



Pathogen transport and fate modeling in the Upper Salem River Watershed using SWAT model



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ABSTRACT

Simulation of the fate and transport of pathogen contamination was conducted with SWAT for the Upper Salem River Watershed, located in Salem County, New Jersey. This watershed is 37 km² and land uses are predominantly agricultural. The watershed drains to a 32 km stretch of the Salem River upstream of the head of tide. This stretch is identified on the 303(d) list as impaired for pathogens. The overall goal of this research was to use SWAT as a tool to help to better understand how two pathogen indicators (*Escherichia coli* and fecal coliform) are transported throughout the watershed, by determining the model parameters that control the fate and transport of these two indicator species. This effort was the first watershed modeling attempt with SWAT to successfully simulate *E. coli* and fecal coliform simultaneously. Sensitivity analysis has been performed for flow as well as fecal coliform and *E. coli*. Hydrologic calibration at six sampling locations indicate that the model provides a “good” prediction of watershed outlet flow ($E = 0.69$) while at certain upstream calibration locations predictions are less representative ($0.32 < E < 0.70$). Monthly calibration and validation of the pathogen transport and fate model was conducted for both fecal coliform ($0.07 < E < 0.47$ and $-0.94 < E < 0.33$) and *E. coli* ($0.03 < E < 0.39$ and $-0.81 < E < 0.31$) for the six sampling points. The fit of the model compared favorably with many similar pathogen modeling efforts. The research contributes new knowledge in *E. coli* and fecal coliform modeling and will help increase the understanding of sensitivity analysis and pathogen modeling with SWAT at the watershed scale.

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1. Introduction

Pathogens are a small subset of microorganisms. Pathogens are most frequently determined and associated with waterborne diseases that can be classified into the three general groups: viruses, protozoans, and bacteria. Pathogen pollution is a serious concern for water resources managers because pathogens can harm human health through contaminated fish and shellfish, skin contact or ingestion of water. In case of entrance to the human body they can cause sickness or even death. Identification of pathogenic organisms in polluted waters is complicated because they are few and highly varied. Thus, health officials generally prefer to monitor nonpathogenic bacteria that are usually associated with pathogens transmitted by fecal contamination but are more easily sampled

and measured (USEPA, 2001). These associated pathogens known as indicator organisms should be easily detected using simple laboratory tests, generally hard to find in unpolluted waters, appear in concentrations that can be correlated with the extent of contamination and have a die-off rate that is not faster than the die-off rate for the pathogens of concern (Thomann and Mueller, 1987). Two commonly used indicator organisms are fecal coliforms and *Escherichia coli* (*Escherichia coli*) (McMurry et al., 1998).

Under section 303(d) of the US Clean Water Act, states, territories and authorized tribes are required to develop lists of rivers, lakes and estuaries that don't meet water quality standards or “impaired”. One third of the length of all impaired streams and rivers in the U.S. are classified as such due to pathogen contamination (USEPA, 2011). The Upper Salem River Watershed (USRW) in Salem County, New Jersey is identified as impaired by pathogens. In order to fulfill state water quality standards, a Total Maximum Daily Load (TMDL) was promulgated for the USRW that requires an 84% reduction of pathogen loads in the USRW (NJDEP, 2003).

At present, there are two methods for tracking pathogen

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pollution in a river system and assessing the effectiveness of the TMDL process in improving water quality of the pathogen impaired waters: field monitoring and mathematical simulation (Shirmohammadi et al., 2006). Field monitoring is the more suitable method to assess TMDL development, but its use is limited because of higher costs and extreme spatial and temporal river variability (Pachepsky et al., 2006). As an alternative to field monitoring, mathematical models can save time, minimize costs, and forecast future conditions of the river under altered management scenarios (Shirmohammadi et al., 2006).

A number of watershed scale models were applied to simulate pathogen for different purposes in the last three decades. Hydrologic Simulation Program FORTRAN (HSPF) model is a widely used model for pathogen fate and transport. Hevesi et al. (2011) applied HSPF to simulate the transport of a pathogen indicator, and evaluate the flow-component and land use contributions to pathogen contamination in the Chino Basin in California. Moyer and Hyer (2003) utilized an HSPF model and pathogen source tracking technique for developing the TMDL for Christians Creek. Loading Simulation Program in C++ (LSPC) is a widely used watershed scale model that was applied by the South Carolina Department of Health and Environment Control (2003) to model fecal coliform contamination in the Twelve Mile Creek watershed. MWASTE was developed by Moore et al. (1989) and is a continuous lumped model that uses Chick's Law to model die-off for both stored and applied waste. The model was intended to simulate waste generation and pathogen concentration in surface runoff from agricultural areas.

Coffey et al. (2007) reviewed 13 quantitative simulation models that could potentially be used for simulating pathogen pollutants in agricultural watersheds. The models were assessed in four main categories: model type, inputs, outputs and functionality. Among the 13 models, the Soil and Water Assessment Tool (SWAT) was ranked first.

SWAT has the capability to simulate fate and transport of pathogens as two different populations: less-persistent pathogens (e.g., FCs) and persistent pathogens (e.g., *E. coli*). The persistent pathogens are characterized by lesser die-off rates whereas the less persistent pathogens have greater die-off rates in the natural environment (Jamieson et al., 2004). This discrepancy in die-off rates leads to the observation of a higher quantity of persistent pathogens in the natural environment compared to pathogens of less persistence (Sadeghi and Arnold, 2002).

Researchers have simulated either FC or *E. coli* as pathogen indicators with the SWAT model in several watersheds in the U.S. (Parajuli et al., 2006, 2009; Chin et al., 2009; Baffaut et al., 2009, 2010), France (Bougeard et al., 2008; Baffaut et al., 2010) and Ireland (Coffey et al., 2010), but no study has been attempted to simulate both indicators and compare them at the watershed scale.

The primary objective of this research was to use SWAT as a tool to help to better understand how two pathogen indicators (*E. coli* and fecal coliform) are transported throughout the watershed, by determining the model parameters that control the fate and transport of these two indicator species.

2. Materials and methods

SWAT is a watershed-scale, distributed, continuous time scale hydrologic model that simulates water, sediment and contaminant flow at daily or hourly time steps. It was developed to predict the effects of water use, sediment, and agricultural chemical yields (Neitsch et al., 2011). The model has nine major components: weather, hydrology, soil characteristics, sediments, plant growth, nutrients, pesticides, pathogens, and land management. The model divides a watershed into several sub-basins, which are then further subdivided into hydrologic response units (HRUs) that consist of

homogenous land use, soil and slope characteristics. The model utilizes an ArcGIS interface for the definition of watershed hydrologic features, which is overlaid by the organization and management of the related spatial and tabular data (Bonham et al., 2006; Neitsch et al., 2011).

In SWAT, hydrology has a major role in fate and transport of any pollutants including pathogens. Surface runoff, evapotranspiration, recharge, and stream flow form all the components of SWAT hydrology. Surface runoff volume and infiltration are computed with the curve number equations or the Green and Ampt method. To calculate the watershed time of concentration and channel flow, SWAT uses Manning's equation (Arnold et al., 1993). Lateral subsurface flow can occur in the soil profile from 0 to 2 m, the groundwater flow contribution to total stream flow is generated by simulating shallow aquifer storage, and flow from the aquifer to the stream is lagged via a recession constant derived from daily streamflow records (Green and Van Griensven, 2007).

2.1. Pathogen model

The SWAT model pathogen simulation component in surface water at the watershed scale was developed by Sadeghi and Arnold (2002). This component has the capability of simulating pathogens for two different populations: non-persistent microorganisms such as FCs and persistent microorganisms such as *E. coli*. In the model, the only difference between these two populations is the die-off rate with the less-persistent population characterized by the more rapid die-off rate. However, the initial quantity of the less-persistent population is usually considered greater than the persistent population (Coffey et al., 2010).

In SWAT, mass balance theory is used to govern pathogen transport and fate processes. These processes comprise: pathogen loading to surface soil layer (manure application and animal waste deposition), pathogen wash-off, pathogen percolation, pathogen decay, pathogen incorporation through tillage, pathogen transport in-stream, pathogen surface run-off, pathogen settling, and pathogen re-suspension. These processes occur in two sub-systems: surface soil layer, soil subsurface top 10 mm, and instream (Baffaut et al., 2010; Neitsch et al., 2011). Equation (1) defines the mass balance theory in change of pathogen loading in the surface soil layer sub-system:

$$\Delta_{\text{surface-pat}} = \text{Pat}_{\text{loading}} + \text{Pat}_{\text{washoff}} - \text{Pat}_{\text{Decay}} - \text{Pat}_{\text{runoff}} - \text{Pat}_{\text{percolation}} - \text{Pat}_{\text{tillage}} \quad (1)$$

where $\Delta_{\text{surface-pat}}$ is the change of pathogen loading in the surface soil layer on a given day; $\text{Pat}_{\text{loading}}$ is the total pathogen loading to the soil layer on a given day; $\text{Pat}_{\text{washoff}}$ is the portion of pathogen on plant foliage washed off during rain event on a given day; $\text{Pat}_{\text{Decay}}$ is the amount of pathogen that decayed on a given day; $\text{Pat}_{\text{runoff}}$ is the amount of pathogen transported by the runoff on a given day; $\text{Pat}_{\text{percolation}}$ is the amount of pathogen transported through percolation into the soil profile on a given day; $\text{Pat}_{\text{tillage}}$ is the amount of pathogen transported through tillage into the soil profile on a given day.

In the instream sub-system, the pathogen mass balance is presented in Equation (2):

$$\Delta_{\text{stream-pat}} = \text{Pat}_{\text{flow-in}} + \text{Pat}_{\text{runoff}} + \text{Pat}_{\text{direct-inputs}} + \text{Pat}_{\text{re-suspension}} - \text{Pat}_{\text{sediment}} - \text{Pat}_{\text{decay}} - \text{Pat}_{\text{flow-out}} \quad (2)$$

where $\Delta_{\text{stream-pat}}$ is the change of pathogen loading in a stream reach on a given day; $\text{Pat}_{\text{flow-in}}$ is the initial amount of pathogen on

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