QMRA as a Compliment to Epidemiologic Studies Estimating Bather Risk at Recreational Beaches



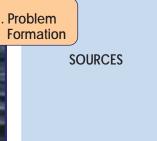
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The US EPA and WHO have set recreational water quality standards based on epidemiologic studies to protect human health at beaches. These studies have largely been limited to sewage-impacted sites and resources are unlikely to be available to assess the myriad of other impacted sites. Here we describe how quantitative microbial risk assessment (QMRA) can be used to assess unstudied pathogen sources in a systematic way to describe risk uncertainty. To illustrate the proposed QMRA comparison an illustrative example is provided focusing on the non-sewage example sources of seagulls and human shedders.

Research Objectives — — — — — — — — —

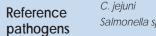
- 1. Compare predicted risk of gastrointestinal (GI) illness from sewage impacted recreational water to non-sewage impacted water using QMRA.
- 2. Identify key uncertain pieces of information in the QMRA estimation of risk to inform future research

Quantitative Microbial Risk Assessment (QMRA) with Monte Carlo sampling of uncertain parameters

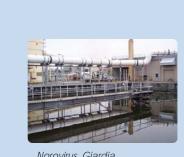


Reference









Cryptosporidium sp. and Salmonella su

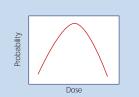
of the count of ENT to the mass of fe nd human shedders (cfu/g) or to the

Monte Carlo Calculation of Pathogen Dose

The pathogen dose μ_{w}^{s} is calculated for ingestion of water with a fecal-indicator bacterial concentration C_{ENT} at the single sample enterococci (ENT) limit of 104 cfu 100mL⁻¹:

$$\mu_{sp}^{s} = \frac{C_{ENT} * F^{s}}{R_{ENT}^{s} * 100} * R_{sp}^{s} * p^{s} * I^{s} * V$$

3. Probability of Gastro-intestinal **Illness for Adults**

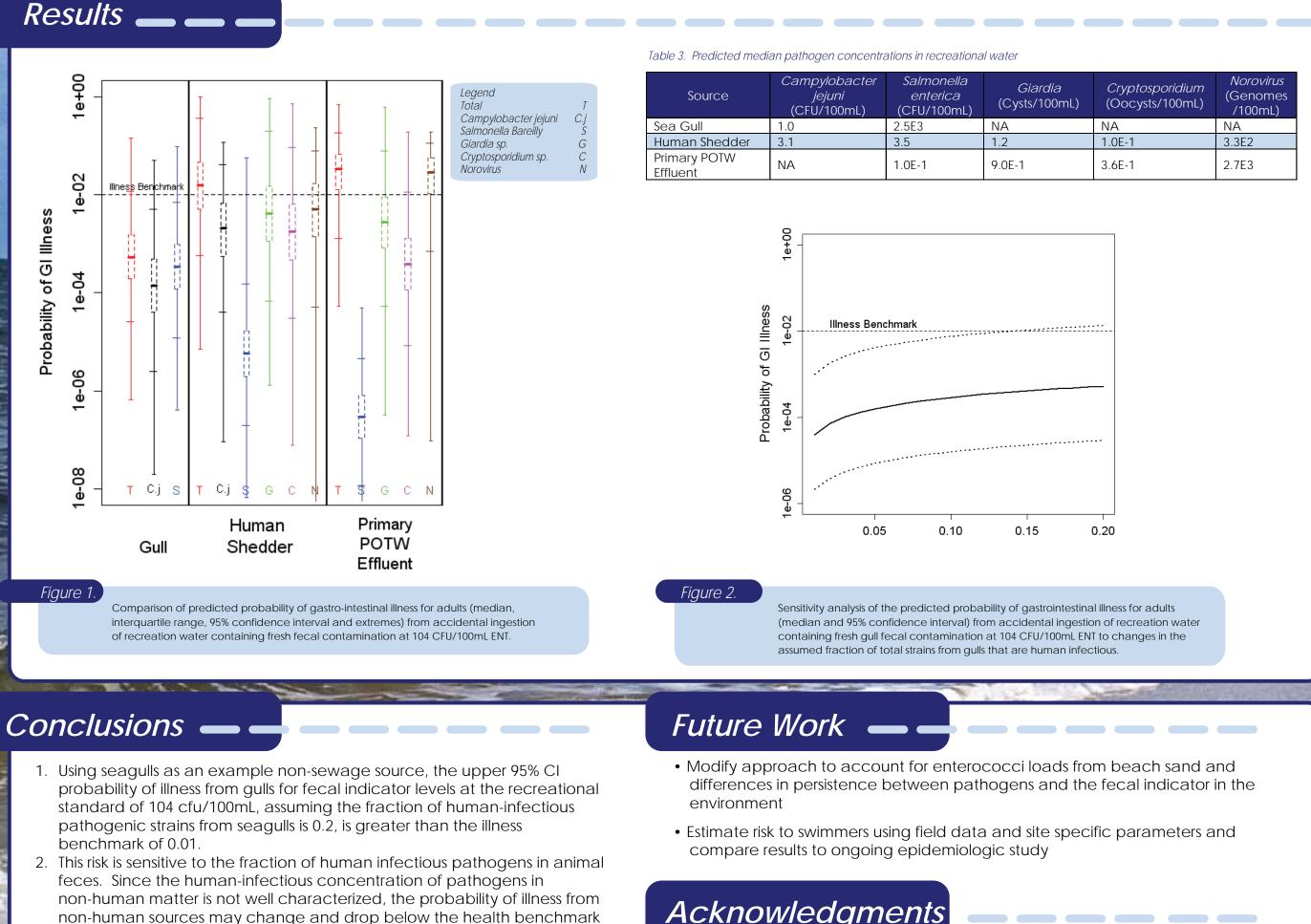


The probabilities of gastro-intestinal illness are calculated using dose-response relationships from the literature with best parameter estimates provided in Table 2.

Table 1. Parameters used of sewage (Sw), human s				dose from sources
Parameter	S	Units	Uniform Distribution	Reference

Parameter	S	Units	Uniform Distribution	Reference
Ratio ENT to source $(R^s_{\scriptscriptstyle ENT})$	Sw	cfu L-1	a = 1E7 $b = 1E8$	(Tschobanoglous et al., 2003)
	Н	cfu g ^{.1}	<i>a</i> = 2E3 <i>b</i> = 3E8	(Slanetz and Bartley, 1957)
	G	cfu g ^{₊1}	a = 1E6 $b = 1E8$	(Fogarty et al., 2003)
Ratio <i>C. jejuni</i> to source $(R_{C,j}^s)$	Н	cfu g ^{.1}	<i>a</i> = 1E6 <i>b</i> = 1E9	(Hindiyeh et al., 2000)
	G	cfu g∙¹	a = 2E3 $b = 1E6$	(Lévesque et al., 2000)
Ratio <i>Salmonella</i> to source (R_s^s)	Sw	cfu L-1	a = 3E0 $b = 1E3$	(Lemarchand, 2003)
	Н	cfu g ^{.1}	<i>a</i> = 1E6 <i>b</i> = 1E9	(Hindiyeh et al., 2000)
	G	cfu g ^{₊1}	a = 2E2 $b = 1E9$	(Lévesque et al., 2000)
Ratio <i>Cryptosporidium</i> to source (R_s^s)	Sw	oocysts L-1	$a = 5E - 1 b = 4E^2$	(Rose et al., 2004)
	Н	oocysts g ⁻¹	a = 1E4 $b = 8E8$	(Okhuysen et al., 1999)
Ratio <i>Giardia</i> to source (R_G^s)	Sw	cysts L-1	a = 7E0 $b = 1E4$	(Rose et al., 2004)
	Н	cysts g ⁻¹	a = 1E4 b = 8E8	(Gerba, 2000)
Ratio Norovirus to source (R_N^s)	Sw	genomes L-1	a = 9E2 $b = 3E7$	(Katayama et al., 2008)
	Н	genomes g ⁻¹	a = 1E7 $b = 1E10$	(Ludwig et al., 2008)
Infection rate of <i>C. jejuni</i> ($I^{s}_{C.j}$)	Н	NA	a = 0.0064 $b = .01$	(Orange County 2008)
Infection rate of Salmonella (I_s^s)	Н	NA	a = 0.0083 $b = .01$	(Orange County 2008)
Infection rate of Cryptosporidium (I_C^s)	Н	NA	a = 0.0003 $b = .000$	(Orange County 2008)
Infection rate of <i>Giardia</i> (I_G^s)	Н	NA	a = 0.0031 $b = .005$	(Orange County 2008)
Infection rate of <i>Norovirus</i> $(I_{\scriptscriptstyle N}^{\scriptscriptstyle S})$	Н	NA	<i>a</i> = 0.04 <i>b</i> = .16	(HMSO 2000)
Fraction of human-infectious	Sw	NA	1	NA
pathogen strains (p^{s})		NA	0.2	(Quessy and Messier, 1992)

Table 2. Parameter Inputs for Dose-Response							
Pathogen	Units	Dose-Response	Reference				
Campylobacter jejuni	cfu	Adult Beta-Poisson $P_{\text{inf}} = 1 - {}_{1}F_{1}(\alpha, \alpha + \beta, -\mu) = 1 - \sum_{n=0}^{\infty} \frac{(\alpha)_{n}}{(\alpha + \beta)_{n}} \frac{(-\mu)^{n}}{n!}$ $a = 0.145 B = 7.59 P_{\text{ill}\beta\text{inf}} = 0.2$	(Black et al., 1988)				
<i>Salmonella enterica</i> serotype Bareilly	cfu	Gompertz $P_{iii} = 1 - \exp(-\exp(-\ln(a) + b \ln(u)))$ $\ln(a) = 11.68$ $b = 0.82$	(Soller JA et al., 2007)				
Cryptosporidium parvum	oocysts	exponential $P_{\text{inf}} = 1 - e^{-E(r)\mu}$ $E(r) = 0.09$ $P_{\text{illfinf}} = 0.7$	(EPA 2005)				
Giardia intestinalis	cysts	exponential $P_{\text{inf}} = 1 - e^{-E(r)\mu}$ $E(r) = 0.0199$ $P_{\text{itlijnf}} = 0.9$	(Perz et al., 1998; Rose et al., 1991)				
Norovirus	genomes	$\begin{aligned} P_{\text{inf}} &= 1 - {}_{2}F_{1}(\alpha, \frac{\mu(1-a)}{a}, \alpha + \beta, -\frac{-a}{1-a}) \\ \alpha &= 0.04 a = 0.0001 \beta = 0.055 \\ P_{\text{iffinf}} &= 1 - (1+\eta\mu)^{-r} \\ \eta &= 2.55\text{E} - 3 r = -0.086 \end{aligned}$	(Teunis and Havelaar, 2000)				



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- with additional information on the content of animal feces.
- impacted water.

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3. Given the current high level of uncertainty in prediction probability of

infection using QMRA, no difference can be concluded between the risk from a sewage impacted water and that of an exclusively seagull

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