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Using SWAT, *Bacteroidales* microbial source tracking markers, and fecal indicator bacteria to predict waterborne pathogen occurrence in an agricultural watershed

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ABSTRACT

Developing the capability to predict pathogens in surface water is important for reducing the risk that such organisms pose to human health. In this study, three primary data source scenarios (measured stream flow and water quality, modelled stream flow and water quality, and host-associated *Bacteroidales*) are investigated within a Classification and Regression Tree Analysis (CART) framework for classifying pathogen (*Escherichia coli* 0157:H7, *Salmonella*, *Campylobacter*, *Cryptosporidium*, and *Giardia*) presence and absence (P/A) for a 178 km^2 agricultural watershed. To provide modelled data, a Soil Water Assessment Tool (SWAT) model was developed to predict stream flow, total suspended solids (TSS), total N and total P, and fecal indicator bacteria loads; however, the model was only successful for flow and total N and total P simulations, and did not accurately simulate TSS and indicator bacteria transport. Also, the SWAT model was not sensitive to an observed reduction in the cattle population within the watershed that may have resulted in significant reduction in *E. coli* concentrations and *Salmonella* detections. Results show that when combined with air temperature and precipitation, SWAT modelled stream flow and total P concentrations were useful for classifying pathogen P/A using CART methodology. From a suite of host-associated *Bacteroidales* markers used as independent variables in CART analysis, the ruminant marker was found to be the best initial classifier of pathogen P/A. Of

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the measured sources of independent variables, air temperature, precipitation, stream flow, and total P were found to be the most important variables for classifying pathogen P/A. Results indicate a close relationship between cattle pollution and pathogen occurrence in this watershed, and an especially strong link between the cattle population and *Salmonella* detections.

1. Introduction

Waterborne pathogens can originate from a variety of point and/or diffuse agricultural, human, and/or wildlife sources in a watershed (Ferguson et al., 2003; Atwill et al., 2012). The risk that these microorganisms pose to human health is an impetus to rapidly increase our understanding of their potential sources, transport mechanisms, and environmental factors governing life cycles. However, even with recent accomplishments, there is still a poor capacity to predict and model the occurrence of these pathogens at policy relevant scales, such as watersheds (Pachepsky et al., 2006; Ferguson et al., 2009).

For simulating watershed scale hydrology, nutrient transport, and suspended sediment movement, spatially distributed deterministic models such as the Soil and Water Assessment Tool (SWAT) are frequently employed, and for such tasks the models generally perform quite well (Moriasi et al., 2007). However, simulating watershed scale fecal indicator bacteria and/or pathogen fate and transport with deterministic methods is highly complex and has so far met with limited success (Benham et al., 2006; Baffaut and Sadeghi, 2010; Cho et al., 2012). The complexity associated with simulating the fate and transport of microorganisms stems from a number of factors, including: complex and variable microorganism life cycles, scarcity of long term datasets required to calibrate and validate such simulations, difficulties characterizing the bacteria spatial and temporal loading patterns, and high levels of uncertainty in modelling inputs and outputs (Benham et al., 2006; Pachepsky et al., 2006; Oliver et al., 2009; Baffaut and Sadeghi, 2010; Bougeard et al., 2011).

As an emerging methodology to identify and target sources of waterborne bacteria and pathogens, microbial source tracking (MST) methods show great promise (Walters et al., 2007; Schriewer et al., 2010; Tambalo et al., 2012; Wilkes et al., 2013). When used in conjunction with spatially distributed watershed models, MST has the potential to bolster our capability to predict pathogen risk in surface water and to identify weaknesses in the underlying modelling mechanisms (Dorner et al., 2006; Parajuli et al., 2009a). However, because of difficulties relating MST markers and fecal indicator bacteria to pathogen occurrence (Jokinen et al., 2012; Marti et al., 2013), there are conceptual challenges to address before spatially distributed watershed models can be routinely incorporated with MST investigations.

Recognizing the strong potential of watershed scale modelling and MST to assist with waterborne pathogen prediction, this study employs the SWAT model in conjunction with a multi-year surface water quality dataset that includes, fecal indicator bacteria, pathogens, and host-associated *Bacteroidales* data, to predict the occurrence and densities of zoonotic pathogens and fecal indicator bacteria in surface waters of an agriculturally dominated watershed. As part of this study, the influence that land use changes have on measured and modelled fecal indicator bacteria levels in surface waters, is investigated. The results elucidate the relative value of MST, fecal indicator bacteria, and observed and modelled water quality data for predicting human health risks associated with fecal contamination of surface water.

2. Methods and materials

2.1. Study area

This study focuses on the 178 km^2 Payne River watershed within the South Nation River basin in eastern Ontario, Canada (Fig. 1). The watershed has an average slope of approximately 2%. Annual precipitation over the 2004–2011 study period ranged from 654 to 1240 mm. Primary land uses are agriculture (58%); forest (39%); and urban (2%), with an estimated population of approximately 2000 people. Fecal pollution sources include livestock manure derived from manure application and grazing, wildlife feces, and failing septic systems (Ruecker et al., 2007; Marti et al., 2013). There are no sewage treatment facilities within the watershed. In 2006 there were an estimated 4805 head of cattle in the watershed, of which approximately 1946 were dairy cattle, and 971 are estimated to be pastured for part of the year (Statistics Canada, 2006). Although there are no large scale swine producers within the watershed, a limited number of swine may be present at any given time on small mixed farming operations, and swine manure from off-watershed sources may be applied on fields in the study area from time to time.

2.2. Data collection

Daily stream flow for the study period was obtained from the Environment Canada hydrometric gauging station located as shown in Fig. 1. Meteorological (MET) data (precipitation, temperature, humidity, solar radiation, and wind speed) were primarily obtained from a weather station located 4.5 km from the watershed. In instances where the primary MET data was errant or missing, data was sourced from weather stations either 16.5 km or 50 km from the watershed. Quantitative water quality parameters (total N, total P, fecal coliform, and *Escherichia coli*) and pathogen (*E. coli* 0157:H7, *Salmonella*, *Campylobacter*, *Cryptosporidium* (oocysts) and *Giardia* (cysts)) presence/absence (P/A) were monitored on a spring – fall