Scenario-based quantitative microbial risk assessment to evaluate the robustness of a drinking water treatment plant

Mohamed A. Hamouda, William B. Anderson, Michele I. Van Dyke, Ian P. Douglas, Stéphanie D. McFadyen and Peter M. Huck

ABSTRACT

While traditional application of quantitative microbial risk assessment (QMRA) models usually stops at analyzing the microbial risk under typical operating conditions, this paper proposes the use of scenario-based risk assessment to predict the impact of potential challenges on the expected risk. This study used a QMRA model developed by Health Canada to compare 14 scenarios created to assess the increase in risk due to potential treatment failures and unexpected variations in water quality and operating parameters of a water treatment plant. Under regular operating conditions, the annual risk of illness was found to be substantially lower than the acceptable limit. Scenario-based QMRA was shown to be useful in demonstrating which hypothetical treatment failures would be the most critical, resulting in an increased risk of illness. The analysis demonstrated that scenarios incorporating considerable failure in treatment processes resulted in risk levels surpassing the acceptable limit. This reiterates the importance of robust treatment processes and the multi-barrier approach voiced in drinking water safety studies. Knowing the probability of failure, and the risk involved, allows designers and operators to make effective plans for response to treatment failures and/or recovery actions involving potential exposures. This ensures the appropriate allocation of financial and human resources.

Key words | drinking water, pathogen, quantitative microbial risk assessment, risk modeling, robustness, treatment

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INTRODUCTION

Water used as a source for drinking water treatment plants may contain pathogenic microorganisms that could cause disease in humans upon ingestion. This is particularly true for water derived from surface water sources (lakes or rivers). One of the main objectives of a water treatment plant is to remove/inactivate pathogens through a series of treatment processes to ensure the supply of safe drinking water to the consumer. Until recently, the common practice was to rely on the compliance of treated water from a water treatment plant by monitoring treatment performance (e.g. turbidity, chlorine residual) and also using microbial pathogen indicators (commonly *Escherichia coli*). However, the lack of real time monitoring techniques for microbial indicators, together with the occasional occurrence of disease outbreaks caused by treated drinking water that passed water quality tests (WHO 2011), has provided the impetus for a more quantitative and rigorous approach to assessing the risk of infection from drinking water. Such an approach is intended to assist with decision making as it pertains to upgrading treatment plants, developing operational strategies, investment planning, and demonstrating the level of consumer protection (Howard *et al.* 2006;

doi: 10.2166/wqrjc.2016.034

Payment & Pintar 2006). Quantitative microbial risk assessment (QMRA) has been developed to quantify the risk to human health resulting from disease caused by being exposed to specific types of waterborne pathogens (Howard *et al.* 2006; Pintar *et al.* 2010; WHO 2011).

The use of QMRA in assessing risk from waterborne pathogens has been described in earlier studies (e.g. Haas *et al.* 1999; Haas & Eisenberg 2001). The main components of the general risk assessment framework are hazard assessment, exposure assessment, dose-response analysis, and risk characterization. Theoretically, a QMRA can be completed for each waterborne pathogen that can be accounted for in source water. However, this would be time-consuming and impractical due to the presence of numerous pathogens and the lack of occurrence data for many of them. Therefore, QMRA models typically use reference organisms that include representatives from the different groups of waterborne pathogens (protozoa, bacteria and viruses) and for which source water, treatment removal, and dose-response data are available. Reference pathogens usually include *Cryptosporidium* for protozoan parasites, pathogenic *E. coli* O157 for bacteria, and rotavirus for viruses (WHO 2011). The results of the risk assessment can take many forms, such as the risk of infection (number of illnesses per population), or a metric representing the burden of disease (economic or otherwise). However, a method that is often used as the unit of measure to characterize risk is the Disability Adjusted Life Year (DALY) (WHO 2011). Ideally, a QMRA process should assess the risk of illness from consuming water at the tap. This would require modeling the change in pathogen concentrations from source water, through treatment, and then through the distribution system and service lines. However, due to the complexity associated with modeling pathogen survival in distribution systems or the potential for contamination associated with cross-connections or intrusion, most QMRA models at present evaluate the risk of illness from consuming the water exiting a treatment plant.

Several studies have implemented QMRA to assess the risks from disease due to consumption of drinking water containing pathogens (e.g. Howard *et al.* 2006; Åström *et al.* 2007; Smeets *et al.* 2008; Hunter *et al.* 2011; Pintar *et al.* 2012). However, only a few attempts have been made to develop generalized computer models in order to make QMRA tools more accessible. Two such generalized QMRA models include QMRAspot (Schijven *et al.* 2011) and Health Canada's QMRA Model (Health Canada 2011, 2012). Both models follow a similar approach to QMRA implementation, and were developed to provide a user-friendly and comparative tool for conducting a risk assessment of water supplies. These interactive models require user input of source water quality, treatment and system data, and then use literature derived values to calculate pathogen removal/inactivation, human exposure and disease risk. Where specific pathogen removal and/or inactivation data is available, these can be incorporated directly into the model to improve the accuracy of risk estimates. Tfaily *et al.* (2015) used Health Canada's QMRA model to measure pathogen removal under average operating conditions at 17 Canadian water treatment facilities, and also assessed the impact of using different modeling strategies on evaluating chemical disinfection. While QMRA assessment under typical operating conditions is useful, these models can also be used for water safety planning by assessing treatment robustness through the evaluation of high risk scenarios including treatment failures and source water challenges.

It is recognized that a strength of implementing QMRA for risk management is that it can be applied using an iterative approach (Medema *et al.* 2006). While there is great value in assessing the full probability distribution of the variability in risk estimates through a rigorous stochastic analysis, this is a very resource-intensive proposition. Thus it is both useful and appropriate to use a tiered approach, particularly for scenario analysis. Scenario analysis can be a more deterministic assessment where the range of variability in each of the model inputs is considered as a set of defined conditions and represented by a point value. The risk can then be calculated for each set of conditions and used to provide an overall picture of the range of expected risks. Thus the focus of this project was to demonstrate the use of a QMRA tool in such a scenario-based approach.

The approach could be useful in improving the understanding of health impacts under normal treatment conditions (e.g. the probability of illness from drinking water under normal treatment plant conditions) but also as a result of a combination of potential challenges to the water supply system. Assessing pathogen removal under

different conditions is important to ensure that a treatment process is robust and can withstand changes in source water quality or potential problems in the treatment system. The specific objectives of this paper are: (a) to explain the principles of the generalized Health Canada QMRA model, (b) to show the usefulness of a scenario-based risk assessment in risk prioritization, and (c) to demonstrate, through a case study, the usefulness of a scenario-based risk assessment using a QMRA model.

METHODS

The Health Canada QMRA model, originally developed in 2007 and updated in 2011 (Version 11_07) was used for this investigation and was developed for Canadian drinking water systems (Health Canada 2011, 2012). In this section, the four main steps implemented to conduct a QMRA on the Holmedale Water Treatment Plant (HWTP) are explained.

Step 1: Hazard assessment

Water system description

The HWTP uses the Grand River as a source and provides drinking water to the City of Brantford. The Grand River watershed is the largest in southern Ontario, encompassing almost 7,000 km^2. In 2007, the total population living in the watershed exceeded 925,000 and it is expected that up to 300,000 more people will be living in the Grand River watershed by the year 2031 (GRCA 2013). The watershed is intensively farmed, with 80% of the land being used for agriculture. The central portion of the watershed is heavily urbanized, with approximately 500,000 people living in the five cities of Brantford, Cambridge, Guelph, Kitchener, and Waterloo (Loomer & Cooke 2011). There are 29 wastewater treatment plants servicing approximately 800,000 people that discharge into the Grand River and its tributaries, half of which treat wastewater to the tertiary level (Loomer & Cooke 2011). Of these wastewater treatment plants, 22 discharge their effluent into rivers upstream of the intake for the HWTP. Other potential sources of pathogen contamination in the Grand River include urban runoff, agriculture, and wildlife (Dorner *et al.* 2004). As a source water, the Grand River would be considered a moderate to heavily impacted surface water, especially given its relatively small average flow rate.

The HWTP plant treatment process includes two process trains, each consisting of: sand-ballasted clarification (SBC), ozone (for taste and odour removal), deep bed biofiltration, UV disinfection, and chlorination (Figure 1). The plant has a design production rate of 100 megalitres of water per day (MLD), with an average plant production of 40 MLD during the present study. Polyaluminum chloride (33 ± 7 mg/L) coagulant and a polymer (0.1–0.2 mg/L Magnafloc™ LT27A, BASF, Mississauga, Canada) were added prior to the SBC process. SBC (ACTIFLO™, Veolia Water Solutions & Technologies) uses microsand, which acts as a seed and ballast for floc formation to improve floc settling velocity and decrease hydraulic retention times (Plum *et al.* 1998; Desjardins *et al.* 2002). Following SBC, ozone was applied at a mean dose of 1 mg/L. Eight deep bed biofilters contained 1.6 m of anthracite (effective size (ES) 1.0–1.2 mm, specific gravity (SG) 1.4) over 0.4 m of sand (ES 0.35–0.45 mm, SG 2.65), and were operated with an average empty bed contact time of 38 min (range 26–51 min). Following filtration, UV was applied at a dose of 20 mJ/cm^2, and then the water was chlorinated with an average free chlorine residual at the end of the chlorine contact chambers of 2.8 mg/L.

Reference pathogen selection

Representative (or reference) microorganisms that are included in the Health Canada model are *Cryptosporidium*, *Giardia*, *Campylobacter* spp., pathogenic *E. coli* O157, and

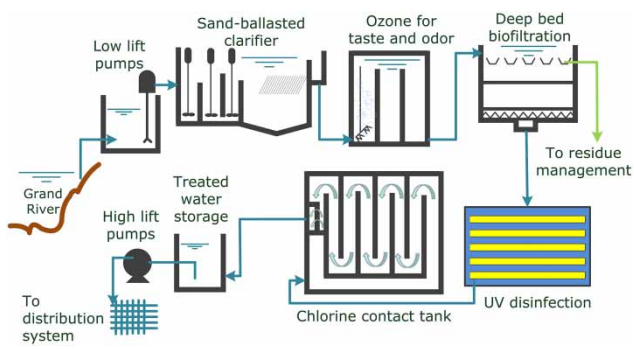

Figure 1 | HWTP process flow diagram.

rotavirus. The selection of these reference organisms was based on several criteria including the following: (1) they have to be commonly detected in source waters; (2) reliable detection methods have to be available; (3) source water concentration data should be available; (4) the group of reference pathogens should represent a broad range of resistance to various drinking water treatment steps, and data on removal through treatment must be available; and (5) they must have a significant human health impact and there has to be dose-response information available. Based on the known inputs into the Grand River and actual confirmed occurrence, it was reasonable to use these reference organisms for this study.

Potential failures and hazard scenarios

Hazard and failure scenarios are intended to capture events that may lead to an increased risk of exposure of consumers to specific pathogenic microorganisms. These can include changes in source water quality or incidents at the treatment plant. Hazardous events or challenges were selected for analysis based on discussions with the HWTP staff and included: (1) higher than average concentration of pathogens in source water, (2) partial or complete failure of the sand-ballasted clarification process, (3) filter breach, (4) lower than required chlorination, (5) low water temperatures, (6) periodic episodes of high ammonia concentration in the raw water, that are known to occur as a result of upstream wastewater treatment plant discharges during periods of ice cover limiting ammonia volatilization as well as slowing its biological transformation, and (7) UV shutdown or failure. Further details on the treatment conditions used for each scenario are provided in Step 2 (Exposure assessment).

Step 2: Exposure assessment

Exposure assessment determines the mean dose of pathogens ingested per capita per day. It is calculated using the following equation:

$$\text{Mean dose of pathogens ingested } (\#/\text{day}) = \text{pathogen concentration}_{(\text{treated})}\ (\#/L) \times \text{daily water consumption } (L/\text{day})$$

The assessment typically uses pathogen concentrations measured in the raw water, and the effectiveness of treatment, to estimate the first factor (pathogen concentration in ingested water). The second factor, the volume of water ingested is estimated from social studies of human behavior. Below is a description of the data used for exposure assessment in this study based on raw water quality data and QMRA model estimates.

Pathogen concentrations in source water at the HWTP

Data on the mean concentration and standard deviation for each reference pathogen are required, and the model then uses this to fit a log-normal distribution. Reference pathogen concentrations can be entered into the Health Canada model in various ways as follows:

(a) When available, specific data on pathogen concentrations in the source water of interest are used. This data is entered as the arithmetic mean and standard deviation (cells, (oo)cysts, or viruses per 100 litres) for each data set.
(b) If the standard deviation is not available or the overall data set is sparse, the standard deviation can be set equal to the mean concentration as a reasonable estimate of variability.
(c) If pathogen concentrations are not known, the model provides default values. These values are based on a qualitative description of the source water (pristine, lightly impacted, moderately impacted, or heavily impacted). The Health Canada model developed these default values using pathogen data from studies conducted on several Canadian source waters in 2007 (Douglas 2011).
(d) If occurrence data are not available for pathogenic *E. coli* O157, then the model estimates *E. coli* O157 as a fraction of total *E. coli* (3.49%) (Martins *et al.* 1993), recognizing that this is likely an overestimation since not all O157 strains will have pathogenic virulence factors.
(e) If recovery values are known for the pathogen test methods, concentrations should be corrected for recovery.
(f) If infectivity data are available for any of the reference pathogens, then the fraction that are human infectious can be entered as a separate value.

In this study, data on pathogen concentrations were available from the City of Brantford for samples collected at the HWTP (Table 1), and were used in the study scenarios to represent average source water conditions. In addition, larger data sets from previous studies were available that measured pathogen concentrations in the Grand River watershed (Table 2), and were used in scenarios to predict worst-case source water conditions (as described below). *Cryptosporidium* and *Giardia* were measured as per USEPA method 1623 (USEPA 2005) in samples collected from the HWTP intake over 12 years (1999–2012) at approximately monthly intervals (Table 1). Average matrix spike data from the laboratory were 50% for *Cryptosporidium* and 48% for *Giardia*; therefore the data were adjusted to account for method recovery. Genotyping data were not available; therefore, it was assumed that all (100%) of the organisms detected were infective to humans. Data on pathogenic *E. coli* O157 were not available at the HWTP intake, therefore total *E. coli* data were used for this calculation. The mean concentration of *E. coli* O157 was calculated to be 4,632 cells/100 L (3.49% of the total *E. coli* values) (Table 1). For rotavirus

Table 1 | Pathogen and indicator concentrations at the Holmedale WTP intake

	Source water pathogen concentrations (# per 100 litres)				
Data source	***Cryptosporidium*[a] HWTP intake (1999–2012)**	***Giardia*[a] HWTP intake (1999–2012)**	***E. coli* O157[b] HWTP intake (2010–2012)**	***Campylobacter* Model default value**	**Rotavirus Model default value**
Mean	9	24	4,632	10,000	10
Standard deviation	8	44	10,374	10,000	10
90th percentile	18	48	9,004		
Number of samples	80	80	142		

[a]Adjusted for 50% recovery.
[b]Based on model estimate using 3.49% of total *E. coli*.

Table 2 | Pathogen and indicator concentrations from previous Grand River studies (Van Dyke *et al.* 2010, 2012)

	Source water pathogen concentration (# per 100 litres)				
Data source	***Cryptosporidium*[a] Grand River (2005–2008)**	***Giardia*[a] Grand River (2005–2008)**	***Campylobacter* Grand River (2005–2008)**	***E. coli* O157[b] Grand River (2005–2008)**	**Rotavirus Model default value**
Mean	37	310	9,980	18,027	10
Standard deviation	52	445	17,595	62,167	
90th percentile	71	717	26,500	28,827	
Number of samples	72	72	82	82	
Summer mean	27	93	6,091	26,354	
Summer standard deviation	18	99	15,140	94,215	
Summer 90th percentile	48	278	15,400	21,778	100
Number of samples	18	18	23	23	
Winter mean	59	634	9,453	17,493	
Winter standard deviation	90	700	15,412	42,683	
Winter 90th percentile	119	1,261	24,800	35,214	100
Number of samples	18	18	18	18	

[a]Adjusted for 50% recovery.
[b]Based on model estimate using 3.49% of total *E. coli*.

and *Campylobacter*, the default values provided in the model for moderately impacted source water were used (10 virions/100 L for rotavirus, and 10,000 cells/100 L for *Campylobacter*) and 100% infectivity was assumed. The default *Campylobacter* value (10,000 cells/100 L) was similar to the mean concentration measured upstream in the Grand River (9,980 cells/100 L) by Van Dyke *et al.* (2010).

In addition to the data provided by the City of Brantford, there have been previous studies that have measured pathogen concentrations in the Grand River watershed. *Campylobacter* (Van Dyke *et al.* 2010), *Cryptosporidium* and *Giardia* (Van Dyke *et al.* 2012) concentrations were monitored at a sampling point in the Grand River located 45 kilometers upstream of the HWTP. These studies collected samples biweekly over a 3-year period, under both average and extreme weather conditions (heavy rains and snow melts). Based on laboratory matrix spike recovery data, *Giardia* and *Cryptosporidium* values were doubled to account for method recovery, and values were not corrected for human infectivity. The mean *E. coli* O157 was calculated as 3.49% of total *E. coli* concentration (Table 2), and the mean value was calculated as 18,027 cells/100 L. Similar to the HWTP intake, rotavirus concentrations were estimated using the default values provided in the model for moderately impacted source water (10 virions/100 L).

By comparing the values in Tables 1 and 2, it is clear that pathogen concentrations from previous Grand River studies at an upstream location are higher than at the intake of the HWTP. *Cryptosporidium* and *E. coli* concentrations were both four-fold higher, and *Giardia* were 10-fold higher. This can be attributed to the fact that the sampling location for the previous studies was 45 km upstream of HWTP, and that the Grand River flow almost doubles between the upstream site and the intake of HWTP. The increased water volume and cell inactivation or settling may have resulted in lower concentrations at Brantford. For this reason, values from Table 2 were only used to create foreseeable worst case scenarios to test the robustness of the HWTP. For *Cryptosporidium*, *Giardia*, *Campylobacter* and *E. coli*, the 90th percentile of winter and summer values were used, calculated using data provided from the previous studies. For rotavirus, the default value in the model for heavily impacted water (100 virions/100 L) was used to estimate the winter and summer 90th percentile values.

Drinking water treatment scenarios

Only the processes that can remove/inactivate pathogens were considered in this analysis, which included: sand-ballasted clarification, deep bed biofiltration, UV disinfection, and chlorination. Since the purpose of this analysis was to outline points of weakness in the systems, it was decided to follow a conservative approach. For example, while the HWTP incorporated an ozone treatment process, it is not intended for disinfection credit (there is no ozone residual in contactor effluent) and as such it was not included in this QMRA.

The Health Canada model estimates pathogen log removal values for each treatment step, calculated using weighted mean values based on literature data reported by KWR Watercycle Research Institute (The Netherlands) (Hijnen & Medema 2007) and data available from extensive literature review (Health Canada 2011, 2012). Levels of pathogen inactivation were calculated using various CT-disinfection equations from literature. Combining the physical log-removal with the log-inactivation, an overall log-reduction was estimated for each pathogen. Pathogen concentrations in treated water entering the distribution system were then calculated by applying the overall log reduction through treatment using the following equation: $\text{Pathogen Conc}_{(\text{treated})} = \text{Pathogen Conc}_{(\text{raw})} \times 10^{-(\log \text{ reduction})}$. The HWTP processes contributing to pathogen removal and the operating parameters used for the scenarios are described as follows:

(a) Sand-ballasted clarification (SBC) pre-treatment, which is considered by the model as a coagulation-flocculation-sedimentation process. The model does not require any operating parameter values for such a process. This process was evaluated under normal operating conditions, and also under conditions in which there was a failure in the sedimentation step only, or a complete failure in the entire process (i.e. the treatment step was removed from the analysis).
(b) Deep bed biofiltration was modeled as a rapid granular filtration process following a coagulation/sedimentation process. The model does not require any operating

values to be entered for this process. This process was evaluated under normal operating conditions, and also under conditions in which there is complete filter failure.

(c) Chlorine disinfection, which requires the input of several operating parameters including chlorine residual concentration, contact time, pH and temperature. Operations data from the HWTP were used to calculate values for typical and challenge scenarios as follows:
   (i) Chlorine residual (taken at the end of the chlorine contact chambers): ranged from 2.3 to 3.0 mg/L with an average of 2.8 mg/L.
   (ii) Contact time: the model recommends using theoretical detention time or T_{50} as the residence time; however, we chose to use the conservative T_{10} in assessing the disinfection effectiveness of chlorine. Tracer tests carried out by the HWTP operating staff showed that the chlorine contact tank T_{10} ranged from 2.35 to 6.68 min with an average of 3.53 min.
   (iii) pH: ranged from 6.0 to 8.4 with an average of 7.2.
   (iv) Temperature: ranged between 0.0 °C (used for worst case scenario) and 28.4 °C with an average of 10.8°C (used for normal operation scenario).

   Chlorine disinfection under average conditions was evaluated (10 mg/min·L at 10.8 °C). As well, conditions that would result in the lowest overall CT values (1.8 mg/min·L at 0 °C) and the lowest winter (6.8 mg/min·L at 0 °C) and summer (15 mg/min·L at 15 °C) values were tested. The effect of high ammonia in the source water on chlorination was also evaluated. In this case, it was assumed that all chlorine would be converted to chloramine (resulting in CT 25.3 mg/min·L of chloramine). This is important since chloramines are less effective disinfectants than chlorine.

(d) UV disinfection. The model requires input of the dose, which is 20 mJ/cm^2 at the HWTP. UV was tested under normal operating conditions, and also in scenarios in which the process was removed from the analysis.

Volume of water consumed and population served

The Health Canada model allows the user to input the amount of water consumed per person in L/day. The model recommends the value of 1.0 L/day as a conservative estimate of per capita unboiled water consumption for Canada, and this was the value used in this study. The population served can also be entered, which was 93,650 according to the City of Brantford 2011 census.

Step 3: Dose-response analysis

The model derives the probability of infection for daily consumption of water following exposure to one or more pathogenic microorganisms from a dose-response model. The conceptual basis for the dose-response model is that exposure of humans to the described pathogen dose leads to the probability of infection as a conditional event; the risk of infection is estimated for each possible ingestion of an organism ranging from 0 to 40 pathogens ingested per day using a dose-response model. A Poisson probability distribution is used to estimate the probability of consuming a certain number of pathogens per day (i.e. chance of consuming 0, 1, 2…etc. up to 40 pathogens per day) given a mean pathogen concentration in the treated drinking water.

The probability of infection for an individual is then calculated using the specific pathogen dose-response model for each ingested dose, ranging from 0 to 40 per day (Douglas 2011; Health Canada 2011, 2012). The Health Canada model was developed using dose-response equations reported in the literature (Table 3), usually based on human experimental data or from actual disease outbreaks.

Step 4: Risk characterization

Risk characterization brings together the data collected on pathogen exposure, dose-response and the incidence and severity of disease. In QMRA, risk characterization calculates the health impact of exposure to pathogens on a target population. Health Canada's model uses the DALY for risk characterization (Health Canada 2011, 2012) as follows:

- The daily probability of infection ($P_{inf,daily}$) for a given pathogen concentration is given by the sum of $\sum[P_{inf}/dose \times P_{dose}]$, which is the sum of probabilities for infection after ingesting a dose range of 0 to 40 pathogens per day.

Table 3 | Dose-response models used in the QMRA assessment

Pathogen	r	α	β	Equation[a]	Reference
Cryptosporidium	0.018			$P_{inf} = 1 - e^{\mu Vr}$	Messner *et al.* (2001)
Giardia	0.01982			$P_{inf} = 1 - e^{\mu Vr}$	Rose & Gerba (1991)
Rotavirus		0.265	0.4415	$P_{inf} = 1 - \left(1 + \frac{d}{\beta}\right)^{-\alpha}$	Haas *et al.* (1999)
Campylobacter		0.024	0.011	$P_{inf} = 1 - \left(1 + \frac{d}{\beta}\right)^{-\alpha}$	Teunis *et al.* (2005)
*E. coli*_O157		0.0571	2.2183	$P_{inf} = 1 - \left(1 + \frac{d}{\beta}\right)^{-\alpha}$	Strachan *et al.* (2005)

[a]d = dose (# of pathogens ingested); μ = mean pathogen concentration (# per Litre); V = volume of water consumed (Litres); r, α, β = probability of infection model coefficients.

- The daily probability of infection is then converted to an annual probability of infection (P_{inf}).
- Not all infected individuals will develop clinical illness; the probability of illness ($P_{illness}$) per year for an individual is calculated by multiplying the $P_{(inf)} \times P_{(illness\ given\ infection)}$. The probability of illness given infection is based on values reported in the literature evaluating the rate of illness observed during disease outbreaks.
- The model then calculates another more comprehensive health index that estimates the impact of illness based on duration and severity of effects (DALY). The DALYs per case of illness are based on the sum of the Years of Life Lost (YLL) due to premature mortality and the Years Lost due to Disability (YLD) for people living with disease caused by a particular pathogen. The DALY risk is then determined by multiplying the $P_{illness}$ × DALY per case of illness.
- The outcome of the analysis provides an estimate of the DALY risk per person per year (DALY/pp/yr) for each type of reference pathogen, and this was the value used to compare scenario outcomes in this study. However, risk can also be calculated for a community by multiplying the individual risk values by the population to determine the annual number of illness cases and burden of disease (DALY) for the population.

RESULTS AND DISCUSSION

A number of scenarios were tested using the automated Health Canada QMRA model to account for varying source water and treatment plant conditions. For each scenario, the data entered into the model were modified to correspond with average or typical values, seasonal variations, low or high range values, and the effect of various treatment failures. Table 4 lists the various scenarios and the values assigned to the main variables.

The first set of scenarios (1–8) used the mean concentration of pathogens from the HWTP monitoring database (Table 1). Mean values for plant operating conditions (e.g. contact time, pH and chlorine dose) were also used. The first scenario is the 'base case' where the treatment plant is under no particular challenge. The remaining seven scenarios were developed to assess the impact of different treatment variations or failures on health risk, including UV disinfection off, partial or complete failure of the SBC and filtration processes, and factors that could affect chlorine CT (Cl_2 concentration or contact time, water temperature or presence of interfering/neutralizing agents such as ammonia).

The robustness challenge scenario (#9) was developed to test the treatment train under conditions of coinciding challenges, including minimum winter CT value and temperature, ineffective sedimentation, and high pathogen concentrations (for all reference pathogens). The higher pathogen concentrations were calculated by using the winter 90th percentile concentration using data from the upstream Grand River monitoring data in Table 2 and by increasing the rotavirus concentration from the model's default value for moderately impacted water to that of heavily impacted water.

The subsequent four 'worst-case' scenarios (#10–13) also used high source water pathogen concentrations, and were developed to test additional challenges such as UV

Table 4 | Scenarios tested to assess risk for the HWTP. Cells in bold represent treatment challenges compared to the base case (scenario 1)

Sc.	Source of pathogen data	UV	Cl_2 CT (mg/min.L)	Temperature (°C)	SBC/filtration
1	HWTP data (mean)	On	Mean (10)	Mean (10.8)	Coag/Floc/Sed/Filt
2	HWTP data (mean)	**Off**	Mean (10)	Mean (10.8)	Coag/Floc/Sed/Filt
3	HWTP data (mean)	On	**Lowest (1.8)**	Mean (10.8)	Coag/Floc/Sed/Filt
4	HWTP data (mean)	On	Mean (10)	Mean (10.8)	**Coag/Floc/Filt**
5	HWTP data (mean)	On	Mean (10)	Mean (10.8)	**Filt only**
6	HWTP data (mean)	On	Mean (10)	Mean (10.8)	–
7	HWTP data (mean)	On	Mean (10)	**Lowest (0.0)**	Coag/Floc/Sed/Filt
8[a]	HWTP data (mean)	On	**NH_2Cl (25.3)**	Mean (10.8)	Coag/Floc/Sed/Filt
9[b]	**GR winter (90th percentile)**	On	**Winter lowest (6.8)**	**Lowest (0.0)**	**Coag/Floc/Filt**
10[c]	**GR winter (90th percentile)**	On	**NH_2Cl (25.3)**	**Lowest (0.0)**	**Coag/Floc/Filt**
11[c]	**GR winter (90th percentile)**	**Off**	**Winter lowest (6.8)**	**Lowest (0.0)**	**Coag/Floc/Filt**
12[c]	**GR winter (90th percentile)**	On	**Winter lowest (6.8)**	**Lowest (0.0)**	**Filt only**
13[c]	**GR winter (90th percentile)**	On	**Winter lowest (6.8)**	**Lowest (0.0)**	–
14[d]	**GR summer (90th percentile)**	**Off**	**Summer Lowest (15)**	Summer lowest (15)	Coag/Floc/Sed/Filt

[a]Ammonia spike scenario, all free chlorine is assumed to be converted to chloramines (equivalent CT 25.3 mg/min·L) in the contact tank.
[b]Robustness challenge scenario.
[c]Worst case scenarios.
[d]Summer challenge scenario.

disinfection off, partial or complete failure of SBC and filtration processes, minimal winter CT and temperature, or a high level of ammonia in the source water. In addition to the scenarios listed, other seasonal variations in source water or treatment plant data were also considered, but are not shown since they resulted in minimal variation in the estimated risk of illness. Finally, a challenge scenario where UV is turned off (#14) is included for the summer season to demonstrate that the UV process is important at high pathogen concentrations under both summer and winter conditions.

The Health Canada QMRA model has various output modules which provide useful information for risk assessment, including: (a) tabulated values for log removal/inactivation of each reference pathogen by each treatment process; (b) tabulated values for probabilities of infection, risk of illness, and DALYs for each pathogen; (c) bar diagrams displaying log removal/inactivation and individual probability of illness and DALYs; and (d) probability distribution graphs for annual risk of illness and DALYs. Results using data from the HWTP were evaluated using these output modules.

Figure 2 provides the model's estimates for log removal (physical process) or inactivation (disinfection processes) through the treatment plant for each of the reference pathogens for the first 8 scenarios. The values show the reductions achieved for each contributing treatment process. Scenario 1 represents average operating conditions at the Holmedale WTP, and results show that for protozoan pathogens, most removal/inactivation was achieved by UV disinfection (3.6 log) and filtration (2–2.5 log). In addition, the contribution of the SBC process was substantial (around 1.7 log) and there was very little inactivation achieved by chlorine disinfection (almost none for *Cryptosporidium*, as expected, and only 0.2 log for *Giardia*). For viruses and bacteria, the treatment process that achieved the highest and most consistent removal/inactivation was chlorine disinfection followed by UV disinfection, with a small contribution from filtration (1 log) and the SBC (1.5 log).

In evaluating log removal values for the various pathogens by chlorination or UV, output from the model cannot exceed a capping value (shown in Table 5), which is equal to twice the maximum experimental values derived from the literature. Thus the estimated log removal is the lesser

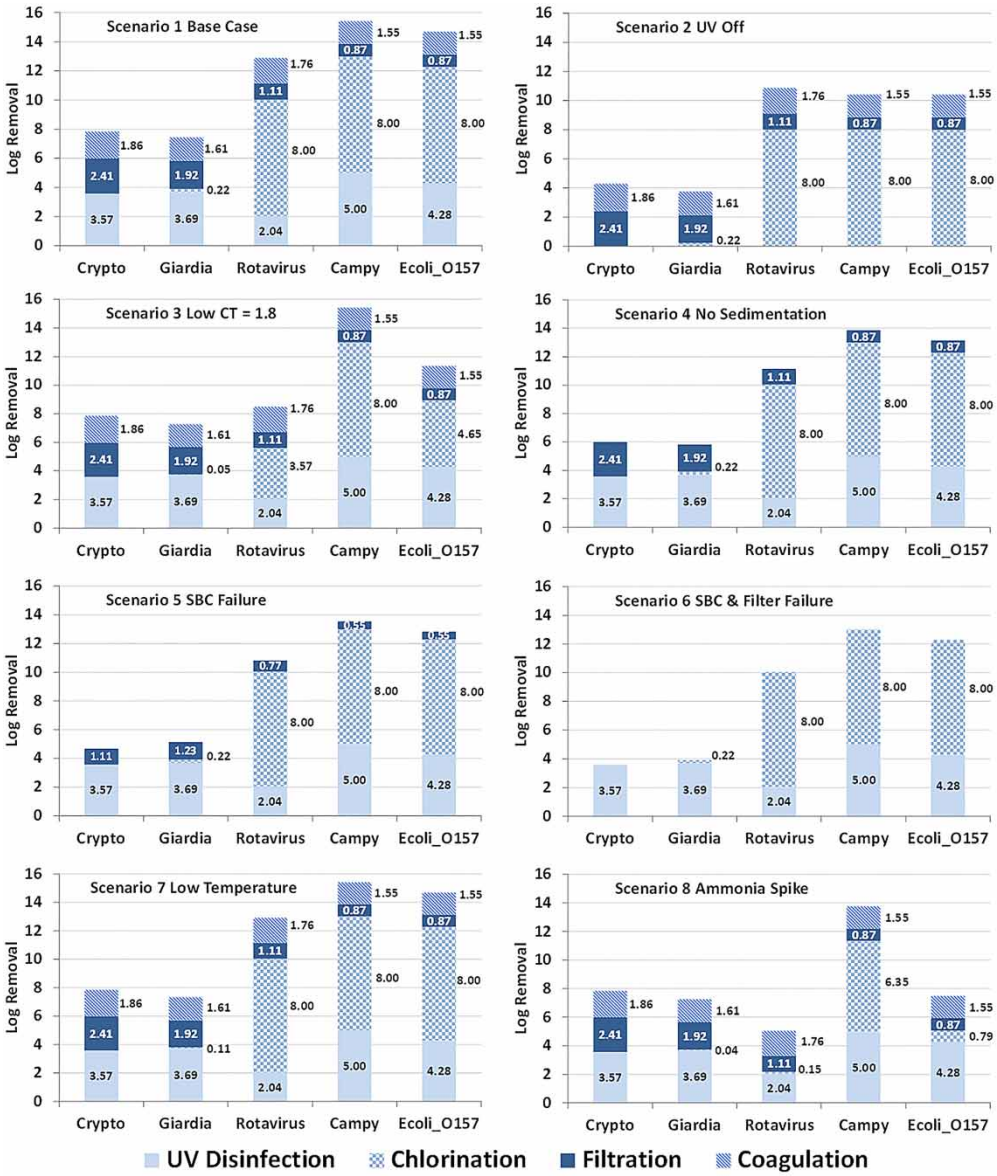

Figure 2 | Estimates for pathogen removal through the drinking water treatment plant for the base case and seven challenge scenarios.

of either the calculated or the capping value. For rotavirus and *Campylobacter* inactivation by chlorination, the calculated log removal in scenario #1 (base case conditions) by the model were actually higher than the capping value, and therefore output for both of these variables was reduced to 8 log. Similarly, *Campylobacter* removal by UV was capped at 5 log. Although the application of a capping value may underestimate true removal values, this approach is important so that the model results are consistent with and can be supported by published experimental data.

By comparing the pathogen removal results for scenarios 1 and 2 (Figure 2), it can be observed that when UV disinfection is off, the log removal of *Cryptosporidium* and *Giardia* through the plant was almost halved. In addition, scenarios 3, 7 and 8, which affected the chlorine disinfection step, were shown to primarily affect rotavirus and bacteria removal, but had no effect on the protozoa. This is expected since it is known that *Cryptosporidium* and *Giardia* are less affected by chlorine than bacteria and viruses (WHO 2011). *Giardia* is more susceptible to chlorine than

Table 5 | Calculated versus capping values for pathogen log inactivation by chlorine and UV disinfection under average operating conditions (scenario #1)

	Log inactivation by chlorine		Log inactivation by UV	
	Calculated value	Capping value	Calculated value	Capping value
Cryptosporidium	0.3×10^{-2}	4.0	3.6	5.0
Giardia	0.2	8.0	3.7	4.0
Rotavirus	20.2	8.0	2.0	5.0
Campylobacter	72.7	8.0	17.6	5.0
E. coli O157	8.0	8.0	4.3	5.5

Cryptosporidium (WHO 2011) but with SBC, filtration, and UV disinfection in the treatment train, the contribution of chlorine is almost negligible. For example, by reducing CT from 10 to 1.8 mg/min.L for the chlorine disinfection process (scenario 3), the overall log removal for rotavirus was reduced from 13 to 8.5 log. Removal of the protozoan pathogens remained unchanged, while removal of *E. coli* was reduced by 3.5 log. Although *Campylobacter* is more sensitive than *E. coli* to the impacts of chlorine (Lund 1996), the decrease in disinfection effectiveness is not reflected in Figure 2. This is because even at the reduced chlorine concentration, *Campylobacter* was inactivated by greater than the capping value of 8 log. Similarly, an ammonia spike in the source water (scenario 8), which would result in the conversion of chlorine to chloramine, did not affect protozoa removal. *Campylobacter* removal was reduced by 1.5 log, while removal for *E. coli* was halved and rotavirus was reduced to almost a third of that during normal operation. Because chlorine disinfection is affected by temperature, viral and bacterial pathogen inactivation by chlorine is expected to decrease when the operating temperatures are lower in the winter; however, a reduction in temperature (scenario 7) had very little impact on pathogen removal. Once again, this is due to the fact that even at the lower temperature, the calculated chlorine inactivation was greater than the capping value of 8 log imposed by the model.

The three scenarios (4, 5, and 6) representing different levels of failure for the SBC and filtration (Figure 2) show that both steps are critical in achieving adequate removal of *Cryptosporidium* and *Giardia*. Sedimentation failure (scenario 4) (e.g. due to short-circuiting) reduced the log removal value of all three groups of microorganisms by approximately 2 log. Similarly a total SBC process failure (scenario 5) reduced the removal of all pathogens by an additional 1 log. Additional filter failure (scenario 6) had more effect on the removal of protozoa (1 log lower), compared with viruses and bacteria, whose removal was only reduced by 0.5 log. Since the overall log removal of protozoan pathogens through the treatment process is less than for other pathogens, factors that affect their removal can prove critical in terms of health risk.

Using the model output modules, the risk associated with the various test scenarios could be evaluated. The model calculated the DALY risk associated with each reference pathogen for each scenario. The results are presented as the normalized probability distribution frequency for the annual DALY risk per person (Figure 3). The calculated DALY risks were then compared to an acceptable level of annual DALY per person of less than 1 in 1,000,000 (10^{-6}) which was established by both the WHO (2011) and adopted in Health Canada's drinking water guidelines for microbiological parameters (Health Canada 2011, 2012) (Figure 3). The base case scenario (scenario 1) shows that the DALY risk from each reference pathogen is well below Health Canada's acceptable level, with a higher risk from *Cryptosporidium* and *Giardia* than from the viral and bacterial pathogens. It can also be observed from Figure 3 that the DALY risk posed by *Cryptosporidium* and *Giardia* in drinking water from the HWTP substantially increased and approached the maximum acceptable level when UV was off (scenario 2) and when sand-ballasted clarification and filtration failed (scenario 6). A change in the primary disinfectant from chlorine to chloramine due to an ammonia spike (scenario 8) increased the risk from rotavirus and bacteria, but it was interesting to see that UV and filtration were capable of keeping the level of risk below the acceptable threshold level.

Figure 4 shows the risk assessment results of the robustness challenge scenario and four worst case scenarios for treatment failure. While these scenarios are quite improbable, they are not impossible. Results showed that the level of DALY risk remained below the threshold even under the robustness challenge (scenario 9), which simulates coinciding challenges of low CT value and temperature, ineffective sedimentation, and high pathogen concentrations. However, it is clear from the various failure scenarios that every treatment process is critical to maintain a robust treatment train. Almost all of the failure scenarios (scenarios

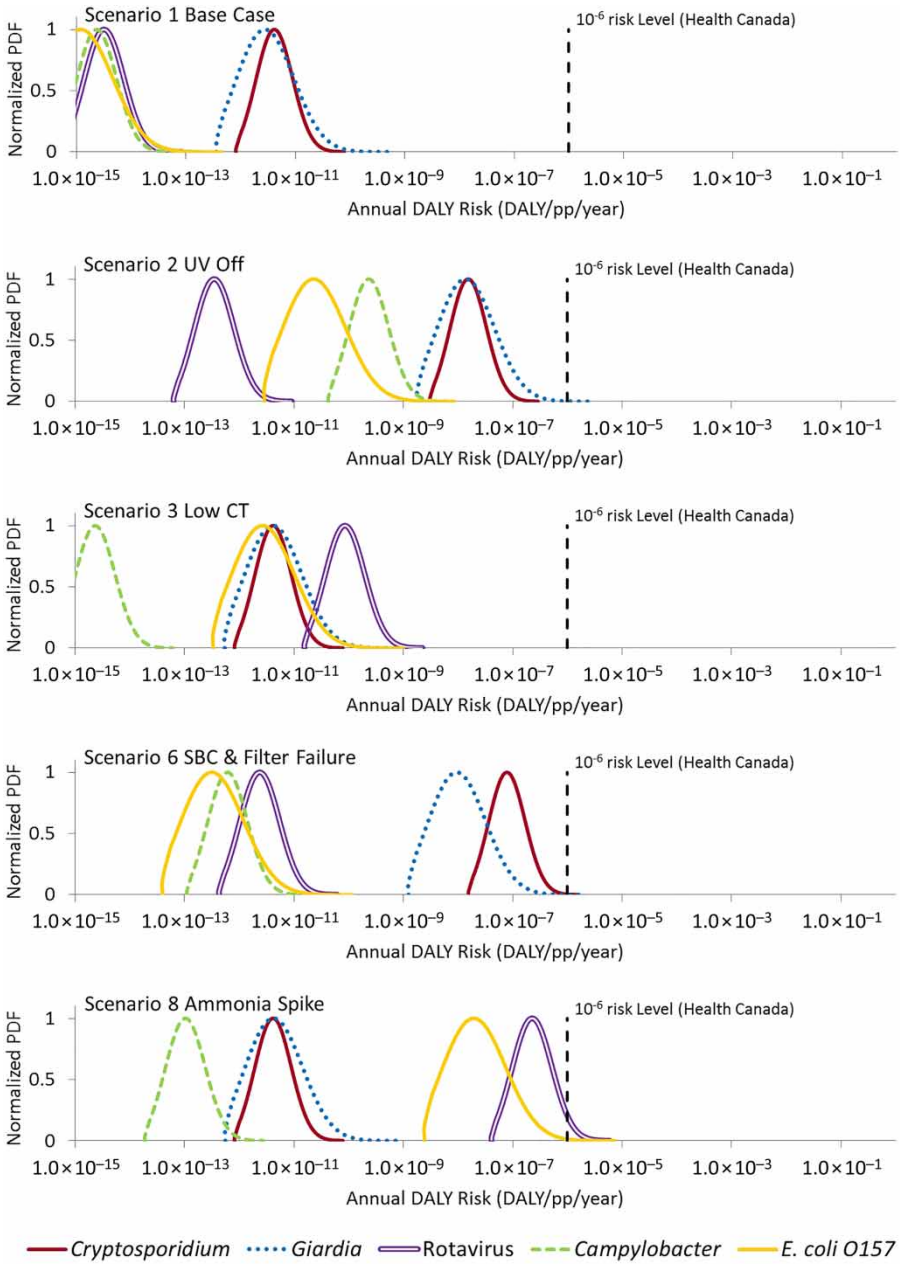

Figure 3 | Probability distribution frequency (PDF) for annual DALY risk per person (pp) from reference pathogens in HWTP treated water for challenge scenarios 1, 2, 3, 6, and 8.

10–13), except for scenario 12, caused the DALY risk levels to surpass the threshold for at least 1 pathogen (scenario 11 illustrates the potential for all three pathogens to surpass the threshold). Figure 5 shows that UV is critical, even in a summer challenge scenario. These challenge scenarios demonstrate that, even at high pathogen concentrations, process robustness is the most critical element in assuring safe drinking water (equivalent to DALYs below the 10^{-6} threshold) which agrees with the results of risk management studies investigating disease outbreaks caused by unsafe drinking water (Hrudey *et al.* 2006).

The summer conditions (scenario 14; Figure 5) were less challenging than the robustness challenge scenario (scenario 9) since the temperatures are higher, pathogen

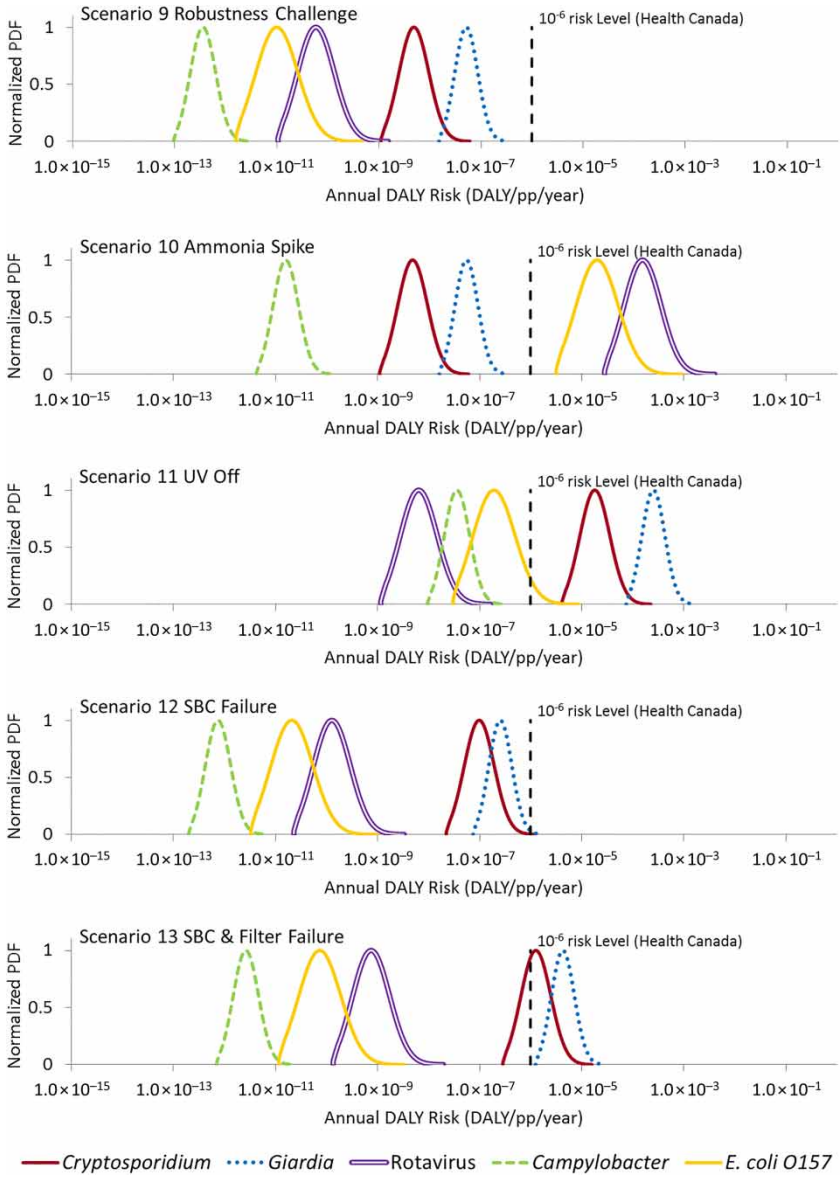

Figure 4 | Probability distribution frequency (PDF) for annual DALY risk per person (pp) for challenge scenarios 9–13.

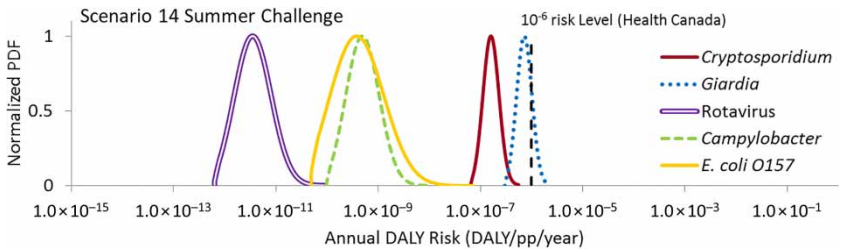

Figure 5 | Probability distribution frequency (PDF) for annual DALY risk per person (pp) from summer challenge (90th percentile pathogen concentration).

concentrations are lower, and no process failure other than UV was included. Nevertheless, under summer conditions with the UV off, the DALY risk from *Giardia* was close to the Health Canada (2011, 2012) threshold, and in fact the tail end of the distribution clearly indicates there could be an increased health risk to the population from *Giardia* under these conditions (Figure 5).

The scenario-based approach contrasts with the QMRA approach of limiting risk evaluation to a single operating or design condition. Examining only a single operating condition may result in overlooking possible treatment challenges. In a more in-depth scenario-based risk assessment approach, it would be helpful to examine the full range on uncertainty and variability in assumptions, including the probabilities of the challenge scenarios actually occurring, in the risk estimate. To fully characterize risk, a dynamic and site-specific system model would be needed. Nevertheless, given the difficulties in implementing a fully probabilistic quantitative risk estimate (particularly when considering the probability variations in source water quality or fully characterizing treatment plant performance variations or failures and the potentially coincidental occurrence of events) the results of the scenario-based QMRA described here can be of substantial benefit in outlining strategic risk management plans and in educating treatment plant operators on the microbial risks under various operating conditions.

This study demonstrates how a scenario-based QMRA can be undertaken with limited amounts of data, and the methodology is transferable amongst a variety of water systems. QMRA in general is of great importance to water utilities implementing water safety plans (WSPs) (Smeets *et al.* 2010). In the current study, results showed how the inclusion of certain treatment processes, such as UV, could provide the necessary level of pathogen removal even when there were challenges with source water quality or treatment inadequacies. Therefore, when provided with information from scenario-based risk assessments, water systems can determine the need for appropriate risk management actions including plans for operations, design, and funding.

CONCLUSIONS

Water utilities have started using QMRA to assess and improve the safety of drinking water. Models have been developed to simplify the task of QMRA as part of the overarching Water Safety Plan (WSP) approach (WHO 2011). This study demonstrated the use of a generalized QMRA tool developed by Health Canada to assess the robustness of the HWTP in the City of Brantford, Canada. Challenges used to create scenarios incorporated potential treatment failures and unexpected variations in water quality and operating parameters. The following was found:

- The treatment plant assessed in this study is producing microbiologically safe water and its treatment process is robust. Under the robustness challenge conditions investigated, the risk of disease to the population is lower than the WHO and Health Canada's acceptable annual per person DALY threshold of 10^{-6}.
- At this treatment plant, UV is an important component to add robustness against protozoan pathogens and ensure year-round drinking water safety (even at the design dose of 20 mJ/cm^2). It is also clear that proper operation of the sand-ballasted clarification and filtration processes are equally critical.
- In most scenarios investigated, the risk from rotavirus, pathogenic *E. coli* or *Campylobacter* was well below the accepted DALY threshold of 10^{-6}. However, one scenario was identified in which virus and bacteria removal could be compromised (combined effect of an ammonia spike in raw water with high pathogen concentration and ineffective sedimentation). As is the case for many treatment plants, particularly those using surface water as a source of water, the protozoa *Giardia* and *Cryptosporidium* are the most challenging from a treatment perspective.
- Monitoring of pathogen concentration is important for risk assessment of water treatment plants. However, this case study demonstrated that, even with challenging pathogen concentrations, only in scenarios simulating considerable failure in treatment processes did the risk level surpass the acceptable limit. This reiterates the importance of robust treatment processes and the multi-barrier approach voiced in drinking water safety studies.

The QMRA approach presented in this study can be used in the comprehensive risk assessment of any water supply system to provide decision support regarding risk management plans. Scenario-based QMRA can be integrated into a more dynamic risk assessment tool to help

outline measures necessary to ensure drinking water safety. As noted by other authors (Pintar *et al.* 2012), the real value in QMRA modelling, whether it be a relatively simple scenario based approach such as that described here, or a more rigorous stochastic process, is not the final mean risk estimate. Indeed, the true value lies in the process: describing the problem, talking with stakeholders, improving everyone's understanding of their source water and treatment system and ultimately informing the decision-making processes. This scenario-based analysis has contributed to a better understanding of the potential risks in this system, and the need for careful and constant attention to a robust and well operated water treatment plant.

ACKNOWLEDGEMENTS

Funding for this research was provided by the Natural Sciences and Engineering Research Council of Canada (NSERC) in the form of an Industrial Research Chair in Water Treatment at the University of Waterloo. The current Chair partners can be found online at www.civil.uwaterloo.ca/watertreatment. Funding was also provided by the Canadian Water Network, and we acknowledge the principal investigator Dr Sarah Dorner (Polytechnique Montréal). We would like to thank Selvi Kongara (Director of Environmental Services), Patrick Halevy, Yonatan Yohannes, and Kelly Hagan from the City of Brantford, Environmental Services, for their assistance and for providing data for analysis. The authors would also like to thank Drs Judith Isaac-Renton and Natalie Prystajecky from the British Columbia Public Health and Reference Laboratory and the University of British Columbia, Drs Katarina Pintar and Frank Pollari from FoodNet Canada (Public Health Agency of Canada), and Dr Susan Weir from the Ontario Ministry of the Environment, for their roles in the acquisition of Grand River pathogen and indicator data.

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First received 22 July 2015; accepted in revised form 18 January 2016. Available online 18 February 2016