



Source specific fecal bacteria modeling using soil and water assessment tool model

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ABSTRACT

Fecal bacteria can contaminate water and result in illness or death. It is often difficult to accurately determine sources of fecal bacteria contamination, but bacteria source tracking can help identify non-point sources of fecal bacteria such as livestock, humans and wildlife. The Soil and Water Assessment Tool (SWAT) microbial sub-model 2005 was used to evaluate source-specific fecal bacteria using three years (2004–2006) of observed modified deterministic probability of bacteria source tracking data, as well as measure hydrologic and water quality data.

This study modeled source-specific bacteria using a model previously calibrated for flow, sediment and total fecal coliform bacteria (FCB) concentration. The SWAT model was calibrated at the Rock Creek sub-watershed, validated at the Deer Creek sub-watershed, and verified at the Auburn sub-watershed and then at the entire Upper Wakarusa watershed for predicting daily flow, sediment, nutrients, total fecal bacteria, and source-specific fecal bacteria. Watershed characteristics for livestock, humans, and wildlife fecal bacterial sources were first modeled together then with three separate sources and combinations of source-specific FCB concentration: livestock and human, livestock and wildlife and human and wildlife. Model results indicated both coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E) parameters ranging from 0.52 to 0.84 for daily flow and 0.50–0.87 for sediment (good to very good agreement); 0.14–0.85 for total phosphorus (poor to very good agreement); –3.55 to 0.79 for total nitrogen (unsatisfactory to very good agreement) and –2.2 to 0.52 for total fecal bacteria (unsatisfactory to good agreement). Model results generally determined decreased agreement for each single source of bacteria (R^2 and E range from –5.03 to 0.39), potentially due to bacteria source tracking (BST) uncertainty and spatial variability. This study contributes to new knowledge in bacteria modeling and will help further understanding of uncertainty that exists in source-specific bacteria modeling.

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1. Introduction

Water quality deterioration associated with non-point source (NPS) pollution has been a great concern for several decades. About 65,000 types of impairments have been reported by the US Environmental Protection Agency (USEPA) as violating different water quality standards such as drinking, swimming and fishing (USEPA, 2006). After mercury, the top three common causes of waterbody impairments are pathogens, sediment and nutrients, representing 13.2%, 10.59% and 8.76% of total listed impaired waterbody segments, respectively (USEPA, 2006). These water quality constituents are responsible for about 21,000 impaired waters. A total of 8522 stream segments have been reported with bacteria impairments, each requiring development and implementation of a TMDL to meet the water quality standard for bacteria in their respective states (USEPA, 2005a). The TMDL program is a watershed management process that inte-

grates watershed planning and remediation with water quality assessment and protection and is mandated by the Clean Water Act (Benham et al., 2006). Hydrologic and water quality models are often used to identify and quantify pollutant sources to develop TMDL. Water quality models help to assess watershed and water bodies to identify the level of impairment and then prioritized for water quality improvement through implementation of best management practices (BMPs).

Often, the source of fecal bacteria contamination in water cannot be determined by standard laboratory analytical methods. Non-point sources, such as livestock, humans and wildlife are possible sources of fecal bacteria contamination. To adequately assess human health risks and develop watershed management plans, it is necessary to know the sources of fecal bacteria contamination. Bacteria source tracking (BST) can identify bacteria source and BST methods are effective determining origins of fecal bacteria contamination of water bodies (Hagedorn et al., 1999). They can also be used to identify the BMPs needed to reduce fecal coliform loading and evaluate the effectiveness of various BMPs. Bacteria models could be useful tools for evaluating watersheds. However,

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no studies have been published using BST data in conjunction with a watershed model to calibrate the model or test model results due to limited data available.

Fecal pathogen contamination of surface waters can result in illness and death and accounts for a majority of the assessed water quality impairments in the United States (USEPA, 2005b). Curriero et al. (2001) found that more than half of the waterborne disease outbreaks in the United States during the past 50 years were preceded by heavy rainfall. Fecal bacteria in surface waters indicates the potential to cause severe illnesses such as typhoid fever, hepatitis, cholera, dermatitis and leptospirosis (Craun and Frost, 2002), globally. Large quantities of FCB can be deposited with manure from heavy grazing, effluent disposal due to failing septic systems, direct deposition of manure in stream or near the stream due to livestock access to the stream, or wildlife. The risk associated with surface water contamination by manure is, in part, a function of manure volume, site topography, hydrology, and proximity to surface waters. This risk can be offset by low rainfall, dryness, minimal land slope, relative isolation of the animal population, and manure application methods. People living in rural non-farm residences depend almost exclusively on individual on-site systems, and on-site system densities also can be quite high in urban developing areas (Pradhan et al., 2004). In the United States, 25% of the total housing units and 33% of all new development use on-site systems (USEPA, 2005b), and the number of on-site systems is increasing every year.

Watershed-based bacteria models could be used to evaluate fecal bacteria sources. Parajuli et al. (2006) calibrated and validated the SWAT 2005 model, but they recommended that the model still needed to be verified for longer periods of time, different landuse distributions and different watershed sizes and using source-specific fecal bacteria data for comparison. The SWAT 2005 model (Sadeghi and Arnold, 2002), which has a microbial sub-model component in it, is a useful tool for bacteria modeling but it needs to be calibrated and verified. Various versions of the SWAT water quality model have been applied, calibrated and validated for parameters including runoff, sediment yield and nutrient losses from watersheds under different geographic locations, conditions and management practices (Gassman et al., 2007; Van Liew et al., 2003; White and Chaubey, 2005; Wang et al., 2006). Limited research has been performed using the SWAT 2005 model for predicting bacteria movement.

Baffaut and Benson (2003) calibrated the SWAT model version 2000, which already had a microbial component (Sadeghi and Arnold, 2002) using daily flow, weekly FCB concentration collected from water quality grab samples. A frequency curve analysis method was used to compare measured versus predicted data for daily flow and FCB concentration. The daily flow curve simulation was reasonable except for over-predictions of peak flow. Then, the SWAT model-predicted values were compared with a frequency distribution of 18 months of weekly measured FCB concentration data using average plus or minus one standard deviation (SD) of measured means for 70% time of the frequency curve. Parajuli et al. (2006), calibrated (Rock Creek watershed) and validated (Deer Creek watershed) the SWAT model 2005 using one year (2004) of measured daily flow, total suspended solids, nutrients and total FCB concentration data. This study modeled source-specific bacteria using a model previously calibrated for flow, sediment and total FCB concentration.

The objectives of this research were to (a) calibrate (Rock Creek watershed) and verify (Deer Creek, Auburn, Upper Wakarusa watersheds) SWAT 2005 model using measured flow, sediment, nutrients and total FCB concentrations and (b) evaluate SWAT 2005 model for source-specific fecal bacteria modeling using three years (2004–2006) of observed modified deterministic probability of source-specific BST data.

2. Methods

2.1. SWAT model

The SWAT 2005 watershed-scale process-based model (Arnold et al., 1998; Neitsch et al., 2002, 2005) operates on a continuous daily time step. It simulates hydrological processes, sediment yield, nutrient loss and pesticide losses into surface/groundwater. The microbial survival and transport sub-model (Sadeghi and Arnold, 2002), originally added in SWAT 2000 (Neitsch et al., 2002), was modified considerably in the 2005 version.

The SWAT 2005 model utilizes geospatially referenced data to satisfy the necessary input parameters. For example, United States Geological Survey (USGS, 1999) 30 m × 30 m digital elevation model (DEM) data was used to delineate the watershed boundaries and topography; the Soil Survey Geographic Database (SSURGO) was used to create a soil database (USDA, 2005) and the Kansas Applied Remote Sensing Program (KARS) Gap Analysis Program (GAP) land-cover data of 2001 that depicts twenty general land-cover classes. Wardlaw and Egbert (2003) evaluated GAP (KARS, 2001) and National Land Cover Data (NLCD) (1992) landuse data for the State of Kansas. The Kansas GAP provided better discrimination of most land-cover classes than NLCD. Specifically, assessment found an overall accuracy of 87% for GAP and 81% for NLCD, and GAP had higher accuracies for most individual land-cover classes. Also, the Kansas GAP and NLCD land-cover products were found to be comparable in terms of characterizing broad scale land-cover patterns, but the Kansas GAP land-cover map appeared to be more appropriate for localized applications that require detailed and accurate land-cover information. The landuse categories were reclassified into eight classes (grazedland, non-grazedland/hay, cropland, woodland, Conservation Reserve Program (CRP), water, urban areas and quarry) based on field-verified landuse conditions (Mankin and Koelliker, 2001; Mankin et al., 2003). Parameters for each Hydrologic Response Unit (HRU) in each watershed were defined on the basis of soil, landuse, and topographic characteristics of the watershed as described in the SWAT 2005 documentation (Neitsch et al., 2005).

The microbial survival and transport sub-model was added to the SWAT model (Sadeghi and Arnold, 2002) and modified in 2005. The SWAT model microbial component considers the fate and transport of organisms for bacterial concentration. The microbial sub-model uses first-order kinetics, as revised by Moore et al. (1989), to model fecal bacteria die-off and re-growth. The first-order decay equation determines the quantity of bacteria that are removed or added by die-off and re-growth, as described in SWAT 2005 (Sadeghi and Arnold, 2002; Neitsch et al., 2005), and is given by Eq. (1):

$$C_t = C_0 \times e^{-K_{20} t \theta^{(T-20)}} \quad (1)$$

where C_t is the bacteria concentration at time t (count/100 mL), C_0 is the initial bacteria concentration (count/100 mL), t_{20} is the first-order die-off rate at 20 °C (per day), t is the exposure time (days), θ is the temperature adjustment factor, and T is the temperature (°C).

2.2. Watershed setting

The Rock Creek watershed (Fig. 1) is located in Douglas and Osage counties and has an area of 75.41 km² in three major landuses: grassland (56%), cropland (37%), and woodland (6%). The silty-clay textured soils are the predominant soil types in this watershed. The model was calibrated in the Rock Creek watershed. The Deer Creek watershed (Fig. 1) is located in Douglas and Shawnee counties and has an area of 51 km² in three major landuses: grassland (51%), cropland (39%), and woodland (9%). The silty-clay

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