MS works to identify an unknown microorganism by detecting an array of biomolecules (nucleic acids, proteins, sugars and other small molecules) and comparing the profile with a reference library (ESR 2018).

Traditionally, coliform bacteria were regarded as including members of the genera *Escherichia*, *Citrobacter*, *Klebsiella* and *Enterobacter*, but the group is more heterogeneous and includes a wider range of genera, such as *Budvicia*, *Erwinia*, *Serratia* and *Hafnia*.

Using MALDI-TOF MS, ESR (2018) identified the following coliform to species/genus level in water samples collected in Christchurch, Selwyn and Hurunui water supplies that had a positive total coliform result: *Butiauxella, Citrobacter, Cronobacter, Enterobacter, Escherichia, Kosakonia, Leclercia, Lelliotia, Pantoea, Pluribacter, Providencia, Rahnella,* and *Serratia.*

Faecal (also known as thermotolerant) coliforms are coliform organisms with the same fermentative properties, but after incubation at 44.5°C.

*E. coli* (see datasheet) is a thermotolerant or faecal coliform organism which ferments lactose (or mannitol) at 44 to 44.5°C with the production of acid and gas within 24 hours, and which also forms indole from tryptophan. *E. coli* also gives a positive result in the methyl-red test, does not produce acetylmethylcarbinol (2 hydroxy-3-butanone) in the Voges-Proskauer test, and cannot utilise citrate as the sole source of carbon.

It should be noted that these are not taxonomic criteria, but practical working definitions based on biochemical tests used for water examination purposes.

Some organisms that are taxonomically within the coliform group will be missed in water examination. They include anaerogenic and non-lactose-fermenting strains of coliform organisms. Such strains are usually outnumbered by those that give typical reactions, so in practice, the interpretation of the results of the coliform test should not be affected. Other organisms, such as aeromonads, which can produce acid and gas from lactose, will be regarded as presumptive coliform organisms unless excluded by subsequent confirmatory tests.

Coliforms can be quantified in drinking-water by using multiple tube dilution (most probable number or MPN), or membrane filtration (MF) techniques for concentration of the organisms from water, followed by growth in or on enrichment/selective media and confirmation by specific tests for the organism/group of organisms. Generally, the MPN test result reports presumptive coliforms (37°C test) or faecal coliforms (44.5°C test). The MPN test result is usually reported as total coliforms (37°C test) or faecal coliforms (44.5°C test). The test result is not explicit without stating the method used.

Today these organisms are often used for environmental studies. For example, the atypical coliforms to total coliforms (AC/TC) ratio compares the background microflora found (identified as atypical colonies (AC) on m-endo agar), with the high numbers of total coliforms (TC) identified in fresh faecal runoff/discharge. Fresh faecal material in the water, therefore, generates a low AC/TC ratio. After discharge into water, the total coliforms progressively die-off and their numbers are lower in comparison to the river microflora suggesting an aged faecal event with a correspondingly higher AC/TC ratio (ESR 2015).

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# Enterobacter

### Maximum Acceptable Value

The DWSNZ do not include a MAV for *Enterobacter*. The WHO Guidelines do not include a GV for *Enterobacter*.

### Sources to drinking-water

Enterobacter species have often been found in biofilms in the distribution system. *E. aerogenes* and *E. cloacae* have been detected in surface and groundwater samples. WHO states there is no evidence that these bacteria are transmitted through drinking-water, although it is plausible that the organism could be present in water of poor quality.

### Health considerations

Several strains of these bacteria are pathogenic and cause opportunistic infections in immunocompromised (usually hospitalised) hosts and in those who are on mechanical ventilation. The urinary and respiratory tracts are the most common sites of infection. Three clinically important species from this genus are *E. aerogenes*, *E. sakazakii* and *E. cloacae*. They have been identified during several outbreaks of hospital-acquired infections in Europe and particularly in France.

WHO (2017) includes a Microbial Fact Sheet for *E. sakazakii*. *Enterobacter sakazakii* has been associated with sporadic cases or small outbreaks of sepsis, meningitis, cerebritis and necrotising enterocolitis. Most of the infections are seen in low-birthweight infants (ie, less than 2 kg) or infants born prematurely (ie, less than 37 weeks of gestation). Mortality has been reported to be as high as 50 percent but has decreased to less than 20 percent in recent years. The organism has been frequently identified in factories that produce milk powder and other food substances and in households.

### New Zealand significance

Enterobacter species are found in natural environments such as water, sewage, soil, and vegetables; some species are found in human and animal species. *Enterobacter cloacae* is a prevalent nosocomial pathogen as it is highly resistant to disinfectants and antimicrobial agents.

*Enterobacter sakazakii* (now *Cronobacter*) has been notifiable in New Zealand since mid-2005.

### Treatment of drinking-water

Standard disinfection procedures are sufficient to inactivate *Enterobacter* sp from water that has a low turbidity.

### Method of identification and detection

*Enterobacter* is a genus of common Gram-negative, facultatively anaerobic, rod-shaped, non-spore-forming bacteria of the family Enterobacteriaceae. The genus *Enterobacter* is a member of the coliform group of bacteria. It does not belong to the faecal coliforms (or thermotolerant coliforms) group of bacteria, unlike *Escherichia coli*, because it is incapable of growth at 44.5°C in the presence of bile salts. However, *Enterobacter* ferments lactose with gas production during a 48-hour incubation at  
35–37°C in the presence of bile salts and detergents so is represented in the “total coliforms”, along with the *Escherichia, Klebsiella, Enterobacter, Serratia,* and *Citrobacter*. It is oxidase-negative, indole-negative, and urease-variable. The *Enterobacter* genus includes over 20 species.

### Derivation of Maximum Acceptable Value

There is no MAV.

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# Enterococci

### Maximum Acceptable Value

The DWSNZ do not include a MAV for *Enterococci*. The WHO Guidelines do not include a GV for *Enterococci*.

### Sources to drinking-water

Enterococci are found in large numbers in the faeces of humans and other warm-blooded animals and can be used to serve as an indicator of recent faecal contamination of water.

Enterococci were detected occasionally in 100 L samples of water abstracted from a shallow aquifer in a natural dune infiltration area of the Netherlands. *Enterococcus moraviensis* was most frequently identified. Because there are no existing reports of faecal sources of *E. moraviensis* and the closely related *E. hemoperoxidus,* the authors aimed to find such sources of these two species in the dunes. Faecal samples from various animal species living in the vicinity of abstraction wells were analysed for enterococci; 1386 enterococci isolates were identified using matrix assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry. *E. moraviensis* was found in the faeces of geese, foxes and rabbits. *E. haemoperoxidus* was isolated from goose faeces. Using hierarchical clustering, the species composition of *Enterococcus* spp. isolated from abstracted water formed one cluster with the species composition found in geese droppings. A sanitary survey supported the indication that feral geese may provide a substantial faecal load in particular parts of this dune infiltration area, close to the water abstraction system. This study confirms the faecal origin of *E. moraviensis* and *E. haemoperoxidus* from specific animals, which strengthens their significance as faecal indicators (Taučer-Kapteijn et al 2017).

### Health considerations

*Enterococcus* is a genus of gram-positive, facultatively anaerobic bacteria of the family Streptococcaceae, formerly classified in the genus [*Streptococcus*.](https://medical-dictionary.thefreedictionary.com/Streptococcus) *E. faecalis* and *E. faecium* are normal inhabitants of the human intestinal tract that occasionally cause urinary tract infections, infective endocarditis, bacteremia, and life-threatening nosocomial infections (vancomycin-resistant *enterococci* infection). *E. avium* is found primarily in the feces of chickens and may be associated with appendicitis, otitis, and brain abscesses in humans. Members of the genus *Enterococcus* were classified as group D [*Streptococcus*](https://en.wikipedia.org/wiki/Streptococcus) until 1984, when genomic DNA analysis indicated a separate genus classification would be appropriate.

Although they occur in faeces at a much lower level than *E. coli*, their persistence means they are an effective indictor of faecal contamination. However, some enterococci are associated with soils and plant material, although there is debate about the extent to which this happens in nature. Many of the issues that concern some workers related to the use of enterococci as an indicator of faecal contamination are less significant in groundwater.

WHO (2004) states in section 11.6.4 (and 2017 in section 11.6):

General description

Intestinal enterococci are a subgroup of the larger group of organisms loosely defined as faecal streptococci, comprising species of the genus *Streptococcus*. These bacteria are Gram-positive and relatively tolerant of sodium chloride and alkaline pH levels. They are facultatively anaerobic and occur singly, in pairs, or as short chains. Faecal streptococci including intestinal enterococci all give a positive reaction with Lancefield’s Group D antisera and have been isolated from the faeces of warm-blooded animals. The subgroup of intestinal enterococci consists of the species *Enterococcus faecalis*, *E. faecium*, *E. durans* and *E. hirae*. This group was separated from the rest of the faecal streptococci because they are relatively specific for faecal pollution. However, some intestinal enterococci isolated from water may occasionally also originate from other habitats, including soil, in the absence of faecal pollution.

Indicator value

The intestinal enterococci group can be used as an index of faecal pollution. Most species do not multiply in water environments. The numbers of intestinal enterococci in human faeces are generally about an order of magnitude lower than those of *E. coli*. Important advantages of this group are that they tend to survive longer in water environments than *E. coli* (or thermotolerant coliforms), are more resistant to drying and are more resistant to chlorination. Intestinal enterococci have been used in testing of raw water as an index of faecal pathogens that survive longer than *E. coli* and in drinking-water to augment testing for *E. coli*. In addition, they have been used to test water quality after repairs to distribution systems or after new mains have been laid.

Source and occurrence

Intestinal enterococci are typically excreted in the faeces of humans and other warm-blooded animals. Some members of the group have also been detected in soil in the absence of faecal contamination. Intestinal enterococci are present in large numbers in sewage and water environments polluted by sewage or wastes from humans and animals.

### New Zealand significance

The presence of intestinal enterococci provides evidence of recent faecal contamination, and detection should lead to consideration of further action, which could include further sampling and investigation of potential sources such as inadequate treatment or breaches in distribution system integrity (WHO 2004/2011).

Enterococci is the preferred bacterial indicator of faecal pollution for marine waters in New Zealand (see MfE 2003), which includes a section on sample collection and testing.

The Massey University Protozoa Research Unit is conducting an ongoing range of studies for the Ministry of Health. Their report for July 2009–June 2010 describes results of a year-long survey of groundwater and surface water samples, testing mainly for *Cryptosporidium* and *Giardia*. Three of the four bore (shallow, non-secure) sites (75 percent) and all surface water sites were positive for *Enterococcus* on at least one occasion, with several samples containing >40 cells per 100 mL and one >200.

Enterococci testing has been added to the Massey survey. To date, 24 samples have been tested; four have been positive, without *E. coli*.

### Treatment of drinking-water

Standard disinfection procedures are sufficient to inactivate enterococci from water that has a low turbidity.

### Method of identification and detection

Enterococci are detectable by simple, inexpensive cultural methods that require basic bacteriology laboratory facilities. Commonly used methods include membrane filtration with incubation of membranes on selective media and counting of colonies after incubation at 35–37°C for 48 hours. Other methods include a most probable number technique using micro-titre plates where detection is based on the ability of intestinal enterococci to hydrolyse 4-methyl-umbelliferyl-b-D-glucoside in the presence of thallium acetate and nalidixic acid within 36 hours at 41°C (WHO 2004; APHA Method 9230).

### Derivation of Maximum Acceptable Value

There is no MAV.

In the European Union (EU), enterococci are used as indicators of drinking water contamination ([The Council of the European Union 1998](https://www.ncbi.nlm.nih.gov/books/NBK190421/)). In the EU, enterococci are not permitted in a 100 mL sample of tested drinking water that flows from a tap, and they are not permitted in a 250 mL sample of bottled water.

The USEPA authorised the use of *E. coli* and enterococci as bacterial indicators of faecal contamination. Enterococci are recommended as one of the indicators for faecally contaminated recreational waters and therefore have widespread use in laboratory testing. Enterococci may be a more sensitive faecal indicator than *E. coli* in certain aquifer settings and therefore may be the preferred indicator in such locations.

The USEPA Ground Water Rule requires that when total coliforms are found the water supplier must test one of three State-specified faecal indicators (*E. coli*, enterococci, or coliphage).

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# *Escherichia coli*

### Maximum Acceptable Value

*Escherichia coli* (*E. coli*) should not be detected in any 100 mL sample of drinking-water. If detected, immediate action should be taken (see Drinking-water Standards for New Zealand).

### Sources to drinking-water

*Escherichia coli* is found in very large numbers in the faeces of humans (up to 109 per gram of faeces) and other warm-blooded animals, and serves as an indicator of recent faecal contamination of water. *E. coli* O157:H7 has been shown to survive for 150 days in soil and 90 days in cattle faeces. It can also survive for at least four months in cattle drinking trough sediment. *E. coli* O157:H7 survives on dry alfalfa seeds for weeks depending on storage temperature (longer survival at lower temperatures). Evidence indicates that low temperature is the primary signal for entry into the viable non‑culturable (VNC) state in water. In relation to cattle water troughs, culturable *E. coli* O157 were used in simulated microcosms, survival in sediments was noted for at least 245 days. Strains that survived more than six months in the contaminated microcosms were infectious to a group of 10-week-old calves with faecal excretion lasting for 87 days after exposure. The authors concluded that water trough sediments contaminated with faeces from infected cattle may serve as a long-term reservoir and source of infection of *E. coli* O157 on farms (MPI 2001/2007).

### Health considerations

*E. coli* is increasingly used as an alternative to faecal coliforms as an indicator of faecal pollution and is the bacterial indicator of choice in the DWSNZ. Some are enteric pathogens in their own right (Payment et al 2003). A number of variants of *E. coli* responsible for diarrhoea are recognised, eg, enteroaggregative (EAEC), enteropathogenic (EPEC), enteroinvasive (EIEC), enterotoxigenic (ETEC) and enterohaemorrhagic (EHEC) strains (Levine 1987).

Enteropathogenic *E. coli* (EPEC) were first recognised as a result of the serological examination of strains of *E. coli* isolated from outbreaks of diarrhoea among infants. Associations of particular serotypes with disease were observed. The pathogenic mechanisms employed by most of these organisms are not understood fully. These strains have been associated particularly with outbreaks of infantile gastroenteritis; experiments in adult volunteers have shown that they also cause disease in adults.

Enteroinvasive *E. coli* (EIEC) produce dysentery by a mechanism similar to *Shigella* spp. These organisms invade the colonic mucosa and cause bloody diarrhoea. The property seems to be restricted to a few O-sero groups. It must be remembered that *Shigella* and *E. coli* are closely related and that genetic material is very readily transferred between the groups.

Though enteropathogenic or enteroinvasive strains may cause serious illness, such epidemiological evidence as is available suggests that enterotoxigenic strains are responsible for most episodes of *E. coli* (or travellers’) diarrhoea, particularly in developing countries. Enterotoxigenic *E. coli* (ETEC) can cause a cholera-like syndrome in infants, children and adults. ETEC produce either a heat-labile enterotoxin (LT), related to cholera enterotoxin, or a heat-stable enterotoxin (ST); some strains produce both toxins. Action of LT is the same as cholera toxin. Production of enterotoxin is controlled by plasmids. The ability of ETEC to cause disease depends not only on the production of enterotoxin but also upon their ability to colonise the small intestine. Various colonisation factors, or adhesions, have been described, which enable the bacteria to attach to the intestinal mucosa.

The fourth class, enterohaemorrhagic *E. coli* (EHEC), was first recognised by the organism’s production of a cytotoxin active against Vero cells; in fact, enterohaemorrhagic *E. coli* (EHEC) was previously called verocytotoxic *E. coli*. Enterohaemorrhagic *E. coli* constitute a subset of serotypes (*E. coli* O157 and some other serogroups) of Shiga toxin (Stx)-producing *E. coli* (STEC). They cause disease ranging from mild diarrhoea to haemorrhagic colitis characterised by blood-stained diarrhoea, usually without fever, and accompanied by abdominal pain. It is also a cause of the life-threatening haemolytic uraemic syndrome, which is most common in the young and elderly, and is characterised by acute renal failure and microangiopathic haemolytic anaemia. *E. coli* O157:H7 is enterohaemorrhagic, causing heamorrhagic colitis. EHEC can grow in temperatures ranging from 7°C to 50°C, with an optimum temperature of 37°C. Most available information relates to serotype O157:H7, since it is easily differentiated biochemically from other *E. coli* strains. The reservoir of this pathogen appears to be mainly cattle and other ruminants such as camels. Although *E. coli* O157:H7 has been isolated from a wide variety of animals sources, most outbreaks of infection have been linked to ruminants. Prevalence of *E. coli* O157 in four cattle studies ranged from 4.91–12.92 percent and for sheep prevalence ranged from 1.35–1.97 percent. Swine were not included because of their low shedding rates and low density in England and Wales (DWI 2015). It is transmitted to humans primarily through consumption of contaminated foods, such as raw or undercooked ground meat products and raw milk. Faecal contamination of water and other foods, as well as cross-contamination during food preparation (with beef and other meat products, contaminated surfaces and kitchen utensils), will also lead to infection. EHEC has also been isolated from bodies of water (ponds, streams), wells and water troughs, and has been found to survive for months in manure and water-trough sediments. Waterborne transmission has been reported, both from contaminated drinking-water and from recreational waters (WHO 2005 and 2012). The incidence of VTEC infections in English and Welsh drinking water has been studied (DWI 2015).

A groundwater supply in Walkerton, Ontario, Canada that became contaminated after heavy rain at the same time that the chlorination system was not operating resulted in seven deaths and 2300 cases of very ill people. The principal causative organism was found to be *E. coli* O157:H7 (Hrudey et al 2002). The drinking-water supply was contaminated by rainwater runoff containing cattle excreta. The CDC estimates 73,500 *E. coli* 0157:H7 illnesses per year in the United States.

Over the period from 1990 to the early 2000s, *E. coli* O157:H7 was identified as the causative agent of approximately 6 percent of the reported drinking water outbreaks in England and Wales and roughly 7 percent of those reported in the United States. With the exception of EHEC, most pathogenic *E. coli* require a high number of bacteria to be ingested in order to produce illness. Infectious dose estimates for non-EHEC strains range from 105 to 1010 organisms. EHEC strains, in contrast, have a very low infectious dose. It has been suggested that ingestion of fewer than 100 cells may be sufficient to cause infection. The onset and duration of pathogenic *E. coli–*related illness will be strain dependent, but symptoms can begin in as little as 8–12 hours and last from a few days up to a few weeks; reported in Health Canada (2013).

The fifth class, enteroaggregative *E. coli* (EAEC), is identified by the adherence of the organisms to Hep-2 cells in a tissue culture. One strain has been shown to cause mild diarrhoea without blood or faecal leucocytes.

### New Zealand significance

Results of a nationwide survey of 10 pathogens and indicators undertaken at 25 freshwater sites in New Zealand over a 15-month period found that *E. coli* were detected in 99 percent of all samples (Till et al 2009).

No studies have been undertaken relating the presence of enterovirulent *E. coli* in drinking-waters with illness in the community. There have been no known cases of waterborne gastrointestinal disease caused by pathogenic *E. coli* in New Zealandalthough VTEC/STEC cases are increasing annually (Sneyd and Baker 2003). Since then (May 2005), a child on the Awatere/Seddon water supply was diagnosed with *E. coli* 0157 infection. Subsequent sampling of the distribution system found *E. coli* 0157.

Verocytotoxigenic *E. coli* (VTEC) has emerged as one of New Zealand’s most important enteric diseases over the last 15 years. The incidence has increased from 0.3 cases in 1987, 1.3 cases in 1998 to 3.2 cases per 100,000 in 2010, placing New Zealand in the upper end of the range reported from other developed countries. The epidemiology of VTEC infections is characterised by farm animal reservoirs, transmission by a wide variety of foods or water, and person-to-person transmission due to its small infection dose of <200 CFU (ESR 2009; MoH int. rep).

Conditions related to verotoxin-producing *E. coli* (VTEC), also known as Shiga toxin-producing *E. coli* (STEC), are notifiable to the Medical Officer of Health. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of VTEC/STEC *E. coli* related cases. A Massey University study (Jaros et al 2013) found that “environmental and animal contact, but not food, are important exposure pathways for sporadic cases of human STEC infection in New Zealand. There are strong indications that dairy cattle and beef cattle are the most important sources of STEC and contact with manure from these animals represents an important exposure pathway. Notably, outbreaks of STEC infections are rare in New Zealand and this further suggests that food is not a significant exposure pathway”.

### Treatment of drinking-water

Standard disinfection procedures are sufficient to inactivate *E. coli* from water that has a low turbidity. Evidence on the susceptibility of *E. coli* O157 to disinfection concluded *E. coli* O157 has the same susceptibility as indicator *E. coli* (DWI 2015).

### Method of identification and detection

*E. coli* is a thermotolerant coliform organism which ferments lactose (or mannitol) at 44.5°C with the production of acid and gas within 24 hours, and which also forms indole from tryptophan. *E. coli* also gives a positive result in the methyl-red test, a negative Voges-Proskauer test, and cannot utilise citrate as the sole source of carbon.

*E. coli* numbers can be determined using multiple tube dilution (MPN) or membrane filtration (MF) techniques for concentration of the organisms from water, followed by growth in enrichment/selective media and confirmation by specific tests (APHA 21st edition). However, neither of these methods is able to distinguish between pathogenic and non-pathogenic strains. Serological techniques can be used to identify some pathogenic strains. The DWSNZ accept presence/absence (P/A) testing as well.

Some pathogenic *E. coli* can be detected by gene probes (Echeverria et al 1982), PCR (Meyer et al 1991), or immunomagnetic-electrochemiluminescent methods (Yu and Bruno 1996). These methods have the advantage of detecting viable non-culturable (VNC) forms, but may not be able to distinguish between live and dead cells. Detection of pathogenic *E. coli* such as O157:H7 in water is possible by confirmation of the colonies after enrichment culture, the process being made more efficient by screening the isolates for *B-*glucoronidase and glutamate decarboxylase (Rice et al1996).

Over the years people have become accustomed to thinking that drinking-water that consistently tests at zero *E. coli* per 100 mL is the same as “water free from *E. coli*”, or even ‘sterile’ water. Water entering the distribution system containing 1 *E. coli* per litre is delivering about 400 to 500 *E. coli* organisms to each house every day. Although the DWSNZ state that *E. coli* should be less than 1 per 100 mL, a good technique, particularly in troubleshooting, is to process a greater volume than the 100 mL (where the method permits). For example, it is possible to filter at least 2 L of low turbidity drinking-water through a membrane filter.

### Derivation of Maximum Acceptable Value

*E. coli* should not be detectable in 100 mL samples taken from water supplies. The presence of *E. coli* indicates faecal contamination and suggests a serious fault in the integrity of the water supply system.

The effect of non-compliance on the community will depend on the *E. coli* strain involved, whether faecal pathogens are also present, the number of organisms, the duration of the non-compliance, and the presence of susceptible individuals.

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# *Helicobacter*

### Maximum Acceptable Value

There is no MAV for *Helicobacter* in the DWSNZ.

### Sources to drinking-water

*Helicobacter pylori*, originally classified as *Campylobacter pylori*, is a Gram-negative, micro-aerophilic, spiral-shaped, motile bacterium that is able to colonise the stomach. There are at least 14 species of *Helicobacter*, but only *H. pylori* has been identified as a human pathogen.

*H. pylori* has been detected in water. Although it is unlikely to grow in the environment, it has been found to survive for 20 to 30 days in water and there is evidence that it can be present in biofilms. In a US study, *H. pylori* was found in a majority of surface water and shallow groundwater samples; its presence was not correlated with the presence of *E. coli*.

### Health considerations

*Helicobacter pylori* is a highly heterogeneous bacterium with a large genomic diversity. In addition, humans may sometimes harbour multiple strains, and *H. pylori* can change genotypically and phenotypically during colonisation in a single host (IARC 2011). Some gastric *Helicobacter*s from animals can infect humans: *H. bizzozeroni*, *H. salomonis*, *H. felis*, *candidatus* *H. suis*. Since they are extremely difficult to grow in cultures, the exact speciation is usually not done.

*H. pylori* is found in the stomach. Although most infections are asymptomatic, people may live their entire lives with the organism. However the organism is associated with chronic gastritis, which may lead to complications such as peptic and duodenal ulcer disease and gastric cancer. It has been estimated that 85–95 percent of ulcers are the result of infection with this organism. The majority of *H. pylori* infections are initiated in childhood and, unless treated, are chronic. Humans appear to be the primary host of *H. pylori*. Other hosts may include domestic cats.

Person-to-person contact within families has been identified as the most likely source of infection through oral-oral transmission. Faecal-oral transmission is considered possible and consumption of contaminated drinking-water has been suggested as a potential source of infection; however, evidence to-date is limited to developing countries and further investigation is required to determine whether waterborne transmission occurs. Consumption of contaminated drinking-water has been suggested as a potential source of infection, particularly in developing countries, but further investigation is required to establish any link with waterborne transmission. There has been less evidence supporting the importance of waterborne transmission in developed owing to the difficulty in isolating *H. pylori* from drinking water with culturable methods (from Health Canada 2013).

*H. pylori* may be more prevalent in biofilm than drinking-water samples (DWI 2003).

In New Zealand, a higher prevalence is noted amongst Maori and Polynesians. Studies show that about 5 percent of European children become infected by the age of 20 years, in contrast to 50 percent of Polynesian children (Fraser 2004).

Although *E. coli* is not a good indicator of *H. pylori*, it is inactivated by chlorination.

IARC (2011) conclude that infection with *Helicobacter pylori* is carcinogenic to humans (Group 1).

### New Zealand significance

See above.

### Treatment of drinking-water

The study (DWI 2004) has demonstrated that although *H. pylori* can be detected by molecular methods in drinking water the organism has not been isolated, despite extensive cultural investigation. Even if viable organisms were present in such low numbers, their successful culture using the presently available culture protocols remains unresolved because of heavy overgrowths of other micro-organisms in the water and biofilms. It is most likely that these organisms are dead or in a viable but non-culturable state. This is because there is considerable evidence for the poor survival of *H. pylori* in water, evidence that disinfection used in treatment and as a residual should prevent its survival, and a lack of any clear evidence that these organisms are viable but non-cultivable.

### Method of identification and detection

See DWI (2004).

### Derivation of Maximum Acceptable Value

There is no MAV.

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# Heterotrophic bacteria

### Maximum Acceptable Value

There is no MAV for heterotrophic bacteria in the DWSNZ.

### Sources to drinking-water

Bacteria, moulds, and yeasts that require organic carbon for growth are known as heterotrophs. Most bacteria, including many of the bacteria associated with drinking water systems, are heterotrophs. Heterotrophic bacteria occur naturally in water, and can enter water with discharges of wastes and in run-off from the land. They can persist for long periods in groundwater as well.

A variety of simple culture-based tests which are intended to recover a wide range of micro-organisms from water are collectively referred to as “heterotrophic plate count” or “HPC test” procedures. Previously called total plate count, TPC or PC.

### Health considerations

HPC can include potentially “opportunistic” pathogens such as *Acinetobacter*, *Aeromonas*, *Alcaligenes*, *Flavobacterium*, *Klebsiella*, *Moraxella*, *Serratia*, *Pseudomonas* and *Xanthomonas*. However, there is no evidence of an association of any of these organisms with gastrointestinal infection through ingestion of drinking-water in the general population. Heterotrophic bacteria in anaerobic groundwater may not grow using the spread plate technique if they are strict anaerobes.

Because heterotrophic bacteria in drinking-water are not considered to cause health problems, their enumeration has been used as an indication of general bacterial condition, rather than faecal contamination. Total plate counts can also be used to indicate bacterial regrowth in the distribution system. See Chapter 5: Microbiological Quality for further discussion. Section 5.3.6 includes an extract from “*Heterotrophic plate counts and drinking-water safety: The significance of HPCs for water quality and the human health*” (WHO 2003), as well as further discussion. Heterotrophic bacteria are also discussed in section 11.6.3 of the WHO (2004) Guidelines.

Chapter 8: Protozoal Compliance discusses the use of heterotrophic bacteria in challenge testing, in lieu of using *Cryptosporidium* oocysts.

### New Zealand significance

The use of heterotrophic plate counts is discussed in Chapters 5 and 6 of these Guidelines.

### Method of identification and detection

The concentration of heterotrophic bacteria in water is measured by the heterotrophic plate count (HPC), also called standard plate count, mesophilic plate count, aerobic plate count, or total plate count, by using membrane filtration, poured plate or spread plate techniques. There are so many different techniques, media, and incubation times and temperatures that it is meaningless to compare results without also defining the methodology. The techniques adopted in most procedures will limit growth to aerobic bacteria. Some fast growing fungi or bacteria may form spreading colonies during the incubation period, preventing other colonies from growing or being seen. Incubation temperatures commonly used vary from 20°C to 37°C and incubation periods range from a few hours to seven days or more; the longer times are usually required when incubating at the lower temperatures.

Because heterotrophic organisms may proliferate in treatment processes such as biologically active sand filters and other filtration systems (such as activated carbon) in the absence of a disinfectant, the test can be a useful process control tool. The test has also been used to monitor regrowth following disinfection by ozone.

### Derivation of Maximum Acceptable Value

There is no MAV.

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# *Klebsiella*

### Maximum Acceptable Value

Coliforms can be used to indicate the possible presence of *Klebsiella* spp. If sought explicitly, *Klebsiella* spp. should not be detected.

### Sources to drinking-water

*Klebsiella* spp. belong to the family Enterobacteriaceae and are inherently environmental organisms that can survive, and sometimes multiply, in suitably enriched waters. They are associated with the roots of plants and can grow to high levels on the leaves of some vegetables. *Klebsiella* spp. are also excreted in the faeces of many healthy humans and animals. They are frequently associated with raw waters and can increase to high levels in waters containing vegetable and pulp mill wastes.

As the organisms have similar sensitivity to disinfection to *E. coli* and some bacterial enteric pathogens, their presence in drinking-water indicates that disinfection has been inadequate.

### Health considerations

Approximately 60–80 percent of all *Klebsiella* spp. isolated from faeces and clinical specimens are *K. pneumoniae*. *Klebsiella oxytoca* has also been identified as a pathogen.

*K. pneumoniae* and *K. oxytoca* are significant opportunistic pathogens in hospitals, but the relationship between infections and drinking-water is, at best, dubious given the wide distribution of members of this genus in the environment.

*Klebsiella* may colonise patients in hospital, being spread mainly by the frequent handling that occurs in intensive care units. Those most at risk are people with impaired defence mechanisms, such as the elderly or the very young, people with burns or excessive wounding, those undergoing immunosuppressive therapy, or those with acquired immune deficiency syndrome (AIDS). From colonisation, invasive infections may occur. On rare occasions they may cause infections, including destructive pneumonia, in apparently healthy people. These problems appear to be associated with *K. pneumoniae* and *K. oxytoca*.

### New Zealand significance

*Klebsiella* spp. have been detected in some New Zealand drinking-waters, but there is no evidence that they have caused disease. It is generally considered to be related to biofilms.

### Treatment of drinking-water

The organisms are reasonably sensitive to disinfectants, and entry into distribution systems can be prevented by adequate treatment. Growth within distribution systems can be minimised by strategies that are designed to minimise biofilm growth, including treatment to optimise organic carbon removal, restriction of the residence time of water in distribution systems and maintenance of disinfectant residuals.

### Method of identification and detection

*Klebsiella* spp. are gram-negative, non-sporing, oxidase-negative, rod-shaped bacteria, capable of aerobic and facultative anaerobic growth in the presence of bile salts of other surface active agents with similar growth-inhibiting properties. They are able to ferment lactose, with the production of acid and gas within 48 hours at 35–37°C, ie, they test as thermotolerant coliforms (total or presumptive).

The genus is heterogeneous and has been difficult to classify. Four species are now included: *K. pneumoniae, K. oxytoca, K. planticola*, and *K. terrigena*. A fifth species, *K. mobilis*, has been proposed, but it remains controversial whether this should be classified in this genus or that of *Enterobacter* (Grimon et al 1991).

Most *Klebsiella* spp. can be quantified in water by either multiple tube dilution or membrane filtration methods for coliforms, followed by suitable tests for identification of the genus (see APHA Method 9222 F and 9225).

### Derivation of Maximum Acceptable Value

*Klebsiella* spp. form a significant proportion of the organisms identified as coliforms in standard tests for indicator bacteria, and these organisms are thus covered by the guideline for coliforms but are not identified by *E. coli* tests.

The presence of these organisms indicates poor water quality, possible faecal contamination, and regrowth in the distribution system.

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# *Legionella*

### Maximum Acceptable Value

No guideline has been set for the presence of *Legionella* in New Zealand drinking-water. Microbial agents (including *Legionella*) are included in the [plan of work of the rolling revision](http://www.who.int/entity/water_sanitation_health/gdwqrevision/en/index.html) of the WHO Guidelines for Drinking-water Quality.

*Legionella* has high political profile (because of the recent drinking water standard introduced in the Netherlands: 50 cfu per litre) but low scientific justification. Analysis of drinking water samples can clearly demonstrate the presence of low numbers of *Legionella.* Being natural water organisms, small numbers will pass through water treatment and survive disinfection, particularly in association with amoebae. The levels in mains water will be low, insufficient to cause infection in aerosols, and it is difficult to see how they can be eradicated. In addition, the organism may be in a viable but non-culturable state that will not be detected by culture techniques. Prevention in buildings relates to good maintenance and cleaning, the use of appropriate plumbing materials and the application of biocide processes. However, given European interest in the need for a standard, the organism has been given high priority status. Should a standard be proposed for *Legionella,* this seems most likely to be included as a mandatory parameter (DWI 2002).

In July 2000 legislation was approved in the Netherlands requiring that cold water should be less than 25°C and hot water more than 60°C. “Dead legs” – parts of the water system that are not used for long periods and remain stagnant – will have to be removed (Weber 2000).

In 2011 the German Federal Ministry of Health published the German drinking water ordinance imposing strict action limits of 1 CFU/mL for total *Legionella* (all *Legionella* species)*,* and ISO 11731-2 (2004) was deemed as the regulatory standard culture method ([German Federal Ministry of Health 2011](http://jwh.iwaponline.com/content/16/1/25#ref-11)).

### Sources to drinking-water

The genus *Legionella*, a member of the family Legionellaceae, has at least 50 species comprising 70 distinct serogroups (52 species are listed in MoH 2011). Legionellae are Gram-negative, rod-shaped, non-spore-forming bacteria that require L-cysteine for growth and primary isolation. *Legionella* spp. are heterotrophic bacteria found in a wide range of water environments and can proliferate at temperatures above 25°C.

Legionellae are widespread in natural sources of fresh water (including hydrothermal waters/springs) and soils, and can appear in some composts and potting mixes. They occur commonly in artificial water systems (such as in hotels and hospitals), particularly in warm to hot water, air-conditioning systems, spa pools and cooling water systems. They can survive in water at temperatures up to 60°C, and can grow in water 20–45°C, more generally 30–43°C. MoH (2011) includes a table showing the effect of temperature.

Being a soil organism, *Legionella* could enter the pipework during repairs or mains laying.

*Legionella* spp. appear to infect humans by inhalation, and their presence in drinking-water *per se* seems irrelevant until they are amplified by growing in specific sites under specific conditions (usually thermal enrichment), from which infective aerosols, and, hence, droplet nuclei, may be created.

Despite disinfection legionellae may be present in reticulated water in very low numbers that are not a health problem. However, in many central hot and cold water services, conditions are conducive for multiplication of these bacteria especially when water remains at temperatures between 20–40°C. *Legionella* found in such services may multiply before the heater, within the heater (particularly near the base) or near hot water outlets such as on tap washers or in shower heads. Biofilms also develop in these water systems and may be dislodged by hydraulic shocks and vibration on the walls of pipes and vessels, markedly increasing the numbers of bacteria in the water.

Conditions in temperature-cooling towers, spas, cold water systems in buildings, hot water systems operated below 60°C, or “dead legs” of hot water systems operated at higher temperatures, may favour the growth of legionellae. Spraying water in cooling towers or water agitated in spas may then produce aerosols; and water from hot water systems is also likely to form aerosols in showers, through nozzle heads, or by splashing in sinks, baths, etc. *Legionella* have been detected in water from thermal areas in New Zealand. The Australian Standard AS 3666 quotes an acceptable limit of <10 CFU per mL temperature-cooling systems.

Less common sources of outbreaks overseas include decorative fountains, a supermarket vegetable misting machine, a machine shop cutting fluid system and ultrasonic nebulisers (National Environmental Health Forum 1996). A possible source of the *Legionella pneumophila* serogroup 1 bacteria responsible for the death at Beachlands (in Manukau City) in 2006 was use of a contaminated water blaster that allowed the organisms to drift on to nearby roofs and enter the water tanks of five houses (Simmons and Jury 2006). *Legionella* had not previously been identified in domestic roof-collected rainwater systems in New Zealand.

Legionellae can be ingested by the trophozoites of certain amoebae (*Acanthamoeba, Hartmanella, Vahlkampfia*, and *Naegleria*) and then grow intracellularly and become incorporated in their cysts. This may explain the difficulty in eradicating legionellae from water systems, and it could be a factor in the aetiology of Pontiac fever.

During 2009–2010, US public health officials from 17 states reported 33 drinking water outbreaks. The outbreaks resulted in 1,040 illnesses, 85 hospitalisations (8.2 percent of cases), and nine deaths. *Legionella* was implicated in 19 outbreaks, 72 illnesses, 58 hospitalisations, and eight deaths. *Legionella* accounted for 58 percent of outbreaks and 7 percent of illnesses, and *Campylobacter* accounted for 12 percent of outbreaks and 78 percent of illnesses. Two of the 19 reported *Legionella* outbreaks occurred at health-care facilities where treatment systems to control *Legionella* growth had been installed, underscoring the limited effectiveness of engineering controls in complex plumbing systems (CDC 2013).

### Health considerations

*Legionella* spp. are not known to cause disease by the ingestion of drinking-water, although this potential has been identified in cases of water contamination. Bartrum et al (2007) state that infection with *Legionella* requires both proliferation and exposure. Potable water systems containing *Legionella* are a significant cause of sporadic cases of legionellosis acquired in the community. Such systems are also the main cause of nosocomial infection (through aspiration or direct infection of wounds, with cases reported in many European countries and in North America. In northern Europe, about 50 percent of cases of legionellosis are associated with travel, and the infection is often associated with hotel water systems.

Legionella infections can be classified into four categories:

subclinical infection (ie, infection with no disease)

non-pneumonic disease (ie, Pontiac fever)

pneumonia (ie, Legionnaires’ disease)

extrapulmonary disease.

Subclincial infections are probably more common. This is indicated by the detection of *Legionella* antibodies in a large percentage of the New Zealand healthy population. The two most common clinical manifestations of legionellosis are Legionnaires’ disease and Pontiac fever; their main symptoms are discussed in MoH (2011).

Legionellosis is a form of pneumonia with an incubation period usually of 2–10 days. Males are more frequently affected than females (2:1), and most cases occur in the 40 to 70 year age group. It occurs more frequently during summer and autumn, ie, when temperatures are higher. Risk factors include smoking, alcoholism, cancer, diabetes, chronic respiratory or kidney disease and severe immuno-suppression, as in transplant recipients. Ten percent or more of cases are fatal (higher in immuno-compromised patients), even though legionellosis can be treated effectively by antibiotics such as erythromycin and rifampicin.

Pontiac fever is a milder disease with a high attack rate. The incubation period is five hours to three days, and symptoms are similar to those of influenza: fever, headache, nausea, vomiting, aching muscles and coughing. No fatal cases have been reported and few outbreaks have been recognised, possibly because the non-specific nature of the symptoms of the disease hinders its detection.

Infection through man-made water systems such as cooling towers and hot water supplies proceeds through inhalation of aerosols which are small enough to penetrate lungs and be retained by the alveoli, the degree of risk depending on four factors: the density of the bacteria in their source, the extent of aerosol generation, the number of inhaled bacteria, and the susceptibility of the exposed individual.

Extrapulmonary disease is a relatively rare manifestation following *Legionella* infection not involving the respiratory system. The bacterium can move from the respiratory system to other sites or organs in the body including the heart, kidney, liver, spleen, digestive tract, and bone tissue.

The number of inhaled bacteria depends on the size of the aerosol generated (<5 micrometres being most dangerous), the dispersal of the aerosol in the air, and the duration of the exposure. Host defence is important in determining whether exposure to legionellae will lead to clinical disease, and differences in susceptibility largely explain the fact that in some cases high counts of *L. pneumophila* in water systems have been reported in the absence of disease, whereas in other cases similar or lower counts have been associated with epidemics. It is also likely, although not yet adequately proven, that differences in virulence between strains account partly for these observations.

In general the sources of legionellae implicated in outbreaks of legionellosis worldwide have been traced to air conditioning plants or to hot water distribution systems that have been incorrectly commissioned or have been poorly maintained. Aerosol drift from cooling tower exhausts may enter doors, windows, ventilation air intakes of buildings, and vehicle washes. Release of aerosols from water distribution systems may occur from shower heads or, to a lesser extent, from water splashing in hand basins or baths. Spa pools are another significant potential hazard. Wherever water is disturbed there is the possibility that it will splash and introduce droplets and aerosols into the air. In Australia major outbreaks have been traced to small cooling towers and to evaporative condensers associated with refrigeration systems. Small numbers of cases have been associated with warm water services and with spa pools (enHealth 2015). Despite records of outbreaks, it is believed that the majority of cases appear to be sporadic. Also, a British study found legionellae in car windscreen wash water that did not include cleaning fluid (WQRA 2010).

With the more recent recognition that legionellosis may be contracted by aspiration of the organism, not only by inhalation of aerosolised legionellae (Muraca et al1998), interest in the presence and significance of legionellae in drinking-water has been rekindled. Recent evidence suggests that aspiration[[1]](#footnote-1) may be a much more common route of infection than inhalation of aerosols from cooling towers (Yu 1996). Aspiration is now regarded as the cause of most *Legionella* infections that are acquired by people who are already in hospitals or nursing homes, and may also be responsible for some of the sporadic cases arising in the community.

*Legionella pneumophila* has been grown from potable water supplies in the UK (Colbourne et al1988; Witherell et al1988), Spain (Canpo and Apraiz 1988), Canada (Marrie et al1992), and USA (Snyderet al1990, and may explain the sporadic nature of legionellosis in these communities.

The reported incidence of Legionnaires’ disease in the US has increased more than four-fold since 2000, and similar increasing trends have been observed in many other countries where surveillance for this infection is carried out. It is not clear to what extent this reflects increased testing and diagnosis, population changes leading to a greater proportion of vulnerable people, or changes in exposure to the pathogen. There are many ways in which changes in drinking water systems, water using devices and human behaviour over the course of recent decades could plausibly have impacted on human exposure to these pathogens and thus influenced infection rates. Examples of such changes include (Health Stream, January 2018):

* growing use of air conditioning systems with wet cooling towers for large buildings
* increases in commercial and residential building sizes with consequent increases in the length and complexity of plumbing systems
* increasing use of spa baths, in both domestic and recreational settings
* changes to household plumbing design, including the use of mixer taps and shared hot/cold water outlets which have created warm temperature zones that did not previously exist
* increasing use of showers rather than baths, and more frequent showering
* changes in shower head design to reduce water use which may have changed the size profile of generated aerosols, potentially leading to increased volumes of water inhalation
* lowering of hot water storage temperatures by consumers in an effort to reduce energy use
* increasing use of humidifiers, misting devices and ice machines.

### New Zealand significance

The family Legionellaceae contains one single genus, *Legionella*, with currently at least 50 reported species, of which *L. pneumophila* serogroups 4, 6 and 8, *L.*longbeachae (the species usually associated with potting mix) and *L. micdadei* are those most frequently associated with human disease in New Zealand. Other serogroups of *L. pneumophila* and occasionally other legionellae have also been reported to cause disease, including *L. pneumophila* serogroup 1 referred to above in relation to the Beachlands incident.

*Legionella* has been found in cooling tower waters in parts of New Zealand. No published reports are available on the presence of *L. pneumophila* in drinking-waters.

Legionellosis is an infectious disease notifiable (since 1980) to a Medical Officer of Health under the Health Act 1956. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of legionellosis. The annual notification data shows there are between 50 and 100 laboratory-confirmed cases each year, giving an annual rate of between 1.3 and 2.3 per 100,000 population, with between 1–5 deaths per annum. The predominant *Legionella* species causing disease in New Zealand differs from that found in other developed countries, with about 30–50 percent of cases due to *L. longbeachae* and a similar percentage due to *L. pneumophila* for any given year, *L. pneumophila* being the more common overseas. From October 2010–2014, Canterbury District Health Board used an enhanced testing strategy to detect cases of Legionnaires’ disease. All lower respiratory samples from hospitalised patients with suspected pneumonia have been tested for *Legionella spp.* by PCR (the diagnostic method of choice), whether specifically requested or not. This approach has resulted in a greater than four-fold increase in case detection and has clearly delineated the local epidemiology of Legionnaires’ disease.

The houses involved in the Beachlands outbreak of legionellosis had their own drinking-water systems, by choice, and were not supplied by piped supplies. Their water supplies thus come under the Building Act 2004, not the Health Act.1956. Under the Building Act (BA) houses are classed as individual dwellings and neither the BA nor the Building Code requires that their drinking-water quality be monitored. As there is no provision in the HA that overrides Section 18 of the BA, the Ministry of Health does not, and under Section 18(1)(a) of the BA legally cannot, carry out routine water quality testing on self-supplied drinking-water systems. Thus investigation of drinking-water quality in individual dwellings by the Ministry of Health under the Health Act only takes place if the Ministry has evidence that insanitary conditions exist in the houses. A case of legionellosis provides such evidence and can trigger an investigation, but this investigation would occur after the event, not prior to it.

### Treatment of drinking-water

Since legionellae can grow in association with many different micro-organisms (Bartrum et al 2007), it is important to control other micro-organisms to reduce the proliferation of legionellae. In general, legionellae in drinking-water can be inactivated quite effectively by most of the common forms of disinfection. Treatment of water with chlorine or chloramines will eliminate these organisms. *Legionella pneumophila* strains isolated from chlorinated water supplies tend to be more resistant to chlorine (Kutcha et al 1983, 1985) and may survive for prolonged periods at low chlorine levels. Therefore, legionellae may be present in drinking-water in the absence of indicator organisms.

Water treatment that does not produce a residual disinfectant level in the distribution system does not prevent bacterial regrowth, consequently treatment of drinking water with ozone or UV may not be sufficient to prevent the growth of *Legionella* in the distribution network. Chlorine breaks down in hot water cylinders.

The *Guidelines for the Control of Legionellosis* (MoH 1995 – see revision 2011) has a section on hot, warm and cold water systems and includes guidelines for decontamination. See also AS/NZS 3666: Parts 1, 2 and 3, *Air-handling and water systems of buildings – Microbial control*, and NZS 4302: *Code of practice for the control of hygiene in air and water systems in buildings.*

EC (2005) developed European guidelines.

Chapter 4 of Bartrum et al (2007) discusses control of legionellae in water supplies and buildings.

Temperature control of hot water cylinders as required by the New Zealand Building Act/Building Code should control the organism in buildings.

It is not advisable to monitor water systems of legionellae routinely or to disinfect all environmental sites where legionellae are detected. The following are generally accepted indications for disinfection:

* sites that are implicated in an outbreak of Legionnaires’ disease or Pontiac fever
* hospital wards housing high-risk patients, such as organ transplant units
* buildings in which the water system has not been used for some time and where high numbers are likely to be found.

Vulnerable systems should be designed and maintained in such a way that colonisation by *Legionella* is prevented or minimised. The main points to consider are:

* preventing the accumulation of sludge, scale, rust, algae and slime and removing such deposits regularly
* maintaining hot water temperatures permanently above 60°C or at intervals above 70°C, and keeping cold water supplies below 20°C
* selecting materials in contact with water which do not release nutrients that support the growth of *Legionella.*

These measures are preferable to, and more effective than, the use of biocides to control legionellae in water supplies within buildings; however, biocides are essential to prevent the build-up of microbial slimes in air conditioning systems that use wet evaporative cooling towers. Such systems should be kept clean and be well-maintained. They should be inspected weekly for fouling and accumulated slimed, scale and for corrosion, and thoroughly cleaned and disinfected twice yearly. Biocides are best used intermittently in clean systems.

It is now recommended practice to incorporate biocides in cooling towers/air-conditioning systems, preferably broad-spectrum types, to reduce the total microbial load. Biocides used in cooling tower water are usually divided into two main groups, oxidising and non-oxidising compounds. Commonly used oxidising antimicrobials for cooling water include chlorine, bromine, stabilised bromine, combinations of bromine and chlorine, chlorine dioxide, peroxy compounds such as hydrogen peroxide, peracetic acid and ozone (Bartram 2007). The most common type of biocidal treatment of cooling tower water is by non-oxidising biocides. As an example, non-oxidising chlorinated phenolic thioether has shown acceptable control. Others include the quaternary ammonium derivatives and isothiazolinones. Carbamates and triazines are considered to have a moderate to low toxicity to aquatic flora and fauna. They should be used instead of hydantoins, isothiazolones and quaternary ammonium compounds, which have a higher toxicity rating. These systems should have no means of cross-connecting with the water supply.

USEPA (2015) discusses the use of chlorine, monochloramine, chlorine dioxide, copper-silver ionisation (CSI), UV disinfection, ozone, and point-of-use treatment. They summarised:

* relatively high doses of chlorine (2 to 6 mg/L) were needed for continuous control of *Legionella* in water systems
* the case studies cited generally support maintaining a chloramine residual in the building water system in the range of 1 to 2 mg/L as an effective means for containing biofilm growth, minimising *Legionella* colonisation, and preventing outbreaks
* chlorine dioxide dosage rates of 0.4 to 0.7 mg/L were reported by systems experiencing successful treatment performance
* high concentrations of both copper and silver have been reported in systems employing CSI, to levels approaching the maximum contaminant level goal and action level for copper (1.3 mg/L) and the secondary maximum contaminant level (SMCL) for silver (0.1 mg/L)
* UV is only effective at inactivating *Legionella* in the water that flows through the UV reactor. For existing facilities with *Legionella* in the piping system downstream of a UV reactor, supplemental controls such as thermal treatment or chemical disinfection will be necessary
* due to the faster decomposition of ozone in warm water, water leaving the ozone contactor with a concentration of 1–2 mg/L may not have a concentration high enough to inactivate *Legionella* when it reaches distal parts of the system
* *Legionella* cells are typically 0.3–0.9 micrometres (μm) wide and 2–20 μm long when grown in laboratory culture; ie, smaller than *Cryptosporidium*. Therefore ultrafiltration or finer will be needed.

### Method of identification and detection

Legionellae are gram-negative, rod-shaped, non-sporing bacteria that require L-cysteine for growth and primary isolation. Cellular fatty acids in legionellae are unique for gram-negative bacilli in that they contain primarily branched chains.

Isolation of legionellae from environmental samples may require pre-concentration if numbers are low. Immunofluorescence techniques may also be used to detect legionellae in the environment. See APHA (2005), Method 9260 J (Legiolert™/Quanti-Tray®); Petrisek and Hall (2018).

### Derivation of Maximum Acceptable Value

No specific guideline value can be established for *Legionella*. The absence of test mechanism does not guarantee the total absence of the organism. Warm water handling systems should always be regarded as being at risk of contamination by *Legionella*.

In Victoria Australia (as at 2015), regulations no longer require testing warm water systems periodically for *Legionella*, but it is recommended that all high-risk facilities undertake a water sampling program as part of a risk management approach. <https://www2.health.vic.gov.au/public-health/water/legionella-risk-management-guidelines/legionella-water-delivery-systems> (accessed March 2018).

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# *Leptospira*

### Maximum Acceptable Value

No MAV has been set for *Leptospira* in New Zealand drinking-water. *Leptospira* are included in the [plan of work of the rolling revision](http://www.who.int/entity/water_sanitation_health/gdwqrevision/en/index.html) of the WHO Guidelines for Drinking-water Quality.

### Sources to drinking-water

The causative organisms have been found in the urine of a variety of both wild and domestic animals, including rodents, possums, insectivores, dogs, cattle, pigs and horses. Pathogenic *Leptospira interrogans* are maintained in the renal tubules of many animal hosts. This can take the form of chronic asymptomatic infections, with excretion persisting for very long periods and even for life. Leptospires have a relatively low resistance to adverse environmental conditions (eg, low pH, desiccation, direct sunlight); in the right circumstances (neutral pH, moderate temperatures), however, they can survive for months in water and damp soil. While domestic animals undergo vaccination, waterways should be fenced off to prevent livestock contaminating them as well as these being a source of infection.

### Health considerations

Leptospires are aerobic spirochetes that are typically 0.1 μm in diameter and 5–25 μm in length. There are two genera: *Leptospira* which includes the pathogenic *L. interrogans*, and *Leptonoma*. *Leptospira interrogans* causes the important zoonotic and widespread disease leptospirosis. More than 200 pathogenic serovars have been identified, and these have been divided into 25 serogroups based on serologic relatedness. See DoL (2007) for a discussion about other species seen in New Zealand.

Leptospirosis is a bacterial disease that affects both humans and animals caused by pathogenic *Leptospira* spp. Human infection occurs through direct contact with the urine of infected animals or by contact with a urine-contaminated environment, such as surface water, soil and plants. Vaccination of animals already infected with *Leptospira* does not reduce their shedding of leptospires and consequently does not reduce the risk of exposure to farm personnel (in McLean et al 2014).

The severity of illness and the types of symptoms vary widely. Infections are often subclinical or so mild that medical attention is not sought. At the other extreme, pulmonary bleeding can result in death. The early stages of the disease may include high fever, severe headache, muscle pain, chills, redness in the eyes, abdominal pain, jaundice, haemorrhages in skin and mucous membranes (including pulmonary bleeding), vomiting, diarrhoea and a rash. Long-lasting sequelae have been identified, including depression, headaches, fatigue and joint pains. Weil disease, characterised by jaundice, renal failure, haemorrhage and myocarditis, has been used as an alternative term for leptospirosis, but it represents a subset of the manifestations. WHO (2004) reports that estimates of case fatalities vary from <5 percent to 30 percent, but the figures are not considered reliable owing to uncertainties over case prevalence. Fatality rates are influenced by the timeliness of treatment interventions. The number of cases is not well-documented as a result of lack of awareness and adequate methods of diagnosis.

Leptospirosis is the world’s most common zoonotic disease, New Zealand’s most common occupationally acquired infectious disease, and its incidence in New Zealand is high in comparison with other temperate developed countries (DoL 2007). In 2015 there were 63 notified cases of leptospirosis in New Zealand.

Leptospires can gain entry to the body through cuts and abrasions in the skin and through mucous membranes of the eyes, nose and mouth, as may occur when bathing or swimming in contaminated water. Human-to-human transmission occurs only rarely.

### New Zealand significance

Water contaminated with urine and tissues of infected animals is an established source of pathogenic leptospires. There is no recorded incidence of leptospirosis arising from drinking-waters in New Zealand.

The disease in New Zealand is generally considered to be work-related. Of the 82 cases in 2005 with recorded occupation, 39 (47.6 percent) worked in the meat processing industry (as either freezing workers, butchers, meat inspectors, meat processing managers, and meat processing cleaning supervisors) and 36 (43.9 percent) were farmers, farm workers, or stock truck drivers. Cases in the 2005 year also included one possum hunter, one market gardener, one contractor (engaged in stock/effluent pond cleaning), one furniture manufacturer (who also had contact with animal manure), one coalmine supervisor (who also had a hobby farm), one concrete cutter, and one plumber. (Taken from DoL 2007.)

Approximately 95 percent of New Zealand dairy herds are vaccinated and all commercial pig producers are mandated to do so.

Leptospirosis is an infectious disease notifiable to the Medical Officer of Health. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of leptospirosis.

In 2016, there were 79 leptospirosis notifications in New Zealand. Provisional data from 2017 showed a large increase to 142 leptospirosis notifications. This increase may be due to increased use of nucleic acid testing by laboratories or inclusion of cases likely acquired overseas in the provisional data. Leptospirosis notification rates were generally higher for males, people aged 45–54 years, Māori, people of European/Other ethnicity, people living in NZDep2013 quintile 3, and people living in rural areas. In 2012–16, the highest leptospirosis notification rates were in Hawke’s Bay, West Coast, Wairarapa, and Whanganui District Health Boards (EHI 2018).

### Treatment of drinking-water

Leptospires are sensitive to disinfectants. No problems are expected when bathing in drinking-water that satisfies the bacterial compliance requirements of the DWSNZ.

### Method of identification and detection

See APHA (2005), Method 9260 I.

### Derivation of Maximum Acceptable Value

There are insufficient data to establish a guideline value for the *Leptosporidia*. Because leptospires are excreted in urine and may persist in favourable environments, *E. coli* (or, alternatively, thermotolerant coliforms) is not a suitable index for the presence/absence of this organism.

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# *Mycobacterium*

### Maximum Acceptable Value

No MAV has been set for *Mycobacterium* in New Zealand drinking-water.

### Sources to drinking-water

The tuberculous or “typical” species of *Mycobacterium*, such as *M. tuberculosis*, *M. bovis*, *M. africanum* and *M. leprae*, have only human or animal reservoirs and are not transmitted by water. In contrast, the non-tuberculous or “atypical” species of *Mycobacterium* are natural inhabitants of a variety of water environments. Tap water has long been known to harbour saprophytic mycobacteria (Collins et al 1984); one of the most commonly occurring species, *M. gordonae*, is also known as the “tap water bacillus”. Opportunistic pathogenic species have also been isolated from tap water. Several mycobacteria, including *M. kansasii, M. zenopi, M. gordonae, M. flavescens, M. fortuitum, M. chelonea* and *M. avium complex,* are found frequently in reticulation systems (Fischeder et al1991*;* von Reyn et al1993; Kubalek and Mysac 1995; Peters et al 1995), some of which were isolated in the course of epidemiological investigations.

In a UK study *Mycobacteria* spp. were isolated from of 19 of the 170 water samples (11 percent) tested. Of these, three were MAC (two *M. avium* isolates, one *M. intracellulare* isolate). MAP was not isolated from any sample. These three MAC positive samples were isolated from the same water treatment and distribution system, once from raw water and twice from water in distribution (DWI 2001). DWI (2003) reported that mycobacteria were isolated from every type of sample in another study, most commonly isolated from showers (67 percent) and least commonly from tap net deposits (17 percent). Ten samples were positive for MAC and these were from shower (three samples) and hot water (four samples) in properties and from reservoir (one sample) and water meter (two samples) deposits. Colonisation by *M. avium* is highest when water temperatures are 40–50°C.

*Mycobacterium lentiflavum* is a species of slow-growing non-tuberculous mycobacterium (NTM) which has been isolated from soil and water samples around the world. Links between environmental sources and human disease attributed to this organism have not been demonstrated. NTM disease (caused by a number of different mycobacterial species) is a notifiable disease in Queensland, Australia. In 2008, there were about 900 isolates of NTM reported. During 2007–2008, potable water was collected from 206 sites in Brisbane’s drinking water system and tested for the presence of *Mycobacterium* species. Mycobacteria were grown from 70 percent of the 206 water sites. The predominant isolates found were *M. gordonae* and *M. kansasii*. *M. lentiflavum* was isolated from 13 sites of which two were reservoirs, one was a treatment plant and remainder were points in the distribution system. Eleven sites had the same groundwater source but were distributed among 10 different reservoir zones (Marshall et al 2010).

WHO (2004) states: Mycobacteria can be recovered from a wide variety of environmental niches and *Mycobacterium avium* Complex (MAC) has been recovered from both fresh water (ponds, lakes, rivers, bogs and swamps), brackish, sea water and wastewater, sometimes in high numbers. MAC has been recovered from drinking-water systems before and after treatment, from the distribution system and from raw source waters. Mycobacterial numbers were higher in the distribution system samples (average 25,000-fold) than in those collected just after treatment, suggesting that they grow in distribution system. Mycobacterial infections linked to contaminated hospital water have been recognised for many years, and MAC has been isolated from hospital waters, particularly hot water systems. The increase in mycobacterial numbers correlated with assimilable organic carbon (AOC) and biodegradable organic carbon levels. MAC are relatively resistant to chlorine, monochloramine, chlorine dioxide and ozone. Soil is also a significant reservoir. Environmental mycobacteria are a frequent cause of infection, and there is a growing body of evidence to show that water is a significant vehicle for the transmission of these organisms.

The ecology of opportunistic mycobacteria in water supplies is poorly understood. The bacteria have been isolated infrequently from treated water or mains water but appear to multiply within the plumbing system in buildings as well as in taps. Increased isolation frequencies have been associated with higher temperatures (hot water systems or cold water pipes in the vicinity of central heating). Older buildings appear to be colonised more frequently than new ones, and distribution of drinking-water over long distances also seemed to increase the numbers of mycobacteria. *Mycobacterium porcinum* was first recognised as a human pathogen in 2004 and is classified as a rapidly growing *Mycobacterium* (RGM). A US study found hospital patients with lung and skin infections; 63 percent of all samples of hospital ice and water contained one or more species of RGM, with 50 percent of samples identified to species level containing *M. porcinum*. Summarised in WQRA (2012).

Survival of *M. bovis* is better under cool conditions. *M. bovis* survived in cow faeces for five months in winter but only two months in summer. It is inactivated by sunlight (MPI 2009). Mycobacteria can survive in water with few nutrients; M. intracellulare was found capable of surviving for over a year in reverse osmosis-deionized water (from Health Canada 2013).

### Health considerations

The pathogenic mycobacteria do not grow in the environment (Portaels 1995). The remaining mycobacteria are regarded as environmental in habitat, and some are considered opportunistic pathogens in a minority of susceptible people. Immunocompromised patients, such as those with AIDS, are particularly susceptible to mycobacterial infections (Portaels 1995).

Most pathogenic species of *Mycobacterium* are found among the slow growers. These comprise the pathogenic species *M. tuberculosis, M. bovis, M. africanum* and *M. leprae*, which are not transmitted by water and have only human or animal reservoirs. Other mycobacterial species, which have been referred to as atypical mycobacteria, have environmental reservoirs. Although many are considered non-pathogenic, several species are opportunistic pathogens for humans. The most important species are the slow growers *M. kansasii, M. marinum, M. avium, M. intracellulare, M. scrofulaceum* and *M. xenopi*; and the rapid growers *M. chelonae* and *M. fortuitum*.

Strictly pathogenic mycobacteria are associated with classical diseases such as tuberculosis and leprosy. The environmental mycobacteria may cause a range of diseases including tuberculous lung disease, and disseminated infections that may also involve the skeleton (*M. kansasii, M. avium* complex), infections of lymph nodes (MAIS complex), infections of the skin and soft tissues (*M. marinum, M. fortuitum* complex). *Mycobacterium avium* subsp. *paratuberculosis* (MAP) is a putative cause of Crohn’s disease (CD), a chronic inflammatory disease of the gastrointestinal tract of humans. The association is poorly understood, and based largely on clinical similarity between Crohn’s disease (CD) and Johne’s disease, a chronic, contagious and lethal disease that effects a wide range of livestock and domestic and wild animals, of which MAP is a known etiological agent (DWI 2005). However, DWI (2005a) found no evidence of an increased risk of CD in association with exposure to two primary hypotheses (drinking water and milk) for transmission pathways of MAP. Consequently this study does not support a role for MAP or drinking water in the aetiology of CD.

*Mycobacterium bovis* enters the body via the intestinal tract in foodborne infections, and primary infection is set up in the associated lymph nodes to form “tubercles”. The infection is often contained at that point, but it can also spread to other parts of the body to cause illness referred to as intestinal tuberculosis or tuberculous enteritis. Symptoms may last for months or years. To-date there is no evidence of transmission by the waterborne route (MPI 2001).

Diseases caused by opportunistic pathogenic mycobacteria are not normally transmitted from person to person but are usually the result of environmental exposure in combination with predisposing factors such as dust retained in the lungs, surgical wounds, or immunosuppression by medication (transplantation patients) or underlying disease (AIDS, malignancies). Mycobacteria are generally resistant to many antimicrobial agents; hence effective treatment may be difficult.

Detections of atypical mycobacteria in drinking-water and the identified routes of transmission suggest that drinking-water supplies are a plausible source of infection. A link between the occurrence of mycobacteria in drinking-water and disease has been suggested in specific incidents. In an investigation of endemic *M. kansasii* infections in Czechoslovakia from 1968, a peak incidence was shown in a small, densely populated district with workers engaged in mining and the heavy or power industry. The organism could also be isolated from shower outlets in collieries, and it was shown later that the drinking-water system in the whole region was contaminated. It was suggested that spread of mycobacteria from drinking-water occurred via aerosols. In Rotterdam in The Netherlands, the frequent isolation of *M. kansasii* from clinical specimens prompted an investigation of the water supply system. The organisms were isolated frequently from tap water and exhibited the same phage type and weak nitratase activity as clinical strains. The increase in number of isolations of the *M. avium* complex in Massachusetts, USA, has also been attributed to their incidence in drinking-water.

It must be noted that in all these cases there is only circumstantial evidence of a causal relationship between the occurrence of bacteria in drinking-water and human disease. The low infectivity of environmental mycobacteria does not warrant standards or eradication programmes.

### New Zealand significance

There is no recorded incidence of mycobacterial disease arising from drinking-waters in New Zealand. Humans are a reservoir of the organism, but human to human infection occurs only rarely. Cattle and other animals are reservoirs of the organism. The possum is a reservoir in New Zealand, making eradication from livestock difficult.

Unpasteurised milk used to be a common vehicle for transmission of *M. bovis*. However, since the introduction of mandatory pasteurisation, milk has largely ceased to be a vehicle. Since 1995, two cases of *M. bovis* infection in New Zealand have reported consuming unpasteurised milk among the risk factors recorded, but in neither case was this vehicle confirmed (MPI 2009).

### Treatment of drinking-water

Atypical *Mycobacterium* spp. multiply in a variety of suitable water environments, notably biofilms. One of the most commonly occurring species is *M. gordonae*. Other species have also been isolated from water, including *M. avium*, *M. intracellulare*, *M. kansasii*, *M. fortuitum* and *M. chelonae*. High numbers of atypical *Mycobacterium* spp. may occur in distribution systems after events that dislodge biofilms, such as flushing or flow reversals. They are relatively resistant to treatment and disinfection and have been detected in well-operated and well-maintained drinking-water supplies with HPC less than 500 per mL and total chlorine residuals of up to 2.8 mg/L. The growth of these organisms in biofilms reduces the effectiveness of disinfection. In one survey, the organisms were detected in 54 percent of ice and 35 percent of public drinking-water samples.

Physical treatment processes need to be effective because mycobacteria are relatively resistant to disinfection. WHO (2004) reports in Chapter 11 a study that examined the disinfection resistance of five strains of *M. avium* to free chlorine, monochloramine, chlorine dioxide and ozone and determined the disinfectant concentration multiplied by the time for a 3 log (99.9 percent) inactivation. Free chlorine values for the *M. avium* strains were 700 to 3000 times greater than that for *E. coli*. Similarly, the 3 log values of the *M. avium* strains for chlorine dioxide and ozone were at least 100- and 50-fold greater (respectively) than the *E. coli* strain.

Free available chlorine residuals of 0.5 to 1.0 mg/L are needed to control the mycobacterial densities in the distribution system.

WHO (2004) includes a table (Table 11.5) based on Taylor et al (2000) that compares C.ts for *Giardia* and *Mycobacterium avium* (see below). WHO (2004) includes discussion in Chapter 11 about the efficacy of other disinfectants.

Comparison of C.ts (3 log in mg.min/L) for *Giardia* cysts and *M. avium*

|  |  |  |
| --- | --- | --- |
| **Disinfectant** | ***Giardia* cysts** | ***M. avium*** |
| chlorine | 46 | 130 |
| monochloramine | 700\* | 580 |
| chlorine dioxide | 11 | 7 |
| ozone | 0.48 | 0.13 |

Data are for pH 7.0, 23 to 25°C. Average *M. avium* data based on Taylor et al2000.

\* Extrapolated.

### Method of identification and detection

*Mycobacterium* spp. are rod-shaped bacteria with a high lipid content in cell walls, which enables them to retain specific dyes in staining procedures that employ an acid wash. They are therefore often referred to as acid-fast bacteria. All mycobacteria are characterised by slow growth (generation times under optimum circumstances 2–20 hours), but within this range they are divided into “slow” and “rapid” growers. Analytical procedures have not been developed specifically for drinking-water although clinical methods can be used (Balows 1991).

A later, and very full, discussion appears in Chapter 5 of WHO (2004). See also DWI (2005) and APHA (2005), Method 9260 M. Mycobacteria are not detected by HPC techniques, and *E. coli* (or, alternatively, thermotolerant coliforms) is not a suitable index for the presence/absence of this organism.

### **Derivation of M**a**ximum Acceptable Value**

There are insufficient data to establish a guideline value for mycobacteria.

When epidemiological associations between the presence of mycobacteria in drinking-water and infections in the community can be demonstrated, an investigation into the source of the contamination, and its removal, should be investigated.

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# *Pseudomonas aeruginosa*

### **Maximum Acceptable Value**

No guideline value has been established for *Pseudomonas aeruginosa* in New Zealand drinking-waters.

### **Sources to drinking-water**

*Pseudomonas aeruginosa* is found commonly in faeces, soil, water and sewage. It cannot be used as an indicator of faecal contamination, as it is not universally present in faeces and sewage, and it may also multiply in an enriched aquatic environment and on the surface of suitable organic materials in contact with water. Its presence, however, can be used to assess the general cleanliness of water distribution systems and the quality of bottled waters.

Some strains of some *Pseudomonas* species have been developed and approved for use as biofungicides or bactericides (see PMEP): *P. aureofaciens*, *P. fluorescens*, *P. syringae*. They do not appear to be registered for use in New Zealand.

### **Health considerations**

*P. aeruginosa* is a classical opportunistic pathogen. *P. aeruginosa* can cause a range of infections but rarely causes serious illness in healthy individuals without some predisposing factor. It rarely becomes established in, and even more rarely infects, the intact host but colonises damaged systems: burn wounds, the respiratory tract of people with underlying disease, physically damaged eyes, etc. From these it may invade the body causing destructive lesions or septicaemia. Immunosuppressed people are at risk.

Contaminated irrigation fluids or pharmaceutical agents (eg, eye drops) delivered to damaged areas have caused severe infection. *Pseudomonas aeruginosa* is a recognised cause of hospital-acquired infections with potentially serious complications. While it is clearly undesirable for water supplies to hospitals to have high counts of this organism (or other opportunistic pathogens), a direct association of hospital infections with drinking-water sources is yet to be established. It has been isolated from a range of moist environments such as sinks, water baths, hot water systems, showers and spa pools. Cleaning of contact lenses with contaminated water can cause a form of keratitis.

High counts of this organism in water of spa and swimming pools have been linked with rashes and superficial infections of the outer ear canal (Jones and Bartlett 1985; Calderon and Mood 1982).

*P. aeruginosa* can display an unusually high degree of antibiotic resistance, which has been linked to its ability to result in unusual phenotypes in stressed environmental conditions.

### **New Zealand significance**

Though *P. aeruginosa* may occur in New Zealand drinking-water supplies, it has only been associated with cases of folliculitis (inflammation of the hair follicles) in health spa whirlpools.

### **Treatment of drinking-water**

*Pseudomonas aeruginosa* is sensitive to disinfection, and entry into distribution systems can be minimised by adequate disinfection. Control measures that are designed to minimise biofilm growth, including treatment to optimise organic carbon removal, restriction of the residence time of water in distribution systems and maintenance of disinfectant residuals, should reduce the growth of these organisms. Free available chlorine residuals of 0.2 to 0.5 mg/L are generally sufficient to control *P. aeruginosa* in water, although higher levels may be required for spa pools.

### **Method of identification and detection**

*P. aeruginosa* is a member of the family Pseudomonadaceae and is a polarly-flagellated, gram-negative rod. It is capable of producing pigments when grown in suitable media. The most significant are the non-fluorescent phenazine pigment, pyocyanin, and fluorescin. Pigment may not be produced by strains of *P. aeruginosa* recovered from clinical specimens and the ability to produce pigment may be lost on subculture. Like other fluorescent pseudomonads that occur in natural waters, *P. aeruginosa* strains produce catalase and oxidase, and produce ammonia from arginine; they grow with citrate as the sole source of carbon; and they are aerobic.

*P. aeruginosa* can grow at 41–42°C. The blue-green pigment it produces differs from the fluorescent pale green pigment (fluorescin) produced by other species of fluorescent pseudomonads found in water. It can also grow anaerobically in stab cultures of nitrate agar. See APHA 2005.

### **Derivation of Maximum Acceptable Value**

Owing to the ubiquitous occurrence of the organism and its opportunistic nature as a pathogen, it is difficult to set a guideline for drinking-water. However, the presence of the organism in drinking-water may indicate a serious deterioration in bacteriological quality, and it is often accompanied by taste, odour and turbidity complaints associated with low rates of flow in the distribution and a rise in water temperature.

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# *Salmonella*

### **Maximum Acceptable Value**

Faecal coliforms (or alternatively *E. coli*) and coliforms are used to indicate the possible presence of salmonellae. If sought explicitly, *Salmonella* should not be detected. If detected, advice should be sought from the relevant health authority.

### **Sources to drinking-water**

Salmonellae (in the family Enterobacteriaceae) are widely distributed in the environment and gain entry into water systems through faecal contamination from livestock, native animals, drainage waters and incompletely treated waste discharges.

Faecal contamination of water that is inadequately treated or inadequately disinfected is the main cause of waterborne outbreaks of salmonellosis. WHO (2004) reports a case of illness associated with a communal rainwater supply where bird faeces were implicated as a source of contamination.

*Salmonella* shed in faeces can contaminate pasture, soil and water. They can survive for months in the soil. Survival in dry environments is a characteristic of the non-typhoid Salmonellae, for example they can survive on surfaces and in chocolate for months. *S. typhi* can survive in seawater for up to nine days, and in sewage for weeks. Survival in groundwater was better than in pond, stream or lake water and this was attributed to less grazing pressure by protozoa (MPI 2001).

### **Health considerations**

There has been much debate about the nomenclature and taxonomy of *Salmonella*, but it is now (WHO 2011) considered that there are actually two species (*Salmonella enterica* and *Salmonella bongori*). Other previously named species, including *S.*Typhi and *S.*Paratyphi, are considered to be serovars. Salmonella enterica is the species of most relevance for human infections, and it can be further broken down into six subspecies, of which one, Salmonella enterica subsp. enterica, contains the majority of serotypes that are associated with cases of human gastroenteritis (from Health Canada 2013). With regard to typhoid (enteric) illness, *Salmonella* spp. can be divided into two fairly distinct groups: the typhoidal species/serovars (*S.*Typhi and *S.*Paratyphi) and the remaining non-typhoidal species/serovars.

*Salmonella* infections typically cause four clinical manifestations: gastroenteritis (ranging from mild to fulminant diarrhoea, nausea and vomiting), bacteraemia or septicaemia (high spiking fever with positive blood cultures), typhoid fever / enteric fever (sustained fever with or without diarrhoea), and a carrier state in persons with previous infections.

Salmonellae, with the exception of those that cause enteric fever in humans (Lloyd 1983), are pathogens of animals that provide important reservoirs for the infection of humans. Typhoid fever is a bacterial infection of the intestinal tract and bloodstream. *Salmonella* serovar Typhi, is a specific human pathogen, humans are the sole reservoir of this organism. In particular, *S*. serovar Typhi, *S*. serovar Paratyphi A, and *S*. serovar Paratyphi B are able to invade tissues and cause a septicaemia with high temperature rather than diarrhoea. This is known as enteric fever. In humans, most of the other serovars cause a transient intestinal infection that results in acute gastroenteritis with diarrhoea. Certain serovars are highly pathogenic for humans, while others appear non-pathogenic. Many *Salmonella* infections are symptomless.

Epidemiological and volunteer studies show that the infective dose of *Salmonella* varies considerably. Method of intake, individual host susceptibility, and virulence of the particular strain are important in determining the dose required to produce an infection.

Symptoms of non-typhoidal gastroenteritis appear from 6 to 72 hours after ingestion of contaminated food or water; non-typhoidal *Salmonella* spp. rarely cause drinking-water-borne outbreaks. Diarrhoea lasts 3–5 days and is accompanied by fever and abdominal pain. Usually the disease is self-limiting. The incubation period for typhoid fever can be 1–14 days but is usually 3–5 days. Typhoid fever is a more severe illness and can be fatal.

*Salmonella* is spread by the faecal–oral route. Infections with non-typhoidal serovars are primarily associated with person-to-person contact, the consumption of a variety of contaminated foods, and exposure to animals. Infection by typhoid species (*Salmonella typhi* and *S.*Paratyphi) is associated with the consumption of contaminated water or food, with direct person-to-person spread being uncommon.

### **New Zealand significance**

As *Salmonella* is a zoonotic pathogen, runoff from agricultural lands can provide a mechanism for the transfer of animal faecal wastes to source waters. *Salmonella* has been isolated from source waters in New Zealand. There are no published associations between the isolation of *Salmonella* from drinking-water and health effects in the community.

Most illnesses resulting from *Salmonella* infection in New Zealand are derived from contaminated foodstuffs, eg, poultry and livestock, and from consuming raw or undercooked contaminated shellfish. Waterborne salmonellae play only a minor role in causing disease today.

Salmonellosis (including typhoid and paratyphoid) is an infectious disease notifiable to the Medical Officer of Health. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of *Salmonella* related cases (salmonellosis and typhoid).

A study of *S*. Typhimurium DT160 was prompted by a marked increase in the number of DT160 human isolates which began in May 2001. Twenty-four cases of *S*. Typhimurium DT160 salmonellosis were reported in the Auckland region, and the first 10 case patients interviewed reported consumption of raw or undercooked egg. The epidemic of *S*. Typhimurium DT160 infection among humans occurred in parallel with illness due to the same pathogen in wild birds, particularly sparrows. Environmental sampling was carried out on roof-collected rainwater supplies from the homes of cases, and egg brands consumed by cases. Twelve case patients had roof-collected water supplies; eight of these sources were sampled and four samples (used by five cases) were contaminated with *S.*Typhimurium DT160. Although untreated water is a recognised risk factor for salmonellosis (in this case possible contamination by bird faeces), this risk factor was not confirmed by the case-control study (MPI 2004).

Results of a nationwide survey of 10 pathogens and indicators undertaken at 25 freshwater sites in New Zealand over a 15-month period found that *Salmonella* were detected in 10 percent of samples) and were most commonly found in August in catchments predominantly impacted by sheep farming (Till et al 2008).

### **Treatment of drinking-water**

Treatment by disinfection using chlorine is usually effective against salmonellae, provided the water has low turbidity.

### **Method of identification and detection**

*Salmonella* are gram-negative, non-sporing rods, which do not ferment lactose; most produce hydrogen sulphide or gas from carbohydrate fermentation. They are a member of the family Enterobacteriaceae.

The numbers of *Salmonella* in water can be determined by concentration followed by enrichment, isolation and confirmation (APHA Water and Wastewater 9260 B, C, D). Note however that *S. typhi* is thought to undergo transition to the viable non-culturable (VNC) state in water.

### **Derivation of Maximum Acceptable Value**

The presence of faecal indicator bacteria is useful to determine the possible presence of salmonellae. However, as with many other pathogens, salmonellae may occasionally be present when indicators are absent, particularly where a supply may have been subject to faecal contamination by amphibians (frogs) and reptiles. It is also important, therefore, to test directly for salmonellae if contamination is suspected.

The direct effect on the community of non-compliance with the guideline will depend on the *Salmonella* spp. involved. The numbers of *Salmonella* may be amplified through contamination of foodstuffs.

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# *Shigella*

### **Maximum Acceptable Value**

Faecal coliforms (or alternatively *E. coli*) and coliforms are used to indicate the presence of pathogenic *Shigella*. If sought explicitly, pathogenic *Shigella* spp. should not be detected. If detected, advice should be sought from the relevant health authority.

### **Sources to drinking-water**

Bacteria of the genus *Shigella* (in the family Enterobacteriaceae) cause bacillary dysentery. There are four species: *S. dysenteriae*, *S. flexneri*, *S. boydii* and *S. sonnei*. Shigella sonnei and Shigella flexneri are the two species of importance as causes of gastrointestinal illness in developed countries. Although infection by *Shigella* is not often waterborne, major outbreaks resulting from waterborne transmission have been described. The isolation of shigellae from drinking-water indicates recent human faecal contamination, but this occurs only rarely. This possibly indicates the limitations of the method rather than absence of the organisms, as there is no useful enrichment or selective medium for isolation of these bacteria. Techniques used have been designed for isolation of salmonellae and are not optimal for shigellae.

Infected humans are the only significant reservoir. As the organisms are not particularly stable in water environments, their presence in drinking-water indicates recent human faecal pollution. Shigellae can survive storage on soil, cheese and herbs for 50 days. It can survive in human faeces for days if the samples remain moist.

### **Health considerations**

Members of the genus have a complex antigenic pattern, and classification is based on their somatic O antigens, many of which are shared with other enteric bacilli, including *E. coli*. They are very similar to *Escherichia coli* and are serologically cross reactive, but have remained a separate species for clinical reasons. Bacteria of the genus *Shigella* cause bacillary dysentery (shigellosis). Shigellae have a low infective dose (as few as 10 to 100 organisms may lead to infection) and are highly pathogenic for humans. They are of crucial public health significance; over two million infections occur each year, resulting in about 600,000 deaths, predominantly in developing countries, and in children under age 10. The incubation period for shigellosis is usually 24 to 72 hours. Characteristic bloody diarrhoea results from the invasion of the colonic mucosa by the bacterium. The process is probably highly species-specific. Shigellae have no natural hosts other than the higher primates, so to all effects, humans are the only source of infection in the New Zealand community. Among the enteric bacterial pathogens, shigellae seem to be the best adapted to cause human disease. Transmission occurs directly between susceptible individuals, and the infectious dose is lower than for other bacteria.

In the United States, *Shigella* accounted for approximately 5 percent of drinking water outbreaks reported from 1991 to 2002, according to US surveillance data. Common causes of waterborne outbreaks by these organisms are poor source water, inadequate treatment or post-treatment contamination; reported in Health Canada (2013).

Among the four species of *Shigella*, *Shigella dysenteriae* type 1 (Sd1) is especially important because it causes the most severe disease and may occur in large regional epidemics. Major obstacles to the control of shigellosis include the ease with which *Shigella* spreads from person to person and the rapidity with which it develops antimicrobial resistance. The low infective dose facilitates person-to-person spread (WHO 2005).

### **New Zealand significance**

No evidence for the transmission of shigellosis through water supplies in New Zealand has been reported. The incidence of infection by *Shigella* in New Zealand is low.

Shigellosis is an infectious disease notifiable to the Medical Officer of Health. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of *Shigella* related cases.

### **Treatment of drinking-water**

Standard disinfection procedures eliminate shigellae from water, provided that the turbidity is low. The control of *Shigella* spp. in drinking-water supplies is of special public health importance in view of the severity of the disease caused.

### **Method of identification and detection**

Shigellae are gram-negative, non-sporing, non-motile rods. Growth occurs both aerobically and anaerobically. Metabolism is both respiratory and fermentative; acid, but usually not gas, is produced from glucose. Lactose is seldom fermented. Catalase is usually produced, except by *Shigella* *dysenteriae* type 1. Oxidase is produced by one serotype only. Nitrates are reduced to nitrites (APHA 2005).

Shigellae are serotyped on the basis of their somatic O-antigens. Both group and type antigens are distinguished, group antigenic determinants being common to a number of related types. Serological typing is adequate for all species except *Shigella* *sonnei*. Do not use salmonella-shigella (SS) agar, as it often inhibits growth of Sd1 (WHO 2005).

Available data on prevalence in water supplies may be an underestimate, because detection techniques generally used can have a relatively low sensitivity and reliability. *Escherichia coli* (or, alternatively, thermotolerant coliforms) is a generally reliable indicator for *Shigella* spp. in drinking-water supplies.

### **Derivation of Guideline**

The isolation of shigellae from drinking-water indicates recent human faecal contamination and, in view of the extreme virulence of the organisms, is of crucial public health significance.

The effect on the community of non-compliance with the guideline will depend on the *Shigella* strain involved, the numbers, and the susceptibility of the population; cases of shigellosis will almost certainly result.

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# *Tsukamurella*

See also Actinomycetes datasheet.

### **Maximum Acceptable Value**

No MAV.

### **Sources to drinking-water**

*Tsukamurella* spp. exist primarily as environmental saprophytes in soil, water and foam (thick stable scum on aeration vessels and sedimentation tanks) of activated sludge. *Tsukamurella* are represented in HPC populations in drinking-water. A South African study found that after *Aeromonas* spp (on 18 percent of plates), *Tsukamurella* were the next commonest bacterium isolated from HPC plates, on 13.3 percent of the plates.

*Tsukamurella* organisms have been detected in drinking-water supplies, but the significance is unclear. There is no evidence of a link between organisms in water and illness. As *Tsukamurella* is an environmental organism, *E. coli* (or, alternatively, thermotolerant coliforms) is not a suitable index for this organism.

### **Health considerations**

*Tsukamurella* spp. cause disease mainly in immunocompromised individuals. Infections with these microorganisms have been associated with chronic lung diseases, immune suppression (leukaemia, tumours, HIV/AIDS infection) and post-operative wound infections. *Tsukamurella* were reported in four cases of catheter-related bacteraemia and in individual cases including chronic lung infection, necrotising tenosynovitis with subcutaneous abscesses, cutaneous and bone infections, meningitis and peritonitis.

### **Method of identification and detection**

The genus *Tsukamurella* belongs to the family Nocardiaceae. *Tsukamurella* spp. are Gram-positive, weakly or variably acid-fast, non-motile, obligate aerobic, irregular rod-shaped, non-spore forming bacteria. They are actinomycetes related to *Rhodococcus*, *Nocardia* and *Mycobacterium*.

The taxon was introduced for actinomycetes previously classified as *Corynebacterium paurometabolum* and *Rhodococcus aurantiacus*. The genus was created in 1988 to accommodate a group of chemically unique organisms characterised by a series of very long chain (68–76 carbons), highly unsaturated mycolic acids, *meso*-diaminopimelic acid and arabinogalactan, common to the genus *Corynebacterium*. The type species is *T. paurometabola*, and the following additional species were proposed in the 1990s: *T. wratislaviensis*, *T. inchonensis*, *T. pulmonis*, *T. tyrosinosolvens* and *T. strandjordae*.

### **Derivation of Maximum Acceptable Value**

No MAV.

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# *Vibrio*

### **Maximum Acceptable Value**

Faecal coliforms (or alternatively *E. coli*) and coliforms are used to indicate the presence of pathogenic *Vibrio*. If sought explicitly, pathogenic *Vibrio* spp. should not be detected. If detected, advice should be sought from the relevant health authority.

### **Sources to drinking-water**

There are a number of pathogenic species, including *V. cholerae*, *V. parahaemolyticus* and *V. vulnificus*. Species are typed according to their O antigens. *Vibrio cholerae* is the only pathogenic species of significance from freshwater environments, the other two being marine organisms, in fact, freshwater can inactivate those organisms. Cholera (caused by *V. cholerae* serotypes O1 and O139), for example, is usually a water-associated disease and numerous such outbreaks have been documented. Foodborne outbreaks, however, are also common. The high numbers required to cause infection make person-to-person contact an unlikely route of transmission; however, person-to-person transmission may occur under conditions of extreme crowding and poor hygiene.

The transmission of cholera has been reviewed extensively, and although water is undoubtedly an important vehicle for transmission, many aspects of the epidemiology of cholera remain open to debate (Miller et al 1985). Evidence has accumulated to suggest that in some circumstances *V. cholerae*, including serotype O1, may occur naturally in some surface waters.

Although *V. cholerae* O1 can be isolated from water in areas without disease, the strains are not generally toxigenic. Toxigenic *V. cholerae* has also been found in association with live copepods as well as other aquatic organisms, including molluscs, crustaceans, plants, algae and cyanobacteria. Numbers associated with these aquatic organisms are often higher than in the water column. Non-toxigenic *V. cholerae* has been isolated from birds and herbivores in areas far away from marine and coastal waters. The prevalence of *V. cholerae* decreases as water temperatures fall below 20°C.

### **Health considerations**

In 1993, *Vibrio cholerae* type O139 was recognised as a potent human pathogen that rapidly achieved pandemic status in southern Asia (Cholera Working Group 1993; Mandal 1993). Hitherto, *V. cholerae* type O1 was considered to be the only cause of cholera. Not all strains of serotypes O1 or O139 possess the virulence factors, and they are rarely possessed by non-O1/O139 strains. Other members of the species are referred to as non-agglutinating strains (Morris 1990). These non-toxigenic strains of *V. cholerae* can cause self-limiting gastroenteritis, wound infections and bacteraemia.

Non-agglutinating strains of *V. cholerae* are part of the normal free-living microbiota in estuarine waters (Roberts et al1982). Non-agglutinating strains of *V. cholerae* have been isolated from sea gulls, poultry and domestic animals (Morris 1990), and asymptomatic carriage by humans has been reported.

*Vibrio* *cholerae* is a well-defined species frequently found in source waters; non-toxigenic *V. cholerae* is widely distributed in water environments, but toxigenic strains are not distributed as widely. While cases of diarrhoea are caused by other types, only the serovar O1 and O139 are associated with the classical cholera symptoms in which a proportion of cases suffer fulminating and severe watery diarrhoea. The O1 serovar has been further divided into “classical” and “El Tor” biotypes, the latter distinguished by the ability to produce a dialysable, heat-labile haemolysin.

In the ‘developed’ world most cases are due to non-O1/non-O139 serotypes. Such incidents are normally associated with the consumption of contaminated seafood. Cholera outbreaks continue to occur in many areas of the developing world. Symptoms are caused by heat-labile cholera enterotoxin carried by toxigenic strains of *V. cholerae* O1/O139. A large percentage of infected persons do not develop illness; about 60 percent of the classical and 75 percent of the El Tor group infections are asymptomatic. Symptomatic illness ranges from mild or moderate to severe disease. The initial symptoms of cholera are an increase in peristalses followed by loose, watery and mucus-flecked “rice-water” stools that may cause a patient to lose as much as 10 to 15 litres of liquid per day. Decreasing gastric acidity by administration of sodium bicarbonate reduces the infective dose of *V. cholerae* O1 from more than 108 to about 104 organisms. Case fatality rates vary according to facilities and preparedness. As many as 60 percent of untreated patients may die as a result of severe dehydration and loss of electrolytes, but well-established diarrhoeal disease control programmes can reduce fatalities to less than 1 percent.

When present in large numbers in the intestinal mucosa, *V. cholerae* O1 and O139 produce an enterotoxin (cholera toxin) that alters the ionic fluxes across the mucosa. This causes catastrophic loss of water and electrolytes in liquid stools. Almost all the organisms that are known to cause epidemic cholera are members of the serogroup O1 and O139, though the very similar *V. mimicus* (sucrose non-fermenter) has been isolated from cases of clinical cholera.

Cholera is typically transmitted by the faecal–oral route, and the infection is predominantly contracted by the ingestion of faecally contaminated water and food. The very high numbers required to cause infection make person-to-person contact an unlikely route of transmission.

### **New Zealand significance**

No cases of cholera originating in New Zealand have been reported, although many travellers have arrived here with it. Non-agglutinating *V. cholerae* is endemic in New Zealand (Baker and Wilson 1993) and has been associated with the consumption of shellfish (Fraser et al 1993).

The occurrence of *V. parahaemolyticus* infection in New Zealand appears to be strongly linked to the personal importation and consumption of seafood by Pacific Islanders. The increasing popularity of raw fish foods, such as sushi, may also make *V. parahaemolyticus* infection more common (MPI 2003).

Cholera is an infectious disease notifiable to the Medical Officer of Health. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of *Vibrio* related cases.

### **Treatment of drinking-water**

*Vibrio cholerae* is highly sensitive to disinfection processes. Within a PHRMP, control measures that can be applied to manage potential risk from toxigenic *V. cholerae* include protection of raw water supplies from human waste, adequate treatment, and protection of water during distribution. *Vibrio cholerae* O1 and non-O1 have been detected in the absence of *E. coli*, and this organism (or, alternatively, thermotolerant coliforms) is not a reliable indicator for *V. cholerae* in drinking-water.

### **Method of identification and detection**

*Vibrio* spp. are non-sporing, slightly curved Gram-negative rods, motile by a single polar flagellum. Their metabolism is both respiratory and fermentative without the production of gas. Their growth is aerobic and facultatively anaerobic. Both catalase and oxidase are formed. Nitrate is reduced to nitrite (APHA Method 9260 H, 2005). Note that *Vibrio* organisms have been shown to undergo a transition to a viable non-culturable (VNC) state.

### **Derivation of Maximum Acceptable Value**

The isolation of *V. cholerae* O1 from water used for drinking is of major public health importance. However, other serotypes of *V. cholerae* are part of the normal flora of some waters. *V. cholerae* and other pathogenic *Vibrio* spp. should be absent from drinking-water supplies.

Microbial agents are included in the [plan of work of the rolling revision](http://www.who.int/entity/water_sanitation_health/gdwqrevision/en/index.html) of the WHO *Guidelines for Drinking-water Quality*. The fourth edition of the WHO Guidelines should contain a brief summary on *Vibrio vulnificus*.

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# *Yersinia*

### **Maximum Acceptable Value**

No guideline value has been established for *Yersinia* in New Zealand drinking-waters. If sought explicitly, pathogenic *Yersinia* spp. should not be detected. If they are detected, advice should be sought from the relevant health authority.

### **Sources to drinking-water**

The genus *Yersinia* is classified in the family Enterobacteriaceae and comprises seven species.

Domestic and wild animals are the principal reservoir for *Yersinia* spp.; pigs are the major reservoir of pathogenic *Y. enterocolitica*, whereas rodents and small animals are the major reservoir of *Y. pseudotuberculosis*. Pathogenic *Y. enterocolitica* has been detected in sewage and polluted surface waters. The major vehicle of transmission is by the faecal–oral route, with the major source probably being food, especially meat and meat products, milk and dairy products (Lloyd 1983). While *Y. enterocolitica* has also been isolated from a variety of environmental samples, especially from water, the isolated serotypes usually differ from those associated with human disease.

Ingestion of contaminated water is also a potential source of infection. Direct transmission from person to person and from animals to people also occurs, but its relative importance has not been clarified. Further research is needed to define the epidemiological importance of environmental strains of *Y. enterocolitica*.

Terrestrial and freshwater ecosystems harbour the pathogen, including soils, vegetation, lakes, rivers, wells and streams. A special feature of *Y. enterocolitica* and *Y. enterocolitica*-like organisms is their capability of growing at temperatures as low as 4°C. Accordingly, long survival of those organisms in water habitats can be demonstrated. For example, *Y. enterocolitica* was detected in ‘sterile’ distilled water for over 18 months at 4°C. Such long survival makes it difficult to reveal the origin of contamination.

### **Health considerations**

The species *Y. pestis*, *Y. pseudotuberculosis* and certain serotypes of *Y. enterocolitica* are human pathogens. *Yersinia pestis* is the cause of bubonic plague through contact with rodents and their fleas. Atypical strains within *Y. enterocolitica*, isolated most frequently from environmental samples, are separated as *Y. enterocolitica*-like organisms. They are not pathogenic for humans and can be subdivided into *Y. intermedia*, *Y. fredereksenii*, *Y. kristensenii*, and *Y. aldovae* by biochemical means.

*Yersinia enterocolitica* penetrates cells of the intestinal mucosa, causing ulcerations of the terminal ilium. Yersiniosis generally presents as an acute gastroenteritis with diarrhoea, fever and abdominal pain, sometimes mistaken for appendicitis; post-infection arthritis may occur in a small proportion of cases. Other clinical manifestations include greatly enlarged painful lymph nodes referred to as “buboes.” The disease seems to be more acute in children than in adults. Not all *Y. enterocolitica* strains can cause human illness. Other human diseases caused by *Y. enterocolitica* are also known. *Y. pseudotuberculosis* also causes gastroenteritis.

No outbreaks of *Yersinia*-related gastroenteritis have been reported for municipal drinking water supplies in North America over the past two decades; reported in Health Canada (2013).

### **New Zealand significance**

Yersiniosis was added to the list of notifiable diseases in New Zealand in June 1996, since when there have been an approximate annual incidence rate of 10 to 12 per 100,000. See Chapter 1: Introduction, Section 1.1.3 for statistics related to the incidence of *Yersinia* related cases.

The first outbreak involving *Y. pseudotuberculosis* in New Zealand was investigated and reported by MPI (2014). A total of 334 cases of yersiniosis were reported, 65 cases were hospitalised. The outbreak was thought to have originated from contaminated vegetables, possibly lettuce or carrots. Amongst the suggested causes for the contamination at the grower stage were:

* crops growing on ground where cattle had recently been grazed
* contaminated irrigation water (surface water, shallow bores or stressed artesian bores)
* contamination with rodent or wild-bird faeces
* contamination with faeces through flooding events.

And at the processor stage:

* use of contaminated wash water or failure of chemical treatment in wash water.

### **Treatment of drinking-water**

Standard disinfection procedures are sufficient to avoid transmission of *Yersinia*, provided the water has a low turbidity when treated. Free chlorine in the range required for water disinfection (0.2 to 0.5 mg/L) for 10 minutes at pH 7 completely inactivates these bacteria. Ozone inactivates the organism after contact with 0.05 mg/L for one minute, regardless of pH.

### **Method of identification and detection**

The genus *Yersinia* is placed currently in the family Enterobacteriaceae and comprises seven species. Strains of *Y. enterocolitica* can cause gastrointestinal disease if ingested. *Y. enterocolitica* is a gram-negative rod, motile at 25°C but non-motile in cultures grown at 37°C (APHA Method 9260 K, 2005).

Owing to the long survival and/or growth of some strains of *Yersinia* spp. in water, *E. coli* (or, alternatively, thermotolerant coliforms) is not a suitable index for the presence/absence of these organisms in drinking-water.

### **Derivation of Maximum Acceptable Value**

Water samples yielding *Y. enterocolitica* often show only light coliform contamination. One study indicates that 25 percent of *Y. enterocolitica*-positive samples were negative for both total and faecal coliforms. Other studies show a close relation between faecal pollution and *Y. enterocolitica* isolation rates. As it is not possible, at this stage, to determine an infectious dose, *Y. enterocolitica* should be absent from drinking-water supplies.

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1. Aspiration is when water goes ‘down the wrong way’ into the respiratory tract when swallowing. [↑](#footnote-ref-1)