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Linking watershed modeling and bacterial source tracking to better assess *E. coli* sources

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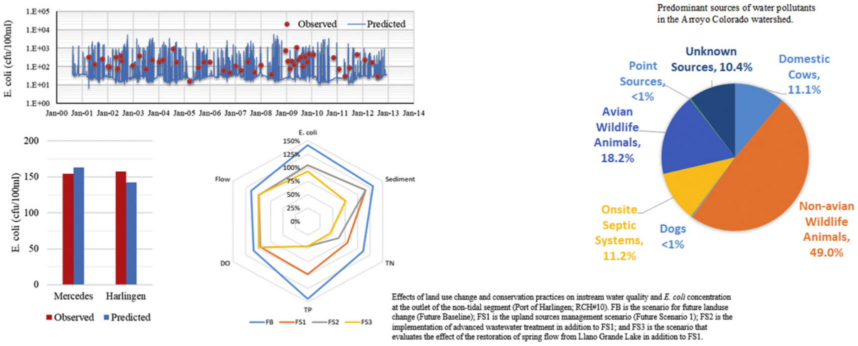
HIGHLIGHTS

- Diffuse sources of *E. coli* identified by a BST assessment were successfully incorporated into SWAT for a watershed scale assessment.
- SWAT was implemented to identify critical source areas of *E. coli* in mixed land uses in south Texas.
- Wildlife contribution is the major source of *E. coli* in streamflow and may remain to be significant after land use change with urbanization.
- A combined effort that implements land managements and advanced treatment is needed to restore water quality for recreational and aquatic life uses.

GRAPHICAL ABSTRACT



Predominant sources of water pollutants in the Arroyo Colorado watershed.

Effects of land use change and conservation practices on instream water quality and *E. coli* concentration at the outlet of the non-tidal segment (Port of Harlingen; RCH#10). FB is the scenario for future landuse change (Future Baseline); FS1 is the upland sources management scenario (Future Scenario 1); FS2 is the implementation of advanced wastewater treatment in addition to FS1; and FS3 is the scenario that evaluates the effect of the restoration of spring flow from Llano Grande Lake in addition to FS1.

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ABSTRACT

Terrestrial fate and transport processes of *E. coli* can be complicated by human activities like urbanization or livestock grazing. There is a critical need to address contributing sources of bacterial contamination, properly assess the management of critical sources, and ultimately reduce *E. coli* concentrations in impaired water bodies. In particular, characterization of wildlife animal contributions and other “background” input sources of microbial pollution are highly uncertain and data are scarce. This study attempts to identify critical sources of *E. coli* and the efficacy of conservation practices for mitigating *E. coli* concentrations in the Arroyo Colorado watershed, Texas, using a process-based hydrologic and water quality model. We propose to incorporate a bacterial source tracking assessment into the modeling framework to fill the gap in data on wildlife and human contribution. In addition, other sources identified through a GIS survey, national census, and local expert knowledge were incorporated into the model as *E. coli* sources. Results suggest that simulated distribution of *E. coli* sources significantly improved after incorporating this enhanced data on *E. coli* sources into the model ($R^2 = 0.90$) compared to the SWAT result without BST ($R^2 = 0.59$). Scenario assessments indicate that wildlife contributions may remain significant despite land use change and urbanization, expected to mostly occur in agricultural and range lands. A combination of nonpoint source management measures, voluntary implementation of advanced treatment by wastewater plants where possible, and installation of aerators in the zone of impairment were demonstrated to be effective measures for restoring the recreation and aquatic life uses of the Arroyo Colorado.

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1. Introduction

Urban and rural streams are increasingly contaminated with pathogenic bacteria. The Texas Commission on Environmental Quality (TCEQ, 2014) has found that over 67% of the streams on the 303(d) list are impaired by pathogenic bacteria, encompassing 27% of all stream segments in the state. Contamination of water by pathogenic organisms sourced to fecal waste is a major environmental concern (USFDA, 1995). Similar to water pollution by excess nutrients, water pollution by microbial pathogens can be caused by point and nonpoint sources (Dadswell, 1993; Garcia-Armisen and Servais, 2007; Jiang et al., 2007).

Fecal Indicator Bacteria (FIB) are used as a proxy for pathogenic bacteria and are, therefore, used to evaluate the ability of a water body to support contact recreation uses. In freshwater, *E. coli* (*Escherichia coli*) is commonly used while enterococcus is typically used in tidal waters. Elevated concentrations of pathogenic bacteria signify an increased risk of contracting a gastrointestinal illness for those recreating in the water body (Neal et al., 1997). Point source fecal contamination of water normally results from direct entry of wastewater from a municipal treatment plant into a water body. It is difficult to identify nonpoint FIB sources, which can originate from animal production, land application of manure, humans through failing on-site sewage facilities (OSSF), or wildlife (Harmel et al., 2010; Garcia-Armisen and Servais, 2007; Parajuli et al., 2009; Pandey et al., 2012). Watersheds highly populated with humans, livestock, and wildlife are prone to water quality impairment due to high FIB concentrations. Terrestrial fate and transport processes and source loads of FIB can be complicated by human activities like urbanization or livestock grazing.

Large quantities of FIB in stormwater runoff are perceived to be one of the most pressing issues in urban watersheds (Hardy and Koontz, 2010). Levels of FIB in stormwater can far exceed recreational water quality guidelines, often by several orders of magnitude, as stormwater picks up and transports a variety of chemicals and human and animal fecal wastes (Parker et al., 2010). OSSFs are designed to treat domestic wastewater using a septic tank for screening and pretreatment and a drain field where pretreated septic effluent is distributed for soil infiltration and final treatment by naturally existing microorganisms (Jeong et al., 2011). Poor installation or maintenance may cause OSSF failure, resulting in release of nutrients and pathogens into nearby water bodies (Ahmed et al., 2005; Siegrist et al., 2005).

Grazing animals and wildlife can also negatively affect the quality of runoff and waterbodies with FIB contamination. The high concentration of FIB in waterbodies increase the risk of infection for people who use the water for drinking or various contact recreation purposes (Hubbard et al., 2004). Although it is well understood that high levels of livestock grazing can negatively impact stream water quality with elevated FIB concentrations (Gary et al., 1983), detailed data on the fate and transport of manure-borne FIB in soils, runoff, and streams remain insufficient (Jamieson et al., 2004; Harmel et al., 2010; Harmel et al., 2013). High populations of animals in preserved wildlife habitats may contribute to high FIB concentrations in streams (Stuart et al., 1971). Weiskel et al. (1996) found that waterfowl contributed 67% of the total annual loading of FIB along the east coast of the U.S. In Texas, non-avian wildlife, such as deer or feral hogs, are commonly found to be significant contributors of FIB to natural streams (Wagner and Moench, 2009).

Process-based hydrologic/water quality models have advantages of simulating environmental outcomes in response to specific management practices (Jones et al., 2009; Guo et al., 2018a). Two commonly used models for FIB modeling are the Soil and Water Assessment Tool (SWAT) (Arnold et al., 1995) and Hydrological Simulation Program—Fortran (HSPF) (Bicknell et al., 1996). Paul et al. (2004) found in a HSPF study that simulated instream fecal coliform concentrations were most sensitive to the first-order decay coefficient in Salado Creek, implying that accurate simulation of FIB's fate and transport in the channels can be significant at the watershed scale. SWAT has an advantage of explicitly partitioning microorganisms into adsorbed and non-adsorbed forms within a spatially explicit GIS framework over other process-based models so that FIB transport processes are explicitly simulated between water-bound and sediment-bound forms (Jones et al., 2009).

Bacterial source tracking (BST) techniques can be useful in identifying FIB sources (Petersen et al., 2005). BST determines the sources of FIB in environmental samples using DNA fingerprints or other phenotyping methods. FIB monitoring data, which are often scarce in quantity, have been complemented by BST assessment (Baffaut and Benson, 2003; Parajuli et al., 2009). BST can provide a groundtruth of the overall contribution of FIB sources to FIB loads at a stream outlet or an estuary; thus, it is expected to help improve watershed-scale FIB analysis and estimates.

There is a critical need to address contributing sources of bacterial contamination of water, properly assess the management of critical sources, and ultimately reduce FIB concentrations in impaired water bodies. Major gaps in knowledge exist in identifying bacterial sources. In particular, characterization of wildlife contributions and other “background” input sources of microbial pollution are highly uncertain (Jamieson et al., 2004). Historically, bacteria models have performed poorly because wildlife is typically underrepresented due to lack of data (e.g., Parajuli et al., 2009; Coffey et al., 2013). In this paper, we attempt to overcome this by incorporating BST results (Casarez and Di Giovanni, 2015) and edge-of-field monitoring data collected in Texas from cropland (Harmel et al., 2013) and urban settings (Jones et al., 2016) into the model. In this study, we attempt to overcome the knowledge gap in identifying sources of FIB for watershed simulation using BST and evaluate if conservation practices can be effective to control FIB loads to streams.

The main goal of this study is to develop a SWAT model to identify significant sources of bacterial contamination and evaluate possible benefits of conservation practice implementation on urban, agricultural, rangelands, and wildlife land uses. Specific objectives are to: 1) identify and quantify significant sources of *E. coli* using GIS, BST, and edge-of-field monitoring results, 2) evaluate a watershed model for *E. coli* concentration and other water quality variables, 3) evaluate the effects of land use changes and conservation practices on the transport of *E. coli*, sediment, and nutrients in the Arroyo Colorado watershed, Texas.

2. Methods and materials

2.1. Description of the SWAT bacteria model

The SWAT model is a watershed-scale, physically-based, continuous simulation model (Arnold et al., 1995). SWAT includes explicit simulation of various terrestrial and instream processes, including agricultural management practices (Christopher et al., 2017; Scavia et al., 2017), plant growth (Guo et al., 2015; Wang et al., 2017; Feng et al., 2017), urban processes (Jeong et al., 2012; Her et al., 2017c), water impoundments (Bosch, 2008), and evaluation of various conservation practices, on water quantity and quality (Cibin et al., 2012; Montgomery et al., 2014; Keitzer et al., 2016). Using a daily time step, SWAT can complete long-term simulations of rainfall-runoff (Wang et al., 2014), soil erosion and nutrient and chemical transport (Niraula et al., 2011; Guo et al., 2018b), algal growth (Millican et al., 2008), and bacteria loads (Sadeghi and Arnold, 2002). The bacteria submodel of SWAT has been extensively tested and validated. Baffaut and Sadeghi (2010) found SWAT reasonably simulated bacteria transport with (Nash-Sutcliffe efficiency) NSE values varying between −6.0 and 0.73 in eight watersheds in the U.S. and France. Kim et al. (2017) suggest that implementing *E. coli* resuspension from sediment improves model performance in their tropical mountain watershed, but the original SWAT model does not simulate *E. coli* during dry seasons.

SWAT incorporates GIS to partition a watershed into multiple subbasins based on the formation of stream networks. Hydrologic and water