GLOBAL WATER PATHOGEN PROJECT

PART FOUR. MANAGEMENT OF RISK FROM EXCRETA AND WASTEWATER

PATHOGEN SPECIFIC PERSISTENCE MODELING DATA

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Citation:

Mitchell, J. and Akram, S. (2017). Pathogen Specific Persistence Modeling Data. In: J.B. Rose and B. Jiménez-Cisneros (eds), *Water and Sanitation for the 21st Century: Health and Microbiological Aspects of Excreta and Wastewater Management (Global Water Pathogen Project)*. (M. Yates (eds), Part 4: Management of Risk from Excreta and Wastewater - Section: Persistence), Michigan State University, E. Lansing, MI, UNESCO. <https://doi.org/10.14321/waterpathogens.53>

Acknowledgements: K.R.L. Young, Project Design editor; Website Design: Agroknow (<http://www.agroknow.com>); K. Dean, E. Willis and A. Wissler, literature review and reviewed and organized data.

Last published: October 26, 2017

Summary

Persistence modeling facilitates the accurate simulation of different stages of growth, survival, and death of microorganisms in environmental matrices by describing the changes in population size of microorganisms over time. The most commonly used model for simulating persistence patterns of pathogens is the first order exponential one-parameter model. However, persistence curves for many microorganisms do not follow this classic linear trend, as evidenced by decades of studies across the growing field of predictive microbiology and for microbes in many different matrices. Therefore, it is essential for an evaluation of linear and non-linear curves (models) in order to provide an accurate description of both pathogen and matrix specific persistence (or inactivation).

Seventeen linear and nonlinear persistence models were used to find the best models for describing the persistence of water microbes - bacteria, viruses, bacteriophages, bacteroidales, and protozoa in human urine, wastewater, freshwater, marine water, groundwater matrices, biosolids and manure. A total number of 30 datasets were used in this study containing 180 different pathogen (or indicator)/matrix combinations to find the best fitting models through linear regression techniques to describe persistence subject to various conditions. Like the exponential decay model, these models contain general parameter(s) to mathematically describe the relationship between reductions in microbial populations with time. The models do not contain explanatory variables to isolate the effects of environmental conditions (i.e. temperature, UV exposure) on inactivation. Overall, three models (JM2, JM1, and Gamma) were found to be the best fitting models across the entire data set and represented 59%, 34% and 25% of the data sets respectively. JM2 fit the persistence data the best across environmental matrices except in human urine, and groundwater in which JM1 performed the best at describing the persistence patterns. Across pathogens, JM2 was the best model for bacteria, bacteriophages, and bacteroidales. However, viruses were best fit by JM1. The models which best describe the persistence pattern of each pathogen or indicator in a matrix under different treatments and their corresponding parameters are presented in this chapter. In addition, T90 and T99 values, which are commonly used to specify the time required for a pathogen concentration to decrease by one and two log units, respectively, is reported for all the datasets and compared between matrices and microorganisms types. While this metric is often used to describe pathogen persistence, it is only relevant in the linear region of the persistence curve and will be misleading if an incorrect model is assumed or a model other than the best fitting model is used to estimate these

values. Therefore, the results in this chapter that contains the best fitting models and parameters along with the associated calculation of T90 and T99 for various pathogen/matrix combinations can reduce uncertainty in estimations of pathogen population size in water environments over time.

1.0 Introduction

Mathematical models are commonly used to describe the microbial inactivation of pathogens persisting in environmental matrices and to predict population sizes for subsequent human health risk calculations, which may lead to treatment decisions. Persistence modeling facilitates the accurate simulation of the stages of growth, survival, and death of microorganisms in different matrices by describing the mathematical relationship between the population size of microorganisms and time through regression techniques to estimate kinetic parameters (constants). While T90 and T99 values are commonly used to indicate the time required for a pathogen concentration to decrease by one and two log units, respectively, these metrics are only relevant in the linear region of a persistence curve and may be misleading if more complex persistence patterns accurately describe a specific pathogen in a specific matrix (i.e. curves with shoulders or tails). The significance of utilizing mathematical models to describe kinetics is in their ability to describe the persistence pattern of specific pathogens in different environments enabling engineers and policy makers to predict the absolute microorganism populations at any given time through interpolation or extrapolation, not just the population size relative to the initial conditions like the T90 or T99.

The most commonly used model for simulating persistence patterns of pathogens is the first order exponential one-parameter model, which was originally developed to describe the inactivation of chemical disinfectants (Chick 1908). However, as predictive microbial modeling has developed as a field over many years, persistence curves for microorganisms in a number of environments were observed that do not follow this classic linear pattern. Therefore, accurate description of non-linear persistence curves is essential. A common explanation for this non-linearity in persistence is that the population of microorganisms may consist of several sub-populations, each with different inactivation kinetics. Along with linear curves, curves with “shoulder” (a delay before attenuation begins), curves with “tailing” (attenuation slows with time), and sigmoidal curves (both a shoulder and a tailing) are the four most typically observed models for bacterial decay (Xiong et al. 1999). Shoulders in curves represent the smooth initial inactivation, while tailing can represent an intrinsic resistance of some microorganisms or that they are protected by various factors. Figure 1 shows a schematic representation of different patterns of persistence of microorganisms.

Figure 1. Schematic representation of four different persistence patterns

As the first order model cannot describe more complex persistence patterns such as shoulders, tailing, and sigmoidal curves noted above, several other models were developed and tested over time.

Table 1 shows the list of the microbial persistence models, which were utilized for the studies described in this chapter as well as their corresponding equations. These models are mostly empirical and have three or fewer model parameters.

Table 1. Models utilized in this study

Model	Abbreviation	Equation ^a	Reference
Exponential	Ep	$\frac{Nt}{N0} = \exp(-k_1 t)$	Chick, 1908
Logistic	lg1	$\frac{Nt}{N0} = \frac{2}{1 + \exp(-k_1 t)}$	Kamau et al., 1990
Fermi	lg2	$\frac{Nt}{N0} = \frac{1}{1 + \exp(-k_1(t - k_2))}$	Peleg, 1995
Exponential damped	Epd	$\frac{Nt}{N0} = 10^{\exp(-k_1 t \times \exp(-k_2 t))}$	Cavalli-Sforza et al., 1983
Juneja and Marks 1	JM1	$\frac{Nt}{N0} = 1 - (1 - \exp(-k_1 t))^{k_2}$	Juneja et al., 2001
Juneja and Marks 2	JM2	$\frac{Nt}{N0} = \frac{1}{1 + \exp(k_1 + k_2 \log(t))}$	Juneja et al., 2006
Gompertz 2	Gz	$\frac{Nt}{N0} = \exp\left[\frac{-k_1}{k_2} \exp((k_2 t) - 1)\right]$	Wu et al., 2004
Weibull	Wb	$\frac{Nt}{N0} = 10^{-((t/k_1)^{k_2})}$	Peleg, 2003
Lognormal	ln	$\frac{Nt}{N0} = 1 - \{(\ln(t) - k_1 / k_2)\}$	Aragao et al., 2007
Gamma	Gam	$\frac{Nt}{N0} = \exp\left\{ (t^{k_1-1}) \exp\left(\frac{-t}{k_2}\right) \right\}$	van Gerwen and Zwietering, 1998
Broken-line	Bi	$\frac{Nt}{N0} = \exp(-k_1 t), t < k_3$	Muggeo, 2003
Broken-line 2	Bi2	$\frac{Nt}{N0} = \exp(-k_1 t + k_2(t - k_3)), t \geq k_3$	Muggeo, 2003
Double exponential	Dep	$\frac{Nt}{N0} = k_3 \exp(-k_1 t) + (1 - k_3) \exp(-k_2 t)$	Gerard Abraham et al., 1990

Model	Abbreviation	Equation ^a	Reference
Gompertz 3	Gz3	$\frac{Nt}{N0} = 10^{k_1 \exp \left[-\exp \left(\frac{-k_2 \exp(1)(k_3 - t)}{k_3} + 1 \right) \right]}$	Gil et al., 2011
Gompertz-Makeham	Gzm	$\frac{Nt}{N0} = 10^{(-k_3 t - k_1 / k_2 (\exp(k_2 t) - 1))}$	Jodrá, 2009
Sigmoid type A	sA	$\frac{Nt}{N0} = 10^{((k_1 t) / \{(1 + k_2 t)(k_3 - t)\})}$	Peleg, 2006
Sigmoid type B	sB	$\frac{Nt}{N0} = 10^{-(k_1 \times t^{k_2}) / (k_2 + t^{k_2})}$	Peleg, 2006

^aNt denotes the number of organisms remaining at time t; N0 denotes the initial number of organisms; k₁, k₂, and k₃ are model parameters. Model parameters, k_i, are constants in each model that have different units depending on the model.

2.0 Best-Fitting Models

A literature review was conducted as described in the previous chapter, “Persistence of Pathogens in Sewage and Other Water Types”. However, it was also expanded to include papers with die-off data presented additional water matrix terms: sludge, urine and manure. For this analysis, raw data of microorganism concentration vs. time was obtained from the original author of the peer-reviewed journal article or digitized from the figures in the publications. A total of 95 studies contained acceptable data for modeling, which contained 304 individual data sets describing a pathogen and matrix combination under various environmental conditions (urine, n=9; freshwater, n=131; wastewater, n=16; biosolids, n=42; marine, n=60; groundwater, n=46). While the environmental conditions - temperature, the presence of UV light or indigenous microbiota, for example - are known to influence decay rates, the focus of this analysis is not to describe empirical data sets with explanatory variables through regression modeling as this is reported in the original papers. The purpose of this chapter is to summarize pathogen specific decay rates using generalized persistence models which best-fit decay data sets for specific water environments

under specific conditions.

Seventeen previously established linear and nonlinear persistence models were evaluated to determine the best models for describing the persistence of different bacteria, viruses, bacteriophages, bacteroidales, and protozoa in human urine, wastewater, biosolids and manure, freshwater, marine water, groundwater matrices. The chapter includes a selected representation of pathogens, marker or indicator data sets across the 6 environmental matrices noted above. A total number of 30 studies are summarized in this chapter which includes 180 different pathogen or indicator/matrix combinations. Indicator bacteria are typically used to detect the level of fecal contamination in environments and are generally not pathogenic to human health while pathogens are microorganisms which can produce diseases. Table 2 shows the best fitting models for all collected data. JM2, JM1, and gamma models were the best fit for 58.7%, 33.7% and 25.0% of the experimental data better than the other tested models respectively. As JM2 fit the persistence data the best in all matrices except in human urine, and groundwater where JM1 performed the best at describing the persistence patterns.

Table 2. Best fitted models to different matrices

Matrices	Model ^a	Percent of the combinations for which the model was the best fit
All Dataset	JM2	58.7
	JM1	33.7
	Gam	25.0
	Epd	20.7
	Dep	20.2
	Ep	19.0
	ln	18.5
Human Urine	JM1	66.7
	Ep	44.4
	Epd	33.3
Wastewater	JM2	50.0
	Gam	33.3
	ln	33.3

Matrices	Model ^a	Percent of the combinations for which the model was the best fit
Freshwater	JM2	76.0
	JM1	34.7
	Epd	21.3
Marine Water	JM2	50.0
	Dep	34.1
	Gam	25.0
Groundwater	JM1	50.0
	Dep	50.0
	ln	50.0
Manure & Biosolids	JM2	47.5
	JM1	35.0
	lg1	30.0

^aModels described in Table 1

Table 3 shows the best fitting models for different bacteria, Bacteriophages, and bacteroidales. For viruses, pathogen and indicator types. JM2 was the best model for JM1 best described the persistence curves.

Table 3. Best fitted models to different types of microorganisms

Microbe Group	Model ^a	Percent of the Combinations for Which the Model was the Best Fit
Bacteria	JM2	54.0
	JM1	31.0
	Gamma	21.8
Bacteriophages	JM2	61.4
	JM1	38.6
	Gamma	29.5
Viruses	JM1	57.1
	Gamma	52.4
	JM2	52.4
Bacteroidales	JM2	74.2
	ln	29.0
	JM1	29.0

^aModels described in Table 1

Table 4 shows the best fitting models for specific pathogens and indicators. The JM2 model best described the persistence curves for *E.Coli*, *Enterococci*, *Salmonella*, and HF183. The persistence was best described for MS2 by the JM1 model, and exponential model was the best fitting model for Adenovirus.

Table 4. Best fitted models to specific pathogens and indicators

Indicator or Pathogen Type	Number of Pathogen and Indicator/Matrix Combinations	Model ^a	Percent of the Pathogen and Indicator/Matrix Combinations for Which the Model was the Best Fit
<i>E. coli</i>	26	JM2	65.4
		Ln	30.8
		JM1	26.9
Enterococci	12	JM2	50.0
		Ep	33.3
		JM1	25.0
<i>Salmonella</i>	18	JM2	31.8
		Gzm	27.3
		Epd	18.2
HF183 ^b	9	JM2	100.0
		JM1	33.3
		Gam	11.1
Adenovirus	7	Ep	57.1
		JM2	42.9
		JM1	42.9
MS2 bacteriophage	15	JM1	80.0
		Epd	53.3
		Gam	53.3

^aFor model description see Table 1; ^b*Bacteroides* human source tracking gene target

3.0 Summary of T90 and T99 data

The time that the concentration of a type of microorganism in a specific environment decreases by one and two log units is called T90 and T99 respectively. These values are calculated and summarized using the best fitting models and their corresponding parameters for every

pathogen (or indicator)/matrix combination. The predicted number of days needed to achieve 90% and 99% decay rates (T90 and T99) of pathogens and indicators in different matrices are summarized in Tables 5 and 6. The tables also show the range of variations and the standard deviations in T90 and T99 values calculated for every pathogen (or indicator)/matrix combination.

Table 5. Range, average and standard deviations in T90 and T99 values in different matrices

Matrix	Number of Pathogen and Indicator/Matrix Combinations		T90 Days	T99 Days
Human Urine	9	Range	0.1 to 2.6	0.3 to 5.1
		Average (SD) ^a	0.7 (0.8)	1.4 (1.5)
Wastewater	11	Range	0.1 to 62.5	0.2 to 85.9
		Average (SD)	21.1 (25.6)	32.6 (33.6)
Freshwater	72	Range	0.1 to 125.8	0.4 to 278.5
		Average (SD)	15.6 (29.4)	31.8 (60.8)
Marine Water	34	Range	0.1 to 127.8	0.2 to 160.8
		Average (SD)	12.1 (24.3)	23.5 (36.1)
Groundwater	5	Range	0.1 to 20.8	0.7 to 99.8
		Average (SD)	11.6 (8.4)	54.0 (40.3)
Manure & Biosolids	38	Range	0.2 to 120.7	0.5 to 290.6
		Average (SD)	8.6 (19.6)	19.3 (46.7)

^aSD: Standard Deviation

Table 6. Range, average and standard deviations in T90 and T99 values for different pathogen or indicator types

Pathogen or Indicator	Number of Pathogen and Indicator/Matrix Combinations		T90 Days	T99 Days
Bacteria	71	Range	0.1 to 127.8	0.2 to 290.6
		Average (SD) ^a	11.9 (23.5)	23.9 (51.3)
Bacteroidales ^b	33	Range	0.4 to 17.2	0.9 to 77.0
		Average (SD)	2.9 (3.0)	7.5 (13.9)
Bacteriophage	43	Range	0.1 to 125.8	0.3 to 251.6
		Average (SD)	17.9 (33.2)	33.4 (62.0)
Protozoa	2	Range	11.4 to 55.2	69.8 to 85.9
		Average (SD)	33.3 (31.0)	77.9 (11.3)
Viruses	18	Range	0.1 to 56.4	0.4 to 121.7
		Average (SD)	13.4 (17.4)	36.6 (35.5)

^aSD: Standard Deviation; ^bGene persistence

4.0 Persistence Modeling in Pathogen/Matrix Combinations

The results from the different studies on the persistence of various types of pathogenic human bacteria, viruses, bacteroidales, protozoa, and bacteriophages in different environments of human urine, wastewater, freshwater, marine water, groundwater, and biosolids were collected to find the best-fit mathematical models for different pathogen (or indicator)/matrix combinations.

4.1 Persistence Modeling in Human Urine

The model parameters for different pathogen combinations in a human urine matrix along with the corresponding fitted parameters are presented in Table 7. Pathogens studied consisted of adenovirus and MS2 bacteriophage. Data were obtained from a yet unpublished study conducted by Dr. Tamar Kohn from Swiss Federal Institute of Technology in Lausanne.

Table 7. Best fitted models and fitting parameters for MS2 bacteriophage (virus indicator) and adenovirus in human urine matrix

Virus Type	T90 (T99) Days	Temp °C	Best Fit Model ^a	k1	k2	Data Points ^b	Other Factors	Other Models ^c
Adenovirus	0.2 (0.4)	35	JM2	9.77	5.36	10	NR	None
MS2	2.6 (5.1)	20	Dep ^d	-0.42	0.90	10	pH=8.47; NH3=15.8	None
MS2	1.1 (1.8)	35	JM1	3.42	4.74	8	pH=8.15; NH3=19.1	None
MS2	0.8 (1.6)	35	Ep	2.92	NA	8	pH=8.19; NH3=24.6	JM1
MS2	0.9 (1.7)	35	JM1	3.10	1.73	4	pH=8.19; NH3=24.4	Epd, Gam, Bi3, Ig1
MS2	0.2 (0.4)	35	JM1	11.62	0.81	6	pH=8.72; EC=33.6; NH3=81	Ep, Epd

Virus Type	T90 (T99) Days	Temp °C	Best Fit Model ^a	k1	k2	Data Points ^b	Other Factors	Other Models ^c
MS2	0.1 (0.3)	35	JM1	10.16	0.22	6	pH=8.79; EC=33.0; NH3=106	Gam
MS2	0.5 (1.0)	35	JM2	4.45	3.71	8	pH=8.49; EC=16.0; NH3=28.2	Bi3, Ep, Epd
MS2	0.3 (0.7)	35	Ep	6.95	NA	10	pH=8.48; EC=33.6; NH3=71.1	JM1, Gam

^aFor model description see Table 1; ^bNumber of data points modeled in the experiment; ^cOther models that provided an equally statistical best-fit; ^dBest fit a model with three parameters, where $k_3 = 0.00000001$

4.2 Persistence Modeling in Wastewater

The model parameters for different pathogen combinations in wastewater matrices along with the

corresponding fitting parameters are presented in Table 8. Studied pathogens consisted of bacteria, viruses, bacteroidales, and protozoa and matrices consisted of treated and untreated wastewaters.

Table 8. Best fitted models and fitting parameters for pathogens in wastewater matrices

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models ^b)	k1	k2	Data Points ^c	Other Factors	Reference
INDICATOR or PATHOGEN								
Enterococci	13.0 (60.1)	10	JM2 (Ep, Epd, ln)	-1.82	1.57	11	Light	Walters et al., 2009
Enterococci	1.5 (2.8)	13	lg1 (Ep)	1.90	NA	9	Light	Walters and Field, 2009
E. coli	9.4 (12.6)	6	Gz3 ^e	-9.50	0.40	7	NR ^d	Czajkowska et al., 2008
E. coli	4.5 (5.8)	24	JM2	-12.55	9.76	7	NR	Czajkowska et al., 2008
Salmonella Thompson	9.7 (19.3)	25	Ep	0.24	NA	14	NR	Ravva and Sarreal, 2014
Salmonella enterica	62.5 (63.1)	15	sA ^f	-703.9	-541.2	14	Darkness	Boehm et al., 2012
Salmonella enterica	0.12 (0.22)	15	JM2 (ln, JM1, Gam)			35	Light	Boehm et al., 2012
Humbac ^g	1.1 (2.0)	10	JM2	1.76	4.20	11	Light	Walters et al., 2009
PROTOZOA AND VIRUSES								
Cryptosporidium parvum	55.2 (85.9)	5.2	Gam	9.69	3.27	7	Sunlight	Jenkins et al., 2013
Norovirus	19.1 (26.6)	20	JM2 (Gz3, Gam, ln, JM1, Sb)	-18.98	7.19	4	NR	Skraber et al., 2009
Norovirus	56.4 (80.1)	4	JM1 (JM2, Gam, ln)	0.10	28.18	4	NR	Skraber et al., 2009

^aFor model description see Table 1; ^bOther models that provided an equally statistical best-fit; ^cNumber of data points modeled in the experiment; ^dNR: Not Reported; ^eBest fit a model with three parameters, where $k_3 = 7.74$; ^fBest fit a model with three parameters, where $k_3 = 63.8$; ^gA gene target

4.3 Persistence Modeling in Manure and Biosolids

The model parameters for different pathogen combinations in different manure and biosolids matrices

along with the corresponding fitting parameters are presented in Table 9. Studied pathogens consisted of bacteria and viruses, bacteroidales, and bacteriophages and matrices consisted of different biosolid types of composted manure, sludge, manure, and freshwaters contaminated with feces.

Table 9. Best fitted models and fitting parameters for indicators and pathogens in manure and biosolids matrices

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models ^b)	k1	k2	Data Points ^c	Other Factors	Reference
BACTERIA								
<i>E.coli</i>	30.3 (46.5)	20	JM1 (ln, Gam, JM2)	0.14	8.43	6	NR ^d	Klein et al., 2011
<i>E.coli</i>	4.5 (14.0)	37	JM1 (Dep)	0.23	0.23	5	NR	Klein et al., 2011
<i>E.coli</i>	0.4 (1.8)	50	JM2 (JM1)	3.52	1.67	6	NR	Klein et al., 2011
<i>E.coli</i>	5.0 (7.4)	24	Ln	1.14	0.37	6	NR	Czajkowska et al., 2008
<i>E.coli</i>	8.3 (13.4)	6	Ln	1.54	0.45	6	NR	Czajkowska et al., 2008
<i>Clostridium sporogenes</i>	120.7 (290.6)	20	Gam (Ep, lg1, Epd, JM1, JM2, ln)	85.39	0.53	4	Composted manure	Klein et al., 2011
<i>Clostridium sporogenes</i>	25.0 (50.0)	37	Ep (lg1, Epd, JM1, Gam)	0.09	N/A ^e	4	Composted manure	Klein et al., 2011
<i>Clostridium sporogenes</i>	11.5 (23.0)	50	Ep (Epd, JM1, lg1)	0.20	N/A	5	Composted manure	Klein et al., 2011
<i>Clostridium sporogenes</i>	3.1 (6.1)	60	Dep ^g (Gzm)	-0.12	0.75	5	Composted manure	Klein et al., 2011
<i>Listeria monocytogenes</i>	30.3 (37.0)	20	JM1 (lg2, JM2, Gam)	0.35	3981.15	6	NR	Klein et al., 2011
<i>Listeria monocytogenes</i>	7.3 (14.5)	37	Ep (JM1, lg1, JM2, Gam)	0.31	NA	6	NR	Klein et al., 2011
<i>Listeria monocytogenes</i>	4.3 (6.6)	50	Epd	0.33	-0.12	4	NR	Klein et al., 2011
Enterococci	4.5 (5.6)	13	jm2	-14.93	11.32	11	In Dark Treatment	Walters and Field, 2009
Enterococci	1.6 (2.8)	13	lg1 (Ep)	1.90	N/A	12	In Light Treatment	Walters and Field, 2009
Enterococci	8.9 (17.4)	Ambient temperature	Gz3 ^h (Dep)	-2.56	0.15	9	Shading	Oladeinde et al., 2014
Enterococci	7.9 (13.4)	Ambient temperature	Gz3 ⁱ	-2.40	0.25	9	No Shading	Oladeinde et al., 2014
BACTERIA SOURCE TRACKING GENE MARKERS^f								
CF128 DNA	1.6 (3.2)	13	Dep (Epd)	-0.57	1.45	29	In Dark Treatment	Walters and Field, 2009

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models ^b)	k1	k2	Data Points ^c	Other Factors	Reference
CF128 DNA	2.6 (3.3)	13	JM2 (ln, Ep, lg1)	-6.63	9.38	24	In Light Treatment	Walters and Field, 2009
CF128 RNA	1.4 (2.9)	13	JM2 (Wb, ln)	1.15	3.21	18	In Dark Treatment	Walters and Field, 2009
CF128 RNA	0.6 9 (1.1)	13	JM2 (ln, JM1)	4.20	3.51	19	In Light Treatment	Walters and Field, 2009
CF193 DNA	1.4 (2.8)	13	Ep (lg1, Bi3)	1.66	N/A	40	In Dark Treatment	Walters and Field, 2009
CF193 DNA	0.6 (1.3)	13	Ln	-1.23	0.63	24	In Light Treatment	Walters and Field, 2009
CF193 DNA	3.1 (4.1)	Ambient temperature	Gam (ln)	0.21	10.31	6	NR	Liang et al., 2012
CF193 RNA	0.4 (0.9)	13	JM2 (ln, Wb)	5.06	3.43	25	In Dark Treatment	Walters and Field, 2009
CF193 RNA	0.6 (0.9)	13	JM2 (ln)	5.16	5.06	25	In Light Treatment	Walters and Field, 2009
CF193 RNA	4.7 (77.0)	Ambient temperature	Ln (JM1, JM2, Gam, Bi3, lg1)	0.22	0.28	5	NR	Liang et al., 2012
Genbac	5.8 (13.2)	Ambient temperature	Dep ^j	0.05	0.41	10	NR	Oladeinde et al., 2014
Cow M3	3.6 (14.5)	Ambient temperature	JM2	-0.01	1.72	10	No shading	Oladeinde et al., 2014
Cow M3	4.5 (14.2)	Ambient temperature	Dep ^k	0.05	0.54	10	Shading	Oladeinde et al., 2014
Rum-2-Bac	2.4 (8.2)	Ambient temperature	JM2	0.48	1.96	10	No shading	Oladeinde et al., 2014
Rum-2-Bac	4.6 (11.6)	Ambient temperature	Dep ^l (JM2)	0.05	0.52	10	Shading	Oladeinde et al., 2014
BACTERIOPHAGE AND VIRUSES								
MS2	0.6 (1.3)	35	Ep (Epd, Gam, JM1, JM2, Wb)	3.63	N/A	7	Manure, pH=8.08; EC=2.0 (mS/cm); NH4=99 (mM)	Decrey and Kohn, 2017
MS2	0.2 (0.5)	35	Epd (JM1, JM2, Gam)	11.94	0.33	9	Manure, pH=8.05; EC=4.6 (mS/cm); NH4=505 (mM)	Decrey and Kohn, 2017
MS2	3.2 (3.6)	35	Bi3 ^m (Epd)	1.75	-3.28	7	Manure, pH=8.23; EC=1.7 (mS/cm); NH4=121(mM)	Decrey and Kohn, 2017
MS2	3.1 (7.3)	35	Ln (Epd, JM1, JM2, Gam)	0.10	0.81	7	Sludge, pH=7.76; EC=6.7 (mS/cm); NH4=28 (mM)	Decrey and Kohn, 2017

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models ^b)	k1	k2	Data Points ^c	Other Factors	Reference
MS2	5.7 (10.0)	35	lg1 (JM1, Gam)	0.54	2.28	11	Sludge, pH=7.76; EC=6.7 (mS/cm); NH4=28 (mM)	Decrey and Kohn, 2017
Adenovirus	13.7 (27.4)	35	Ep (lg1)	0.17	N/A	13	Manure, pH=8.23; EC=1.7 (mS/cm); NH4=121(mM)	Decrey and Kohn, 2017
Adenovirus	2.4 (4.8)	35	Ep (lg1)	0.97	N/A	10	Sludge, pH=7.76; EC=6.7 (mS/cm); NH4=28 (mM)	Decrey and Kohn, 2017

^aFor model description see Table 1; ^bOther models that provided an equally statistical best-fit; ^cNumber of data points modeled in the experiment; ^dNot reported; ^eN/A not applicable as model only has one parameter; ^fBelonging to the order of the Bacteroidales; ^gBest fit a model with three parameters, where $k_3=0.000001$; ^hBest fit a model with three parameters, where $k_3=2.14$; ⁱBest fit a model with three parameters, where $k_3=3.84$; ^jBest fit a model with three parameters, where $k_3=0.01$; ^kBest fit a model with three parameters, where $k_3=0.02$; ^lBest fit a model with three parameters, where $k_3=4.17$; ^mEC Electrical conductivity

4.4 Persistence Modeling in Freshwater

The model parameters for different pathogen combinations in different freshwater matrices along with

the corresponding fitting parameters are presented in Tables 10a, 10b, and 10c. Studied pathogens consisted of bacteria, viruses, bacteroidales, bacteriophages, and protozoa and matrices consisted of different freshwater types of lakes and rivers.

Table 10a. Best fitted models and fitting parameters for bacteria indicators and pathogens in freshwater matrices

Indicator or Pathogen	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models ^b)	k1	k2	Data Points ^c	Other Factors	Reference
<i>E. coli</i>	0.01 (0.4)	14.1	JM1 (Gam, JM2)	0.16	0.00	4	Indigenous Microbiota and Ambient Sunlight	Korajkic et al., 2014
<i>E. coli</i>	6.6 (9.6)	14.1	JM2 (JM1, ln, Gam, Epd)	0.79	20.42	4	Indigenous Microbiota	Korajkic et al., 2014
<i>E. coli</i>	2.7 (6.6)	14.1	Dep (Ep, Epd, JM2)	-3.97	0.85	4	Ambient Sunlight	Korajkic et al., 2014
<i>E. coli</i>	0.01 (0.4)	14.1	lg1 (Ep, JM1, ln)	0.25	N/Ad	4	Without a Treatment	Korajkic et al., 2014
<i>E. coli</i>	11.8 (21.2)	25	Ln (Epd, JM2)	3.80	0.14	5	Control	Dick et al., 2010
<i>E. coli</i>	1.1 (2.0)	25	JM2	1.63	4.32	5	Light	Dick et al., 2010
<i>E. coli</i>	1.2 (2.4)	25	JM2	1.65	3.33	5	Sediment	Dick et al., 2010
<i>E. coli</i>	1.1 (2.7)	15	Epd (JM2)	2.24	0.10	5	N/A ^d	Dick et al., 2010

Indicator or Pathogen	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Other Factors	Reference
<i>E. coli</i>	3.2 (6.1)	25	JM2	-2.11	3.72	5	Reduced Predation	Dick et al., 2010
Enterol1a ^e	3.8 (5.4)	14.1	JM2 (Gam, JM1)	-7.19	6.99	4	Indigenous Microbiota and Ambient Sunlight	Korajkic et al., 2014
Enterol1a ^e	4.1 (5.6)	14.1	JM2 (JM1, Gamma, lg1)	-8.76	7.74	4	Indigenous Microbiota	Korajkic et al., 2014
Enterol1a ^e	3.9 (5.5)	14.1	JM2	-6.77	6.65	4	Ambient Sunlight	Korajkic et al., 2014
Enterol1a ^e	4.2 (5.6)	14.1	JM2 (JM1)	-8.97	7.83	4	Without a Treatment	Korajkic et al., 2014
Enterococci	0.9 (2.0)	14.1	Epd (JM1, JM2, Gam)	2.63	0.07	4	Indigenous Microbiota and Ambient Sunlight	Korajkic et al., 2014
Enterococci	2.5 (3.7)	14.1	JM2 (Ep, Lg1)	-3.53	6.14	4	Indigenous Microbiota	Korajkic et al., 2014
Enterococci	0.6 (3.0)	14.1	JM1 (Gam)	0.80	0.11	4	Ambient Sunlight	Korajkic et al., 2014
Enterococci	4.0 (6.1)	14.1	JM2 (JM1)	-6.03	5.88	4	Without a Treatment	Korajkic et al., 2014
Fecal streptococci	2.6 (2.8)	24	Epd	0.0002	-3.15	6	Phosphate buffered freshwater with sunlight	Fujioka et al., 1981
<i>Salmonella enterica</i>	80.1 (82.1)	15	sA ^f (Dep, Gzm, sB)	-820.2	-201.7	16	Dark	Boehm et al., 2012
<i>Bacteroides fragilis</i>	17.2 (31.0)	10		0.17	NA	5	NR ^g	Balleste and Blanch, 2010

^aFor model description see Table 1; ^bOther models that provided an equally statistical best-fit; ^cNumber of data points modeled in the experiment; ^dN/A not applicable as model only has one parameter; ^eMolecularly based fecal indicator bacteria; ^fBest fit a model with three parameters, where $k_3=84.2$; ^gNR: Not Reported

Table 10b. Best fitted models and fitting parameters for bacterial indicator and microbial source tracking genes in freshwater matrices

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Other Factors	Reference
BACTERIA								
ENT 23s	23.5 (278.5)		41	JM2 (ln, Ep, Epd)	-0.87	0.97	11	In Dark Treatment Walters et al., 2009
ENT 23s	13.0 (60.1)	41	JM2 (Ep, ln, Epd)	-1.82	1.57	11	In Light Treatment Walters et al., 2009	
BACTERIA SOURCE TRACKING GENETIC MARKERS ^d								

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Other Factors	Reference
GenBac3	3.5 (4.4)	14.1	JM2 (JM1)	-10.65	10.30	4	Indigenous Microbiota and Ambient Sunlight	Korajkic et al., 2014
GenBac3	3.5 (4.5)	14.1	JM2 (JM1)	-9.84	9.57	4	Indigenous Microbiota	Korajkic et al., 2014
GenBac3	3.6 (4.8)	14.1	JM2	-8.30	8.23	4	Ambient Sunlight	Korajkic et al., 2014
GenBac3	3.8 (5.1)	14.1	JM2	-9.30	8.57	4	Neither	Korajkic et al., 2014
HF183	3.2 (3.9)	14.1	JM2	-12.26	12.29	4	Indigenous Microbiota and Ambient Sunlight	Korajkic et al., 2014
HF183	3.3 (4.1)	14.1	JM2 (JM1)	-9.86	10.22	4	Indigenous Microbiota	Korajkic et al., 2014
HF183	3.2 (4.0)	14.1	JM2	-10.01	10.58	4	Ambient Sunlight	Korajkic et al., 2014
HF183	3.4 (4.4)	14.1	JM2 (JM1)	-10.01	9.92	4	Neither	Korajkic et al., 2014
HF183	0.5 (1.3)	25	JM2	3.92	2.37	5	Control	Dick et al., 2010
HF183	0.6 (1.4)	25	JM2	3.58	3.09	5	Light	Dick et al., 2010
HF183	0.6 (1.3)	25	JM2	3.88	2.95	5	Sediment	Dick et al., 2010
HF183	0.6 (2.0)	15	JM2 (Gam, JM1)	3.12	2.09	5	Reduced Temperature	Dick et al., 2010
HF183	1.5 (2.6)	25	JM2	0.60	4.24	5	Reduced Predation	Dick et al., 2010
HumM2	3.2 (4.3)	14.1	JM2	2.26	153.58	4	Indigenous Microbiota and Ambient Sunlight	Korajkic et al., 2014
HumM2	3.5 (4.4)	14.1	JM2 (JM1)	-10.27	10.04	4	Indigenous Microbiota	Korajkic et al., 2014
HumM2	3.2 (4.0)	14.1	JM2	-10.15	10.55	4	Ambient Sunlight	Korajkic et al., 2014
HumM2	3.5 (4.5)	14.1	JM2 (JM1)	-10.37	9.96	4	Neither	Korajkic et al., 2014
BifAd	4.07(8.26)	Ambient temperature	JM2	-2.56	3.39	7	NR ^e	Jeanneau et al., 2012
Humbac	0.66(21.06)	Ambient temperature	Epd	3.80	0.14	4	NR	Dick et al., 2010
<i>B. thetaitomicron</i>	6.7 (13.3)	10	Ep (JM1, Gam, ln, JM2)	0.34	NA	8	NR	Balleste and Blanch, 2010

^aFor model description see Table 1; ^bOther models that provided an equally statistical best-fit; ^cNumber of data points modeled in the experiment; ^dBelonging to the order of the Bacteroidales; ^eNR: Not Reported

Table 10c. Best fitted models and fitting parameters for bacteriophage and viruses in freshwater

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Reference
VIRUSES							
Enterovirus	12.9 (25.7)	37	Ep (JM1, lg1, Epd)	0.18	N/A ^d	11 ^e	Walters et al., 2009
Enterovirus	4.3 (21.2)	37	JM1 (Gam)	0.12	0.11	10 ^f	Walters et al., 2009
Rotavirus	31.1 (60.3)	15	JM2 (Epd, Bi)	-10.27	3.63	8	Espinosa et al., 2008
BACTERIOPHAGE							
F+DNA, f1	32.2 (60.6)	4	JM2	-11.00	3.80	12	Long and Sobsey, 2004
F+DNA, f1	2.7 (5.4)	20	Dep ^g	0.18	0.85	9	Long and Sobsey, 2004
F+DNA, fd	31.1 (50.5)	4	JM2	-14.86	4.96	10	Long and Sobsey, 2004
F+DNA, fd	3.5 (5.5)	20	JM2	-4.72	5.47	7	Long and Sobsey, 2004
F+DNA, M13	104.8 (188.4)	4	lg1 (Ep, ln, JM2, JM1)	0.03	N/A	10	Long and Sobsey, 2004
F+DNA, M13	13.4 (28.9)	20	Epd (JM2, Gam)	0.18	0.00	11	Long and Sobsey, 2004
F+DNA, OW	104.8 (188.4)	4	lg1 (Ep, ln, JM2, JM1, Gam)	0.03	N/A	12	Long and Sobsey, 2004
F+DNA, SD	9.8 (16.1)	4	JM2	-8.92	4.87	9	Long and Sobsey, 2004
F+DNA, SD	2.0 (3.0)	20	JM2	-1.82	5.89	5	Long and Sobsey, 2004
F+DNA, ZJ2	37.0 (69.3)	4	JM2	-11.63	3.83	11	Long and Sobsey, 2004
F+DNA, ZJ2	3.3 (6.7)	20	Dep ⁱ (JM2)	0.00	0.69	7	Long and Sobsey, 2004
F+RNA, Dm3	1.7 (6.6)	4	JM1 (Gam, Dep, Epd)	0.43	0.16	8	Long and Sobsey, 2004
F+RNA, Dm3	32.8 (42.3)	20	Epd	3.62	0.10	7	Long and Sobsey, 2004
F+RNA, Go1	125.8 (251.6)	4	Ep (Bi, JM2)	0.02	N/A	11	Long and Sobsey, 2004
F+RNA, Go1	8.0 (13.3)	20	JM2 (Gz3)	-7.63	4.73	11	Long and Sobsey, 2004
F+RNA, MS2	109.8 (197.4)	4	lg1	0.03	N/A	12	Long and Sobsey, 2004

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Reference
F+RNA, MS2	9.1 (18.9)	20	Dep	0.09	0.26	11	Long and Sobsey, 2004
F+RNA, SG1	69.0 (138.1)	4	Bi (Epd, JM2, Wbl, ln, Gam, JM1)	0.03	0.03	12	Long and Sobsey, 2004
F+RNA, SG1	7.2 (13.1)	20	JM2	-5.80	4.04	10	Long and Sobsey, 2004
F+RNA, SG4	2.5 (5.0)	4	Dep ^j (Gz3)	0.00	0.92	8	Long and Sobsey, 2004
F+RNA, SG4	0.4 (0.9)	20	JM2	4.77	2.77	5	Long and Sobsey, 2004
F+RNA, SG42	1.4 (3.4)	4	JM2	1.32	2.69	9	Long and Sobsey, 2004
F+RNA, SG42	0.5 (1.0)	20	JM2	4.75	4.08	3	Long and Sobsey, 2004
F+RNA, sp2	19.3 (37.3)	4	JM2 (Dep)	-8.56	3.63	12	Long and Sobsey, 2004
F+RNA, sp2	4.2 (8.5)	20	Dep ^k	0.05	0.54	9	Long and Sobsey, 2004
FRNAPH	3.76 (16.62)	18.5	JM2	0.06	1.61	3	Jeanneau et al., 2012

^aFor model description see Table 1; ^bOther models that provided an equally statistical best-fit; ^cNumber of data points modeled in the experiment; ^dN/A not applicable as model only has one parameter; ^eExperiment conducted in the dark; ^fExperiment conducted in the light; ^gBest fit a model with three parameters, where $k_3=0.0008$; ^hBest fit a model with three parameters, where $k_3=0.000005$; ⁱBest fit a model with three parameters, where $k_3=0.00017$; ^kBest fit a model with three parameters, where $k_3=0.00005$

4.5 Persistence Modeling in Marine Water

The model parameters for different pathogen combinations in different marine water matrices along with

the corresponding fitting parameters are presented in Table 11. Studied pathogens consisted of bacteria and viruses, and matrices consisted of different marine water types of seawater, laboratory prepared saltwater and isolated estuarine waters.

Table 11. Best fitted models and fitting parameters for indicators and pathogens in marine water matrices

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Other Factors	Reference
BACTERIA								
<i>Clostridium perfringens</i>	2.1 (3.6)	22-24	Gz3 ^e	-2.41	0.91	11	Beach Sand Microcosms	Zhang et al., 2015

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Other Factors	Reference
<i>Clostridium perfringens</i>	2.0 (3.9)	22-24	JM2 (Dep)	-0.16	3.51	11	Seawater Microcosms	Zhang et al., 2015
<i>E. coli</i>	1.4 (2.6)	20	JM2	0.70	4.00	5	NR ^d	Chandran and Hatha, 2005
<i>E. coli</i>	0.4 (5.1)	30	JM2	2.99	0.98	5	NR	Chandran and Hatha, 2005
<i>E. coli</i>	1.1 (2.1)	Ambient temperature	JM2	1.70	3.79	5	Sunlight	Chandran and Hatha, 2005
<i>E. coli</i>	21.7 (22.9)	27	Dep ^f	-0.02	-0.03	12	NR	Miyagi et al., 2001
<i>E. coli</i>	20.0 (22.6)	27	Dep ^g	0.02	0.00	12	NR	Miyagi et al., 2001
<i>E. coli</i>	38.0 (68.3)	21	lg1 (Bi2)	0.08	N/A	20	No UV radiation	Beckinghausen et al., 2014
<i>E. coli</i>	19.5 (33.1)	21	JM2 (JM1, ln, Gam, Wb, sB, lg1)	-11.26	4.53	7	UV radiation and algae association	Beckinghausen et al., 2014
<i>E. coli</i>	9.8 (13.6)	21	Epd (Dep)	0.48	0.07	7	UV radiation and no algae association	Beckinghausen et al., 2014
<i>E. coli</i>	3.8 (8.9)	Ambient temperature	JM2 (Ep, ln, lg1)	-1.65	2.86	6	Water column	Korajkic et al., 2013
<i>E. coli</i>	13.8 (39.3)	Ambient temperature	JM2 (ln, Ep, sB, JM1, Gam, lg1)	-3.83	2.30	6	Sediments	Korajkic et al., 2013
Enterococci	5.3 (10.7)	22-24	Dep ^h	-0.29	0.43	11	Beach Sand Microcosms	Zhang et al., 2015
Enterococci	2.0 (2.9)	22-24	JM2	-2.45	6.60	11	Seawater Microcosms	Zhang et al., 2015
Fecal streptococci	5.9 (10.2)	24 ± 2	JM1 (Gam, lg1, Dep, JM2)	0.54	2.44	5	Without Sunlight	Fujioka et al., 1981
Fecal streptococci	2.3 (2.7)	24 ± 2	sB ⁱ (Wb, Gam)	53402.75	1026397.77	5	With Sunlight	Fujioka et al., 1981
<i>Salmonella</i> <i>Heidelberg</i>	0.1 (0.2)	15	Ep	27.79	N/A	21	In Light Treatment	Boehm et al., 2012
<i>Salmonella</i> <i>Mbandaka</i>	7.9 (13.4)	15	Dep ^j (Bi, Gzm)	0.01	0.01	14	In Dark Treatment	Boehm et al., 2012
<i>Salmonella</i> <i>Mbandaka</i>	0.1 (0.2)	15	lg1 (JM2)	22.66	N/A	22	In Light Treatment	Boehm et al., 2012
<i>Salmonella</i> <i>Typhimurium</i>	127.8 (160.8)	15	Epd	0.00	-0.01	13	In Dark Treatment	Boehm et al., 2012
<i>Salmonella</i> <i>Typhimurium</i>	1.8 (2.6)	20	sB ^k	2.77	17.34	5	NR	Chandran and Hatha, 2005
<i>Salmonella</i> <i>Typhimurium</i>	0.4 (1.0)	30	JM2 (JM2)	4.56	2.88	5	NR	Chandran and Hatha, 2005
<i>Salmonella</i> <i>Typhimurium</i>	0.8 (1.7)	Ambient temperature	Ep (JM2, Epd)	2.76	N/A	5	Sunlight	Chandran and Hatha, 2005
<i>Salmonella</i> <i>Typhimurium</i>	103.9 (113.3)	43	jm1	0.25	18201386478	50	Seawater w/o Alginic Acid	Davidson et al., 2015
<i>Salmonella</i> <i>Typhimurium</i>	61.9 (70.4)	43	jm2	-75.18	18.75	45	Seawater with Alginic Acid	Davidson et al., 2015
<i>Salmonella</i> <i>Typhimurium</i>	108.0 (121.0)	43	Epd	0.00	-0.04	60	Filtered Seawater w/o Alginic Acid	Davidson et al., 2015

Agent	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	k1	k2	Data Points ^c	Other Factors	Reference
<i>Salmonella</i> <i>Typhimurium</i>	132.5 (145.8)	43	Ln (Wb, Gam, Bi3, Gz3, Gzm)	4.82	0.09	86	Filtered Seawater with Alginic Acid	Davidson et al., 2015
<i>Salmonella</i> <i>Typhimurium</i>	100.9 (201.9)	12	Bi (Bi3)	0.02	-0.36	44	Unfiltered seawater with Alginic acid	Davidson et al., 2015
<i>Salmonella</i> <i>Typhimurium</i>	61.9 (70.4)	12	JM2 (ln, JM1, Gam)	-75.18	18.75	44	Unfiltered seawater without Alginic acid	Davidson et al., 2015
<i>Salmonella</i> <i>Typhimurium</i>	41.3 (82.6)	21	Epd	0.22	0.10	20	No UV radiation	Beckinghausen et al., 2014
<i>Salmonella</i> <i>Typhimurium</i>	416.2 (832.5)	21	Gzm ¹ (Dep)	0.01	-4*10 ⁻⁷	7	UV radiation and algae association	Beckinghausen et al., 2014
<i>Salmonella</i> <i>Typhimurium</i>	15.7 (21.3)	21	lg2	0.43	10.55	7	No UV radiation and algae association	Beckinghausen et al., 2014
<i>Vibrio</i> <i>fluvialis</i>	3.9 (18.2)	Ambient temperature	JM2 (Dep, Bi3)	0.11	1.55	12	Sediment	Amel et al., 2008
<i>Vibrio</i> <i>fluvialis</i>	1.0 (2.0)	Ambient temperature	Dep	0.03	2.29	12	No Sediment	Amel et al., 2008
<i>Helicobacter</i> <i>pylori</i>	9.4 (16.8)	37	lg1 (Dep, Gam, JM1, JM2, ln)	0.06	-0.24	7	NR	Konishi et al., 2007
VIRUSES								
Adenovirus	55.7 (121.7)	37	JM1 (Gam, JM2, Dep)	0.03	0.67	6	No UV irradiation	de Abreu Correa et al., 2012
Adenovirus	0.1 (4.6)	37	JM1 (Gam, Dep)	0.06	0.01	6	UV irradiation	de Abreu Correa et al., 2012
Hepatitis A	0.2 (55.6)	37	JM1 (Gam, JM2, Dep)	0.02	0.02	6	No UV irradiation	de Abreu Correa et al., 2012
Hepatitis A	0.1 (9.6)	37	JM1 (Gam, JM2, Bi3, Dep)	0.02	0.01	6	UV irradiation	de Abreu Correa et al., 2012
Murine Norovirus-1	0.1 (31.2)	37	JM1 (Gam, ln, JM2, Epd)	0.02	0.01	6	No UV irradiation	de Abreu Correa et al., 2012
Murine Norovirus-2	1.7 (4.7)	37	JM2	0.87	2.39	4	UV irradiation	de Abreu Correa et al., 2012
Poliovirus	8.9 (17.9)	15	Ep (Epd, JM1, Gam)	0.26	NR	5	NR	Enriquez et al., 1995

a For model description see Table 1; b Other models that provided an equally statistical best-fit; cNumber of data points modeled in the experiment; ^dNot Reported; ^eBest fit a model with three parameters, where $k_3=0.97$; ^fBest fit a model with three parameters, where $k_3=6.94$; ^gBest fit a model with three parameters, where $k_3=2.70$; ^hBest fit a model with three parameters, where $k_3=0.000002$; ⁱBest fit a model with three parameters, where $k_3=3.61$; ^jBest fit a model with three parameters, where $k_3=2.24$; ^kBest fit a model with three parameters, where $k^3=4.0$; ^lBest fit a model with three parameters, where $k_3=0.000003$; The T90 and T99 values were eliminated in decay rate analysis (section 2.0) due to considerably different experimental conditions.

4.6 Persistence Modeling in Groundwater

The model parameters for different pathogen

combinations in different groundwater matrices along with the corresponding fitting parameters are presented in Table 12. Studied pathogens consisted of viruses, a protozoa, and a bacteriophage.

Table 12. Best fitted models and fitting parameters for pathogens in groundwater

Indicator or Pathogen Agent	Group	T90 (T99) Days	Temp °C	Best Fit Model ^a (Other Models) ^b	K1	K2	Data Points ^c	Reference
<i>Cryptosporidium</i>	Protozoa	11.4 (69.8)	NR ^d	Dep ^e	0.04	1.04	8	Sidhu and Toze, 2012
Adenovirus	Virus	18.1 (99.8)	NR	JM2 (ln, Epd, JM1, Gam, Dep, Ep)	-1.87	1.40	5	Sidhu and Toze, 2012
Echovirus	Virus	20.9 (75.2)	12	JM2 (Ep, ln)	-3.49	1.87	10	Yates et al., 1990
Poliovirus	Virus	7.5 (24.6)	12	Gam (JM1, ln, Dep)	10.24	0.24	13	Yates et al., 1990
MS2	Bacteriophage	0.1 (0.7)	NR	JM1 (Wb)	0.95	0.01	6	Yates et al., 1990

^aFor model description see Table 1; ^bOther models that provided an equally statistical best-fit; ^cNumber of data points modeled in the experiment; ^dNR: Not reported; ^eFit the model with three parameters $K_3=0.16$

5.0 Models and Methodological Approach

As the first order model could not describe the persistence pattern of various pathogen/matrix combinations, several other models were developed and tested over time. The logistic model was developed originally to describe the sigmoid shaped decay curves in microbiology (Kamau et al. 1990). The Fermi model was applied originally to describe the influence of electric field intensity on the persistence of a microbial population (Peleg 1995). In addition, an exponentially damped polynomial model can be used to describe tailing survival curves (Cavalli-Sforza et al. 1983). Juneja and Marks developed two models, denoted here as JM1 and JM2, to describe the fate of foodborne pathogens in food processing operations (Juneja et al. 2003; Juneja et al. 2006). JM1 was mostly utilized to simulate the decay which had a convex shape and describe the tail in decay curves over long periods. JM2 was frequently used to simulate the non-linear persistence curves of thermal inactivation rates. Different variations of Gompertz models, denoted Gz2 and Gz3, were developed to predict the number of microorganisms persisting under stressed environmental conditions (Wu et al. 2004; Gil et al. 2011). Along with the logistic model, Gompertz functions are frequently used to fit sigmoidal kinetics (Membre et al. 1997). Gz2 and Gz3 models can describe log-linear kinetics, shoulders, and tailing effects (Zwietering et al. 1990; Chhabra et al. 1999). Weibull and

lognormal models are commonly used for thermal and non-thermal disinfection in different matrices. Weibull model can predict linear, concave, and convex and sigmoidal curves (Coroller et al. 2006). The other commonly used persistence model is Gamma. This is a simple model with few parameters and is commonly being utilized to simulate the microbial persistence in water matrices under varying environmental conditions (van Gerwen & Zwietering 1998). The broken line models of Bi and Bi2 were originally developed to simulate multiple break-points in decay curves (Muggeo 2003). The double exponential model that was originally developed to simulate thermal inactivation is able to represent linear and biphasic persistence curves (Abraham et al. 1990). On the other hand, sigmoidal models of sA and sB are typically being used to describe concave inactivation curves (Peleg 2006).

This chapter specifies and discusses the most appropriate mathematical models to describe the persistence patterns of various types of pathogens in different matrices, and compares the best fit models and decay rates in the specific pathogen (or indicator)/matrix combinations.

Maximum likelihood estimation and Bayesian Information Criterion (BIC) values were used in order to assess the goodness of fit among the 17 persistence models which were fit to each pathogen (or indicator)/matrix

combination. The models with the lowest absolute BIC values were selected as the best fitting models. Differences less than 2 in BIC values are not considered strong evidence for model selection. If the difference between the lowest BIC values of some models in a pathogen/matrix combination was less than 2, all these models were considered as the best fit models in this chapter.

BIC is defined as:

$$BIC = k \ln(n) - 2 \ln(L_m)$$

where k is the total number of parameters, n is the number of data points in the observed data (x), and L_m is

the maximum likelihood of the model. L_m is defined as:

$$L_m = p(x|\theta, M)$$

where θ are the parameter values which maximize the likelihood function, and M is the model used.

Raw data from different studies were obtained/extracted, analyzed, and fit to various persistence models using R statistical language (R Development Core Team, 2013). Data-capturing software, GetData Graph Digitizer (<http://www.getdata-graph-digitizer.com>), was used to digitize figures in the published papers where data values were not specifically stated.

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