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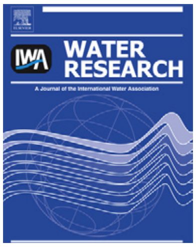

Evaluating the importance of faecal sources in human-impacted waters☆

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ABSTRACT

Quantitative microbial risk assessment (QMRA) was used to evaluate the relative contribution of faecal indicators and pathogens when a mixture of human sources impacts a recreational waterbody. The waterbody was assumed to be impacted with a mixture of secondary-treated disinfected municipal wastewater and untreated (or poorly treated) sewage, using *Norovirus* as the reference pathogen and enterococci as the reference faecal indicator. The contribution made by each source to the total waterbody volume, indicator density, pathogen density, and illness risk was estimated for a number of scenarios that accounted for pathogen and indicator inactivation based on the age of the effluent (source-to-receptor), possible sedimentation of microorganisms, and the addition of a non-pathogenic source of faecal indicators (such as old sediments or an animal population with low occurrence of human-infectious pathogens). The waterbody indicator density was held constant at 35 CFU 100 mL^{-1} enterococci to compare results across scenarios. For the combinations evaluated, either the untreated sewage or the non-pathogenic source of faecal indicators dominated the recreational waterbody enterococci density assuming a culture method. In contrast, indicator density assayed by qPCR, pathogen density, and bather gastrointestinal illness risks were largely dominated by secondary disinfected municipal wastewater, with untreated sewage being increasingly less important as the faecal indicator load increased from a non-pathogenic source. The results support the use of a calibrated qPCR total enterococci indicator, compared to a culture-based assay, to index infectious human enteric viruses released in treated human wastewater, and illustrate that the source contributing the majority of risk in a mixture may be overlooked when only assessing faecal indicators by a culture-based method.

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1. Introduction

Numerous epidemiology studies have generated evidence of adverse health outcomes attributed to swimming in municipal disinfected wastewater effluent-impacted waters, or what we will call here, human-impacted waters (Prüss, 1998; Wade et al., 2006; Zmirou et al., 2003). Other epidemiology studies have focused on bather risk from non-human sources of faecal contamination, and are summarized in reviews by Sinton et al. (1998) and updated by Soller et al. (2010b). In 2012, the U.S. Environmental Protection Agency (EPA) will issue new or revised recreational water quality criteria. Although the

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Nomenclature

S	source of the indicator (i.e. POTW, Raw, or Other) or the pathogen (i.e. POTW or Raw)
$D_w{}^p$	density of pathogen (*p*) in the waterbody (*w*)
$D_S{}^p$	density of pathogen (*p*) in a source (S)
V_s	volume of waste from a source (S)
$F_S{}^p$	fraction of pathogen (*p*) from a source (S) that sediments out of the waterbody
t_s	age of the waste from a source (S) when mixed into the waterbody
k_p	decay coefficient of the pathogen (*p*) in the waterbody
$D_w{}^I$	density of indicator (*I*) by culture method in the waterbody (*w*)
$D_S{}^I$	density of indicator (*I*) by culture method in a source (S)
$D_S{}^{qPCR}$	density of indicator (*I*) by qPCR method in a source (S)
V_F	volume of water in the waterbody
$F_S{}^I$	fraction of indicator (*I*) from a source (S) that sediments out of the waterbody
K^I	decay coefficient of the indicator (*I*) by culture method in the waterbody
K^{qPCR}	decay coefficient of the indicator (*I*) by qPCR method in the waterbody
L^I	load of indicator (*I*) from a non-pathogenic, environmental source (S)
$P_S{}^V$	percent of the total waterbody volume from a source (S)
$P_S{}^I$	percent of the total indicator (*I*) load from a source (S)
$P_S{}^p$	percent of the total pathogen (*p*) load from a source (S)
V_i	volume of waterbody ingested over duration of one swimming event
$u_w{}^p$	pathogen dose ingested over duration of one swimming event
$P(ill\|inf)$	conditional probability of illness given infection
$P_{inf}(\alpha,\beta,-u)$	dose-response function for pathogen (*p*) with parameters (α,β)
$P_{ill}{}^T$	total probability of illness
$P_{ill}{}^S$	probability of illness attributable to a source (S).

existing epidemiology studies are extremely valuable in this process, there are many faecal source mixtures unstudied, and indeed, some may not be possible to study through current epidemiology approaches.

In previous work, we used quantitative microbial risk assessment (QMRA) as a complement to the epidemiology evidence to further understand the potential risks from a variety of faecally contaminated waterbodies (Schoen and Ashbolt, 2010; Soller et al., 2010a,b; U.S. EPA, 2010). We presented a QMRA approach for predicting and comparing the potential probability of gastrointestinal (GI) illness from accidental ingestion of recreational water impacted by alternative sources of faecal contamination (Schoen and Ashbolt, 2010). Waterbodies impacted by seagull excreta and primary sewage effluent were compared at the same faecal indicator bacterial density with the result of a lower predicted illness risk from seagull-impacted waters. The same approach was extended to compare the relative risks from exposure to recreational waters impacted by direct contamination by gulls, chickens, pigs, and/or cattle and those associated with human-impacted waters (Soller et al., 2010b; U.S. EPA, 2010). The primary finding from this work was that the predicted illness risk associated with non-sewage impacted beaches was dependent on the source of contamination. Generally, the existing QMRA work has estimated GI risks for recreational water exposures from a single source of faecal contamination, with the exception of an illustrative example of a seagull and primary sewage impacted recreational beach presented in Schoen and Ashbolt (2010).

Here, we used QMRA to model mixtures of faecal contamination and compare different ways to interpret the mixture. Our attention was first on human-impacted waters because the existing epidemiology and QMRA studies provide estimates of GI risk. In previous work, we used QMRA to evaluate the etiological agents potentially responsible for the reported epidemiology results in human-impacted waters (Soller et al., 2010a). The results of that work indicated that human enteric viruses and in particular, *Norovirus* represented the vast majority of the observed swimming-associated GI illnesses in the human-impacted freshwaters studied. The epidemiology studies that supported the 1986 Ambient Water Quality Criteria (AWQC) (Cabelli et al., 1982; Dufour et al., 1984) probably resulted from a combination of both well treated, disinfected municipal wastewater and less well treated or untreated sewage contamination (directly from swimmers, poorly operating septic systems, sewage bypassing treatment etc.) (Soller et al., 2010a). Here we simulate possible mixtures of untreated (or poorly treated) sewage and secondary-treated disinfected municipal wastewater and then apply QMRA, using *Norovirus* as the reference pathogen, to estimate each source contribution to the total GI risk.

The main objective was to synthesize the various approaches commonly used to describe a mixture of two (or more) sources of faecal contamination. The least complicated way to describe a mixture is to report and compare the mass or volume of waste from each source. A second way to describe a mixture is to estimate the portion of the total indicator load from a source, such as in microbial source tracking (Wang et al., 2010). Rarely does a study attempt to determine the actual pathogen or risk contribution from each source in a mixture of sources. Hence, four approaches were used to describe mixtures: (a) the percent of the total waterbody volume from each source, (b) the percent of total faecal indicator load by traditional culture and rapid methods from each source, (c) the percent of the waterbody index pathogen load from each source, and (d) the probability of illness attributable to each source. All four measures are synthesized in the discussion to provide context for understanding mixtures of sources in human-impacted waters.