Coupling a continuous watershed-scale microbial fate and transport model with a stochastic dose-response model to estimate risk of illness in an urban watershed

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HIGHLIGHTS

- Compliance with numerical FIB criteria may be insufficient to protect public health.
- Climatic variations influence risk of illness.
- Improved estimation of human fecal sources is vital in watershed remediation plans.

GRAPHICAL ABSTRACT
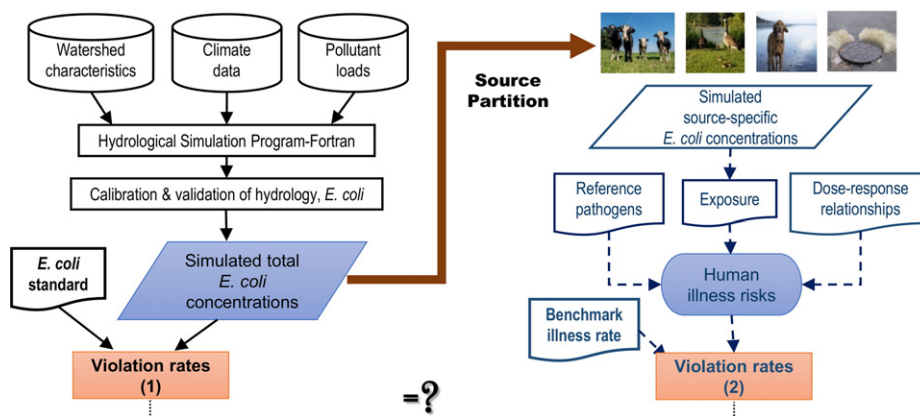
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ABSTRACT

Within the United States, elevated levels of fecal indicator bacteria (FIB) remain the leading cause of surface water-quality impairments requiring formal remediation plans under the federal Clean Water Act's Total Maximum Daily Load (TMDL) program. The sufficiency of compliance with numerical FIB criteria as the targeted endpoint of TMDL remediation plans may be questionable given poor correlations between FIB and pathogenic microorganisms and varying degrees of risk associated with exposure to different fecal pollution sources (e.g. human vs animal). The present study linked a watershed-scale FIB fate and transport model with a dose-response model to continuously predict human health risks via quantitative microbial risk assessment (QMRA), for comparison to regulatory benchmarks. This process permitted comparison of risks associated with different fecal pollution sources in an impaired urban watershed in order to identify remediation priorities. Results indicate that total human illness risks were consistently higher than the regulatory benchmark of 36 illnesses/1000 people for the study watershed, even when the predicted FIB levels were in compliance with the *Escherichia coli* geometric mean standard of 126 CFU/100 mL. Sanitary sewer overflows were associated with the greatest risk of illness. This is of particular concern, given increasing indications that sewer leakage is

ubiquitous in urban areas, yet not typically fully accounted for during TMDL development. Uncertainty analysis suggested the accuracy of risk estimates would be improved by more detailed knowledge of site-specific pathogen presence and densities. While previous applications of the QMRA process to impaired waterways have mostly focused on single storm events or hypothetical situations, the continuous modeling framework presented in this study could be integrated into long-term water quality management planning, especially the United States' TMDL program, providing greater clarity to watershed stakeholders and decision-makers.

1. Introduction

Pathogen contamination is the leading cause (14%) of surface water-quality impairments in the United States (USEPA, 2015). Identified water quality impairments are primarily addressed through the development of basin-specific Total Maximum Daily Load (TMDL) restoration plans in accordance with the 1972 Clean Water Act's sections 303(d) and 305(b) (USEPA, 2015). During the TMDL processes, elevated levels of fecal indicator bacteria ("FIB", e.g. *Escherichia coli* and enterococci) are used to assess potential human health risks based on the assumption that FIB behave similarly to pathogenic organisms with respect to incidence, fate, and transport in the environment (Yates, 2007). Although TMDL development requires extensive hydrodynamic modeling of FIB concentrations over time, it is important to note that only total (i.e. not source-specific) FIB concentration is predicted, and compliance with relevant numerical criteria remains the sole desired TMDL endpoint (e.g. minimal exceedance of a given concentration). The sufficiency of this goal has been questioned given several recent scientific research findings: 1) poor correlation between levels of FIB and actual human pathogens (Field and Samadpour, 2007; Wu et al., 2011; Harwood et al., 2014); 2) differences between patterns of contamination in inland and coastal waters, which renders the broad application of standards developed based on epidemiology studies at sewage-impacted coastal sites not universally appropriate (Wade et al., 2003; Dorevitch et al., 2010); and 3) substantial variation in risks associated with a given level of FIB exposure among sources (e.g. human vs. animal) (Schoen and Ashbolt, 2010; Soller et al., 2010; USPEA, 2010; Soller et al., 2014). Given that waterborne disease is estimated to be responsible for over 40,000 hospitalizations per year with a direct health-care cost of $970 million annually in the United States (Collier et al., 2012), it is critical to target remediation plans to directly minimize potential human health risks.

In response to these concerns, several recent studies have attempted to survey surface waters for human pathogens with relatively well established dose-response relationships in order to estimate human illness risks within a quantitative microbial risk assessment (QMRA) framework (McBride et al., 2013; Ishii et al., 2014; Sales-Ortells and Medema, 2014). QMRA is a mathematical strategy that links environmental exposure to illness risk via epidemiological relationships (Haas et al., 2014). Given the time and expense associated with direct pathogen monitoring, and the number of waters that require protection, USPEA (2010) has proposed a "reference pathogens" approach to QMRA: a set of eight reference pathogens (Norovirus, Rotavirus, Adenovirus, *Cryptosporidium* spp., *Giardia lamblia*, *Campylobacter* spp., *Salmonella* spp., and *E. coli* O157:H7) are considered representative of the fate and transport of waterborne pathogens of concern from particular sources of surface water fecal contamination. This strategy has been applied to investigations of gastrointestinal (GI) illness risks associated with recreational contact in a variety of waterbodies impacted by both human and animal sources (Schoen and Ashbolt, 2010; Soller et al., 2010; McBride et al., 2013; Soller et al., 2014). While useful in demonstrating the "reference pathogens" approach, in past cases these QMRA efforts were conducted mainly based on exposure during a limited period of time, i.e. there have been no attempts previously to apply this strategy over temporal or climatic changes. This is appropriate for short-term surface water management decisions (e.g. beach closures), but long-term watershed remediation efforts (e.g. TMDLs), generally consider compliance and risk over multiple years in conjunction with deterministic watershed-scale models to determine appropriate interventions and societal investments.

The aim of the present study was to quantitatively estimate human health risks associated with potential exposure to waterborne pathogens by coupling an existing watershed-scale model widely used in TMDL development with a stochastic dose-response model in order to identify potential discrepancies in FIB levels and GI illness risks. It was hypothesized that because risk has proven highly source-dependent in previous studies (Schoen and Ashbolt, 2010; Soller et al., 2010; USPEA, 2010), periods of high human health risks would likely not always coincide with periods of high FIB concentrations. Specific objectives were to: 1) estimate doses of human pathogens by source; 2) quantify source-specific and total human illness risks; and 3) compare violations of *E. coli*-based criteria and equivalent illness rate.

2. Methods

2.1. Study area

This study targets the 31-km^2 instrumented upper Stroubles Creek watershed within the Ridge and Valley ecoregion of Virginia, USA (Fig. 1), which has been described extensively in previous work (Thompson et al., 2012; Liao et al., 2014; Liao et al., 2015a; Liao et al., 2015b). The Town of Blacksburg, which encompasses the majority of the residential area within the watershed, is served by separate storm and sanitary sewer systems. An 11-km segment of Stroubles Creek is currently included on the 303(d) list of impaired waters (VADEQ, 2015a) due to violations of Virginia's *E. coli* standard (SWCB, 2010). Potential pollutant sources of concern include discharges from municipal separate storm sewer systems (MS4), pet waste, livestock (grazing or feeding operations), wet weather discharges, wildlife, and other unspecified domestic waste (VADEQ, 2015a).

2.2. Modeling source-specific E. coli concentrations

The Hydrologic Simulation Program – Fortran (HSPF, version 12.2) was used to predict in-stream *E. coli* concentrations. This is a continuous, deterministic, lumped-parameter, watershed-scale model that is currently recommended for TDML development by the USEPA (Bicknell et al., 2005; Benham et al., 2006). Hydrologic and microbial water quality calibration and validation of the HSPF model for the Stroubles Creek watershed is provided in Supplementary Data (Appendix A) and further detailed in Liao et al. (2015b). The daily in-stream *E. coli* concentrations at the outlet of the upper Stroubles Creek watershed for the entire period of 1/1/2010–12/31/2014 were simulated via the previously calibrated and validated HSPF model, which facilitated the subsequent analysis in this study. The overall daily in-stream *E. coli* concentrations were partitioned into four major pollutant sources: wild waterfowl (duck and geese), livestock (cattle), pets (dog), and human (failing septic systems and sanitary sewer overflows). Major pollutant watershed sources of concern were selected based on presence in this watershed and the availability of literature data for subsequent risk calculations. Other potential sources (e.g. raccoons, muskrats, deer, and swine) were assumed to have negligible