Quantification of pathogen inactivation efficacy by free chlorine disinfection of drinking water for QMRA

S. R. Petterson and T. A. Stenström

ABSTRACT

To support the implementation of quantitative microbial risk assessment (QMRA) for managing infectious risks associated with drinking water systems, a simple modeling approach for quantifying Log_{10} reduction across a free chlorine disinfection contactor was developed. The study was undertaken in three stages: firstly, review of the laboratory studies published in the literature; secondly, development of a conceptual approach to apply the laboratory studies to full-scale conditions; and finally implementation of the calculations for a hypothetical case study system. The developed model explicitly accounted for variability in residence time and pathogen specific chlorine sensitivity. Survival functions were constructed for a range of pathogens relying on the upper bound of the reported data transformed to a common metric. The application of the model within a hypothetical case study demonstrated the importance of accounting for variable residence time in QMRA. While the overall Log_{10} reduction may appear high, small parcels of water with short residence time can compromise the overall performance of the barrier. While theoretically simple, the approach presented is of great value for undertaking an initial assessment of a full-scale disinfection contactor based on limited site-specific information.

Key words | disinfection, drinking water, free chlorine, pathogen inactivation, QMRA

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INTRODUCTION

The framework for safe drinking water promotes the management and mitigation of water-related infectious risks through systematic assessment of a water supply from catchment to tap (Bartram *et al.* 2001; WHO 2009, 2011). Quantitative microbial risk assessment (QMRA) is a powerful tool for supporting the systematic assessment of drinking water supplies (Medema & Smeets 2009; Smeets *et al.* 2010). A key component of this assessment is the evaluation of drinking water treatment barriers including both their expected performance (Hijnen *et al.* 2006; Teunis *et al.* 2009; Hijnen & Medema 2010), and potential vulnerabilities (Westrell *et al.* 2003; Hunter *et al.* 2009).

Chlorination continues to be the most widely used water treatment globally, and is effective at low doses for a broad range of micro-organisms. The efficacy depends on numerous site-specific factors related to water quality (temperature, pH, and organic constituents), dosage and contact time and does vary between micro-organisms (Haas 1999; LeChevallier & Au 2004). Fecal coliform bacteria, historically used to ensure water safety, are much more readily inactivated by free chlorine in comparison to some more persistent viruses and protozoa (Ashbolt *et al.* 2001). Therefore, absence of indicator bacteria in finished water is a poor measure of disinfection performance.

Measuring the inactivation of pathogens by chlorine at full scale is difficult if not impossible and therefore modeling is an essential tool for assessing disinfection performance. Modeling approaches rely on quantifying the dose of chlorine (defined as Ct: Chlorine concentration ($mg\ L^{-1}$) × time (min)) and predicting the pathogen kill associated with that dose. Modeling approaches vary in their simplicity from generic point estimates (USEPA 2003a) to detailed site-specific models (Bellamy *et al.* 1998). Simple point

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estimate models are limited in their capacity to describe barrier variability, and hence have limited value to support management of the waterborne risks. Detailed models are preferred, however they require significant investment of time and resources to develop and calibrate. There is a need for a simple modeling approach that can be used to quantify disinfection efficacy for QMRA as part of a screening level risk assessment, which allows for the key risk drivers to be explored. The approach needs to rely on the best available scientific literature, and require limited site-specific information.

The objective of this study was therefore as follows:

- Review the published studies in the literature on pathogen and indicator sensitivity to free chlorine in order to quantitatively compare pathogen sensitivity both within and between pathogen groups.
- Develop a model to quantify Log_{10} reduction across a contactor accounting for variability in residence time, and drawing on the pathogen specific chlorine sensitivity from the literature. The model should support the needs of water safety managers at the screening level and rely on limited site-specific information.
- Compare the calculations from this new approach with other comparable screening level methods (Ct calc, continuously stirred tank reactor (CSTR) equation).

MATERIAL AND METHODS

The study was undertaken in three stages: firstly, review of the laboratory studies published in the literature; secondly, development of a conceptual approach to apply the laboratory studies to full-scale conditions; and finally, implementation of the calculations for a hypothetical case study system and compare with alternate approaches.

Literature review

Peer reviewed published laboratory studies on the sensitivity of human enteric pathogens and indicators to free chlorine were collated and reviewed. This was based on a systematic search beginning with the citation list of selected drinking water treatment reference documents (USEPA 2003a; LeChevallier & Au 2004; WHO 2011), extended with database searches including Science Direct, PubMed, Google scholar and selected medical, and technical journals. Articles were limited to those addressing free chlorine inactivation only (not in combination with other agents) in drinking water of enteric pathogens and selected indicator organisms. When reviewing the reported data, attention was given to the experimental conditions including temperature and pH, chlorine dosage, organism strain, and method of statistical analysis. For comparison between published studies, it was necessary to translate reported results into a common measure. The selected common measure was the required Ct for a 1, 2, 3, 4, and 5 Log_{10} reductions, up to the maximum demonstrated reduction for each particular study. For some studies, this required a reanalysis of the reported results and/or visual reading off published graphs. The methods used to reach the common metric are summarized in Table 1.

Conceptual model

The conceptual model relied on a simple dose-response relationship to describe pathogen inactivation. The dose was defined as the Ct delivered across the chlorine contactor, which is expected to be variable depending on the residence time distribution and the chlorine concentration. The response was described by a pathogen specific survival function S(Ct) (probability of survival as a function of Ct).

The conceptual model therefore required quantification of three components:

1. the residence time distribution of the contactor;
2. the free chlorine concentration across the contactor;
3. pathogen specific survival functions based on the results of the literature review.

Combining parts (1) and (2) provided a distribution of the Ct for the full-scale contactor.

The residence time distribution

The residence time distribution is unique to any particular disinfection contactor; however, a simple theoretical

Table 1 | Method of transformation applied to published data in order to achieve common metric

Adaptation method Number	Reported results	Calculations undertaken	References
A	Graph of Log_{10} percentage surviving versus contact time (min) Chlorine concentration at the beginning and the end of the experiment (mg L^{-1})	Contact time for each Log_{10} reduction was read from an enlarged graph First-order decay of chlorine was assumed over the duration of the experiment Ct was calculated by integrating the chlorine concentration over the time to the required Log_{10} reduction and multiplying by time	Grabow *et al.* (1983)
B	Graph of Log_{10} percentage surviving versus contact time (min) Chlorine concentration at the beginning of experiment	Contact time for each Log_{10} reduction was read from an enlarged graph Ct was calculated using contact time and initial chlorine dose	Lund (1996)
C	Time for 99% inactivation (min) Concentration of free chlorine during the experiment (mg L^{-1})	Ct99 calculated from time for 99% reduction and the measured chlorine concentration at the end of the experiment Linear interpolation was used to calculate Ct for other Log_{10} reductions up to the maximum observed reduction in the study	Engelbrecht *et al.* (1980); Berman & Hoff (1984)
D	Graph of Log_{10} pfu surviving versus time Concentration of HOCL at pH 6 and OCL^- at pH 10 in uM	Contact time for each Log_{10} reduction was read from the published graphs Concentration of HOCL or OCL was stoichiometrically converted to free chlorine concentration mg L^{-1} assuming at pH 6, 95% of free chlorine is HOCl and at pH 10, 99.7% of free chlorine is OCl^- Ct was the direct multiplication of chlorine dose and contact time	Jensen *et al.* (1980); Sharp & Leong (1980)
E	Percentage surviving after 1, 10, 100, and 1,000 min of contact Initial chlorine concentration (0.4 mg L^{-1}) and concentration after 16 hours (0.1 mg L^{-1})	Assumed linear interpolation between each reported point value Numerical transformation to calculate min for each Log_{10} reduction Chlorine decay was assumed to follow first-order kinetics and fit using the two point estimates reported in the paper Ct calculated by integrating the chlorine concentration over the exposure time, and multiplying by exposure time (min)	Payment *et al.* (1985b)
F	Starting concentration and $-Log_{10}$ surviving fraction at 0.5, 1, 2 or 5 min Initial chlorine concentration	Assumed linear interpolation between each reported point value Numerical transformation to calculate time for each Log_{10} reduction Ct calculated using initial chlorine concentration over the exposure time (min)	Blaser *et al.* (1986); Rice & Clark (1999)
G	Percentage inactivation at 10, 30, and 60 min Initial chlorine dose	Assumed linear interpolation between each reported point value Numerical transformation to calculate min for each Log_{10} reduction Ct calculated using initial dose and multiplying by exposure time	Li *et al.* (2002)

approximation can be made assuming that the contactor consists of CSTRs in series (Nauman & Buffham 1983; Do-Quang *et al.* 2000a, b). The theoretical distribution of residence times is represented by $E(t)$, where t is the time inside the contactor. For a number of CSTRs in series $E(t)$ is given by

$$E(t) = \frac{t^{n-1}}{(n-1)!\tau_i^n} e^{(-t/\tau_i)} \quad (1)$$

where n is the number of CSTRs in series and is selected to be equal to the number of cells separated by simple baffles, and τ is the mean residence time (MRT) of each CSTR. Optimal hydraulic behavior for a contactor is theoretical plug flow where all water parcels achieve an identical contact time (number of CSTRs is assumed to be very high).

The free chlorine concentration

The chlorine concentration across the contactor is influenced by the magnitude, method and location of dosing; the mixing characteristics of the contactor; the chlorine demand and the chlorine dissociation rate. A simplified approach for quantifying chlorine concentration over the contactor was selected. Following initial losses, the free chlorine residual was assumed to follow first-order dissociation ($C_t = C_0 e^{-kt}$) where k is the chlorine dissociation rate, C_0 is the initial chlorine residual and C_t is the chlorine concentration at time t).

Pathogen specific survival functions

By relying on pathogen sensitivity results reported from laboratory scale experiments in the literature, a survival curve (probability of survival versus Ct) was constructed for each pathogen. For each bacteria and virus, required Cts for 1, 2, 3, 4, 5 Log_{10} reduction (up to the maximum of reported observations) were selected based on the most conservative result over the entire pH and temperature range, rounded up to one significant figure. The survival function was then constructed by linear interpolation between each Ct value (note: $P_{Survival} = 10^{-Log_{10}reduction}$).

Case study: comparison between three approaches

The Log_{10} reductions for five selected reference pathogens (*Campylobacter*, *Escherichia coli* O157:H7, rotavirus, norovirus, *Giardia*) were calculated across a hypothetical chlorine contactor with assumed initial chlorine residuals of 0.4 and 1.5 mg L^{-1}; a MRT of 12 min and a chlorine dissociation rate of 0.1 min^{-1}. The hydraulic behavior was classified as poor, medium or good, and calculations of treatment efficacy were undertaken based on the following three approaches.

Approach 1: The Ct_{calc} method

The Ct_{calc} method is a simplified approach recommended by the USEPA for benchmarking disinfection processes. Contact time was calculated as the MRT × baffling factor (BF) (USEPA 2003a). BF equaled 0.3 for poor hydraulics, 0.6 for medium hydraulics and 1.0 for perfect plug flow. Rather than select the chlorine concentration at the outlet of the contact tank, to compare between approaches, the chlorine concentration was integrated over the contact time of the contactor. For the calculated Ct, the k_{10} (the first-order inactivation coefficient for each pathogen on a Log_{10} scale) was used to predict the Log_{10} reduction. To facilitate comparison with approach 3 (see below), the survival functions were used to quantify the inactivation rate on a Log_{10} scale, assuming Log-linear reduction: $k_{10} = (n/Ct_n)$ where $Ct_n$was the C_t required to achieve Log_{10} reduction n (maximum demonstrated Log_{10} reduction for each pathogen).

Approach 2: CSTR approach

The CSTR equation has been applied in drinking water treatment for ozone disinfection contactors (USEPA 2003b; Smeets *et al.* 2006). The Log_{10} reduction was quantified using the following equation:

$$Log_{10}\,\text{reduction} = -\sum_{i=1}^{n} Log_{10}\left(\frac{1}{1 + 2.3 \times k_{10} \times Cl_i \times t_i}\right) \quad (2)$$

where k_{10} is the first-order inactivation coefficient for the pathogen on a Log_{10} scale; n is the number of CSTRs; Cl_i is the chlorine concentration in CSTR i, in mg L^{-1} (calculated assuming first-order inactivation across previous CSTRs with assumptions consistent with approach 1 and 3), and t_i is the hydraulic residence time for CSTR i. For poor hydraulics, two CSTRs were selected, medium-good hydraulics six CSTRs, and for near perfect plug flow 20 CSTRs.

Approach 3: The method proposed

The residence time distribution based on the theoretical tanks-in-series Equation (1) for two CSTRs, six CSTRs, and

20 CSTRs was applied. The Ct distribution for the contactor was calculated based on a Monte Carlo simulation with 10,000 random samples drawn from the residence time distribution; for each sample, the chlorine concentration was integrated over the residence time resulting in a sample of the Ct. For each sample from the Ct distribution, the Log_{10} reduction for each respective pathogen was predicted using the survival function. Quantiles (0.001, 0.01, 0.05, 0.5, 0.95) of the sample Log_{10} reductions were calculated to show the variability in treatment efficacy. In addition, the overall Log_{10} reduction assuming complete mixing of flow following the disinfection contactor was calculated.

RESULTS

Review

The collation of published laboratory studies on inactivation of human enteric pathogens and indicators due to free chlorine, translated to the common metric of required Ct for 1, 2, 3, 4, and 5 Log_{10} reduction, are summarized in Table 2 for the bacteria, Table 3 for viruses and Figure 1 for *Giardia*. Since the experimental conditions were variable with respect to factors including (but not limited to) temperature, pH, chlorine dose, spiking concentrations, and laboratory strains, the results for each organism were pooled across all experimental conditions and plotted against the probability of survival (Figures 2 and 3) (note the probability of micro-organism survival is related to the Log_{10} reduction of the microbial population: $P_{Survival} = 10^{-Log_{10}reduction}$). This was done to compare the overall range of expected sensitivity of different pathogens and indicators (for experiments mainly in demand-free buffer). The results demonstrate that in general, bacteria are the most sensitive to chlorine with Ct for 3 Log_{10} reduction ranging up to 0.54 min mg L^{-1} (*E. coli* O157:H7 (Rice & Clark 1999)); followed by enteric viruses up to 127 min mg L^{-1} (CoxsackieB5 (Payment *et al.* 1985a)); and *Giardia* were the most persistent.

Within individual bacterial species, studies were reviewed that compared the resistance among different strains. The wild-type strains of *E. coli* from cattle manure tested by Rice & Clark (1999) appeared more resistant to chlorination in comparison to values reported for laboratory strains (Blaser *et al.* 1986; Lund 1996). Wild-type *E. coli* strains required a Ct of 0.52–0.63 min mg L^{-1} (pH = 7; $T = 5\ ^{\circ}C$; Cl = 1.1 mg L^{-1}) for 3 Log_{10} reduction in comparison to 0.21 min mg L^{-1} (pH = 8; $T = 4\ ^{\circ}C$; Cl = 0.1 mg L^{-1}) (Blaser *et al.* 1986) and 0.073 min mg L^{-1} (pH = 6.5; $T = 4\ ^{\circ}C$; Cl = 0.2 mg L^{-1}) (Lund 1996), however the concentration of chlorine was much higher in the wild-type study.

There was considerable variability in persistence between virus types (Table 3, Figures 3 and 4). These compilations and illustrations show that adenoviruses, reoviruses, simian rotaviruses and caliciviruses were susceptible to chlorine with Ct for 3 Log_{10} inactivation typically less than 0.5 min mg L^{-1}. Enteroviruses were more resistant with a required Ct for 3 Log_{10} inactivation of ~20, ~90, and ~130 min mg L^{-1} for echoviruses, coxsackievirus B4 and coxsackievirus B5, respectively. The particularly high resistance to chlorine and high variability between strains was observed by Payment *et al.* (1985a) using environmental strains, with the most resistant strain originating from raw sewage (all experiments performed in demand free water). Two later studies on coxsackievirus B5 reported comparable results with each other, but lower persistence than Payment *et al.* (1985a), for example Ct 3 Log = 5.5 (Black *et al.* 2009) and 8.4 min mg L^{-1} (Cromeans *et al.* 2010) at pH 7 and 7.5, respectively, using the same laboratory strain (Faulkner strain). The feline caliciviruses and murine noroviruses (suggested as surrogates for human noroviruses, since the latter cannot be cultivated) were easily inactivated by free chlorine. Of the two bacteriophages included (Table 3), coliphage V1 was up to an order of magnitude more resistant to free chlorine inactivation than the MS2 phage.

Berman & Hoff (1984) specifically investigated the impact of cell-association on survival of simian rotavirus, and observed higher persistence for cell-associated viruses (Table 3). It is difficult to quantify the magnitude of the protective effect at pH 6 since the unassociated viruses were so quickly inactivated; however, if the Ct for 3 Log_{10} inactivation was assumed to be at the limit of detection (0.025 mg L^{-1}), then the required Ct for 3 Log_{10} inactivation was increased by an order of magnitude due to cell association; at pH 10, the required Ct for 2 Log_{10} inactivation (3 Log_{10} inactivation was not observed in the unassociated virus) was increased by a factor of three.

Table 2 | Reported studies on susceptibility of bacteria to free chlorine inactivation

Micro-organism	pH	T °C	Approximate chlorine dose (mg L^{-1})	Ct for Log_{10} reduction (min mg L^{-1}) 1	2	3	4	5	Max red	Data transformation[a]	Reference
E. coli	6	4	0.1	0.019	0.037	0.068			3.89	F	Blaser *et al.* (1986)
	6	25	0.1	0.022	0.044	0.079			3.39	F	Blaser *et al.* (1986)
	6.5	4	0.2	0.028	0.046	0.073	0.16	4.02	5.00	B	Lund (1996)
	6.5	10	0.2	0.022	0.026	0.043	0.081	1.32	5.20	B	Lund (1996)
	8	4	0.1	0.043	0.079	0.207	0.497		4.01	F	Blaser *et al.* (1986)
	8	25	0.1	0.058	0.183	0.366			3.73	F	Blaser *et al.* (1986)
E. coli (wild type)	7	5	1.1	0.18 (0.17–0.19)[b]	0.35 (0.34–0.38)	0.53 (0.52–0.63)	0.94 (0.83–2.16)	NM – 1.94	4.95 (4.74–5.14)	F	Rice & Clark (1999)
Pathogenic *E. coli*											
E. coli O157:H7	7	21	0.4–0.5				0.13				Chauret *et al.* (2008)
	8	21	0.4–0.5				~9[c]				Chauret *et al.* (2008)
E. coli O157:H7	7	5	1.1	0.17 (0.17–0.18)[d]	0.34 (0.33–0.36)	0.51 (0.50–0.54)	1.06 (0.93–1.36)	2.06 ((2.02–2.11)	4.74 (4.01–5.13)	F	Rice & Clark (1999)
Campylobacter											
Campylobacter jejuni PEN 1	6	4	0.1	0.012	0.024	0.036	0.049		> 4.12	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 2	6	4	0.1	0.014	0.027	0.041	0.086		> 4.60	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 3	6	4	0.1	0.011	0.021	0.032	0.043		> 4.70	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 1	6	25	0.1	0.035	0.087				2.04	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 2	6	25	0.1	0.019	0.039				2.88	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 3	6	25	0.1	0.011	0.022	0.033	0.044		> 4.5	F	Blaser *et al.* (1986)
Campylobacter jejuni 1	6.5	4	0.2	0.024	0.032	0.066	0.28	0.79	5.80	B	Lund (1996)
Campylobacter jejuni 1	6.5	10	0.2	0.027	0.043	0.061	0.15	0.58	5.30	B	Lund (1996)
Campylobacter jejuni PEN 1	8	4	0.1	0.064	0.078	0.092	0.483		> 4.02	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 2	8	4	0.1	0.023	0.047	0.073			3.70	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 3	8	4	0.1	0.014	0.029	0.043	0.072		> 4.70	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 1	8	25	0.1	0.146	0.474				2.08	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 2	8	25	0.1	0.017	0.034				> 2.93	F	Blaser *et al.* (1986)
Campylobacter jejuni PEN 3	8	25	0.1	0.152	0.294	0.436			3.45	F	Blaser *et al.* (1986)

All results are from batch studies

[a]See Table 1 for transformation method.

[b]Range across four different strains.

[c]Approximate from published graph.

[d]Range across seven different strains.

Table 3 | Reported studies on susceptibility of viruses to free chlorine inactivation

Micro-organism	Batch (B) or continuous (C)	pH	T °C	Approximate chlorine dose (mg L^{-1})	Ct for Log_{10} reduction (min mg L^{-1}) 1	2	3	4	5	Max red	Data transformation[a]	Reference
Adenoviruses												
Adenovirus 2	B	7	5	0.2		0.02	0.06	0.15		4.5	–	Cromeans *et al.* (2010)
	B	8	5	0.2		0.04	0.12	0.27		5	–	Cromeans *et al.* (2010)
	B	7	5	0.2			0.035–0.10				–	Kahler *et al.* (2010)
	B	8	5	0.2			0.037–0.12				–	Kahler *et al.* (2010)
	B	7	15	0.2			<0.040–0.063				–	Kahler *et al.* (2010)
	B	8	15	0.2			<0.02–0.061				–	Kahler *et al.* (2010)
Adenovirus 40	B	6	5	0.17		0.05 (0.04–0.13)	0.11 (0.09–0.17)	0.22 (0.17–0.34)			–	Thurston-Enriquez *et al.* (2003)
	B	7	5	0.17		0.15 (0.04 –0.17)	0.38 (0.34–0.85)	0.75			–	Thurston-Enriquez *et al.* (2003)
	B	7	5	0.2		<0.02	<0.02	<0.04			–	Cromeans *et al.* (2010)
	B	8	5	0.31		0.11 (<0.08–0.16)	0.17 (0.16–0.23)	0.24 (0.16–0.23)			–	Thurston-Enriquez *et al.* (2003)
	B	8	5	0.2		<0.02	<0.02	<0.04			–	Cromeans *et al.* (2010)
Adenovirus 41	B	7	5	0.2		0.005	0.01	ND			–	Cromeans *et al.* (2010)
	B	8	5	0.2		<0.02	<0.02	<0.03			–	Cromeans *et al.* (2010)
Reoviruses												
Reovirus 3	B	6	25	0.4	0.1	0.16	0.39	1.8	2.3	5.2	A	Grabow *et al.* (1983)
	B	8	25	0.4	0.1	0.16	0.20	0.74	1.3	4.2	A	Grabow *et al.* (1983)
	B	10	25	0.4	0.12	0.2	0.24	0.32	0.40		A	Grabow *et al.* (1983)
Rotaviruses												
SA-11 Simian rotavirus	B	6	5	0.1	<0.025	<0.025	<0.025	<0.025		4	C	Berman & Hoff (1984)
	B	10	5	0.5	0.45	0.60				2.7	C	Berman & Hoff (1984)
	B	8	25	0.4	0.1	0.12	0.16	0.20	0.30	4.5	A	Grabow *et al.* (1983)
	B	10	25	0.4	0.08	0.20	0.28	0.40	0.70		A	Grabow *et al.* (1983)
SA-11 Simian rotavirus – cell associated	B	6	5	0.5	0.25	0.88	2.3			3	C	Berman & Hoff (1984)
	B	10	5	0.5	0.15	1.8	2.8			3	C	Berman & Hoff (1984)
Enteroviruses												
Coxsackievirus A9	B	6	5	0.5	0.075	0.15	0.22			3	C	Engelbrecht *et al.* (1980)
	B	10	5	0.5	0.38	0.75				2.5	C	Engelbrecht *et al.* (1980)
Coxsackievirus B3	C	6	20	0.5	0.02	0.26	0.35	0.43		4	D	Jensen *et al.* (1980)
	B	7	5	0.2		0.97	1.4	2.9		4.5	–	Cromeans *et al.* (2010)
	B	8	5	0.2		0.65	1.1	1.7		4.5	–	Cromeans *et al.* (2010)
	C	10	20	0.5	2.2	4.5	6.8			3.7	D	Jensen *et al.* (1980)
Coxsackievirus B4	B	7	5	0.4	0.28–0.30	2.4–26	21–84			3.9	E	Payment *et al.* (1985a)
Coxsackievirus B5	B	6	5	0.5	0.88	1.8				1.8	C	Engelbrecht *et al.* (1980)
	C	6	20	0.5	0.11	0.22	0.33	0.44		4	D	Jensen *et al.* (1980)
	B	7	5	0.4	1.3–52	21–59	72–127	101	130	3.1–5	E	Payment *et al.* (1985a)
	B	7	5	0.2		3.6	5.5	7.4		3.2	–	Cromeans *et al.* (2010)
	B	7.5	5	1		5.4	8.4	12			–	Black *et al.* (2009)
	B	7.8	5	0.5	1.1	2.3				2.9	C	Engelbrecht *et al.* (1980)
	B	8	5	1		4.7	7.6	10		4.5	–	Cromeans *et al.* (2010)
	B	9	5	1		14	19	23			–	Black *et al.* (2009)
	C	10	20	0.5	1.9	4.0				2.1	D	Jensen *et al.* (1980)
	B	10	5	0.5	17	34				2.2	C	Engelbrecht *et al.* (1980)
	B	7	5	0.2			3.2–5.2				–	Kahler *et al.* (2010)
	B	8	5	0.2			2.3–7.9				–	Kahler *et al.* (2010)
	B	7	15	0.2			1.0–2.0				–	Kahler *et al.* (2010)
	B	8	15	0.2			0.73–3.6				–	Kahler *et al.* (2010)

(*continued*)

Table 3 | continued

Micro-organism	Batch (B) or continuous (C)	pH	T °C	Approximate chlorine dose (mg L^{-1})	Ct for Log_{10} reduction (min mg L^{-1}) 1	2	3	4	5	Max red	Data transformation[a]	Reference
Poliovirus 1	C	6	20	0.3	0.07	0.18				2.2	D	Sharp & Leong (1980)
				1.1	0.15	0.27	0.38	0.51		4.2		
	B	6	5	0.5	0.51	1.0	1.5			3.4	C	Engelbrecht *et al.* (1980)
	B	6	5	~1		0.93 (1.0–2.8)	2.9 (1.0–5.0)	6.7 (<10)			–	Thurston-Enriquez *et al.* (2003)
	B	7	5	0.4	0.19–0.47	0.39–3.9	2.1–27	3.9–68	40–130	5.0	E	Payment *et al.* (1985a)
	B	7.5	5	1		1.4	3.0	5.3			–	Black *et al.* (2009)
	B	7.8	5	0.5	0.33	0.66	0.99			nr	C	Engelbrecht *et al.* (1980)
	B	9	5	1		8.2	15	22			–	Black *et al.* (2009)
	C	10	20		0.54	1.1	1.6			3	D	Sharp & Leong (1980)
	B	10	5	0.5	5.5	11	16			3.2	C	Engelbrecht *et al.* (1980)
Poliovirus 2	B	6	5	0.5	0.31	0.61	0.92			3	C	Engelbrecht *et al.* (1980)
	B	6	25	0.4	0.1	0.16	0.20	0.68	1.4	5.2	A	Grabow *et al.* (1983)
	B	7	5	0.4	0.14–0.23	0.28–0.8	0.59–4.0	2.3–71	4.0–130	5.0	E	Payment *et al.* (1985a)
	B	8	25	0.4	0.1	0.28	0.50	0.74	1.0	4.7	A	Grabow *et al.* (1983)
	B	10	5	0.5	16	32				2.5	C	Engelbrecht *et al.* (1980)
	B	10	25	0.4	0.16	0.78	3.0			3.8	A	Grabow *et al.* (1983)
Poliovirus 3	B	7	5	0.4	0.10–0.35	0.20–1.6	0.30–3.1	0.40–71		4.5	E	Payment *et al.* (1985a)
Echovirus 1	B	6	5	0.5	0.12	0.25	0.37			Nr	C	Engelbrecht *et al.* (1980)
	B	7	5	0.2		0.96	1.3	1.5		3.2	–	Cromeans *et al.* (2010)
	B	7.5	5	1		1.6	3.5	6.2			–	Black *et al.* (2009)
	B	7.8	5	0.5	0.29	0.59	0.88			3.2	C	Engelbrecht *et al.* (1980)
	B	8	5	0.2		0.99	1.3	1.6		5.8	–	Cromeans *et al.* (2010)
	B	9	5	0.2		3.3	8.5	17			–	Black *et al.* (2009)
	B	10	5	0.5	25	49	73			3.2	C	Engelbrecht *et al.* (1980)
	B	7	5	0.2			0.49–0.84				–	Kahler *et al.* (2010)
	B	8	5	0.2			0.66–1.2				–	Kahler *et al.* (2010)
	B	7	15	0.2			0.29–0.48				–	Kahler *et al.* (2010)
	B	8	15	0.2			0.30–0.84				–	Kahler *et al.* (2010)
Echovirus 5	B	6	5	0.5	0.32	0.64	0.96			nr	C	Engelbrecht *et al.* (1980)
	B	7.8	5	0.5	0.47	0.94	1.4			3.5	C	Engelbrecht *et al.* (1980)
	B	10	5	0.5	6.9	14	21			nr	C	Engelbrecht *et al.* (1980)
Echovirus 11	B	7	5	0.2		0.82	1.0	1.1		4	–	Cromeans *et al.* (2010)
	B	8	5	0.2		0.54	0.97	1.4		4	–	Cromeans *et al.* (2010)
Echovirus 12	B	7.5	5	1		2.1	4.4	7.4			–	Black *et al.* (2009)
	B	9	5	1		8.4	19	32			–	Black *et al.* (2009)
Hepatitis A	B	6	25	0.4	0.1	0.16	0.2	0.28	0.36		A	Grabow *et al.* (1983)
	B	7	?	5	>300					0.97	G	Li *et al.* (2002)
				10	~100	< 300				nr		
				20	~80	< 600				nr		
	B	8	25	0.4	0.1	0.16	0.2	0.24	0.39	3	A	Grabow *et al.* (1983)
	B	10	25	0.4	0.08	0.2	0.47	0.97	1.5	4	A	Grabow *et al.* (1983)

(*continued*)

Table 3 | continued

Micro-organism	Batch (B) or continuous (C)	pH	T °C	Approximate chlorine dose (mg L^{-1})	Ct for Log_{10} reduction (min mg L^{-1})					Max red	Data transformation[a]	Reference
					1	2	3	4	5			
Caliciviruses												
Feline Calicivirus	B	6	5	0.17		0.02 (<0.04)	0.07 (0.04–0.08)	0.19 (0.11–0.15)			–	Thurston-Enriquez *et al.* (2003)
	B	7	5	0.16		0.05 (<0.08)	0.06 (<0.08)	0.07 (<0.08)			–	Thurston-Enriquez *et al.* (2003)
	B	8	5	0.16		0.18 (<0.32)	0.23 (<0.32)	0.27 (<0.32)			–	Thurston-Enriquez *et al.* (2003)
Murine Norovirus	B	7	5	0.2		<0.02	<0.02	<0.07			–	Cromeans *et al.* (2010)
	B	7.2	5	0.19		0.14	0.25	0.31		2.5	–	Lim *et al.* (2010)
	B	7.2	20	0.18		0.061	0.18	0.29		3	–	Lim *et al.* (2010)
	B	8	5	0.2		<0.02	<0.02	<0.08			–	Cromeans *et al.* (2010)
	B	7	5	0.2			0.016–0.023				–	Kahler *et al.* (2010)
	B	8	5	0.2			0.024–0.034				–	Kahler *et al.* (2010)
	B	7	15	0.2			<0.010— 0.015				–	Kahler *et al.* (2010)
	B	8	15	0.2			<0.020 –0.021				–	Kahler *et al.* (2010)
Bacteriophage												
Coliphage V1	B	6	25	0.4	1.2	1.9	2.8			3.0	A	Grabow *et al.* (1983)
	B	8	25	0.4	1.0	2.9				2.5	A	Grabow *et al.* (1983)
	B	10	25	0.4	0.24	1.5	3.9			3.4	A	Grabow *et al.* (1983)
Coliphage MS2	B	6	25	0.4	0.12	0.28	0.57	1.2	1.8	4.7	A	Grabow *et al.* (1983)
	B	7.2	5	0.17		0.24	0.36	0.44		4	–	Lim *et al.* (2010)
	B	7.2	20	0.17		0.080	0.14	0.18		5	–	Lim *et al.* (2010)
	B	8	25	0.4	0.2	0.39	0.70	1.1	1.6	5	A	Grabow *et al.* (1983)
	B	10	25	0.4	0.16	0.32	0.47	0.67	0.90	5.3	A	Grabow *et al.* (1983)

nr, not reported.

All studies identified infectious viruses by ability to infect host cells in tissue culture/plaque assay procedures.

Except where stated otherwise, all strains used in studies were laboratory strains.

[a]Data transformations explained in Table 1, '–' indicates that results are as reported in the original publication.

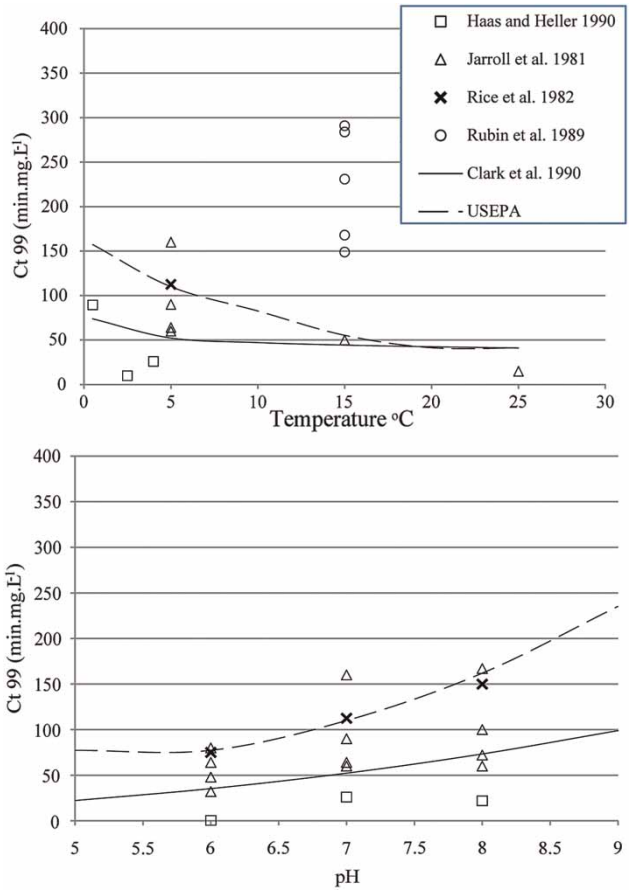

Figure 1 | Illustration of published *Giardia* susceptibility data, and best-fit (solid line) model from Clark *et al.* (1990) and upper uncertainty bound (dashed line) applied in the USEPA long-term surface water treatment rule.

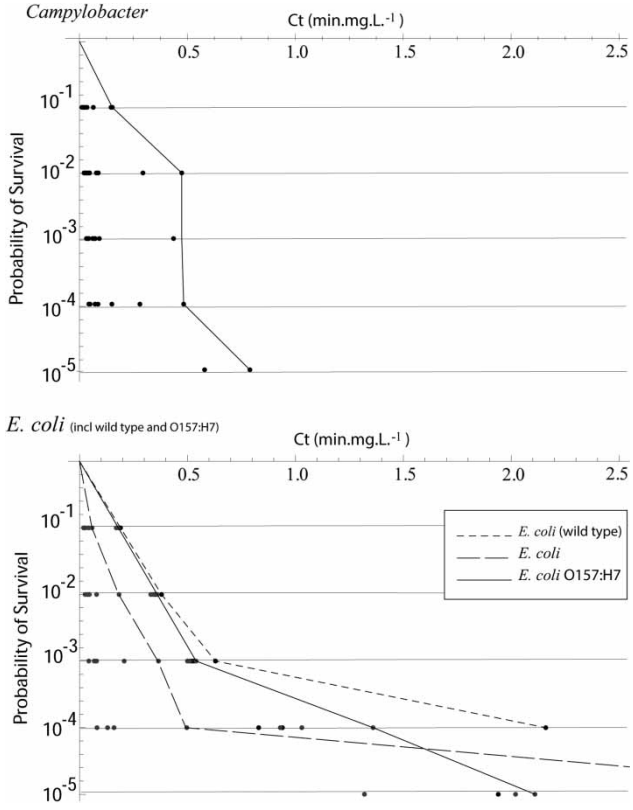

Figure 2 | Illustration of pooled and transformed data for *Campylobacter* (above) and *E. coli* O157 (below) susceptibility to free chlorine inactivation from the literature. Lines indicate upper bound of persistence from reported data.

Giardia is much more resistant to inactivation by free chlorine than bacteria and viruses and has therefore been used as a conservative reference pathogen for disinfection, most notably in the USEPA long-term 1 surface water treatment rule (LT1SWTR) (USEPA 2003a). As a result, more detailed research and modeling has been undertaken on *Giardia* in order to quantify the Ct requirements for 4 Log_{10} inactivation under different dosing, temperature, and pH conditions. Clark *et al.* (1990) fitted a numerical model to two large datasets from *Giardia lamblia* (Jarroll *et al.* 1981; Hibler *et al.* 1987) (the first using excystation as an endpoint, the second using animal infectivity) in order to estimate the model parameters. The resulting equation with best-fit model parameters is given by: $\text{Ct} = 0.12I^{-0.27}C^{0.19}\text{pH}^{2.54}\text{temp}^{-0.15}$ (Clark *et al.* 1990) where I is the ratio of organisms remaining at time t to organisms at time zero, C is the concentration of chlorine (mg L^{-1}), and temp is the temperature (°C). To obtain a conservative level for the surface water treatment rule, the upper 99% confidence interval at the 4 Log_{10} inactivation level was calculated, and then first-order kinetics were assumed so that the line passed through 1 (no reduction) at $\text{Ct} = 0$. The best-fit curve and the upper 99% confidence interval used for the LT1SWTR are illustrated in Figure 1.

Results from three other experimental studies on *Giardia* (Rice *et al.* 1982; Leahy *et al.* 1987; Rubin *et al.* 1989) were also identified in this review and are also illustrated for comparison in Figure 1. Results from Rice *et al.* (1982) yielded results consistent with the EPA model that were above the best-fit line but below the LT1SWTR line. While Rubin *et al.* (1989) reported a higher resistance than other studies, the cysts used in their study were harvested from gerbils in contrast to previous studies that had used cysts from humans. The best-fit curve of the Clark *et al.* (1990) model was applied in the QMRA calculations.

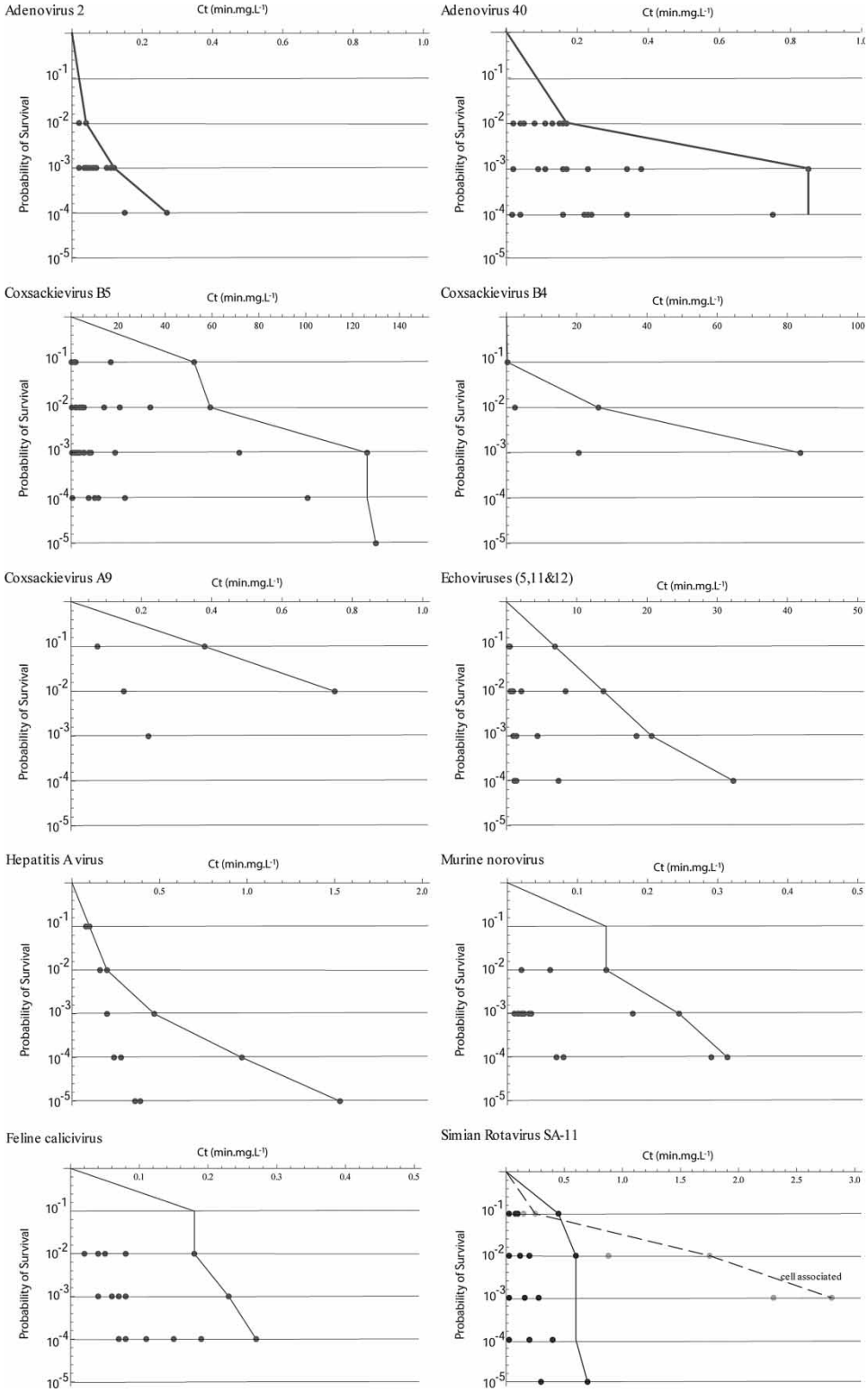

Figure 3 | Illustration of pooled and transformed data for human enteric viruses and surrogates susceptibility to free chlorine inactivation from the literature. Lines indicate upper bound of persistence from reported data. *Note:* scale of the *x*-axis varies between figures.

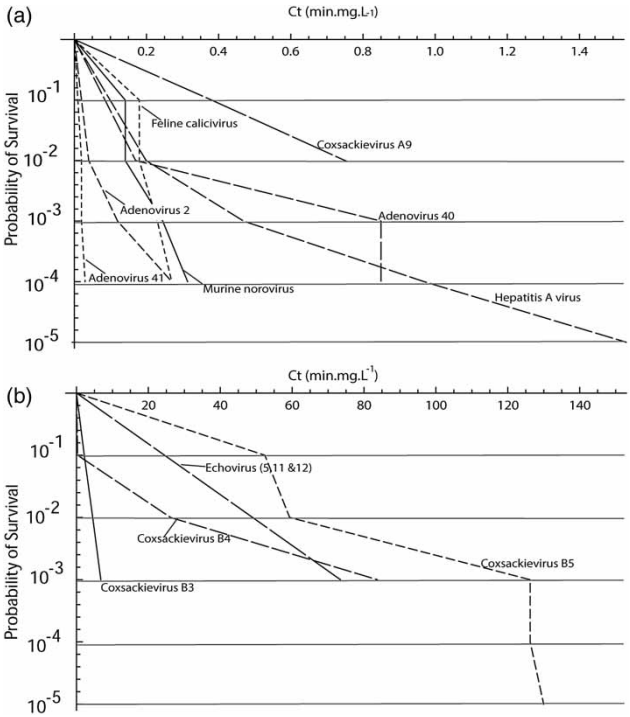

Figure 4 | Comparative illustration of survival functions from Figure 2 representing (a) less resistant and (b) more resistant human enteric viruses and surrogates. Lines indicate upper bound of persistence from reported data.

Conceptual model

The conceptual model accounts for variability in the residence time of the disinfection contactor, chlorine decay across the contactor and for pathogen specific survival functions. The residence time distribution represented by the theoretical tanks in series model (MRT = 12 min) is illustrated in Figure 5 with three hydraulic assumptions (two, six, and 20 CSTRs). With few CSTRs (two) the residence time is highly variable, with some portions of flow exhibiting a very short residence time (<1 min). As the hydraulics are assumed to improve with increasing CSTRs (approaching plug flow), the variability in residence time is reduced, and hence the portion of flow that is able to short-circuit the contactor with minimal residence time is reduced.

The survival functions were used to predict the Log_{10} reduction for each pathogen, given a quantified chlorine dose (Ct), as illustrated in Figure 6. The survival functions constructed for the bacterial and viral reference pathogens are illustrated in Figure 7. The functions are constructed from Ct values reported in Table 4 which were selected

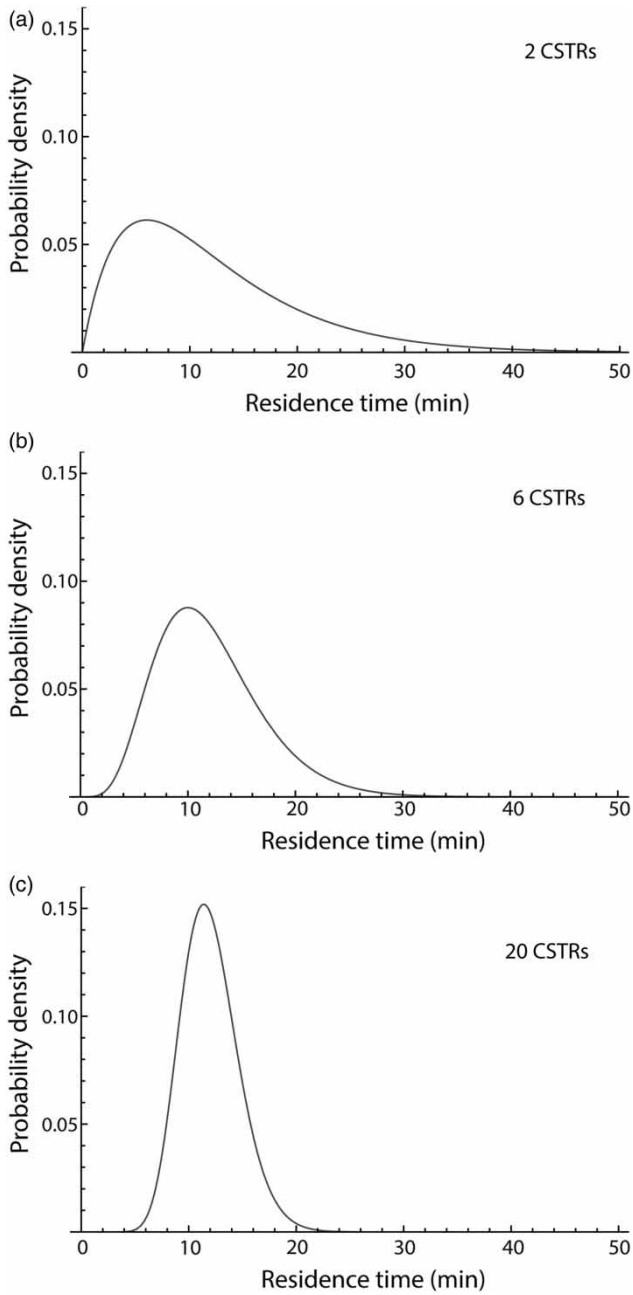

Figure 5 | Influence of assumed number of CSTRs on the residence time distribution applied in the QMRA tool.

from the following publications: *Campylobacter* (Blaser *et al.* 1986; Lund 1996); *E. coli* O157 (Rice & Clark 1999); rotavirus based on results for non-cell associated SA-11 simian rotavirus (Grabow *et al.* 1983; Berman & Hoff 1984); norovirus based on feline calicivirus (Thurston-Enriquez *et al.* 2003) and murine norovirus (Cromeans

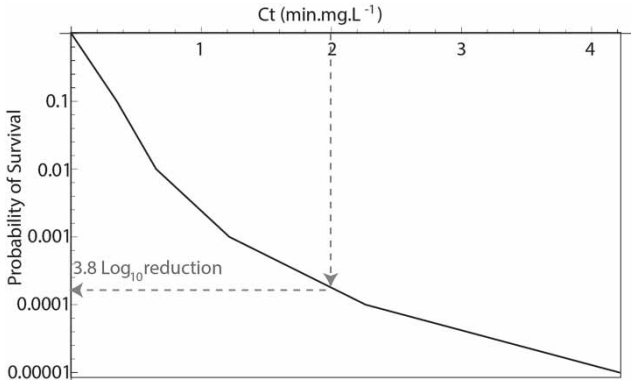

Figure 6 | Generic example of a survival function S(Ct) illustrating the relationship between Ct, probability of survival and the Log_{10} reduction.

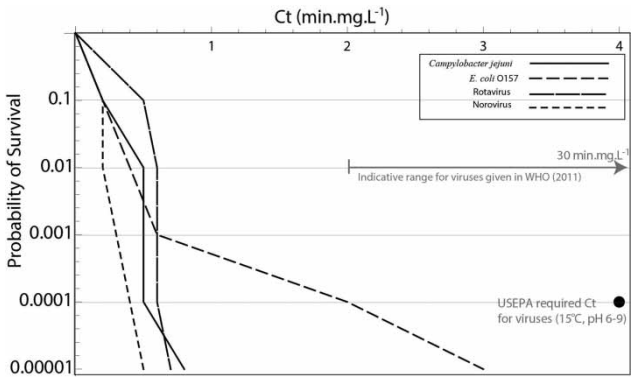

Figure 7 | Selected survival functions S(Ct) for reference viruses and bacteria in QMRA tool, with comparisons to the indicative ranges given in the WHO drinking water guidelines (2011) (indicated by the arrow bar 2–30 min mg L^{-1}) and the USEPA Ct requirements.

et al. 2010; Kahler *et al.* 2010; Lim *et al.* 2010). For *Giardia*, the best-fit model parameters published by Clark *et al.* (1990) that formed the basis for Ct requirements of the USEPA surface water treatment rule was used. While not possible for other pathogens, the pH, dose and temperature dependence was therefore incorporated into the QMRA model for *Giardia*.

Hypothetical case study

A comparison of Log_{10} reduction performance for the hypothetical contactor, using each of the three proposed approaches is given in Table 5 (initial residual of 0.4 mg L^{-1}) and Table 6 (initial residual of 1.5 mg L^{-1}). In each case, as the hydraulics of the contactor was assumed to be improved, the predicted Log_{10} reduction increased. For *Campylobacter* at a dosage of 0.4 mg L^{-1} (Table 5), with approach 1, increasing the BF from 0.3 to 1 increased the calculated Log_{10} reduction from 4.5 to 15.1. For approach 2, increasing the assumed number of CSTRs from 2 to 20 increased the calculated Log_{10} reduction from 2.4 to 9.2. For approach 3, the flow weighted mean Log_{10} reduction was similar and increased from 2.8 to 9.0 Log_{10}.

The proposed method (approach 3) for quantifying contactor performance explicitly accounted for variability in residence time distribution. When hydraulic performance was assumed to be poor, very low Log_{10} reductions were predicted for a portion of flow. For example, consider the quantiles of Log_{10} reduction of *Campylobacter* with an initial chlorine residual of 1.5 mg L^{-1} in Table 6. While the Ct calc method predicted 17 Log_{10} reduction, results from method 3 predicted that 0.1% of flow may only achieve less than 1.9 Log_{10} reduction. Improving the hydraulic

Table 4 | Selected Ct values for defining the reference pathogen specific survival functions

	Ct required for reduction					
Reference pathogen S(Ct)	**1 Log_{10} 0.1**	**2 Log_{10} 0.01**	**3 Log_{10} 0.001**	**4 Log_{10} 0.0001**	**5 Log_{10} 0.00001**	**k_{10}**
Campylobacter	0.2	0.5	0.5	0.5	0.8	2.1
E. coli O157:H7	0.2	0.4	0.6	2	3	0.6
Rotavirus	0.5	0.6	0.6	0.6	0.7	2.4
Norovirus	0.2	0.2	0.3	0.4	~	3.3
Giardia[a]	$Ct = 0.12I^{-0.27}Cl^{0.19}pH^{2.54}temp^{-0.15}$					
at pH7, 15 °C, 0.4 mg L^{-1}	17.5	32.6	60.8	113.2	210.7	0.024
at pH7, 15 °C, 1.5 mg L^{-1}	22.5	42.0	78.1	145.5	270.9	0.018

[a]Model developed by Clark *et al.* (1990).

Table 5 | Results from three different approaches for quantifying Log_{10} reduction efficacy by free chlorine disinfection for QMRA (initial chlorine residual 0.4 mg L^{-1}, MRT = 12 min)

	1: Ct calc		2: CSTR equation		3: Proposed method with residence time distribution						
						Quantiles of Log_{10} reduction					
Reference pathogen	BF[a]	Log_{10} reduction	*n*	Log_{10} reduction	*n*	0.001	0.01	0.05	0.50	0.95	Overall mean[b] (Log_{10} reduction)
Campylobacter	0.3	4.5	*2*	2.4	*2*	0.5	1.6	3.6	9.7	13.7	2.8
	0.6	9.1	6	5.0	6	4.1	5.3	6.7	10.4	13.1	6.5
	1	15.1	20	9.2	20	6.5	7.7	8.6	10.6	12.2	9.0
E. coli O157:H7	0.3	1.2	2	1.4	*2*	0.5	1.6	3.0	4.2	9.2	2.8
	0.6	2.4	6	2.4	6	3.0	3.0	3.1	3.9	9.1	3.7
	1	4.0	20	3.6	20	3.0	3.1	3.2	3.8	4.3	3.7
Rotavirus	0.3	5.2	2	2.5	2	0.2	0.7	3.8	22.2	34.0	2.1
	0.6	10.3	6	5.3	6	5.4	9.0	13.1	24.3	32.3	7.5
	1	17.2	20	9.9	20	12.6	16.2	18.9	24.8	29.6	15.4
Norovirus	0.3	7.2	2	2.7	2	0.5	2.3	5.8	24.2	36.0	2.9
	0.6	14.5	6	6.1	6	7.4	11.0	15.1	26.3	34.3	9.5
	1	24.1	20	12.0	20	14.6	18.2	20.9	26.8	31.6	17.4
Giardia	0.3	0.02	2	0.05	2	0.01	0.02	0.04	0.14	0.21	0.13
	0.6	0.03	6	0.06	6	0.05	0.07	0.09	0.16	0.20	0.15
	1	0.06	20	0.06	20	0.09	0.11	0.13	0.16	0.19	0.16

[a]BF, baffling factor from (USEPA 2003a).
[b]Assuming complete mixing following the contactor.

Table 6 | Results from three different approaches for quantifying Log_{10} reduction efficacy by free chlorine disinfection for QMRA (initial chlorine residual 1.5 mg L^{-1}, MRT = 12 min)

	1: Ct calc		2: CSTR equation		3: Proposed method with residence time distribution						
						Quantiles of Log_{10} reduction					
Reference pathogen	BF[a]	Log_{10} reduction	*n*	Log_{10} reduction	*n*	0.001	0.01	0.05	0.50	0.95	Overall mean[b] (Log_{10} reduction)
Campylobacter	0.3	17.0	2	3.5	2	1.9	5.4	9.8	32.8	47.6	4.3
	0.6	34.0	6	8.1	6	11.8	16.3	21.5	35.4	45.5	13.6
	1	56.6	20	18.0	20	20.9	25.4	28.8	36.0	42.1	23.6
E. coli O157:H7	0.3	4.5	2	2.4	2	1.9	3.2	4.1	10.5	14.9	4.2
	0.6	9.1	6	5.0	6	4.1	5.5	7.0	11.2	14.2	6.5
	1	15.1	20	9.2	20	6.9	8.2	9.2	11.4	13.2	9.4
Rotavirus	0.3	19.4	2	3.6	2	0.7	9.2	22.3	91.5	135.7	3.3
	0.6	38.8	6	8.4	6	28.4	41.8	57.4	99.3	129.4	27.1
	1	64.7	20	19.0	20	55.6	69.1	79.3	101.1	119.2	57.8
Norovirus	0.3	27.2	2	3.9	2	2.7	11.2	24.3	93.5	137.7	4.5
	0.6	54.3	6	9.3	6	30.4	43.8	59.4	101.3	131.4	29.1
	1	90.5	20	21.7	20	57.6	71.1	81.3	103.1	121.2	59.8
Giardia	0.3	0.05	2	0.13	2	0.02	0.05	0.11	0.42	0.62	0.40
	0.6	0.10	6	0.17	6	0.14	0.20	0.27	0.45	0.59	0.44
	1	0.17	20	0.19	20	0.26	0.32	0.37	0.46	0.54	0.46

[a]BF, baffling factor from (USEPA 2003a).
[b]Assuming complete mixing following the contactor.

performance (increasing the assumed CSTRs to 6 and 20) reduced the impact of this small portion of flow.

DISCUSSION

A large number of studies reporting the sensitivity of human enteric pathogens to free chlorine inactivation have been reviewed and compared by transforming reported results to a common metric. A statistical meta-analysis of all data was not adopted due to the variation between studies and the many unquantifiable uncertainties underlying the data, including the following:

- The experimental conditions such as temperature, pH, suspension media, and chlorine dosage. For example, Blaser *et al.* (1986) investigated *Campylobacter jejuni* inactivation at pH 6 and 8, temperatures of 4 and 25 °C and used a dosage of 0.1 mg L^{-1}; while Lund (1996) investigated *Campylobacter jejuni* inactivation at pH 6.5, temperatures of 4 and 10 °C and used a dosage of 0.2 mg L^{-1}.
- The selection of experimental strains. Recent independent studies on coxsackievirus B5 reported comparable results, for example $Ct_{99.9} = 5.5$ (Black *et al.* 2009) and 8.4 mg L^{-1} min^{-1} (Cromeans *et al.* 2010) at pH 7 and 7.5, respectively, using the same laboratory strain (Faulkner strain). However, older work undertaken by Payment *et al.* (1985a) using environmental strains of coxsackievirus B5 reported much higher overall persistence, and higher variability in persistence between strains, with the most resistant strain originating from raw sewage ($Ct_{99.9} = 126$ mg L^{-1} min^{-1}).
- The interpretation and analysis of experimental data. An example is the kinetic modeling approaches that accounted for chlorine decay over the course of the experiment (Thurston-Enriquez *et al.* 2003; Black *et al.* 2009; Cromeans *et al.* 2010) whereas earlier studies often only provided data plots, e.g. Sharp & Leong (1980), Grabow *et al.* (1983) and Berman & Hoff (1984).

Rather than to statistically aggregate all results into a single estimate for each reference pathogen with some quantitative representation of variability and uncertainty, the results from the literature are tabulated and the upper bound of the reported range was selected for characterizing the pathogen specific survival functions. This approach was deliberately selected to maintain transparency of the underlying scientific data. It was concluded that quantifying uncertainty bounds on these numbers would not provide a meaningful representation of the true variability and uncertainty underlying the reported data. We expect that for specific conditions or risk scenarios, and as additional scientific evidence becomes available, risk assessors should and will select alternative survival functions.

Shielding of micro-organisms due to the presence of organic matter is expected to lead to a reduction in disinfection efficacy. Only one study in the review looked specifically at the difference between free and cell-associated organisms (Berman & Hoff 1984), demonstrating around one order of magnitude difference in required Ct. Clogging as well as particle association related to chlorine resistance is poorly characterized and not well accounted for in QMRA calculations, yet is very important for assessing the risk associated with full-scale disinfection of drinking water. In particular, during episodes of poor plant performance, when conventional treatment may be sub-optimal, the disinfection barrier is expected to be challenged with micro-organisms that are associated with organic matter or chemical floc. Understanding the effectiveness of disinfection during such events are of critical importance as the need for the disinfection barrier is increased and the expected performance of the barrier is reduced. Clearly more quantitative scientific evidence is needed to better understand drinking water safety during sub-optimal treatment events. It is very important to recognize that the survival functions characterized based on the evidence reported in this review do not account for micro-organism shielding. A safety factor to account for this shielding could be included in the model. The requirements of the LT1SWTR (USEPA 2003a) for enteric viruses are based on Hepatitis A Virus inactivation studies performed by Sobsey *et al.* (1988) multiplied by a safety factor of 3. It may be that to account for shielding, the safety factor needs to be as high as 10.

Previously published QMRA investigations that have quantified Log_{10} reduction of pathogens by chlorine disinfection have relied on reported ranges from the literature, and did not consider site-specific characteristics or operational factors. Storey & Ashbolt (2003) assumed free chlorine disinfection (dose and residence time unspecified) would achieve

2 Log_{10} inactivation of enteric viruses (in general) over the contact chamber, followed by 0.5 Log_{10} reduction in the distribution system citing (Storey & Ashbolt 2003; Jacangelo *et al.* 1995; Rose *et al.* 1996; Payment 1999). Westrell *et al.* (2003) used triangular distributions (defined by min, mode, and maximum) to describe Log_{10} inactivation (residual concentration = 0.2 mg L^{-1} and average residence time of 2 days in distribution) for *Cryptosporidium* (T(0, 0.4, 1.0) citing results of Korich *et al.* (1990) and Finch *et al.* (1997), the same triangular distribution was then later applied by Signor & Ashbolt (2006)); for rotavirus (T(1.5, 2.0, 3.0) citing Sobsey (1989)); and for *Campylobacter* (T(2.5, 3.5, 5.0) citing Sobsey (1989)). In these studies, several factors were unclear. Firstly, the scientific justification for the selection of reported ranges and parameters of the triangular distributions were ambiguous. Secondly, the site-specific characteristics including plant design and contact time were not explicitly considered. Thirdly, it was not possible to quantitatively explore the impact of process management decisions on the consumer safety including a change in chlorine dose or increase in contact time.

The conceptual model presented overcomes the limitations of previously published methods for quantifying chlorine disinfection efficacy for QMRA, and has two significant additional advantages. Firstly, even within a screening level QMRA, the model accounts for variability in residence time of a disinfection contactor. Contact time is critical for effective chlorine disinfection, and therefore small fractions of flow that receive a low chlorine dose may have important implications for public health. It is of great value to be able to explore this conceptually within the QMRA model. For the example reported in Table 6 for *Campylobacter*, the predicted Log_{10} reduction using the Ct_{cal} method would have implied a very high level of consumer protection (17 Log_{10} reduction with BF = 0.3). However, when considering the variability in residence time (approach 3), 0.1% of flow was calculated to achieve less than 1.9 Log_{10} reduction. For a 1 ML per day drinking water treatment plant, this equates to 1,000 L per day of water. For water treatment plants with limited clear water tank storage, and for consumers located close to the water treatment plant, this water could be directly distributed to the consumer. The model results demonstrate that characterizing the hydraulic performance of the disinfection contactor and storage tank are critical for ensuring that the minimal Log_{10} reductions are adequate to ensure safety for the entire population.

The model describes the residence time distribution using the theoretical tanks-in-series model. The residence time distribution of any real full-scale contactor will however deviate (at least to some extent) from this theoretical distribution. For a more detailed site-specific study the residence time distribution should be locally quantified using tracer testing (Haas *et al.* 1998; Peplinski & Ducoste 2002)) and/or computational fluid dynamics (Greene *et al.* 2006). In addition to residence time, mixing behavior within contactors has also been shown to affect disinfection efficacy and needs to be considered for a detailed analysis (Haas 1988). The theoretical model presented is not an alternative to these approaches, but rather provides a generic approach to be applied as a first screening step, allowing the residence time distribution to be predicted based on general inputs such as MRT and baffle structure.

Validation (how well do the predicted Log_{10} reductions reflect actual full-scale plant performance?) is an important consideration of any proposed modeling approach. In the case of full-scale disinfection performance of human enteric pathogens, direct validation is typically not possible. Previous studies have compared the predicted Log_{10} reductions by alternative modelling methods with those calculated from measured *E. coli* concentration at bench scale (Smeets *et al.* 2006) and pilot scale (Pfeiffer & Barbeau 2014). In each case, conclusions regarding the preferred modeling method were based on which method predicted a Log_{10} reduction closest to those calculated from observations. This apparently logical approach does not give adequate consideration to the mechanistic assumptions behind each approach and why each may lead to different predictions. The CSTR equation (approach 2) resulted in similar Log_{10} predictions to the flow weighted mean result achieved with approach 3. While both approach 2 and approach 3 consider the contactor as a series of CSTRs in series, they are based on different assumptions. Approach 2 (a widely applied equation in many fields of environmental and engineering processes) applies a materials balance approach and simplifies exponential inactivation as a single step for each CSTR. The reduction in predicted Log_{10} inactivation between approach 1 and approach 2 is

caused by the limited number of steps of inactivation that are quantified when the CSTR equation is applied. In contrast, approach 3 applies the theoretical residence time distribution for a series of CSTRs and therefore explicitly accounts for the impact of variability in residence time on the overall Log_{10} reduction. Approach 3 does not simplify the microbial inactivation as a step function, but quantifies inactivation according to a defined survival function. Approach 3 should therefore be preferred for QMRA because the impact of contact time on consumer risk can be explicitly explored. When more detailed site-specific information on the residence time distribution is available, the theoretical distribution can be replaced in the model with the site-specific residence time distribution.

Secondly, the model accounted for reference pathogen specific survival functions. Reported ranges in review and guidance documents are typically intended to be indicative only, referring broadly to the performance across each of the pathogen groups: viruses, bacteria and protozoa. For example, the WHO drinking water guidelines report a Ct_{99} for viruses to be 2–30 min mg L^{-1} at 0–10 °C and pH 7–9; for bacteria to be 0.04–0.08 min mg L^{-1} at 5 °C and pH 6–7; and for protozoa (identified as mainly *Giardia*) to be 25–245 min mg L^{-1} at 0–25 °C and pH 7–8. Slightly broader but similar ranges were reported by LeChevallier & Au (2004). The literature review data summarized in Tables 2 and 3 show the documented considerable variability between pathogens in their sensitivity to chlorine. Reference pathogens are selected for QMRA under the assumption that they are conservative models for all pathogens in their respective microbial group. If the water treatment operation is designed to protect the consumer from the reference pathogen, then it is assumed that the consumer will also be protected from all pathogens within that group. The reference pathogens used in the model were not conservative choices for chlorine disinfection, but were selected due to their high prevalence in the community, and high infectivity. When undertaking QMRA of systems that use free chlorine disinfection, it may be more reasonable to consider the resistance of enteroviruses such as echovirus or coxsackievirus. While less prevalent and (assumed to be) less infectious, enteroviruses can lead to very significant health outcomes including meningitis and myocarditis. Some dose-response data are available for Echovirus 12 (Schiff *et al.* 1984) and mouse infectivity data for coxsackievirus B4 (Suptel 1963), both of which have been previously applied for water-related QMRA (Mena *et al.* 2003; Åström *et al.* 2007; van Lieverloo *et al.* 2007).

The approach for quantifying chlorine concentration across the contactor was very simplistic. Different approaches for modeling chlorine decay have been reviewed by Clark & Sivaganesan (2002). Particularly in the initial stages of disinfection, the first-order relationship has been shown to be appropriate; however, the first-order model is not capable of reproducing the higher decay rates often observed in the initial stages of chlorination nor the slow tailing off of the decay at very long reaction times (Haas & Karra 1984a, b). The residence times of disinfection contactors are in practice relatively short (<30 min) in comparison to long-term deviations (>4 h) from linear inactivation kinetics, and therefore first-order decay may be appropriate for considerations within the contact itself. Better predictions of required chlorine dosage would require a site-specific appreciation of the mixing characteristics of the contact chamber, the compositions of the reactive compounds in the water, and factors such as temperature that drive the reaction kinetics. In addition, longer term chlorine decay rates within the distribution network combined with travel time to consumers would provide a better overall appreciation of Log_{10} reductions beyond the contact chamber itself.

CONCLUSIONS

This paper presents a screening level approach for quantifying the efficacy for free chlorine disinfection across a full-scale contactor taking into consideration the variability in residence time and the pathogen specific chlorine sensitivity. Quantitative review of the breadth of laboratory studies on pathogen and indicator sensitivity to free chlorine was a challenge due to differences in experimental conditions (pH, temperature, dosing), micro-organism strains and spiking density, and data reporting protocols, however survival functions were constructed for a range of pathogens relying on the upper bound of the reported data. The residence time distribution for a full-scale contactor was quantified based on limited local information regarding

the geometry and flow rate. The application of the model within a hypothetical case study demonstrated the importance of accounting for variable residence time in QMRA. While the overall Log_{10} reduction may appear high, small parcels of water with short residence time can compromise the overall performance of the barrier. QMRA is an emerging tool for the assessment, management and communication of water-related infectious risks. While theoretically simple, the approach presented is of great value for undertaking an initial assessment of a full-scale disinfection contactor based on limited site-specific information.

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