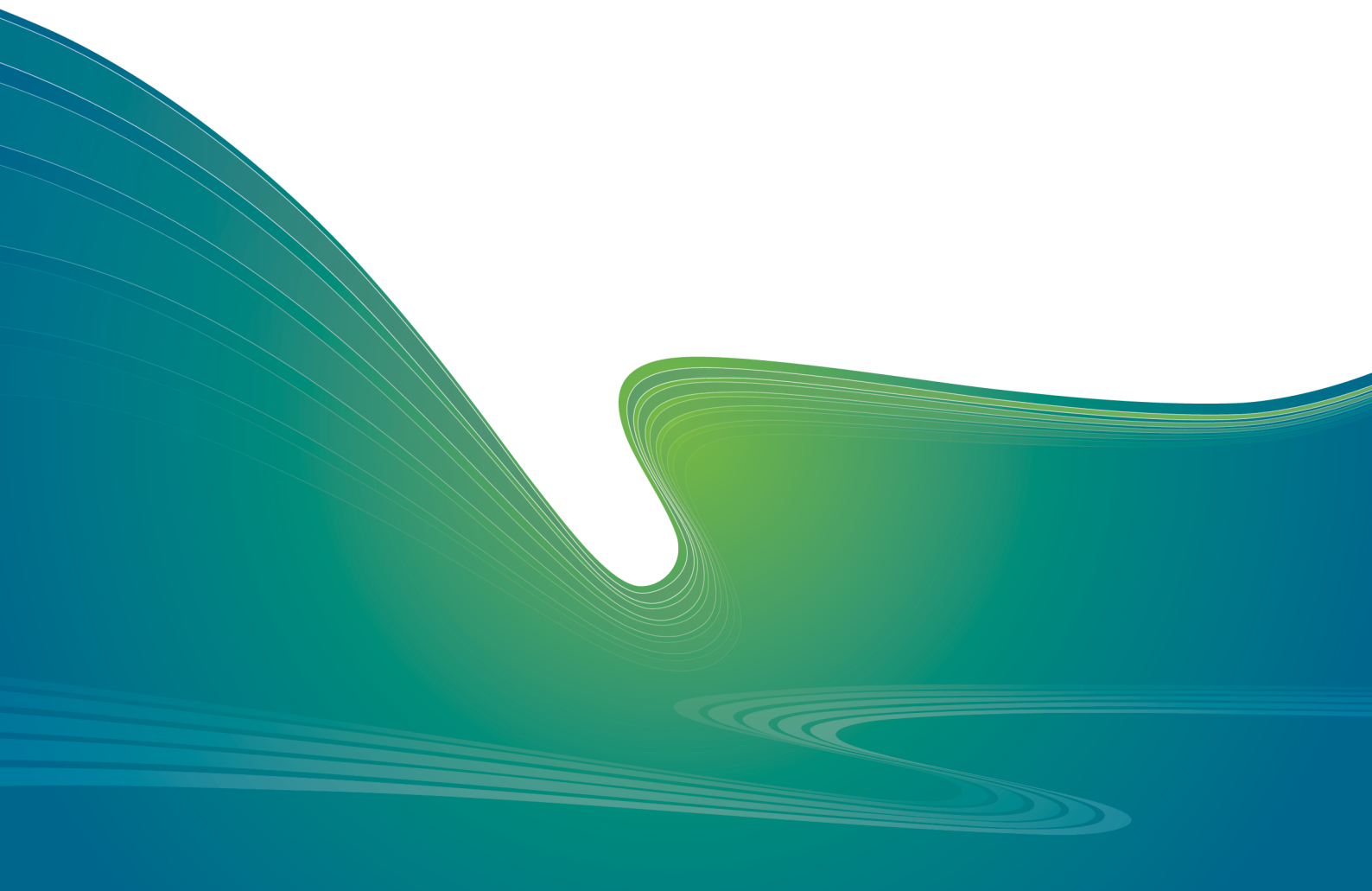
Appendix J: **A Quantitative Microbiological Risk Assessment of the Porirua WWTP Discharge & Receiving Environment**

Streamlined ENVIRONMENTAL

A Quantitative Microbial Risk Assessment of the Porirua WWTP Discharge and Receiving Environment



Action	Name	Date
Draft prepared by	John Oldman, Christopher A. Dada	30th October 2019
Draft internally reviewed by	Mike Stewart, Malcolm Green	7th October 2019
Draft externally reviewed by	NIWA	
Final prepared by	John Oldman, Christopher A. Dada	May 2020

Report DHI1901
Prepared for Stantec
By DHI and SEL
May 2020

Oldman, J.W. & Dada A.C (2020) A Quantitative Microbial Risk Assessment of the Porirua WWTP discharge and receiving environment. DHI1901, Streamlined Environmental, Hamilton, 58 pp.

DHI/SEL

Contents

Executive Summary

As part of the process of renewing the consent for the Porirua Wastewater Treatment Plant (WWTP) marine shoreline discharge, a Quantitative Microbiological Risk Assessment (QMRA) has been prepared to assess the viral enteric illness risks related to contact recreation and consumption of harvested shellfish , as well as the acute febrile illness (respiratory) risks associated with potential inhalation of spray droplets following discharge from the outfall. The QMRA is a fundamental part of the discharge application, not only because it provides an assessment of the health risks associated with the outfall discharge, but also because it provides an indication of the WWTP virus treatment/disinfection requirements.

Presented in this report are information on all water-related enteric and respiratory illnesses whose causative agents have an established dose-response formulation. Consistent with other previous QMRAs, for environmental waters impacted by treated wastewater, the ideal pathogens considered for this human risk assessment are the viruses norovirus, enterovirus and adenovirus. Typical concentrations of these viruses in untreated wastewater, as have been documented in previous New Zealand QMRAs, were used to assess risks associated with ingestion of potentially polluted water and inhalation of aerosolised pathogens e.g. during water-skiing or people accessing the shore close to the outfall being subject to wave/wind driven spray. In addition to recreational exposure, this QMRA also assessed three established shellfish gathering sites for risks related to consumption of raw shellfish. Pathogen concentrations arising from the discharge of treated wastewater from an outfall into the ocean near Porirua were predicted at these sites using a hydrodynamic model calibrated by DHI. The following scenarios were considered:

(i) A baseline case, i.e. no expansion in current discharge levels and the existing (2018) population (flow of 306 L/s based on 84,000 population equivalents [PE] is discharged from the outfall); and
(ii) Long term (2043), i.e. flow of 440 L/s based on a future population of 121,000 PE.

Four scenarios of virus removal in the existing treatment systems at the Porirua WWTP were modelled, these being 1-log, 2-log, 3-log and 4-log reductions corresponding to 10-, 100-, 1,000- and 10,000-fold reductions in virus concentrations. For each of these assumed virus removal efficacies, this QMRA assessed risks that would be associated with the discharge.

In order to optimize public health protection, this QMRA applied a precautionary approach all through the entire process, for instance through the inclusion of occasional very high influent virus concentrations that occur during on-going but undetected viral illness outbreak in the community.

Hydrodynamic Modelling Results

A calibration of the hydrodynamic model prepared by DHI Ltd was undertaken (DHI, 2018), which included a comparison of model performance against measured water levels and currents and the mixing of the treated wastewater plume and oceanic waters near the discharge point. A good calibration was achieved, and the model was deemed fit for purpose with regard to predicting the hydrodynamics of the area offshore of the discharge point, Porirua Harbour and the behaviour of the treated wastewater plume. Time series of virus dilutions were extracted from the year-long 2018 simulation for the 15 selected exposure sites and subsequently applied in the QMRA to assess the risk of illness to swimmers and individuals who consume raw shellfish.

QMRA Results

The modelling results suggest that if wastewater treatment/disinfection reduces virus concentrations in the Porirua WWTP discharge by 3-log, then risks in relation to inhalation, ingestion during swimming and consumption of shellfish harvested at all exposure sites will reduce to levels below the no observable adverse effects level (NOAEL), even under the worst-case scenario of future 2043 flows (121,000 PE).

Statement on health risk associated with the discharge

Projected log reductions that will be achieved at the Porirua WWTP are higher than levels required in the QMRA results. Stantec and Connect Water have advised that:

- more than 3.0, 5.0 and 7.0 log removals of adenovirus, norovirus and enterovirus, respectively, will be achieved by the Porirua WWTP plant at current and future average weather flows of 306 L/s & 440 L/s.

Consequently, and in line with the results of this QMRA, this level of treatment at the Porirua WWTP is sufficient to reduce health risks of the discharge below the “no observable adverse effects level” during average flows.

1. Introduction

As part of the process of renewing the resource consent for the Porirua Wastewater Treatment Plant (WWTP) marine shoreline discharge, a Quantitative Microbiological Risk Assessment (QMRA) has been prepared to address enteric illness risks related to contact recreation and consumption of harvested shellfish, as well as the acute febrile illness risks (respiratory) associated with potential inhalation of spray water from the discharge. The QMRA is a fundamental part of the discharge application, not only because it interfaces with the hydrodynamic studies, but because it provides some feedback loop to WWTP treatment/disinfection requirements.

This QMRA report is presented in topical sections. Section 2 presents a general summary of the hydrodynamic modelling which provides an overview of the dynamics of the wastewater plume in the receiving environment. Section 3 captures a discussion on the approach used in the QMRA modelling, while Sections 4 and 5 report and discuss the results of risks associated with ingestion, inhalation and consumption of shellfish at sites potentially impacted by the treated WWTP outfall discharge. Section 6 provides a comparison of log reductions required in the QMRA to reduce health risk below the "no observable adverse effects level" versus the achievable log reduction at the Porirua WWTP. Section 7 concludes.

2. Hydrodynamic model

2.1 Overview

This section provides details of the model simulations carried out for the assessment of the public health risk associated with the Porirua WWTP discharge (Figure 1).

Previous modelling (DHI, 2018), assessed a number of alternative discharge options which included a shoreline discharge to the south of the existing discharge point (Round Point) and two long offshore outfalls at 10 and 15 m depths (Figure 1). For the purposes of the assessment of alternatives, a representative six-week period was modelled which provided quantification of how the alternative discharge options performed in terms of achievable dilutions relative to the existing discharge.

Figure 1. Location of existing WWTP shoreline discharge and alternative discharge options considered.

Taking account of the outcome of a multi-criteria analysis process, a decision has to been made by Wellington Water to retain the existing shoreline outfall but to limit the proposed application term to 20 years to meet the water quality improvements objectives of the Te Awarua-o-Porirua Whaitua. Details of the model bathymetry, mesh, freshwater inflows, salinity, wind, current and water level data and open ocean boundaries data are described in a DHI (2018).

To carry out a public health risk assessment for the preferred existing discharge option, longer term model simulations were required compared to the assessment of the alternative discharge options. This allows the distribution of achievable dilutions at key sites to be fully quantified.

The overall dilution achieved is a combination of the near-field mixing as well as dilution achieved in the far-field as the plume disperses. To quantify the dilution achieved, both conservative[1] and non-conservative[2] tracers were modelled. However, only the dilution achieved in the conservative tracer was used for the QMRA modelling.

[1] In the conservative tracer run, UV-based inactivation is exempted from the hydrodynamic modelling.

[2] The non-conservative modelling approach includes dilution, dispersion, UV irradiation and temperature-based inactivation of pathogens in the receiving marine environment. Viruses were modelled assuming worst case of somatic phages. Dark (night-time) inactivation coefficients for summer and winter of 0.044 h^{-1} and 0.015 h^{-1} respectively, while the daytime coefficients were assumed to be 0.33 h^{-1} and 0.045 h^{-1} for summer and winter respectively. These inactivation coefficients were derived from data presented in Sinton et. al (1999). The seasonal and daily variation for inactivation rates for viruses were derived based on the above dark and light inactivation rates. The seasonal variation in the maximum dark and light rates were derived using a sigmoidal variation based on the number of days to and from winter solstice. Lastly, the light inactivation rate was modulated on an hourly basis based on the observed solar radiation for 2018. The actual inactivation rate was assumed to be the predicted maximum daily inactivation rate (from above formula) multiplied by the ratio of the observed hourly solar radiation to the maximum clear sky solar radiation for the day being considered. These methods are consistent with previous hydrodynamic modelling studies in New Zealand e.g. NIWA's Akaroa Harbour Modelling (Bell et al 2014) and earlier NIWA Clarks Beach work (McBride 2016).

The reasons for the exclusion of the dilutions achieved in the non-conservative tracer are supported by arguments related to UV inactivation in published literature (e.g. see Silverman 2013, Linden et al 2007; Jin & Flury 2002). The effectiveness of sunlight inactivation of waterborne viruses depends on complex and variable environmental factors (e.g. the intensity and spectrum of sunlight), characteristics of the water containing the virus particles (e.g. pH, DO, ionic strength, source and concentration of photosensitizers), and peculiarities of the virus particles (e.g. virus structures, genome type and prevalence of sites susceptible to photo-transformation; protein capsid composition and structure). For instance, several previous studies (Anders 2006; Havelaar 1993; Hijnen et al 2006; Kohn and Nelson 2007; Kohn et al. 2007; Love et al. 2010; Romero et al. 2011; Sinton et al. 1999; Sinton et al. 2002) that have reported on sunlight inactivation of viruses relied on MS2 and other bacteriophages as models for human viruses due to their similar structure and size. While bacteriophage MS2 are a good conservative surrogate for representing the UV inactivation of many viruses, they are not reliable surrogates for adenovirus (Shin et al 2005). Furthermore, bacteriophages are not usually human pathogens, hence, they may not accurately model human virus inactivation under all environmental conditions. There are also uncertainties regarding the extent to which viruses are associated with particles from water treatment and the effects of particle association and clumping of viruses on UV inactivation (Linden et al 2007). These uncertainties present a core challenge in accurately modelling virus inactivation rates. It is thus difficult to simply compare or apply experimental UV irradiation values across different studies (Silverman 2013). For these reasons, it is not possible to reliably predict mechanisms or rates of inactivation of viruses of public health concern based on current knowledge of bacteriophage inactivation.

Despite the uncertainties associated with estimating the actual rates of UV inactivation that would take place in the receiving environment, it is certain that ultraviolet inactivation will occur. Our approach to exclude solar radiation-based ultraviolet inactivation from the hydrodynamic module (as was applied in the conservative tracer model run) is thus, a highly precautionary approach, from a public health protection perspective. Consequently, the reported risks from this QMRA include the worst-case scenario and may be overstated.

For the purpose of the 20-year consent term, a discharge flow of 0.306 m^3/s has been assumed for the current average daily flow. With an allowance for 44% population growth in the period to 2043, the average daily flow for the future discharge regime is assumed to be 0.440 m^3/s.

2.2 Selection of exposure assessment sites

The project team identified potential exposure sites for the purposes of modelling. Fifteen key sites (see Figure 2 and Table 1) where contact recreation and shellfish gathering occur (or may occur) were identified. Selection of sites was generally informed by:

- direction of pathogen contaminants following dilution (i.e. virus distribution following discharge from existing shoreline outfall) as predicted in an initial DHI hydrodynamic modelling report (DHI 2018)
- previously published studies, including the GWRC marine bathing sites[3], cockle transects in the Michael and Wells (2017) study[4], cockle density by transect, Pautahanui inlet[5], Strava heat map data for water sports[6], and the Greater Wellington Regional Council microbial forecast model sites, as reported in the Rob Greenaway & Associates (2018) Porirua WWT recreation review.

Based on the outcomes of the Te Awarua-o-Porirua Whaitua Study (DHI, 2019) inner harbour sites (towards the south of the Onepoto Arm and the east of the Pauatahanui Inlet) are unlikely to be significantly impacted by the WWTP discharge and any public health risk associated with these sites will be driven more by catchment derived discharges that occur directly to the harbour. Contact Recreation 7 site is not a shellfish gathering site but was included (given its peculiar location at the inlet of the Pauatahanui Arm of the Te Awarua-o-Porirua) to capture risks due to shellfish gathering in the Pauatahanui Arm (see Figure 2). Therefore, only three sites within the harbour (i.e. SF4, SF5 and CR7) have been included in the shellfish risk assessment modelling.

Table 1 Geographical coordinates of the exposure sites under consideration.

S/No	Site	Latitude	Longitude
1	Ti Korohiwa Rocks (monitoring site)	-41.106338°	174.816576°
2	200m South-west of the discharge point (monitoring site)	-41.106256°	174.820829°
3	200m East of the discharge point (monitoring site)	-41.104887°	174.825126°
4	200m Offshore of the discharge point	-41.104228°	174.822159°
5	Titahi beach (monitoring site)	-41.103398°	174.833546°
6	Titahi beach (S) (monitoring site)	-41.106411°	174.830947°
7	Contact Recreation 1 (CR1)	-41.105721°	174.834494°
8	Mount Cooper (monitoring site)	-41.097678°	174.834485°
9	Tirau Bay	-41.111040°	174.808230°
10	Shellfish 4 (SF4)	-41.108384°	174.855473°
11	Shellfish 5 (SF5)	-41.105221°	174.864626°
12	Contact Recreation 3 (CR3)	-41.092273°	174.854664°
13	Contact Recreation 4 (CR4)	-41.088228°	174.865808°
14	Contact Recreation 5 (CR5)	-41.083562°	174.864340°
15	Contact Recreation 7 (CR7)	-41.102897°	174.870941°

[3] as cited in the Rob Greenaway & Associates (2018) Porirua WWT recreation review, page 27.
[4] as reported in the Porirua WWT recreation review, page 38.
[5] as reported in the Porirua WWT recreation review, page 39
[6] as reported in the Porirua WWT recreation review, page 51.

Figure 2 Location of the fifteen selected exposure sites.

2.3 95th percentile spatial plots

The 95th percentile exceedance plots for virus concentrations during the conservative tracer model runs are presented in Figure 3. 95th percentile values for concentration and 5th percentile values for dilution are presented in Table 2a and b.

A concentration of 10 corresponds to a dilution of 100, a concentration of 1 corresponds to a dilution of 1,000 and a concentration of 0.1 corresponds to a dilution of 10,000.

95th percentile dilutions in the receiving environment ranged from 4 at the site 200 m South West of the WWTP outfall to greater than 6,000 at Site Shellfish (SF4, see Table 2b).

2.4 Time-series at the 15 exposure sites

Time series of virus concentrations and dilutions were extracted from the year-long 2018 simulation for selected locations shown in Figure 2. Time series of virus dilutions were later applied in the QMRA to assess the risk of illness to swimmers and individuals who consume raw shellfish (in Section 3).

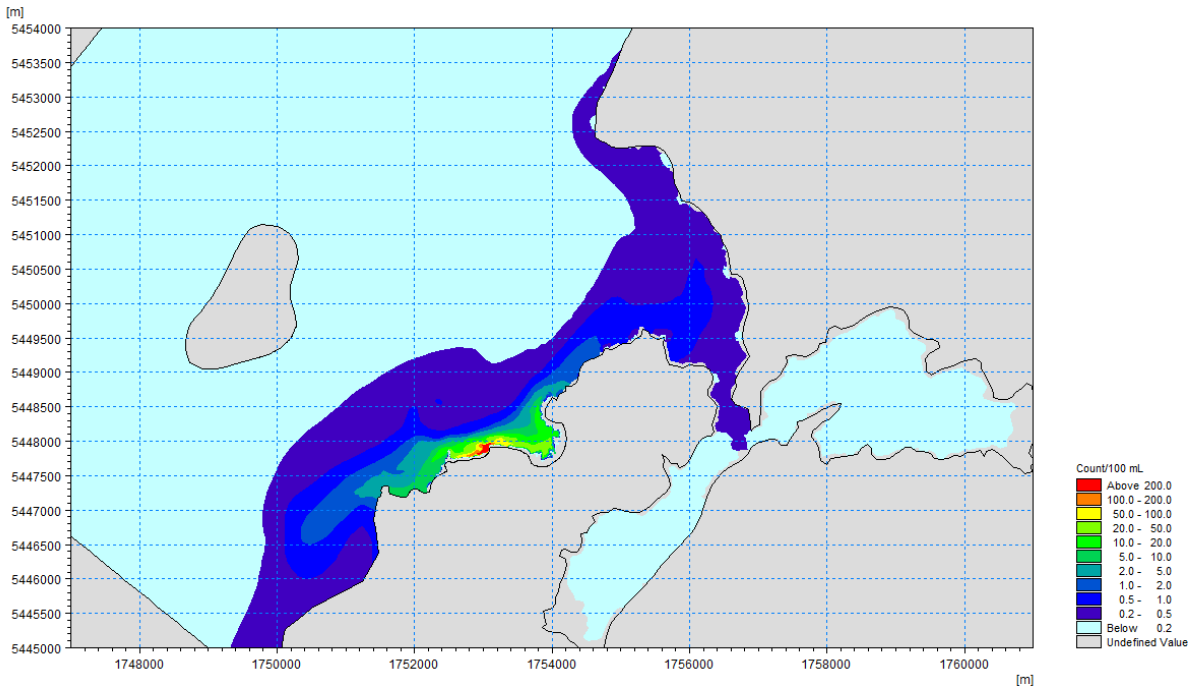


Figure 3 95th percentile concentration for a conservative tracer under current discharge regimes. Source concentration is assumed to be 1000 units/100 mL.

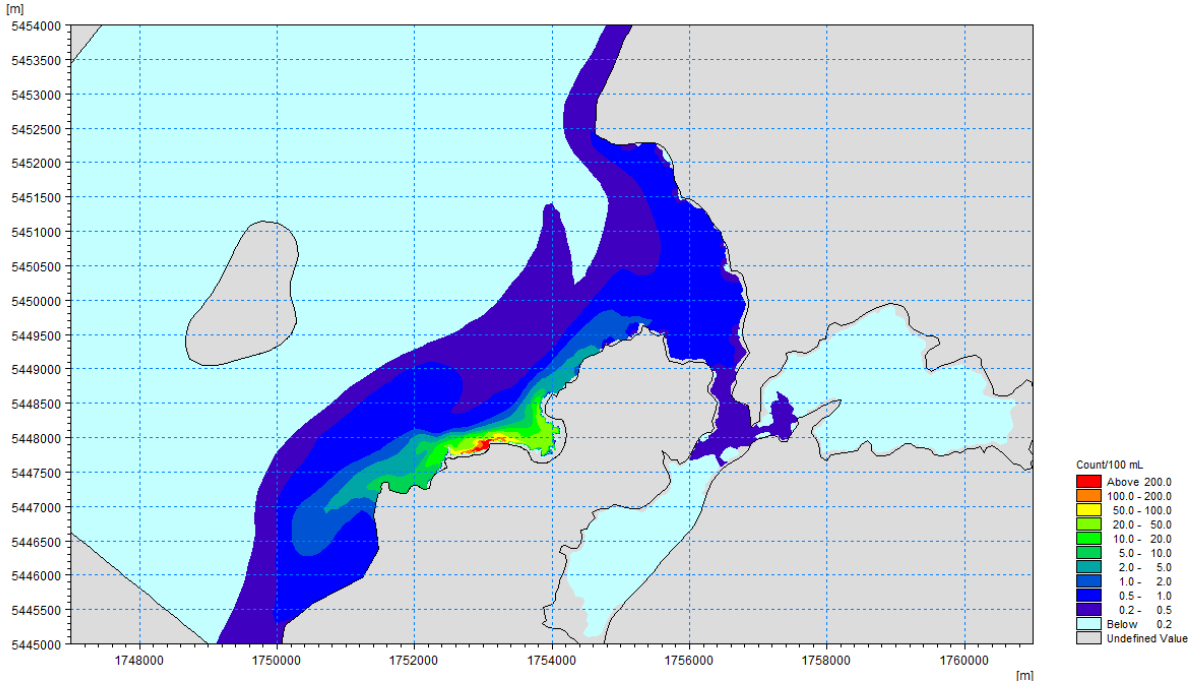


Figure 3b 95th percentile concentration for a conservative tracer under future discharge regimes. Source concentration is assumed to be 1000 units/100 mL.

Table 2a 95th percentile concentrations from the annual simulation of a conservative tracer (virus) at the QMRA sites (Figure 2). Sites are ordered highest to lowest predicted 95th percentile concentration. Source concentration is assumed to be 1000 units.

Scenario	200m SW	200m E	Ti Korohiwa Rocks	Titahi Beach (S)	Contact Recreation 1	Titahi Beach	200m Offshore	Tirua Bay	Mount Cooper	Contact Recreation 3	Contact Recreation 4	Contact Recreation 5	Contact Recreation 7	Shellfish 5	Shellfish 4
Current Average Daily Flow	156.46	78.69	35.10	29.91	21.79	17.60	7.32	5.78	2.52	0.46	0.37	0.33	0.17	0.17	0.10
Future Average Daily Flow	223.91	108.29	52.61	42.52	33.29	27.64	11.45	8.56	4.24	0.71	0.58	0.50	0.26	0.26	0.15

Table 2b 95th percentile dilution from the annual simulation of a conservative tracer at the QMRA sites (Figure 2). Sites are ordered lowest to highest predicted 5th percentile dilution.

Scenario	200m SW	200m E	Ti Korohiwa Rocks	Titahi Beach (S)	Contact Recreation 1	Titahi Beach	200m Offshore	Tirua Bay	Mount Cooper	Contact Recreation 3	Contact Recreation 4	Contact Recreation 5	Contact Recreation 7	Shellfish 5	Shellfish 4
Current Average Daily Flow	6.4	12.7	28.5	33.4	45.9	56.8	136.6	173.1	396.9	2166.9	2676.4	3039.7	5833.1	5918.0	9916.8
Future Average Daily Flow	4.5	9.2	19.0	23.5	30.0	36.2	87.3	116.8	235.8	1413.8	1730.3	1990.8	3814.5	3866.2	6486.9

3. Quantitative Microbial Risk Assessment

3.1 Overview

Quantitative Microbial Risk Assessment (QMRA) is a framework that applies information and data incorporated into mathematical models to assess the potential public health risks from pathogens after discharge in a receiving environment such as water[7]. While quantitative risk assessment was initially designed to assess risks of exposure to various hazards, particularly chemicals, it has since been modified to incorporate risks related to exposure to microbial pathogens (NRC 1983). Risk is the combination of the likelihood of identified hazards causing harm in exposed populations in a specified time frame and the severity of the consequences (Hrudey, Hrudey, and Pollard 2006).

Typically, four steps are involved in a QMRA (Haas, Rose, and Gerba 1999). These are: hazard identification, exposure assessment, dose-response analysis, and risk characterization.

[7] It is important to note that the assessment only relates to the risk from a particular discharge, i.e. it doesn't take into account the risks associated with other discharges (for example, stormwater or non-point source discharges) that may be in the area.

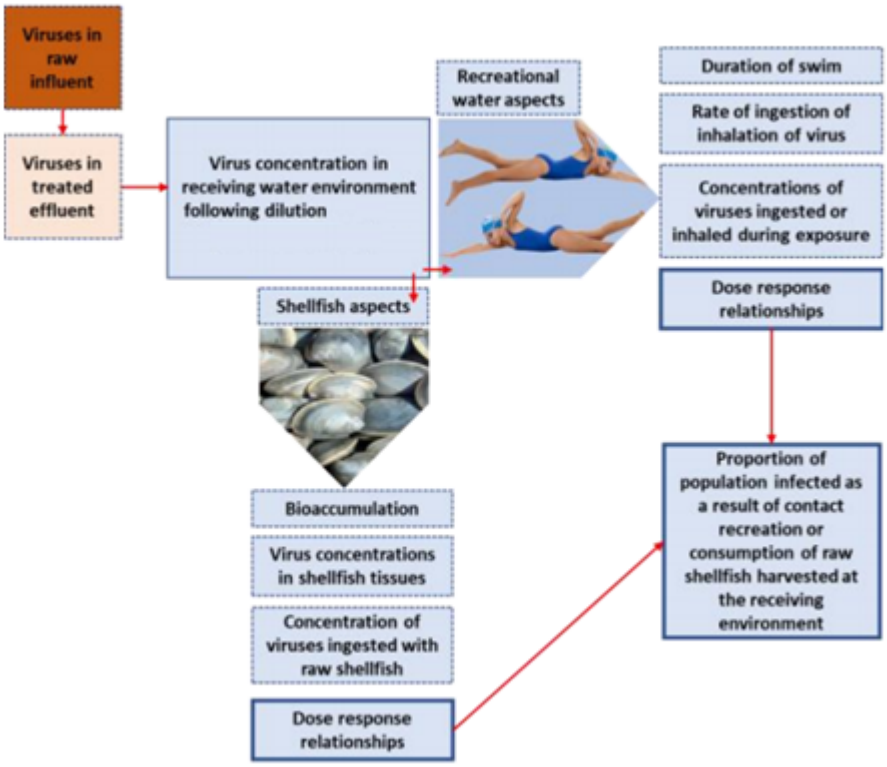


Figure 4 Stages in a QMRA.

3.2 Hazard analysis

Wastewater may contain several pathogenic species (Jacangelo et al. 2003; McBride 2007). The majority of pathogens in wastewater are enteric, that is, they affect the digestive system, and may present a serious health risk if ingested (Hai et al. 2014). These pathogens include: protozoans, which can cause life-threatening diseases including giardiasis, cryptosporidiosis, dysentery and amoebic meningoencephalitis (Bitton 2010); viruses, which can cause paralysis, meningitis, respiratory disease, encephalitis, congenital heart anomalies and upper respiratory and gastrointestinal illness (Melnick, Gerba, and Wallis 1978; Toze 1997; Okoh, Sibanda, and Gusha 2010); and bacteria, consisting of the enteropathogenic and opportunistic bacteria which cause gastrointestinal diseases such as cholera, dysentery, salmonellosis, typhoid and paratyphoid fever (Toze 1997; Cabral 2010).

Because the tests for pathogens are time-consuming and expensive, it is not practical to implement such testing on a routine basis. Instead, regulatory bodies support testing for faecal indicator bacteria (FIB) (e.g. enterococci and faecal coliforms) as a cost-effective means to assessing the presence of faecal contamination and the quality of treated effluent. These generally non-pathogenic bacteria are contained in the gut of warm-blooded animals, including humans, in large concentrations.

Research shows that most pathogens die at the same rate as FIB, and hence the numbers of FIB in the treated effluent can be used to indicate the presence of pathogens.

While focus has been placed on enterococci concentrations for regulatory purposes, limitations associated with the use of conventional FIB as an indicator for viruses is well documented (Wade et al. 2008, Wade et al. 2010, USEPA 2015). Furthermore, as most standard wastewater treatment and disinfection processes vary in their efficiency in eliminating viruses, treated effluent may still contain concentrations of enteric viruses that present a significant public health risk (Lodder et al. 2010; Okoh, Sibanda, and Gusha 2010). Several enteric viruses have been described in published literature as associated with outbreaks due to exposure to polluted recreational water (Jiang et al., 2007; Sinclair et al., 2009, USEPA 2015). These include noroviruses, adenoviruses, hepatitis A viruses, echoviruses and Coxsackie viruses (Hauri et al. 2005; Lodder et al. 2010). Literature has also suggested that the greatest public health risk linked with the discharge of treated wastewater relates mainly to viruses (Courault et al. 2017; Prevost et al. 2015). A unique characteristic of viral infections is that a high proportion of the exposed populations could be potentially affected, often leading to very high incidences of gastroenteritis that can then be spread by person-to-person contact to other individuals who were not directly exposed to the polluted waters (Patel et al. 2008; Widdowson, Monroe, and Glass 2005). For instance, a single vomiting incident from an individual infected with norovirus could expel up to 30 million virus particles (Tung-Thompson et al. 2015). In community settings, this could result in contamination of surfaces with large numbers of viruses, effectively promoting the further spread of the pathogens.

For environmental waters impacted by treated wastewater, the ideal reference pathogens considered for human risk assessment are the viruses: norovirus, enterovirus and adenovirus (McBride 2016a,b). These viruses have been used as representative viruses for previous studies in New Zealand (McBride 2011, 2012, 2016a,b). While norovirus and enterovirus are significant contributors to enteric infections, adenovirus (Type 4) can cause respiratory illnesses via inhalation of aerosols from contaminated water during swimming, skiing or other water-related recreational activity. Hence, in this study, norovirus and enterovirus were used as reference QMRA pathogens for primary contact recreation and shellfish consumption. For secondary contact recreation, which includes activities such as shoreline walking, jogging, paddling, wading, boating and fishing, in which there may be some direct contact but the chance of swallowing water is unlikely, only adenovirus (Type 4) was used as reference pathogen for assessing risks associated with inhalation of potentially polluted water (e.g. from wind or wave-induced spray) containing aerosolised pathogens. Other technical reasons that warranted the choice of these reference pathogens are detailed in Appendix 5. Typical concentrations of these reference viruses in untreated wastewater are presented in Table 4 (see Section 5.3)

and are in line with values have been documented in several previous New Zealand QMRAs (e.g. McBride 2011, 2016a, b).

3.3 Exposure Assessment

Exposure assessment involves identification of populations that could be affected by pathogens. The main individuals at risk of exposure to pathogens in the receiving environment of the Porirua WWTP are those that engage in any sort of contact recreation or those who consume raw shellfish collected from any site potentially impacted by the discharge. In order to assess the potential level of exposure, the following were considered:

- proximity of the QMRA site[8] to the discharge outlet;
- the possible exposure pathways that allow the pathogen to reach people and cause infection (through the air, through ingesting polluted water, consuming shellfish etc.);
- range (minimum, maximum and median) of pathogen concentrations in treated effluent;
- discharge volumes of the treated wastewater;
- the environmental fate of the microbial contaminants in the receiving environment: dilution of viral pathogens in the receiving marine environment;
- how much water a child[9] will ingest or inhale over a period of time during a particular recreational activity;
- how much raw shellfish harvested from the impact sites that an individual will consume at one sitting; and
- estimation of the amount, frequency, length of time of exposure, and doses for an exposure.

3.3.1 Porirua WWTP influent and effluent virus concentrations

A limited (3 sample) virus monitoring programme carried out by Wellington Water in September 2019 indicated that the Porirua WWTP influent virus concentrations could be as high as 10^7 genomes per L (Table 3). This is a snapshot sampling and does not adequately reflect the year-round variabilities in influent virus concentrations. Notwithstanding this, the monitoring data fall within the range of concentrations reported in previous New Zealand QMRAs (e.g. McBride 2016a,b). Influent virus concentrations (minimum, maximum and median) applied in this QMRA were thus based on previous documented ranges (see Table 4). To estimate final concentration of viral pathogens for each of the 15 exposure sites, the dilution factors[10] from the

[8] The Porirua WWTP Project team was responsible for identifying potential exposure sites for the QMRA.
[9] A child is considered the worst-case risk because studies show that ingestion rates for children are twice as much as for adults (e.g. Dufour et al.2006) as reported in McBride (2017) QMRA for Bell Island WWTP outfall.
[10] sampled from the entire 1-year range using a "riskcumul" function. This is a cumulative distribution which uses the parameters (minimum, maximum, range of values i.e. spread between the 10th and 99.9th percentile, and the

hydrodynamic modelling was multiplied by the hockey-stick fitted concentrations of viruses in the sewage discharging from the outfall diffuser. In accordance with previous QMRA reports and international literature (e.g. McBride 2016a,b reports for Warkworth WWTP QMRA and Snells Beach QMRA), minimum, median and maximum virus concentrations were bounded in the hockey-stick distribution in a way that the resulting data are strongly right skewed with a hinge at the 95%ile. The RiskGeneral function was used to generate the random draws from the right-skewed distribution of virus concentrations. This, therefore, presents in the same population the generally predominant lower virus concentrations (i.e. having higher probabilities) alongside the extreme concentrations (which could be said to be rare but substantial). In this way, the QMRA aligns with the Resource Management Act which defines an "effect" to include considerations for instances of rare (i.e. low probability of occurrence) but high potential impact . These "low probability events" (such as periods of infectious outbreaks in the community or WWTP system malfunction) coupled with elevated virus concentrations are effectively captured in the hockey-stick distribution.

The literature reveals that viral reductions in effluents (i.e. after treatment) could be as low as no reduction (in the case of a complete treatment failure) to as high as 5-log reduction (i.e. a 100,000-fold reduction) (McBride 2016a, b). Depending on the existing WWTP treatment process, each of these range of possible reductions is critical for a robust microbial risk assessment. In this study, 1-, 2-, 3- and 4-log reductions were incorporated into the QMRA modelling.

cumulative probabilities of each value in range i.e. spread between 0.1 and 0.999). This is consistent with previous NIWA QMRAs.

Table 3 Porirua WWTP Influent virus monitoring results (September 2019).

Sampling date	Virus	Influent (genomes per L)
9th September 2019	Norovirus Genogroup I	4.80E+05
	Norovirus Genogroup II	1.00E+07
	Enterovirus	8.40E+04
	Adenovirus	3.30E+05
16th September 2019	Norovirus Genogroup I	8.20E+04
	Norovirus Genogroup II	4.90E+06
	Enterovirus	5.20E+04
	Adenovirus	2.30E+05
23rd September 2019	Norovirus Genogroup I	8.30E+04
	Norovirus Genogroup II	4.70E+06
	Enterovirus	1.50E+05
	Adenovirus	1.00E+06

*Results sheets in Appendix 1

3.3.2 Discharge volumes of treated Porirua WWTP effluent

Stantec and the WWTP operators have provided a range of population equivalents [PE] during baseline (2018) and future (2043) conditions. Based on these data, different WWTP discharge scenarios were considered in this QMRA:

1. A baseline case, i.e. no expansion in current discharge levels and the existing (2018) population (flow of 306 L/s based on 84,000 PE is discharged from the outfall); and
2. Long term (2043), i.e. flow of 440 L/s based on a future population of 121,000 PE.

3.3.3 Predicting exposure doses

The dose of the pathogen that an individual ingests, inhales or comes in contact with is an important component of the dose-response models used to predict the probability of infection or illness. In order to convert pathogen concentrations into doses, reference was made to the influent virus concentrations, the ingestion or inhalation rates for the water users (adults and children, in the case of swimming or other contact recreation), as well as shellfish bioaccumulation factors (in the case of shellfish harvesters). Details of dose-response models are presented in Appendices 2 to 4.

For risks due to swimming, water ingestion rates applied in the QMRA (Table 4) were based on previous studies that have applied biochemical procedures to trace a decomposition product of chlorine-stabilizing chloroisocyanurate, which passes through swimmers' bodies unmetabolized (Dufour et al. 2006, McBride 2016).

In order to assess risks due to consumption of raw harvested shellfish, ingestion rates used were in line with estimates of daily intake of 98 consumers of mussels, oysters, scallops, pipi and tuatua in the 1997 National Nutrition Survey, as reported in previous New Zealand QMRAs (e.g. Dada 2018a,b, Stewart et al.2017, McBride 2005, 2016a,b).

It is important to note that previous QMRA reports (e.g. McBride 2016 a, b) have assessed risks due to ingestion of raw shellfish tissue using bivalve molluscs as the vector. This is because bivalve molluscs are very common and accessible in New Zealand waters, are very frequently consumed raw; and because they are known to 'bioaccumulate' pathogens, hence the additional multiplier effect called the pathogen bioaccumulative factor (PBAF, see Table 4) applied in our model (Bellou, Kokkinos, and Vantarakis 2013; Hanley 2015; Hassard et al. 2017)

Table 4 Distributions and inputs for the QMRA (Adapted from McBride 2016 a, b).

Parameter	QMRA Statistics applied	Comments
Influent concentration, Adenovirus (per litre)	Minimum = 2,000 Median = 5,000 Maximum = 30,000,000	Hockey stick distribution, as previously described (McBride 2007, 2011; 2012; 2016 a,b). Norovirus harmonization factor of 18.5 was included, in line with McBride 2011 and 2017)
Influent concentration, Norovirus (per litre)	Minimum = 100 Median = 10,000 Maximum = 10,000,000	
Influent concentration, Enterovirus (per litre)	Minimum = 500 Median = 4,000 Maximum = 50,000,000	
Duration of swim (hours)	Minimum = 0.1 Median = 0.25 Maximum = 2	For child or adult (McBride 2007, 2011; 2012; 2016 a,b)
Swimmers water ingestion rate, mL per hour	Minimum = 20 Median =50 Maximum = 100	PERT distribution for a child rate. Typically, adult rate is half the child rate (Dufour et al, 2006)
Water inhalation rate, mL per hour	Minimum = 10 Median =25 Maximum = 50	PERT distribution for an adult, assumed as half of child rate (McBride 2007, 2011; 2012; 2016 a,b)
Dose response parameters	Enterovirus (beta-binomial model, α = 1.3, β =75) Prob(illness/infection)=1	Dada 2018a; 2018b; McBride 2007, 2011; 2012; 2016; Stewart et al. 2017, Soller et al. 2010a,b
	Adenovirus Type 4 (simple binomial model, r = 0.4142). Only 3-10% of adenoviruses cause respiratory illnesses. Prob(illness/infection)=0.5	Dada 2018a; 2018b; McBride 2007, 2011; 2012; 2016; Stewart et al. 2017, Soller et al. 2010 a,b, Kundu et al. 2013
	Norovirus (beta-binomial model, α = 0.04, β =0.055) Prob(illness/infection)=0.6	Dada 2018a; 2018b; McBride 2007, 2011; 2012; 2016; Stewart et al.2017, Soller et al. 2010 a,b
Shellfish size	α = 2.2046 β = 75.072 γ = -0.903	Loglogistic distribution between 5g and 800g, based on estimates of daily intake of consumers of raw shellfish (see McBride 2005, McBride 2007, 2011; 2012; 2016, Russel et al.1999)
Pathogen bioaccumulation factor (PBAF)	Mean = 49.9 Standard deviation = 20.93	Normal distributions around mean. Pathogen dose upon consumption of 100 grams of shellfish is a product of the PBAF and the number of pathogens in an equivalent volume of water (see Burkhardt & Calci 2000, McBride 2007, 2011; 2012; 2016)

3.3.4 Dose-response models

Dose-response models estimate the risk of a response (for example, infection or illness) given a known dose of a pathogen. Dose-response models are mathematical functions which describe the dose-response relationship for specific pathogens, transmission routes and hosts. Additional dose-response details are presented in Appendix 5.

3.3.5 Risk characterization

Information from the previous steps was incorporated into Monte Carlo simulations to determine the likelihood of illness from exposure to pathogens. The Monte Carlo simulation is a randomization method that applies multiple random sampling from distributions assigned to key input variables in a model, in a way that incorporates the uncertainty profiles of each key input variable into the uncertainty profile of the output.

Typically, in a Monte Carlo model run, 100 individuals who do not have prior knowledge of existing contamination in the water are 'exposed' to potentially infectious water on a given day and this exposure is repeated 1,000 times. Therefore, the total number of exposures is 100,000. The result of the analysis is a full range of possible risks, including average and worst-case scenarios, associated with exposure to pathogens during the identified recreational activities or following consumption of raw shellfish. Monte Carlo simulations were undertaken using @Risk software (Palisade, NY). QMRA results are reported in terms of both infection and illness. It is noted however, that not all individuals that become infected eventually become ill. Although pathogen-dose response models in literature were determined based on infection endpoint, illness endpoint can be estimated simply using a uniform probability for illness as was done in several previous QMRAs (e.g. McBride 2011, 2017). Infection/illness ratios of 0.6 and 0.5 were applied for noroviruses and adenoviruses (McBride 2016), respectively. Due to the relative unavailability of dose-response and morbidity data for enterovirus, a precautionary approach was used in this study, that is, it was assumed that every individual who contracted enterovirus infections also became ill, hence a conservative infection/illness ratio of 1 was applied. This is in line with methods applied in previous New Zealand QMRAs (e.g. McBride 2011, 2016).

The predicted risk is reported as the IIR (individual illness risk), calculated as the total number of infection cases divided by the total number of exposures, expressed as a percentage. The IIR is then compared with thresholds defined in the New Zealand "*Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas*" (MfE/MoH 2003). Depending on the risk being examined, the applicable NZ thresholds differ.

In the case of risk due to enteric illnesses as a result of ingestion of polluted water while swimming or consumption of raw shellfish harvested from the impacted sites, the following **thresholds** apply:

- high illness risk (>10% GI illness);
- moderate illness risk (5-10% GI illness);
- low illness risk (1-5% GI illness);

- NOAEL (<1%); the 1% IIR threshold, also referred to as the 'no observable adverse effects level (NOAEL), is the widely-accepted threshold when assessing the effect of wastewater discharge on recreational health risk (Dada 2018a; 2018b; McBride 2016a,b, 2017; Stewart et al.2017).

In the case of acute febrile illness risks due to inhalation of pathogens in spray water, near or at the impacted sites, comparatively lower thresholds apply:

- high illness risk (>3.9% AFRI illness);
- moderate illness risk (1.9-3.9% AFRI illness);
- low illness risk (0.3-<1.9% AFRI illness);
- NOAEL (<0.3%).

4. QMRA Results

The Individual's Illness Risk[11] (IIR) results of the QMRA analysis for individuals exposed to a range of reference pathogens under the various proposed discharge scenarios are presented in Table 7 to Table 9**.** The 95th predicted number[12] of illness cases is also presented in Appendix 6 and 7.

Consistent with previous New Zealand QMRAs, the average IIR% (as presented in Table 7 to Table 9), is recommended for comparison with thresholds defined in the New Zealand 2003 "*Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas*" (see IIRs and MfE/MoH comparable level of risk listed above).

[11] for a group of 100 recreational users exposed on any random occasion, expressed as a percentage.

[12]We note that means, like other central tendency statistics can hide some larger short-term risks, hence the reason for the inclusion of the 95th percentile data in the appendix.

4.1 Risks associated with ingestion of potentially polluted recreational water

Table 5. Child's enteric illness risk (annual[13]) at fifteen identified sites impacted by enteroviruses during different Porirua WWTP discharge scenarios[14].

Virus Log Reduction	Exposure site	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	200m E	3.63	4.23
	200m Offshore	0.42	0.55
	200m SW	4.83	5.09
	Contact Recreation 1	2.45	2.72
	Contact Recreation 3	0.17	0.22
	Contact Recreation 4	<0.1	0.11
	Contact Recreation 5	0.15	<0.1
	Mount Cooper	0.15	0.26
	Ti Korohiwa Rocks	3.94	4.84
	Titahi Beach (S)	3.21	3.80
	Titahi Beach	1.44	1.72
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	1.17	1.36
2 Log Reduction	200m E	1.52	1.89
	200m Offshore	<0.1	<0.1
	200m SW	2.42	2.82
	Contact Recreation 1	0.71	0.83
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	<0.1	<0.1
	Ti Korohiwa Rocks	1.09	1.24
	Titahi Beach (S)	0.96	1.10
	Titahi Beach	0.47	0.56
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	0.40	0.49
3 Log Reduction	200m E	0.31	0.35
	200m Offshore	<0.1	<0.1
	200m SW	0.46	0.67
	Contact Recreation 1	<0.1	0.15
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	<0.1	<0.1
	Ti Korohiwa Rocks	0.41	0.43
	Titahi Beach (S)	0.32	0.36
	Titahi Beach	0.11	0.12
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	<0.1	<0.1
IIR> 10%	High illness risk		
IIR (5.0-10%)	Moderate illness risk		
IIR (1.0-4.99%)	Low illness risk		
IIR <1%	No illness risk		

[13] Averaged out IIR, consistent with previous NZ QMRAs.

[14] There is no need to present results for 4-log reductions as the 3-log reductions are mostly associated with IIRS < 0.1% at most of the exposure sites. Additionally, at 3-log reductions at all sites, the IIRs were far less than the 1% threshold (i.e. NOAEL).

Table 6. Child's enteric illness risk (annual) at fifteen identified sites impacted by noroviruses during different Porirua WWTP discharge scenarios.

Virus Log Reduction	Exposure site	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	200m E	7.46	8.76
	200m Offshore	0.97	0.99
	200m SW	13.15	14.79
	Contact Recreation 1	1.93	2.22
	Contact Recreation 3	0.20	0.38
	Contact Recreation 4	0.17	0.23
	Contact Recreation 5	0.17	0.27
	Mount Cooper	0.42	0.55
	Ti Korohiwa Rocks	3.07	3.32
	Titahi Beach (S)	2.28	2.54
	Titahi Beach	1.34	1.69
	Contact Recreation 7	0.23	0.25
	Shellfish 4	<0.1	0.12
	Shellfish 5	<0.1	0.15
	Tirua Bay	1.30	1.42
2 Log Reduction	200m E	1.68	2.01
	200m Offshore	0.30	0.35
	200m SW	3.17	3.94
	Contact Recreation 1	0.78	0.85
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	0.12	0.19
	Ti Korohiwa Rocks	1.06	1.17
	Titahi Beach (S)	0.85	0.97
	Titahi Beach	0.48	0.54
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	0.35	0.50
3 Log Reduction	200m E	0.59	0.61
	200m Offshore	<0.1	<0.1
	200m SW	0.76	0.82
	Contact Recreation 1	0.26	0.29
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	<0.1	<0.1
	Ti Korohiwa Rocks	0.31	0.34
	Titahi Beach (S)	0.27	0.31
	Titahi Beach	<0.1	0.13
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	<0.1	<0.1
IIR> 10%	High illness risk		
IIR (5.0-10%)	Moderate illness risk		
IIR (1.0-4.99%)	Low illness risk		
IIR <1%	No illness risk		

4.2 Risks associated with inhalation of potentially polluted recreational water

Table 7 Child's acute febrile illness risk at fifteen identified sites impacted by adenoviruses during different Porirua WWTP discharge scenarios.

Virus Log Reduction	Exposure site	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	200m E	1.62	1.92
	200m Offshore	0.50	0.69
	200m SW	2.19	2.44
	Contact Recreation 1	1.03	1.20
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	<0.1	<0.1
	Ti Korohiwa Rocks	1.29	1.68
	Titahi Beach (S)	1.34	1.59
	Titahi Beach	0.61	0.80
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	0.53	0.66
2 Log Reduction	200m E	0.69	0.75
	200m Offshore	<0.1	0.12
	200m SW	1.27	1.49
	Contact Recreation 1	0.23	0.29
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	<0.1	<0.1
	Ti Korohiwa Rocks	0.45	0.48
	Titahi Beach (S)	0.33	0.48
	Titahi Beach	<0.1	0.11
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	<0.1	<0.1
3 Log Reduction	200m E	<0.1	<0.1
	200m Offshore	<0.1	<0.1
	200m SW	0.20	0.23
	Contact Recreation 1	<0.1	<0.1
	Contact Recreation 3	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1
	Mount Cooper	<0.1	<0.1
	Ti Korohiwa Rocks	<0.1	<0.1
	Titahi Beach (S)	<0.1	<0.1
	Titahi Beach	<0.1	<0.1
	Contact Recreation 7	<0.1	<0.1
	Shellfish 4	<0.1	<0.1
	Shellfish 5	<0.1	<0.1
	Tirua Bay	<0.1	<0.1
IIR> 3.9%	High AFR illness risk		
IIR (1.9-3.9%)	Moderate AFR illness risk		
IIR (0.3-<1.9%)	Low AFR illness risk		
IIR <0.3%	No AFR illness risk		

*AFR = Acute Febrile Respiratory

4.3 Risks associated with shellfish harvesting and consumption

Table 8. Individual's illness risk (%) associated with consumption of raw shellfish collected from the shellfish harvesting sites potentially contaminated with enteroviruses during different Porirua WWTP discharge scenarios.

Virus Log Reduction	Exposure site	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	Contact Recreation 7	2.59	3.11
	Shellfish 4	2.36	2.67
	Shellfish 5	3.44	3.43
2 Log Reduction	Contact Recreation 7	0.66	0.83
	Shellfish 4	0.63	0.81
	Shellfish 5	0.97	1.28
3 Log Reduction	Contact Recreation 7	<0.1	0.14
	Shellfish 4	<0.1	<0.1
	Shellfish 5	0.14	0.22
IIR> 10%	High enteric illness risk		
IIR (5-10%)	Moderate enteric illness risk		
IIR (1-4.99%)	Low enteric illness risk		
IIR <1%	No enteric illness risk		

*Contact Recreation 7 site is not a shellfish gathering site but was included (given its peculiar location at the inlet of the Pauatahanui Arm) to capture risks due to shellfish gathering in the Pauatahanui Arm (see Figure 2).

Table 9. Individual's illness risk (%) associated with consumption of raw shellfish collected from the shellfish harvesting sites potentially contaminated with noroviruses during different Porirua WWTP discharge scenarios

Virus Log Reduction	Exposure site	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	Contact Recreation 7	2.52	3.22
	Shellfish 4	1.9	2.56
	Shellfish 5	2.45	3.15
2 Log Reduction	Contact Recreation 7	0.76	1.03
	Shellfish 4	0.77	0.94
	Shellfish 5	0.99	1.11
3 Log Reduction	Contact Recreation 7	0.19	0.2
	Shellfish 4	0.24	0.31
	Shellfish 5	0.19	0.36
IIR> 10%	High enteric illness risk		
IIR (5-10%)	Moderate enteric illness risk		
IIR (1-4.99%)	Low enteric illness risk		
IIR <1%	No enteric illness risk		

*Contact Recreation 7 site is not a shellfish gathering site but was included (given its peculiar location at the inlet of the Pauatahanui Arm) to capture risks due to shellfish gathering in the Pauatahanui Arm (see Figure 2).

5. Discussion

5.1 Overview

In order to optimize public health protection, a precautionary approach to this QMRA has been applied through the entire process. For instance, using a hockey-stick distribution fitting, the QMRA included considerations for very high influent virus concentrations that occasionally occur during illness outbreaks in the community. While these high concentrations are rare, they have a high potential impact on the estimated risks. Another precautionary approach in this QMRA is to report the children's illness risk as opposed to the generally lower adults' risk. This is consistent with previous QMRAs e.g. the Bell Island QMRA (McBride 2017). This QMRA also included a dilution-only scenario which does not include solar ultraviolet-based inactivation of viruses, to capture risks posed to early-morning recreational water users. Therefore, the reported risks from this QMRA include the worst-case scenario and may be overstated.

5.2 QMRA Results for contact recreation

The QMRA results (Table 7- Table 9) generally indicate that individual illness risks (IIR) increase with increasing wastewater flows, which are based on population estimates, i.e., 2018 < 2043. In terms of the extent of impact of the proposed discharge on the assessment sites, risks due to swimming in waters potentially contaminated with viruses are generally in this order: greatest risk at 200 m SW > 200 m E > Ti Korohiwa Rocks > Titahi Beach (S) > Contact Recreation 1 > Titahi Beach > 200 m Offshore > Tirua Bay > Mount Cooper > Contact Recreation 3 > Contact Recreation 4 > Contact Recreation 5 > Contact Recreation 7.

Illness risks associated with ingestion of polluted water during swimming, or inhalation of aerosolized pathogens at the study sites, were reduced below the NOAEL when the WWTP reduces the viral concentrations by 1,000-fold (i.e. 3-log reduction) before discharge. For instance, during worst-case conservative tracer scenarios of future flows and wastewater treatment that reduces the adenovirus concentrations by 1,000-fold, the acute febrile illness risk was less than 0.3% at all the fifteen exposure sites (Tables 7 and 8). Similarly, enteric illness risk associated with ingestion of water potentially containing enterovirus or norovirus was reduced at all the study sites to below the NOAEL when a 3-log reduction of the wastewater viral concentrations is achieved before discharge (see Table 7 - Table 9).

5.3 QMRA Results for shellfish gathering

Table 10 and Table 11 show predictions of the IIR among 100 individuals who consume raw shellfish harvested from the selected exposure sites in the receiving marine environment following discharge at Titahi Bay WWTP.

If a 2-log reduction in enterovirus and norovirus concentrations is achieved at the WWTP before discharge, enteric illness risks is low among individuals who consume raw shellfish collected at the shellfish harvesting sites. We however note that IIRs associated with consumption of raw shellfish are only fractionally above the 1% threshold for NOAEL.

If a 3-log reduction in enterovirus and norovirus concentrations is achieved at the WWTP before discharge, enteric illness risks among individuals who consume raw shellfish collected at the shellfish harvesting sites (i.e. sites SF4, SF5 and CR7) are reduced below the NOAEL at all these sites, despite the increased flow associated with future discharges. Previous surveys have shown that many shellfish harvesting sites are located in the Pauatahanui Arm (see Figure 2). This explains why a contact recreation site (CR7) at the inlet of the Pauatahanui Arm was included in the shellfish risk assessment. Results of this QMRA indicates that enteric illness risk as a result of the WWTP discharge is below the NOAEL in Porirua Harbour, including in Pauatahanui Arm (see Figure 2).

6. Statement on health risks due to the Porirua WWTP discharge

This section compares the log reductions required in the QMRA to reduce health risk below the “no observable adverse effects level” versus the achievable log reduction at the Porirua WWTP. On the whole, log reduction required to reduce health risk below the “no observable adverse effects level” are summarised in Table 10.

Table 10 Summary of log removals required to reduce risk below the “no observable adverse effects level” based on QMRA

Scenario	Virus Log Reduction	Norovirus	Enterovirus	Adenovirus
2018 (84,000 PE)	Contact recreation	3	3	3
	Shellfish	3	3	N/A
2043 (121,000 PE)	Contact recreation	3	3	3
	Shellfish	3	3	N/A

Stantec and Connect Water have assessed the likely norovirus, enterovirus and adenovirus reduction through the Porirua WWTP (including through the secondary and UV disinfection processes), using available relevant information including the results of studies from similar secondary processes, and by calculating the dose and

inactivation of viruses through the UV disinfection process (see Appendix N WWTP Virus Reduction & Disinfection Performance). Results from the study showed that more than 3.0, 5.0 and 7.0 log removals of adenovirus, norovirus and enterovirus, respectively, will be achieved by the Porirua WWTP plant at current and future average weather flows of 306 L/s & 440 L/s.

It is important to note that the projected log reductions that will be achieved at the Porirua WWTP are higher than levels required in the QMRA results (see comparison in Table 11). Consequently, and in line with the results of this QMRA, this level of treatment at the Porirua WWTP is sufficient to reduce health risks of the discharge below the "no observable adverse effects level" during average flows.

Table 11 Comparison of log removals of norovirus, enterovirus and Adenovirus achieved in the plant versus log removals required to reduce health risks below "no observable adverse effects level"

Pathogen	Scenario	2018 (84,000 PE i.e. 306 L/S)		2043 (121,000 PE i.e. 440 L/s)	
		Contact recreation	Shellfish	Contact recreation	Shellfish
Norovirus	Log reduction required based on QMRA results	3.0	3.0	3.0	3.0
	Log reduction achieved in the Porirua WWTP (average flows)	>5.0			
Enterovirus	Log reduction required based on QMRA results	3.0	3.0	3.0	3.0
	Log reduction achieved in the Porirua WWTP (average flows)	>7.0			
Adenovirus	Log reduction required based on QMRA results	3.0	N/A	3.0	N/A
	Log reduction achieved in the Porirua WWTP (average flows)	>3.0			

7. Conclusion

The QMRA shows that wastewater treatment that reduces virus concentrations in the WWTP discharge by 3-log reduction will reduce health risks associated with the discharge (in relation to inhalation, ingestion during swimming and consumption of shellfish harvested) at all exposure sites, to levels below the NOAEL, even during a worst-case flow scenario (i.e. 121,000 PE in the 2043 scenario).

Projected log reductions that will be achieved at the Porirua WWTP are higher than levels required in the QMRA results. Consequently, and in line with the results of this QMRA, this level of treatment at the Porirua WWTP is sufficient to reduce health risks of the discharge below the "no observable adverse effects level" during average flows.

8. References

Abel, Nicole, Mary E Schoen, John C Kissel, and J Scott Meschke 2017 Comparison of Risk Predicted by Multiple Norovirus Dose–response Models and Implications for Quantitative Microbial Risk Assessment. Risk Analysis 37(2): 245–264.

Ahmed, Sharia M, Benjamin A Lopman, and Karen Levy 2013 A Systematic Review and Meta-Analysis of the Global Seasonality of Norovirus. PloS One 8(10): e75922.

Ahmed, W., Hamilton, K. A., Lobos, A., Hughes, B., Staley, C., Sadowsky, M. J., & Harwood, V. J. (2018). Quantitative microbial risk assessment of microbial source tracking markers in recreational water contaminated with fresh untreated and secondary treated sewage. Environment international, 117, 243-249.

Albinana-Gimenez, Nestor, Marize P Miagostovich, Byron Calgua, et al. 2009 Analysis of Adenoviruses and Polyomaviruses Quantified by qPCR as Indicators of Water Quality in Source and Drinking-Water Treatment Plants. Water Research 43(7): 2011–2019.

Amahmid, O, S Asmama, and K Bouhoum 2002 Urban Wastewater Treatment in Stabilization Ponds: Occurrence and Removal of Pathogens. Urban Water 4(3): 255–262.

Anders, R. (2006). Virus fate and transport during field-scale infiltration. University of California, Irvine.

Azuma, Kenichi, Iwao Uchiyama, and Jiro Okumura 2013 Assessing the Risk of Legionnaires' Disease: The Inhalation Exposure Model and the Estimated Risk in Residential Bathrooms. Regulatory Toxicology and Pharmacology 65(1): 1–6.

Bambic, Dustin G, Beverly J Kildare-Hann, Veronica B Rajal, et al. 2015 Spatial and Hydrologic Variation of Bacteroidales, Adenovirus and Enterovirus in a Semi-Arid, Wastewater Effluent-Impacted Watershed. Water Research 75: 83–94.

Bellou, M, P Kokkinos, and A Vantarakis 2013 Shellfish-Borne Viral Outbreaks: A Systematic Review. Food and Environmental Virology 5(1): 13–23.

Bitton, Gabriel 2010 Pathogens and Parasites in Domestic Wastewater. Wastewater Microbiology, Fourth Edition: 119–172.

Burkhardt, W. & Calci, K. R. (2000). Selective accumulation may account for shellfish-associated viral illness. Applied and environmental microbiology, 66(4), 1375–1378. doi:10.1128/aem.66.4.1375-1378.2000

Cabral, João PS 2010 Water Microbiology. Bacterial Pathogens and Water. International Journal of Environmental Research and Public Health 7(10): 3657–3703.

Carducci, Annalaura, Gabriele Donzelli, Lorenzo Cioni, and Marco Verani 2016 Quantitative Microbial Risk Assessment in Occupational Settings Applied to the Airborne Human Adenovirus Infection. International Journal of Environmental Research and Public Health 13(7): 733.

CDC 2014 Centers for Disease Control and Prevention. Reported Norovirus Outbreaks by Primary Transmission Mode and Month of Onset. Https://Www.cdc.gov/Norovirus/Reportedoutbreaks.html. Last Accessed August 2017.

Centers for Disease Control and Prevention. (2015). Norovirus-U.S. Trends and Outbreaks. Tam, C. C., Rodrigues, L. C., Viviani, L., Dodds, J. P., Evans, M. R., Hunter, P. R., et al. (2012). Longitudinal study of infectious intestinal disease in the UK (IID2 study): incidence in the community and presenting to general practice. *Gut, 61*(1), 69–77.

Choi, Samuel, and Sunny C Jiang 2005 Real-Time PCR Quantification of Human Adenoviruses in Urban Rivers Indicates Genome Prevalence but Low Infectivity. Applied and Environmental Microbiology 71(11): 7426–7433.

Costan-Longares, A, L Mocé-Llivina, A Avellon, J Jofre, and F Lucena 2008 Occurrence and Distribution of Culturable Enteroviruses in Wastewater and Surface Waters of North-eastern Spain. Journal of Applied Microbiology 105(6): 1945–1955.

Couch, Robert, Thomas Cate, Gordon Douglas Jr, Peter Gerone, and Vernon Knight 1966 Effect of Route of Inoculation on Experimental Respiratory Viral Disease in Volunteers and Evidence for Airborne Transmission. Bacteriological Reviews 30(3): 517.

Courault, D, I Albert, S Perelle, et al. 2017 Assessment and Risk Modeling of Airborne Enteric Viruses Emitted from Wastewater Reused for Irrigation. Science of The Total Environment 592: 512–526.

Dada, A.C. (2018a) Quantitative Microbial Risk Assessment for the discharge of treated wastewater into Whitford Embayment through Turanga Creek, LCL1702, Streamlined Environmental, Hamilton, 41 pp.

Dada, A.C. (2018b) Quantitative Microbial Risk Assessment for the discharge of treated wastewater at Army Bay. Report WSL1701, Streamlined Environmental, Hamilton, 73 pp.

DHI 2018. Porirua Outfall Options. Report 44801313 prepared for Wellington Water.

DHI 2019. Porirua Harbour - Modelling for Whaitua Collaborative Modelling Group. Report 44800943/01 prepared for Greater Wellington Regional Council

Donzelli, Gabriele, Marco Verani, Giandomenico Mastroeni, Lorenzo Cioni, and Annalaura Carducci 2015 Quantitative Microbial Risk Assessment in Occupational Settings: The Airborne Infectious Biological Risk.

Dufour, A.P.; Evans, O.; Behymer, T.D.; Cantú, R. (2006). Water ingestion during swimming activities in a pool: A pilot study. Journal of Water Health 4(4): 425–430.

Farkas, K., Peters, D. E., McDonald, J. E., de Rougemont, A., Malham, S. K., & Jones, D. L. (2017). Evaluation of two triplex one-step qRT-PCR assays for the quantification of human enteric viruses in environmental samples. Food and environmental virology, 9(3), 342-349.

FSANZ 2002 Australia New Zealand Food Standards Code Standard 1.6.1. Microbiological Limits for Food. Food Standards Australia and New Zealand.

Greenaway & Associates 2018. Porirua Wastewater Programme Recreation Assessment. Report prepared for Wellington Water and Stantec.

Haas, Charles N 2002 Conditional Dose-Response Relationships for Microorganisms: Development and Application. Risk Analysis 22(3): 455–463.

Haas, Charles N, Joan B Rose, and Charles P Gerba 1999 Quantitative Microbial Risk Assessment. John Wiley & Sons.

Hai, Faisal I, Thomas Riley, Samia Shawkat, Saleh F Magram, and Kazuo Yamamoto 2014 Removal of Pathogens by Membrane Bioreactors: A Review of the Mechanisms, Influencing Factors and Reduction in Chemical Disinfectant Dosing. Water 6(12): 3603–3630.

Hanley, Kaitlyn Terese 2015 Human Noroviruses in the Coastal Environment: Association with Aquatic Macroaggregates and the Risk of Infection by Raw Shellfish Consumption. University of California, Davis.

Hassard, Francis, Jasmine H Sharp, Helen Taft, et al. 2017 Critical Review on the Public Health Impact of Norovirus Contamination in Shellfish and the Environment: A UK Perspective. Food and Environmental Virology 9(2): 123–141.

Havelaar, A.H., Van Olphen, M. & Drost, Y.C. (1993) F-specific RNA bacteriophages are adequate model organisms for enteric viruses in fresh water. Appl. Environ. Microbiol. 59, 2956–2962.

Hauri, AM, M Schimmelpfennig, M Walter-Domes, et al. 2005 An Outbreak of Viral Meningitis Associated with a Public Swimming Pond. Epidemiology & Infection 133(2): 291–298.

Health Canada 2012 Guidelines for Canadian Drinking Water Quality: Guideline Technical Document — Enteric Protozoa: Giardia and Cryptosporidium. Water, Air and Climate Change Bureau, Healthy Environments and Consumer Safety Branch, Health Canada, Ottawa, Ontario. (Catalogue No H129-23/2013E-PDF).

Hewitt, Joanne, Gail E Greening, Margaret Leonard, and Gillian D Lewis 2013 Evaluation of Human Adenovirus and Human Polyomavirus as Indicators of Human Sewage Contamination in the Aquatic Environment. Water Research 47(17): 6750–6761.

Hijnen, W.A.M., Beerendonk, E.F. & Medema, G.J. (2006) Inactivation credit of radiation for viruses, bacteria and protozoan (oo)cysts in water: A review. Water Res. 40, 3-22.

Hrudey, Steve E, Elizabeth J Hrudey, and Simon JT Pollard 2006 Risk Management for Assuring Safe Drinking Water. Environment International 32(8): 948–957.

Jacangelo, JG, P Loughran, B Petrik, D Simpson, and C McIlroy 2003 Removal of Enteric Viruses and Selected Microbial Indicators by UV Irradiation of Secondary Effluent. Water Science and Technology 47(9): 193–198.

Jiang, S.C., Chu, W., He, J.W. 2007. Seasonal detection of human viruses and coliphage in Newport Bay, California. Applied and Environmental Microbiology, 73(20): 6468-6474.

Jin, Y., & Flury, M. (2002). Fate and transport of viruses in porous media. In Advances in agronomy (Vol. 77, pp. 39-102). Academic Press.

Kohn, T. & Nelson, K.L. (2007) Sunlight-mediated inactivation of MS2 coliphage via exogenous singlet oxygen produced by sensitizers in natural waters. Environ. Sci. Technol. 41, 192–197.

Kohn, T., Grandbois, M., McNeill, K. & Nelson, K.L. (2007) Association with natural organic matter enhances the sunlight-mediated inactivation of MS2 coliphage by singlet oxygen. Environ. Sci. Technol. 41, 4626–4632.

Kundu, Arti, Graham McBride, and Stefan Wuertz 2013 Adenovirus-Associated Health Risks for Recreational Activities in a Multi-Use Coastal Watershed Based on Site-Specific Quantitative Microbial Risk Assessment. Water Research 47(16): 6309–6325.

Linden, K. G., Thurston, J., Schaefer, R., & Malley, J. P. (2007). Enhanced UV inactivation of adenoviruses under polychromatic UV lamps. Appl. Environ. Microbiol., 73(23), 7571-7574.

Lodder, WJ, HHJL Van Den Berg, SA Rutjes, and AM de Roda Husman 2010 Presence of Enteric Viruses in Source Waters for Drinking Water Production in The Netherlands. Applied and Environmental Microbiology 76(17): 5965–5971.

Lofranco, Cassandra Diane 2017 Occurrence of Human Norovirus GII and Human Enterovirus in Ontario Source Waters.

Lopman, Benjamin A, Duncan Steele, Carl D Kirkwood, and Umesh D Parashar 2016 The Vast and Varied Global Burden of Norovirus: Prospects for Prevention and Control. PLoS Medicine 13(4): e1001999.

Love, D.C., Silverman, A. & Nelson, K.L. 2010 Human virus and bacteriophage inactivation in clear water by simulated sunlight compared to bacteriophage inactivation at a Southern California beach. Environ. Sci. Technol. 44, 6965–6970.

Maunula, Leena, Ilkka T Miettinen, and Carl-Henrik Von Bonsdorff 2005 Norovirus Outbreaks from Drinking Water. Emerging Infectious Diseases 11(11): 1716.

Mara, D., & Sleigh, A. 2010. Estimation of norovirus infection risks to consumers of wastewater-irrigated food crops eaten raw. *Journal of Water and Health*, *8*(1), 39-43.

McBride, G. 2017 Bell Island Wastewater Treatment Plant: Quantitative Microbial Risk Assessment. Report Prepared by NIWA for Stantec. 2017350HN.

McBride, G. 2016a Quantitative Microbial Risk Assessment for the Discharge of Treated Wastewater: Warkworth Wastewater Treatment Plan. Report Prepared by NIWA for Watercare Services Limited. HAM2016-037.

2016b Quantitative Microbial Risk Assessment for the Discharge of Treated Wastewater: Snells Beach Wastewater Treatment Plan. Report Prepared by NIWA for Watercare Services Limited. HAM2016-038.

McBride, Graham 2007 Microbial Risk Assessment Modeling. Statistical Framework for Recreational Water Quality Criteria and Monitoring: 135–151.

McBride, Graham B, Rebecca Stott, Woutrina Miller, Dustin Bambic, and Stefan Wuertz 2013 Discharge-Based QMRA for Estimation of Public Health Risks from Exposure to Stormwater-Borne Pathogens in Recreational Waters in the United States. Water Research 47(14): 5282–5297.

McBride, G. 2011 A Quantitative Microbial Risk Assessment for Napier City's ocean outfall wastewater discharge. Report Prepared by NIWA for Napier City Council. HAM2011-016.

Melnick, J. L., C. P. Gerba, and C. Wallis 1978 Viruses in Water. Bulletin of the World Health Organization 56(4): 499–508.

MfE/MoH (2003) Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas. Joint Report of the Ministry for Environment and Ministry of Health. ME number: 474

Moore J. (2014) Basics of UV Disinfection, Local Section Seminar, Michigan Water Environment Association. Available at: https://www.mi-wea.org/docs/Joe%20Moore-Basics%20of%20UV%20Disinfection%20for%20website.pdf

Noble, R.T., Lee, I.M. and Schiff, K.C. 2004. Inactivation of indicator micro-organisms from various sources of faecal contamination in seawater and freshwater. Journal of Applied Microbiology 2004, 96, 464–472

NRC 1983 Risk Assessment in the Federal Government: Managing the Process Working Papers. National Academies Press.

Okoh, Anthony I, Thulani Sibanda, and Siyabulela S Gusha 2010 Inadequately Treated Wastewater as a Source of Human Enteric Viruses in the Environment. International Journal of Environmental Research and Public Health 7(6): 2620–2637.

Patel, Manish M, Marc-Alain Widdowson, Roger I Glass, et al. 2008 Systematic Literature Review of Role of Noroviruses in Sporadic Gastroenteritis. Emerging Infectious Diseases 14(8): 1224.

PHAC 2015 Public Health Agency of Canada. (2015). Canada Communicable Disease Report CCDR. Volume 41 S-1, February 20, 2015. Http://Www.phac-Aspc.gc.ca/Publicat/Ccdrrmtc/15vol41/Dr-rm41s-1/Review-Revue-Eng.php#figure-1).

Prevost, Benoit, FS Lucas, Alexandre Goncalves, et al. 2015 Large Scale Survey of Enteric Viruses in River and Waste Water Underlines the Health Status of the Local Population. Environment International 79: 42–50.

Rajab, Ahmed Rahomi, Mohd Razman Salim, Johan Sohaili, Aznah Nur Anuar, and Sivarama Krishna Lakkaboyana 2017 Performance of Integrated Anaerobic/Aerobic Sequencing Batch Reactor Treating Poultry Slaughterhouse Wastewater. Chemical Engineering Journal 313: 967–974.

Romero, O.C., Straub, A.P., Kohn, T. & Nguyen, T.H. (2011) Role of temperature and suwannee river natural organic matter on inactivation kinetics of rotavirus and bacteriophage MS2 by solar irradiation. Environ. Sci. Technol. 45, 10385–10393.

Ryan, Michael O, Charles N Haas, Patrick L Gurian, et al. 2014 Application of Quantitative Microbial Risk Assessment for Selection of Microbial Reduction Targets for Hard Surface Disinfectants. American Journal of Infection Control 42(11): 1165–1172.

Sassoubre, Lauren M, Kara L Nelson, and Alexandria B Boehm 2012 Mechanisms for Photoinactivation of Enterococcus Faecalis in Seawater. Applied and Environmental Microbiology 78(21): 7776–7785.

Schijven, Jack, Martijn Bouwknegt, Roda Husman, et al. 2013 A Decision Support Tool to Compare Waterborne and Foodborne Infection And/Or Illness Risks Associated with Climate Change. Risk Analysis 33(12): 2154–2167.

Stott, R. 2012. Viral Monitoring Review for Warkworth Wastewater Treatment Plant 2010-2011. Report Prepared for Watercare Services Limited.

Sedmak, Gerald, David Bina, and Jeffrey MacDonald 2003 Assessment of an Enterovirus Sewage Surveillance System by Comparison of Clinical Isolates with Sewage Isolates from Milwaukee, Wisconsin, Collected August 1994 to December 2002. Applied and Environmental Microbiology 69(12): 7181–7187.

Shin G-A, Linden KG, Sobsey MD. Low pressure ultraviolet inactivation of pathogenic enteric viruses and bacteriophages. Journal of Environmental Engineering and Science 2005;4(S1):S7-S11.

Silverman, A. I. (2013). Sunlight Inactivation of Waterborne Viruses: Mechanisms, Modeling, and Application to Surface Waters and Wastewater Treatment (Doctoral dissertation, UC Berkeley).

Simmons, Fredrick J, David H-W Kuo, and Irene Xagoraraki 2011 Removal of Human Enteric Viruses by a Full-Scale Membrane Bioreactor during Municipal Wastewater Processing. Water Research 45(9): 2739–2750.

Simpson, D, J Jacangelo, P Loughran, and C McIlroy 2003 Investigation of Potential Surrogate Organisms and Public Health Risk in UV Irradiated Secondary Effluent. Water Science and Technology 47(9): 37–43.

Sinclair, R.G., Jones, E.L., Gerba, C.P. 2009. Viruses in recreational water-borne disease outbreaks: a review. Journal of Applied Microbiology, 107(6): 1769-1780

Sinton, L.W., Davies-Colley, R.J., and Bell, R.G. 1994. Inactivation of enterococci and fecal coliforms from sewage and meatworks effluents in seawater chambers. Applied and Environmental Microbiology 2040–2048.

Sinton, L.W., Finlay, R.K., Lynch, P.A. 1999. Sunlight Inactivation of Fecal Bacteriophages and Bacteria in Sewage-Polluted Seawater. Applied and Environmental Microbiology 3065-3613.

Sinton, L.W., Hall, C.H., Lynch, P.A. & Davies-Colley, R.J. (2002) Sunlight inactivation of fecal indicator bacteria and bacteriophages from waste stabilization pond effluent in fresh and saline waters. Appl. Environ. Microbiol. 68, 1122-1131.

Soller, J.A.; Bartrand, T.; Ashbolt, N.J.; Ravenscroft, J.; Wade, T.J. (2010a). Estimating the primary etiologic agents in recreational freshwaters impacted by human sources of Water Research 44(16): 4736–4747.

Soller, J.A.; Schoen, M.E.; Bartrand, T.; Ravenscroft, J.E.; Ashbolt, N.J. (2010b). Estimated human health risks from exposure to recreational waters impacted by human and non-human sources of faecal contamination. Water Research 44(16): 4674–4691.

Stewart, M, Cooke, J, Dada, A.C. (2017) Assessment of ecological effects on the receiving environment associated with the discharge from the proposed membrane bioreactor wastewater treatment system. Option 1: Treatment of all wastewater generated by Te Kauwhata (current and future), Springhill Prison (current and future) and the Lakeside development. Report LDL1701–FINAL, Streamlined Environmental, Hamilton, 168 pp.

Teunis, P. F. M., Moe, C. L., Liu, P., Miller, S. E., Lindesmith, L., Baric, R. S., Le Pendu, J. & Calderon, R. L. 2008 Norwalk virus: how infectious is it? J. Med. Virol. 80(8), 1468–1476

Teunis, P., Schijven, J., Rutjes, S., 2016. A generalized dose-response relationship for adenovirus infection and illness by exposure pathway. Epidemiol. Infect. 144, 3461–3473.

Toze, Simon 1997 Microbial Pathogens in Wastewater: Literature Review for Urban Water Systems Multi-Divisional Research Program. CSIRO Land and Water Australia.

Tung-Thompson, Grace, Dominic A Libera, Kenneth L Koch, L Francis III, and Lee-Ann Jaykus 2015 Aerosolization of a Human Norovirus Surrogate, Bacteriophage MS2, during Simulated Vomiting. PloS One 10(8): e0134277.

USEPA 1999 USEPA, Wastewater, Technology Fact Sheet: Sequencing Batch Reactors, U.S Environmental Protection Agency, Office of Water, Washington, D.C., EPA 932-F-99-073. 1999.

USEPA. (2010). Quantitative Microbial Risk Assessment to Estimate Illness in Freshwater Impacted by Agricultural Animal Sources of Fecal Contamination. EPA 822-R-10-005.

US EPA. (2015). Review of coliphages as possible indicators of fecal contamination for ambient water quality. 820-R-15-098

Verbyla, Matthew E, and James R Mihelcic 2015 A Review of Virus Removal in Wastewater Treatment Pond Systems. Water Research 71: 107–124.

Vergara, GGRV, JB Rose, and KYH Gin 2016 Risk Assessment of Noroviruses and Human Adenoviruses in Recreational Surface Waters. Water Research 103: 276–282.

Wade, T.J., Calderon, R.L., Brenner, K.P., Sams, E., Beach, M., Haugland, R., Wymer, L., Dufour, A.P. 2008. High Sensitivity of Children to Swimming-Associated Gastrointestinal Illness – Results Using a Rapid Assay of Recreational Water Quality. Epidemiology 19(3): 375383.

Wade, T.J., Sams, E., Brenner, K.P., Haugland, R., Chern, E., Beach, M., Wymer, L., Rankin, C.C., Love, D., Li, Q., Noble, R., Dufour, A.P. 2010. Rapidly Measured Indicators or Recreational Water Quality and Swimming-Associated Illness at Marine Beaches: A Prospective Cohort Study. Environmental Health 9: 66.

Widdowson, Marc-Alain, Stephan S Monroe, and Roger I Glass 2005 Are Noroviruses Emerging? Emerging Infectious Diseases 11(5): 735.

WHO (2016) Quantitative microbial risk assessment: application for water safety management. World Health Organization. ISBN 978 92 4 156537 0

Wyer, Mark D, A Peter Wyn-Jones, David Kay, et al. 2012 Relationships between Human Adenoviruses and Faecal Indicator Organisms in European Recreational Waters. Water Research 46(13): 4130–4141.

Appendices

Appendix 1 Monitoring data: Influent and effluent virus concentrations

Sample Details: **Water**

Influent
Porirua WWTP

ID No: **NA**

Referring Lab No: **NA**

Order No: **NA**

Environmental and Food Virology Laboratory

Laboratory Manager: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Specimen Type: Water
Site:

Date Collected: 23 Sep 2019 ESR Lab No: FEV19/113
Received In Lab: 23 Sep 2019 Episurv No:

Test	Results
Norovirus RT-PCR	GI positive, GII positive
Enterovirus RT-PCR	Positive
Adenovirus PCR	Positive

Reported by: Joanne Hewitt, Senior Scientist

Issued 11:15 on 03 Oct 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

ESR Lab No: FEV19/113

Comments

Norovirus detected by norovirus genogroup I and II RT-qPCR.

Concentration of norovirus genogroup I is 4.9 $\log_{10}$ (8.3×10^4) genome copies/L as determined by qPCR.

Concentration of norovirus genogroup II is 6.7 $\log_{10}$ (4.7×10^6) genome copies/L as determined by qPCR.

Enterovirus detected by RT-qPCR.

Concentration of enterovirus is 5.2 $\log_{10}$ (1.5×10^5) genome copies/L as determined by qPCR.

Adenovirus detected by qPCR.

Concentration of adenovirus is 6.0 $\log_{10}$ (1.0×10^6) genome copies/L as determined by qPCR.

Testing commenced 23 September 2019

Please note: this test is not covered by our IANZ 17025 accreditation.

Reported by: Joanne Hewitt, Senior Scientist — Issued 11:15 on 03 Oct 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

Sample Details: **Water**

Effluent
Porirua WWTP

ID No: **NA**

Referring Lab No: **NA**

Order No: **NA**

Environmental and Food Virology Laboratory

Laboratory Manager: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Specimen Type: Water
Site:

Date Collected: 23 Sep 2019 ESR Lab No: FEV19/114
Received In Lab: 23 Sep 2019 Episurv No:

Test	**Results**
Norovirus RT-PCR	GI positive, GII positive
Enterovirus RT-PCR	Positive
Adenovirus PCR	Positive

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 10:34 on 03 Oct 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

---

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

ESR Lab No: FEV19/114

Comments

Norovirus detected by norovirus genogroup I and II RT-qPCR.

Concentration of norovirus genogroup I is 2.8 $\log_{10}$ (6.7 $x10^2$) genome copies/L as determined by qPCR.

Concentration of norovirus genogroup II is 3.6 $\log_{10}$ (3.8 $x\ 10^3$) genome copies/L as determined by qPCR.

Enterovirus detected by RT-qPCR.

Concentration of enterovirus is <1.7 $\log_{10}$ (<50) genome copies/L as determined by qPCR.

Adenovirus detected by qPCR.

Concentration of adenovirus is 4.2 $\log_{10}$ (1.5 $x10^4$) genome copies/L as determined by qPCR.

Testing commenced 23 September 2019

Please note: this test is not covered by our IANZ 17025 accreditation.

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 10:34 on 03 Oct 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

Sample Details: **Water**

Influent
Porirua WWTP

ID No: **NA**

Referring Lab No: **NA**

Order No: **NA**

Environmental and Food Virology Laboratory

Laboratory Manager: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Specimen Type: Water
Site:

Date Collected: 9 Sep 2019
Received In Lab: 9 Sep 2019

ESR Lab No: FEV19/109
Episurv No:

Test	**Results**
Norovirus RT-PCR	GI positive, GII positive
Enterovirus RT-PCR	Positive
Adenovirus PCR	Positive

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:44 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

ESR Lab No: FEV19/109

Comments

Norovirus detected by norovirus genogroup I and II RT-qPCR.

Concentration of norovirus genogroup I is 5.7 $\log_{10}$ (4.8 x10^5) genome copies/L as determined by qPCR.

Concentration of norovirus genogroup II is 7.0 $\log_{10}$ (10^7) genome copies/L as determined by qPCR.

Enterovirus detected by RT-qPCR.

Concentration of enterovirus is 4.9 $\log_{10}$ (8.4 x10^4) genome copies/L as determined by qPCR.

Adenovirus detected by qPCR.

Concentration of adenovirus is 5.5 $\log_{10}$ (3.3 x10^5) genome copies/L as determined by qPCR.

Testing commenced 9 September 2019

Please note: this test is not covered by our IANZ 17025 accreditation.

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:44 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

Sample Details: **Water**

Effluent
Porirua WWTP

ID No: **NA**

Referring Lab No: **NA**

Order No: **NA**

Environmental and Food Virology Laboratory

Laboratory Manager: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Specimen Type: Water | Date Collected: 9 Sep 2019 | ESR Lab No: FEV19/110

Site: | Received In Lab: 9 Sep 2019 | Episurv No:

Test	**Results**
Norovirus RT-PCR	GI positive, GII positive
Enterovirus RT-PCR	Positive
Adenovirus PCR	Positive

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:44 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

---

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

ESR Lab No: FEV19/110

Comments

Norovirus detected by norovirus genogroup I and II RT-qPCR.

Concentration of norovirus genogroup I is 4.2 $\log_{10}$ (1.7 x10^4) genome copies/L as determined by qPCR.

Concentration of norovirus genogroup II is 4.7 $\log_{10}$ (5.6 x 10^4) genome copies/L as determined by qPCR.

Enterovirus detected by RT-qPCR.

Concentration of enterovirus is 2 $\log_{10}$ (10^2) genome copies/L as determined by qPCR.

Adenovirus detected by qPCR.

Concentration of adenovirus is 4.8 $\log_{10}$ (5.7 x10^4) genome copies/L as determined by qPCR.

Testing commenced 9 September 2019

Please note: this test is not covered by our IANZ 17025 accreditation.

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:44 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

Sample Details: **Water**

Influent
Porirua WWTP

ID No: **NA**

Referring Lab No: **NA**

Order No: **NA**

Environmental and Food Virology Laboratory

Laboratory Manager: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Specimen Type: Water
Site:

Date Collected: 16 Sep 2019 ESR Lab No: FEV19/111
Received In Lab: 16 Sep 2019 Episurv No:

Test	**Results**
Norovirus RT-PCR	GI positive, GII positive
Enterovirus RT-PCR	Positive
Adenovirus PCR	Positive

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:44 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

---

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

ESR Lab No: FEV19/111

Comments

Norovirus detected by norovirus genogroup I and II RT-qPCR.

Concentration of norovirus genogroup I is 4.9 $\log_{10}$ (8.2 x10^4) genome copies/L as determined by qPCR.

Concentration of norovirus genogroup II is 6.7 $\log_{10}$ (4.9 x 10^6) genome copies/L as determined by qPCR.

Enterovirus detected by RT-qPCR.

Concentration of enterovirus is 4.7 $\log_{10}$ (5.2 x 10^4) genome copies/L as determined by qPCR.

Adenovirus detected by qPCR.

Concentration of adenovirus is 5.4 $\log_{10}$ (2.3 x10^4) genome copies/L as determined by qPCR.

Testing commenced 16 September 2019

Please note: this test is not covered by our IANZ 17025 accreditation.

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:44 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

Sample Details: **Water**

Effluent
Porirua WWTP

ID No: **NA**

Referring Lab No: **NA**

Order No: **NA**

Environmental and Food Virology Laboratory

Laboratory Manager: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Specimen Type: Water
Site:

Date Collected: 16 Sep 2019 ESR Lab No: FEV19/112
Received In Lab: 16 Sep 2019 Episurv No:

Test	**Results**
Norovirus RT-PCR	GI positive, GII positive
Enterovirus RT-PCR	Positive
Adenovirus PCR	Positive

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:45 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003

ESR Lab No: FEV19/112

Comments

Norovirus detected by norovirus genogroup I and II RT-qPCR.

Concentration of norovirus genogroup I is 3.8 $\log_{10}$ (6.1 $x10^3$) genome copies/L as determined by qPCR.

Concentration of norovirus genogroup II is 4.8 $\log_{10}$ (6.3 $x\ 10^4$) genome copies/L as determined by qPCR.

Enterovirus detected by RT-qPCR.

Concentration of enterovirus is 1.7 $\log_{10}$ (50) genome copies/L as determined by qPCR.

Adenovirus detected by qPCR.

Concentration of adenovirus is 4.6 $\log_{10}$ (3.6 $x10^4$) genome copies/L as determined by qPCR.

Testing commenced 16 September 2019

Please note: this test is not covered by our IANZ 17025 accreditation.

Final Report

Reported by: Joanne Hewitt, Senior Scientist
Issued 16:45 on 25 Sep 2019

Enquiries: Joanne Hewitt, (04) 914 0690, joanne.hewitt@esr.cri.nz

Return Address:
Christopher Dada
Streamlined Environmental Ltd
PO Box 7003
HAMILTON 3247

Porirua WWTP influent and effluent virus concentrations

Sampling date	Virus	Influent (genome/L)	Effluent (genome/L)	Virus Log Removals
9th September 2019	Norovirus Genogroup I	4.80E+05	1.70E+04	1.5
	Norovirus Genogroup II	1.00E+07	5.60E+04	2.3
	Enterovirus	8.40E+04	1.00E+02	2.9
	Adenovirus	3.30E+05	5.70E+04	0.8
16th September 2019	Norovirus Genogroup I	8.20E+04	6.10E+03	1.1
	Norovirus Genogroup II	4.90E+06	6.30E+04	1.9
	Enterovirus	5.20E+04	5.00E+01	3.0
	Adenovirus	2.30E+05	3.60E+04	0.8
23rd September 2019	Norovirus Genogroup I	8.30E+04	6.70E+02	2.1
	Norovirus Genogroup II	4.70E+06	3.80E+03	3.1
	Enterovirus	1.50E+05	5.00E+01	3.5
	Adenovirus	1.00E+06	1.50E+04	1.8

Appendix 2 Additional notes on choice of QMRA reference pathogens

We selected noroviruses as the first representative viral pathogen for this QMRA because:

1. Noroviruses are host-specific, present mostly in human waste. This makes them ideal candidates for tracking primary sources of human-related faecal contamination in the environment (Ahmed et al., 2010; Mara and Sleigh, 2010).
2. Human noroviruses are now the most common cause of gastroenteritis outbreaks in children in developed countries worldwide, implicated in >90% of nonbacterial and ≈50% of all-cause epidemic gastroenteritis worldwide (Lopman et al. 2016; Lofranco 2017). They are unquestionably the most common viral cause of gastroenteritis[15] for which dose-response data are available (Mara and Sleigh, 2010; Teunis et al., 2008, CDC 2015, Farkas et al.2017).
3. As with other enteric viruses, they are often symptomatic or pauci-symptomatic[16]; they can even present a high risk of morbidity and mortality in vulnerable (high-risk) populations such as young children, elderly individuals and immunocompromised patients (Prevost et al., 2015).
4. Noroviruses often present higher illness risks than other viruses ((Vergara, Rose, and Gin 2016). Also, noroviruses have a much lower ID_{50} (the minimum dose of norovirus pathogens that can cause infection in 50% of exposed and susceptible subjects) than other viruses. Dose-response relationships suggest that a single norovirus particle can cause infections in more than 40% of susceptible individuals, a rate much higher than other viruses (McBride, 2011).
5. Norovirus outbreaks can occur throughout the year, but have been reported to occur more frequently during the colder winter seasons in temperate climates (Lofranco 2017; CDC 2014; Maunula, Miettinen, and Von Bonsdorff 2005; Ahmed, Lopman, and Levy 2013). A similar observation was made in the scoping and surrogate study on virus concentration at Mangere WWTP influent, New Zealand (Simpson et al.2003).

We selected enterovirus as a second representative viral pathogen for this QMRA because:

1. Enterovirus, one of the largest genera of viruses classified within the Picornaviridae family, represents a significant burden to public health globally (Lofranco 2017).

[15] norovirus mainly affects children under the age of three
[16] i.e. presenting few symptoms.

2. Enteroviruses target either intestinal or upper respiratory tract cells resulting in an upper respiratory tract infection or gastrointestinal illness. Enterovirus types can cause a wide spectrum of diseases within humans and present a broad range of symptoms.
3. Enteroviruses are also transmissible via sewage contaminated waters (Lofranco 2017; Health Canada 2012).
4. Although human enterovirus outbreaks can occur throughout the year depending on the strain, in temperate climates, enterovirus infections are most prevalent during summer months (Sedmak, Bina, and MacDonald 2003; Costan-Longares et al. 2008; PHAC 2015).

We selected adenovirus as the third representative viral pathogen for this QMRA because:

1. Adenovirus, a double-stranded DNA virus, is often detected in these same environments as noroviruses and enteroviruses (Choi and Jiang 2005; Sassoubre, Nelson, and Boehm 2012). However, compared to other viruses, it has been reported to have prolonged survival time and increased resistance to disinfection e.g. UV treatments (Albinana-Gimenez et al. 2009; Wyer et al. 2012; Kundu, McBride, and Wuertz 2013; Hewitt et al. 2013).
2. This pathogenic virus has a low infectious dose and is thus of great importance in public health (Donzelli et al. 2015). Human adenoviruses (HAdVs) cause numerous symptomatic and asymptomatic infections affecting the respiratory tract, the eyes, and the gastrointestinal tract (Carducci et al. 2016). They can be excreted in the faeces, urine, and respiratory secretions and transmitted via contact with the eyes, the faecal-oral route, or inhalation (Bambic et al. 2015)..
3. HAdVs have a number of features that justify their use as index pathogens for air in occupational settings possibly contaminated by faecally-excreted pathogens (Donzelli et al. 2015).

Appendix 3 Additional notes on dose-response characterization

A rich discussion on dose-response functions already exists in published literature (e.g. See McBride 2011, 2016a, Vergara et al.2016, USEPA 2010, WHO 2016). Dose-infection curves for the viral pathogens used have been established from clinical test results of subsets of volunteers challenged with laboratory-prepared aliquots of viral suspensions at varying serial dilutions of known mean[17] doses of viruses (Haas et al.1999). These were based primarily on two assumptions. This first assumption is the 'single-hit' hypothesis, which is that a single viral pathogen would evade the host defense mechanisms and reach its potential infection site, establish itself and then cause infection. The second assumption is based on a Poisson distribution of the viral pathogens in the laboratory-prepared viral aliquot, which better reflects a random, well-mixed population. These assumptions can be described with probability distributions.

When the probability of ingesting a dose of pathogens is Poisson-distributed and all of the ingested pathogens have an equal probability of initiating infection, the exponential dose-response model is appropriate:

$$P_{\inf(d;r)} = 1 - e^{-rd} \qquad \text{....eqn(1)}$$

where $P_{\inf}$ is the probability of infection, d is dose (number of pathogens), e represents the standard exponential constant, 2.7183, and r is a parameter of the distribution equal to the probability that an individual pathogen initiates infection.

When the probability of ingesting pathogens is Poisson-distributed and the probability that individual pathogens initiate infection is beta-distributed, the beta-Poisson model is appropriate:

$$P_{\inf(d;\alpha,\beta)} = 1 - {}_1F_1(\alpha, \alpha+\beta, -d) \qquad \text{....eqn(2)}$$

where α and β are parameters of the Beta distribution and ${}_1F_1$ denotes a confluent hypergeometric function. A commonly used approximation to the beta-Poisson may be used when β >> 1 and β >> *α*, which is usually so in most cases. This approximation is:

$$P_{\inf(d;\alpha,\beta)} = 1 - (1 + \frac{d}{\beta})^{-\alpha} \qquad \text{....eqn(3)}$$

where $P_{\inf}$ is the probability of infection, d = mean dose, *α* and β are 'nonnegative shape' and location parameters, respectively. This approximation however is inadequate for noroviruses because the fitted α and β parameters *(i.e* β = 0.055, *α = 0.04)* do not comply with the condition β >> 1 and β >> *α ,* hence the push for the use

[17] Doses in individuals' challenges are not measured, instead the average dose given to each member of a group is known.

of the much-more-difficult-to-evaluate hypergeometric equation (2) (as argued in McBride 2011).

One approach to QMRA is to use individual exposure per exposure occasion to represent a group visiting a polluted beach. This approach often produces unrealistic risk profiles. A very robust QMRA approach is to expose multiple people on each exposure occasion. In this case, it is possible to assign individual doses, thus eliminating the need for the Poisson averaging. Hence, for the constant r, the simple one-parameter exponential model is easily replaced by the simple bionomial model:

$$P_{inf} = 1 - (1 - r)^{i} \quad \text{....eqn(4)}$$

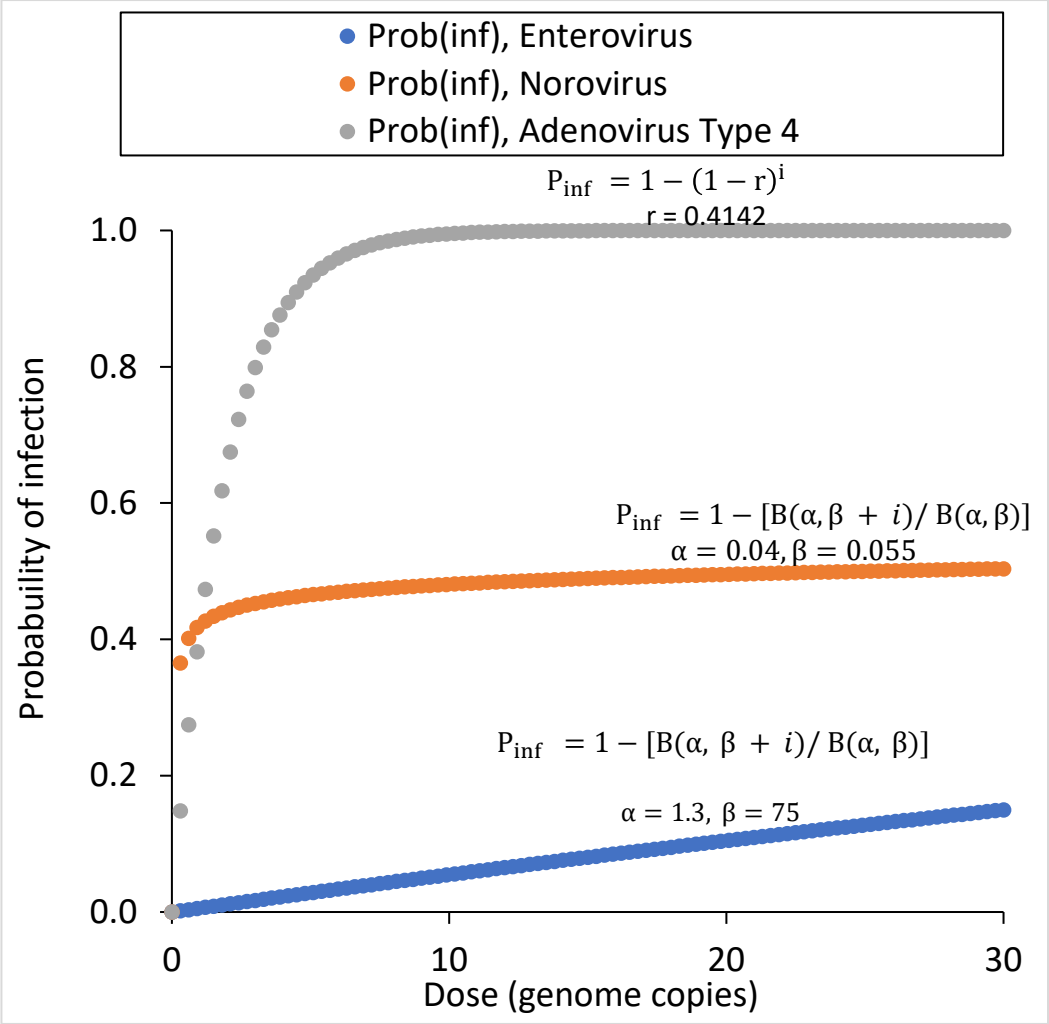
where *i* is the individual dose. Similarly, the two-parameter beta-Poisson model (eqn 2) becomes replaced with the beta-bionomial model, below, which is easily executed using the natural logarithm of the gamma function in Excel[18]:

$$P_{inf} = 1 - [B(\alpha, \beta + i) / B(\alpha, \beta)] \quad \text{....eqn(5)}$$

where P(i) is probability of infection, β is a standard beta function (Abramowitz and Stegun, 1964; Teunis et al., 2008), α and β are shape and location parameters and *i* represents a dose received by an individual.

[18] Prob of infectin $= 1 - \text{EXP}\{\text{GAMMALN}(\beta + i) + \text{GAMMALN}(\alpha + \beta) - [\text{GAMMALN}(\alpha + \beta + i) + \text{GAMMALN}(\beta)]\}$ (as in McBride 2011)

Appendix 4 Dose-response curves applied in this QMRA



Plots of individual dose response curve for adenovirus type 4, enterovirus and norovirus used in this QMRA

Appendix 5 Estimation of combined log reduction of viruses during conditions of WWTP overflows

To estimate the combined log reduction for each pathogen during instances when part of the wastewater is released as bypasses, the following formula was applied:

$$Combined\ combined\ logremoval = \frac{\text{Treated\%} * \text{RVC}_\text{t}}{100} + \frac{\text{Bypass\%} * \text{RVC}_\text{b}}{100}$$

where :

- $\text{Bypass\%}$ is the median proportion of bypass compared to daily influent flow.
- $\text{Treated\%}$ is the median distribution of the proportion of treated wastewater compared to daily influent flow.
- RVC_t is the resultant effluent concentration following treatment of non-bypass wastewater. This parameter was estimated by the formula:

$$RVC_t = \frac{\text{influent virus concentrations}}{10^{\text{log removal achieved during treatment}}}$$

  where log reduction achieved during treatment is the median log reduction achieved for each virus, based on monitoring data (see Table 5).

- RVC_b is the resultant effluent concentration following discharge of untreated bypass wastewater. During overflow conditions, the wastewater undergoes primary treatment but is bypassed around secondary treatment before UV disinfection. The combined log removals achievable, should some proportion of the wastewater be released as WWTP bypasses, are much lower compared to when all the wastewater is fully treated at the WWTP. Hence, on the average, the log removal achieved during treatment of the bypass is at least 1 log lower than would have been achieved, if fully treated. (a nominal influent virus concentration of 1,000,000 units was applied)

Appendix 6 Predicted Individual Illness risks (expressed as percentages and based on the 95th Percentiles) following inhalation or ingestion of potentially polluted recreational water [19]

Virus Log Reduction	Exposure site	Adenovirus		Enterovirus		Norovirus	
		2018 (84,000 PE)	2043 (121,000 PE)	2018 (84,000 PE)	2043 (121,000 PE)	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	200m E	1.0	2.0	2.0	3.0	14.0	15.0
	200m Offshore	<0.1	<0.1	<0.1	1.0	2.0	2.0
	200m SW	2.0	3.0	2.0	5.0	20.0	22.0
	Contact Recreation 1	1.0	1.0	1.0	1.0	6.0	8.0
	Contact Recreation 3	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1	<0.1	<0.1	<0.1	1.0
	Contact Recreation 5	<0.1	<0.1	<0.1	<0.1	<0.1	1.0
	Mount Cooper	<0.1	<0.1	<0.1	1.0	1.0	2.0
	Ti Korohiwa Rocks	1.0	1.0	2.0	2.0	9.0	10.0
	Titahi Beach (S)	1.0	1.0	1.0	1.0	10.0	10.0
	Titahi Beach	<0.1	1.0	1.0	1.0	4.0	6.0
	Contact Recreation 7	<0.1	<0.1	<0.1	<0.1	<0.1	1.0
	Shellfish 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 5	<0.1	<0.1	<0.1	<0.1	<0.1	1.0
	Tirua Bay	<0.1	1.0	1.0	1.0	2.0	3.0
2 Log Reduction	200m E	<0.1	1.0	1.0	1.0	2.0	2.0
	200m Offshore	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	200m SW	<0.1	1.0	1.0	1.0	3.0	4.0
	Contact Recreation 1	<0.1	<0.1	<0.1	<0.1	1.0	2.0
	Contact Recreation 3	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Mount Cooper	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Ti Korohiwa Rocks	<0.1	<0.1	1.0	1.0	2.0	3.0
	Titahi Beach (S)	<0.1	<0.1	<0.1	1.0	2.0	2.0
	Titahi Beach	<0.1	<0.1	<0.1	<0.1	1.0	1.0
	Contact Recreation 7	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 5	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Tirua Bay	<0.1	<0.1	<0.1	<0.1	1.0	1.0
3 Log Reduction	200m E	<0.1	<0.1	<0.1	<0.1	1.0	1.0
	200m Offshore	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	200m SW	<0.1	<0.1	1.0	1.0	1.0	1.0
	Contact Recreation 1	<0.1	<0.1	<0.1	<0.1	<0.1	1.0
	Contact Recreation 3	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Mount Cooper	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Ti Korohiwa Rocks	<0.1	<0.1	<0.1	<0.1	1.0	1.0
	Titahi Beach (S)	<0.1	<0.1	<0.1	<0.1	<0.1	1.0
	Titahi Beach	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 7	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 5	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Tirua Bay	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
4 Log Reduction	200m E	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	200m Offshore	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	200m SW	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 3	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 5	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Mount Cooper	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Ti Korohiwa Rocks	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Titahi Beach (S)	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Titahi Beach	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Contact Recreation 7	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 4	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Shellfish 5	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1
	Tirua Bay	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1

[19] Adenovirus- QMRA reference pathogen for acute febrile illness risks, Enterovirus and Norovirus- QMRA reference pathogen for gastrointestinal illness (primary water contact).

Appendix 7 Predicted Individual Illness risks (expressed as percentages and based on the 95th Percentiles) following consumption of potentially polluted raw shellfish

Virus Log Reduction	Exposure site	Enterovirus		Norovirus	
		2018 (84,000 PE)	2043 (121,000 PE)	2018 (84,000 PE)	2043 (121,000 PE)
1 Log Reduction	Contact Recreation 7	1.0	1.0	9.0	10.0
	Shellfish 4	1.0	1.0	5.0	9.0
	Shellfish 5	1.0	1.0	10.0	15.0
2 Log Reduction	Contact Recreation 7	<0.1	<0.1	2.0	3.0
	Shellfish 4	<0.1	<0.1	1.0	2.0
	Shellfish 5	<0.1	<0.1	2.0	3.0
3 Log Reduction	Contact Recreation 7	<0.1	<0.1	1.0	1.0
	Shellfish 4	<0.1	<0.1	1.0	1.0
	Shellfish 5	<0.1	<0.1	1.0	1.0
4 Log Reduction	Contact Recreation 7	<0.1	<0.1	<0.1	<0.1
	Shellfish 4	<0.1	<0.1	<0.1	<0.1
	Shellfish 5	<0.1	<0.1	<0.1	<0.1