

Effect of streambed bacteria release on *E. coli* concentrations: Monitoring and modeling with the modified SWAT

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ABSTRACT

Streambed sediment has been attracting attention as a reservoir for bacteria, including pathogenic strains. Soil and Water Assessment Tool (SWAT) has been augmented with a bacteria transport subroutine in SWAT2005 in which bacteria die-off is the only in-stream process. The purpose of this study was to develop the partial model of sediment-associated bacteria transport in stream and to evaluate the potential significance of streambed *Escherichia coli* (*E. coli*) release and deposition within the SWAT microbial water quality simulations. Streambed *E. coli* release and deposition were simulated based on the sediment resuspension and deposition modules in SWAT. The modified SWAT was applied to the Little Cove Creek watershed, Pennsylvania, which has forestry and dairy pasture landuses. Temporal changes in sediment *E. coli* concentrations were derived from monitoring data rather than from a streambed bacteria population model. Sensitivity analyses and calibrations were separately conducted for both hydrologic and bacteria parameters. Hydrologic calibration characterized soils in the watershed as pervious and thus the surface runoff was only moderately contributing to the streamflow. However, the surface runoff carried large numbers of *E. coli* to the stream, and sediment resuspension contributed to the persistent concentration of *E. coli* in stream water. Although the uncertainty of *E. coli* concentrations in streambed sediments and from wildlife probably affected the performance of the modified SWAT model, this study qualitatively confirmed the significance of modeling *E. coli* release from streambed and deposition for the SWAT microbial water quality simulations. Further developments should include modeling dynamics of bacteria populations within streambeds.

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1. Introduction

Improved characterization of bacteria sources is needed to advance modeling bacteria fate and transport at the watershed scale (Benham et al., 2006). Nonpoint sources of bacteria are much more difficult to control as compared to point sources. Runoff from fields, pastures, etc. and natural inputs from wildlife are often mentioned as the nonpoint sources of bacteria in rural watersheds. Recently, streambed sediment has been increasingly attracting attention as a reservoir of bacteria, including pathogenic strains. Sediments serve as a hospitable environment for bacterial survival due to the availability of soluble organic matter and nutrients, protection from predators such as protozoa, and shielding from exposure to the UV sunlight (Davies et al., 1995; Decamp and Warren, 2000; Jamieson et al., 2004; Koirala et al., 2008). Survival of fecal coliforms and fecal streptococci organisms was demonstrated

to be significantly longer in sediment-laden waters than in those without sediment (Sherer et al., 1992).

Numerous authors have observed that concentrations of fecal coliform bacteria in sediments are multiple-fold higher than in the water column. For example, van Donsel and Geldreich (1971) noted that concentrations of sediment fecal coliforms were 100–1000 times greater than that of overlying waters in various aquatic environments. Davies-Colley et al. (2004) analyzed data from agricultural streams in New Zealand and concluded that most of the time the water in the agricultural streams contained only a tiny fraction (about 1/1000) of the total fecal coliform contamination in the stream; the rest resided in the streambed from where it could be released during high-flow events.

Amounts of streambed microorganisms that can be released to water as sediments resuspend are large (Byappanahalli et al., 2003; Muirhead et al., 2004; Giddings and Oblinger, 2004; Cinotto, 2005). The direct method to observe the effect of sediment resuspension on bacteria concentration in water was proposed by McDonald et al. (1982) who carried out multiple releases of water from reservoir to a stream in North Yorkshire. They observed one to two-orders of magnitude increase of bacteria concentration during the water release due to *Escherichia coli* (*E. coli*) resuspension. Two-orders

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of magnitude increase were observed during the artificial flood experiments carried out by Nagels et al. (2002) and Muirhead et al. (2004) in New Zealand. Wilkinson et al. (1995) monitored changes in fecal coliform concentrations during and after controlled release of water in Wales streams and developed the first quantitative conceptual model of streambed bacteria release, settling, and die-off during a high-flow events.

Recently most of modeling bacteria fate and transport in streams and lakes has been done for *E. coli*. This organism has been used in recent environmental research and regulations as the common indicator of fecal contamination and microbial water quality of surface waters.

Models of *E. coli* fate and transport that did not account for the streambed or lake bottom bacteria release and deposition successfully captured spatial trends, but appeared to be incapable of explaining changes in bacteria concentrations in water during and after rainfall events (Hellweger and Masopust, 2008). McCorquodale et al. (2004) simulated bacteria fate and transport following storm water discharges in a coastal lake, and included in the model the description of bacteria deposition but not release. The authors indicated that the possibility of bacteria release due to waves, currents, or human swimming activity is a concern that needs to be addressed in the models.

Several in-stream modeling works addressed the sediment-associated bacteria fate and transport. In earlier studies, no distinction was made between free-floating and suspended sediment-associated bacteria. Tian et al. (2002) simulated the watershed scale bacteria fate and transport and considered sediment-associated bacteria release and deposition. These authors defined a threshold flowrate value that separated the release and the deposition flow regimes: bacteria in water settled to the streambed if the flowrate was less than the threshold flowrate, otherwise bacteria in streambed sediments were released to water. Collins and Rutherford (2004) assumed that bacteria release from streambed and deposition back to streambed were proportional and inversely proportional to flowrate, respectively, following power law functions. Jamieson et al. (2005a) demonstrated that bacteria release occurred when the streambed shear stress was larger than a critical value. Bacteria release rate was proportional to the streambed bacteria concentration and the average flowrate during the sediment resuspension period. In the work of Wu et al. (2009), the concentration of resuspended bacteria was computed as a simple empirical power law function of flowrate, based on the assumption that the streambed supplied an unlimited source of bacteria.

Recently, the distinction between free-floating and suspended sediment-associated bacteria has been made in bacteria fate and transport models. Jamieson et al. (2005b) simulated bacteria deposition during steady-state flow conditions by partitioning bacteria to free-floating and sediment-associated. The deposition rate of sediment-associated bacteria was computed according to the sediment net settling velocity. The irreversible bacteria adsorption to sediments was assumed and the settling velocity of free-floating bacteria was assumed to be negligible in the work. Bai and Lung (2005) partitioned fecal bacteria to free-floating and sediment-associated bacteria in water using a linear attachment isotherm. The authors assumed that only sediment-associated bacteria were deposited when the streambed shear stress was lower than a critical value for deposition, whereas both free-floating and sediment-associated bacteria were released when the streambed shear stress was higher than the critical value for sediment resuspension.

Soil and Water Assessment Tool (SWAT), the watershed-scale, physically-based and continuous-time model, has been developed to simulate fate and transport of pollutants from nonpoint sources and has been augmented with the bacteria transport subroutine by

Sadeghi and Arnold (2002). The main sources of bacteria in SWAT are grazing operations and manure application to croplands. Bacteria can be partitioned into foliage and soil solution, where bacteria can either grow or die depending on the temperature. Bacteria on foliage can be washed off by rainfall, and these bacteria along with bacteria from the soil solution can reach streams in surface runoff as free-floating and/or sediment-associated organisms. The sediment transport in surface runoff is computed using the Modified Universal Soil Loss Equation (MUSLE). After bacteria reach the stream, the temperature-dependent bacteria die-off is the only fate and transport of bacteria included in the current SWAT2005 version of SWAT (Neitsch et al., 2005).

Recently, the SWAT model has been expanded and improved in its various components, such as riparian wetland hydrology (Liu et al., 2008), surface runoff retention (White and Arnold, 2009), nutrients losses (Pohler et al., 2007; Baffaut and Benson, 2009), pesticide losses (Holvoet et al., 2008), etc. Limitations of current SWAT microbial sub-model for the bacteria fate and transport were pointed out in the study of modeling source-specific fecal bacteria (Parajuli et al., 2009). The purpose of this study was to augment SWAT bacteria module with sediment-associated bacteria transport in stream and to evaluate the potential significance of streambed bacteria release and deposition for the SWAT simulations of daily *E. coli* concentrations. Flow and *E. coli* monitoring data from the Little Cove Creek, Pennsylvania, were used for the application of the newly developed module.

2. Materials and methods

2.1. Study area and monitoring sites

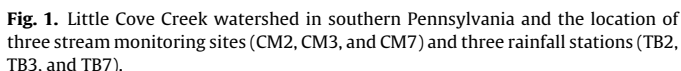
The study area was the Little Cove Creek watershed located in Franklin County, Southern Pennsylvania within the Chesapeake Bay watershed and surrounded by the Appalachian Mountains (Fig. 1). Little Cove Creek, after merging with Licking Creek, flows into the Potomac River near Hancock, Maryland. The headwater of Little Cove Creek is located in a forested area and flows for approximately 2.5 km through forest before entering a campground area and subsequently into an agricultural area where grazing dairy cows, cattle, and horses can be found. The watershed has the total population of 470 in 168 households.

Three stream monitoring sites, CM2, CM3, and CM7, have been established within the watershed at the distances of 7.2 km, 12.1 km, and 17.7 km from the stream source, respectively. The contributing areas of these monitoring sites are 18.8 km², 36.8 km², and 68.0 km², respectively. The site CM2 marked the beginning of agricultural inputs to the streams. Streambed sediments were of a sandy texture. The CM3 site was located in the area of slow moving water with a high sediment load due to a bridge and cattle ford just below the site that partially impounds flow. In the spring, flow may be artificially constricted by beaver dams. Streambed sediments were of sandy to silty texture. The CM7 site was beneath a newly constructed bridge in 2007 with a pier constricting flow. The bottom was sandy with a deep (~1 m) and meandering channel just upstream of the bridge at CM7.

2.2. Monitoring data acquisition

2.2.1. Rainfall

Rainfall was measured hourly at three tipping bucket (Onset Hobo S-RGB-M002) rainfall stations (TB2, TB3, and TB7) located near each stream monitoring site (Fig. 1) in 2007 and 2008. The hourly rainfall data were summed and transformed to the daily data to conform to the time step of SWAT input. Due to the intermittent malfunction of the rainfall stations, the missing daily rainfall data



2.2.2. Streamflow

Periodic streamflow measurements were collected according to standard USGS methods (Rantz et al., 1982) by measuring water

2.2.3. *E. coli* in streambed sediments and stream water

In 2005–2006, composite water (1–2 L) and sediment (about 100 g from the top 1 cm layer) samples were collected weekly at each stream monitoring site and transported on ice to the Beltsville Agricultural Research Center (BARC), Beltsville, Maryland, or Wilson College Biology Department in Chambersburg, Pennsylvania, where they were processed within 24 h. Generic *E. coli* were quantified using the Colilert Assay (Idexx Laboratories, Inc., Westbrook, MA). For water samples, 100 mL of sample and distilled water were mixed with nutrients and incubated at 37 °C in Colilert “trays”. For sediment samples, 10 g (wet weight) were blended with 100 mL of sterile water for 2 min. After allowing sand and silt particles to settle for ~2 h, 100 mL of supernatant (or 10-fold dilutions) were mixed with nutrients and incubated at 37 °C in Colilert “trays”.

2.3. Spatial data acquisition

The soil map of the Little Cove Creek watershed was obtained using the State Soil Geographic (STATSGO) database of the U.S. Department of Agriculture (USDA) Natural Resources Conservation Service (NRCS) (USDA, 2009). The predominant soil texture within the watershed was silt loam (93%) corresponding to PA055 as the map unit identifier (MUID) in STATSGO database (<http://soildatamart.nrcs.usda.gov/Survey.aspx?State=PA>, accessed on February 14, 2010). The landuse within the watershed was characterized from the National Land Cover Data 1992 (NLCD 92) which was provided by USGS (2009a). The major landuses within the watershed include pasture (25.0%) and forest (71.9%: Deciduous 66.7%, Evergreen 1.0%, and Mixed 4.2%). The high fraction of forest may lead to bacteria from the wildlife which is difficult to quantify (Benham et al., 2006). Accordingly, this study, which did not consider the *E. coli* inputs from the wildlife due to lack of information, could underestimate the *E. coli* concentration in stream water. In this study, since there was no commercial landuse (except a campground near the upstream) within the watershed, surface runoff of *E. coli* from landuse within the water-

Table 1
Number of HRU in each subbasin.

Subbasin number						Number of HRU					
S1	6	S8	19	S15	21	S22	21	S29	13	S36	21
S2	5	S9	12	S16	23	S23	11	S30	27	S37	9
S3	10	S10	12	S17	16	S24	12	S31	34	S38	5
S4	6	S11	15	S18	7	S25	11	S32	12	S39	16
S5	6	S12	17	S19	14	S26	22	S33	24	S40	14
S6	7	S13	17	S20	21	S27	10	S34	7	S41	17
S7	5	S14	13	S21	23	S28	14	S35	16	Avg.	14

shed was assumed to be only from manure application in grazing operation.

The Little Cove Creek watershed boundaries and topography were delineated using 30-m National Elevation Dataset (NED) provided by United States Geological Survey (USGS, 2009b). Based on the auto-delineation in AVSWAT-X (Di Luzio et al., 2005a), the watershed area (68 km²) was divided into 41 subbasins (Fig. 1). The total numbers of hydraulic response units (HRU) in each subbasin are listed in Table 1. The total length and the average slope of the main second-order stream (Little Cove Creek) were 17.7 km and 0.014 m/m, respectively. The average slope of tributaries of Little Cove Creek was 0.035 m/m. The stream including both main stream and tributaries were partitioned into 41 stream segments, which were relevant to 'subbasins' in SWAT, based on the topography delineation. In each stream segment, the hydrologic properties and in-stream water quality were assumed to be homogeneous.

Some SWAT modeling results are known to be sensitive not only on the parameter values but on delineation of HRUs. For example, Bingner et al. (1997) found that the number of subwatersheds affected predicted sediment yields; FitzHugh and Mackay (2000), Jha et al. (2004), and Chen and Mackay (2004) found similar results when varying both HRUs and subwatersheds. However flow predictions are much less sensitive to that delineation. Bingner et al. (1997), Manguerra and Engel (1998), FitzHugh and Mackay (2000), Jha et al. (2004), and Chen and Mackay (2004) demonstrated that SWAT flow predictions were generally insensitive to HRU and/or subwatershed delineations, with no changes in input data. Overland bacteria transport in SWAT with runoff is controlled by both runoff volumes and amount of sediment (Sadeghi and Arnold, 2002). Little bacteria are associated with sediment in runoff with typical values of parameters. This is in agreement with recent results of experiments and simulations of manure-borne bacteria transport at different scales (Stout et al., 2005; Kouznetsov et al., 2007; Pachepsky et al., 2006; Guber et al., 2009). Therefore flow predictions rather than sediment in runoff predictions are essential for bacteria transport simulations. Because the SWAT flow simulations are relatively insensitive to HRU and/or subwatershed delineations, the standardized delineation method (Di Luzio et al., 2005b) that we have applied was expected to be sufficient.

2.4. In-stream sediment and bacteria modules in SWAT

2.4.1. Sediment resuspension and deposition

The in-stream sediment transport model in SWAT includes sediment resuspension and deposition as a function of the peak stream velocity which is the stream velocity (v_{ch} , m/s) multiplied by the peak rate adjustment factor (PRF). The maximum concentration of sediment ($conc_{sed,max}$, ton/m³) that can be transported from a stream segment to the next downstream segment was computed by an empirical function, the simplified Bagnold's stream power equation (Neitsch et al., 2005):

$$conc_{sed,max} = SPCON \cdot (PRF \cdot v_{ch})^{SPEXP} \quad (1)$$

where $SPCON$ and $SPEXP$ are user-defined linear and exponent parameters, respectively. Suggested ranges of these values were from 0.0001 to 0.01 and from 1 to 2 for $SPCON$ and $SPEXP$, respectively. If the initial concentration of sediment in a stream segment for a time step ($conc_{sed,i}$) was smaller than $conc_{sed,max}$, streambed sediments would be resuspended and the amount of resuspended sediments ($M_{S,res}$) would be the function of the channel erodibility factor (K_{ch}) and the channel cover factor (C_{ch}):

$$M_{S,res} = (conc_{sed,max} - conc_{sed,i}) \cdot Q \cdot K_{ch} \cdot C_{ch} \quad (2)$$

where Q is the volume of water in the stream segment (m³). Otherwise, suspended sediments would be deposited to the streambed

and the amount of deposited sediments ($M_{S,dep}$) would be the function of the streamflow:

$$M_{S,dep} = (conc_{sed,i} - conc_{sed,max}) \cdot Q \quad (3)$$

2.4.2. Streambed *E. coli* release and deposition

The SWAT bacteria module was modified in terms of streambed *E. coli* release and deposition which were computed based on the sediment resuspension and deposition modules in SWAT. When streambed sediments were resuspended, the amount of the released *E. coli* ($M_{B,res}$, CFU) was determined as:

$$M_{B,res} = M_{S,res} \cdot C_{B,B} \quad (4)$$

where $M_{S,res}$ is the mass of resuspended sediment (ton) computed by Eq. (2) and $C_{B,B}$ is the *E. coli* concentration in streambed sediments (CFU/g sediment) which includes both free-floating *E. coli* in sediment pores and sediment-associated *E. coli*.

The *E. coli* suspended in stream water ($M_{B,W}$) were partitioned into free-floating ($M_{B,free}$) and sediment-associated *E. coli* based on the Bai and Lung's (2005) assumption about the linear relationship between them, and the sediment-associated *E. coli* were partitioned again into *E. coli* attached to the suspended sediments ($M_{B,sus}$) and *E. coli* attached to the deposited sediments ($M_{B,dep}$) satisfying the following equation:

$$\frac{M_{B,free} + M_{B,sus} + M_{B,dep}}{M_{B,W}} = \frac{1 + K_p \cdot conc_{sed,sus} + K_p \cdot conc_{sed,dep}}{1 + K_p \cdot conc_{sed,i}} \quad (5)$$

where $conc_{sed,sus}$ is the concentration of the suspended sediments, $conc_{sed,dep}$ is the concentration of the deposited sediments, and K_p is the partitioning coefficient of *E. coli* between the sediments and water (m³/ton or mL/g). Using Eq. (5), the net amount of *E. coli* settled from stream water can be calculated as:

$$M_{B,dep} = M_{B,W} \cdot \frac{K_p \cdot M_{S,dep}}{Q + K_p \cdot M_{S,W}} \quad (6)$$

where $M_{B,dep}$ is the number of *E. coli* deposited (CFU), $M_{B,W}$ is the number of *E. coli* in water (CFU), $M_{S,dep}$ ($= Q \cdot conc_{sed,dep}$) is the mass of deposited sediments computed from Eq. (3) (ton), and $M_{S,W}$ ($= Q \cdot conc_{sed,i}$) is the mass of sediments in water (ton). Values of K_p were computed from the regression equation (Pachepsky et al., 2006):

$$\log K_p = (-1.6 \pm 0.9) + (1.98 \pm 0.7) \cdot \log CLAY \quad (7)$$

where $CLAY$ is the percentage of clay in sediment (%), $2\% < CLAY < 50\%$. The value of $CLAY$ was defined as an input parameter of the modified SWAT module and assumed to be constant throughout the streambed in the watershed.

2.5. Empirical dependence of sediment *E. coli* concentrations on time

The streambed sediments *E. coli* concentrations, $C_{B,B}$, sampled at three sites were plotted versus time (Fig. 2) and the sine function was fitted to yield daily records for model input. The fitted function was

$$\log C_{B,B} = c_1 \cdot \sin \left(c_2 \cdot \frac{Days - c_3}{366} \cdot \pi \right) + c_4 \quad (8)$$

where $c_1 = 1.543$ is the amplitude, $c_2 = 2.194$ is the angular frequency, $c_3 = 187$ is the phase, and $c_4 = 3.870$ is the bias. The R^2 of the curve-fit was 0.66. The daily $C_{B,B}$ values from Eq. (8) were used as the input in the modified bacteria module of SWAT (Eq. (4)).

2.6. Sensitivity analysis and calibration in SWAT

Sensitivity analysis was performed by the LH-OAT method (van Griensven et al., 2006) which combines the Latin Hypercube (LH) sampling and One-factor-At-a-Time (OAT) design. LH sampling is

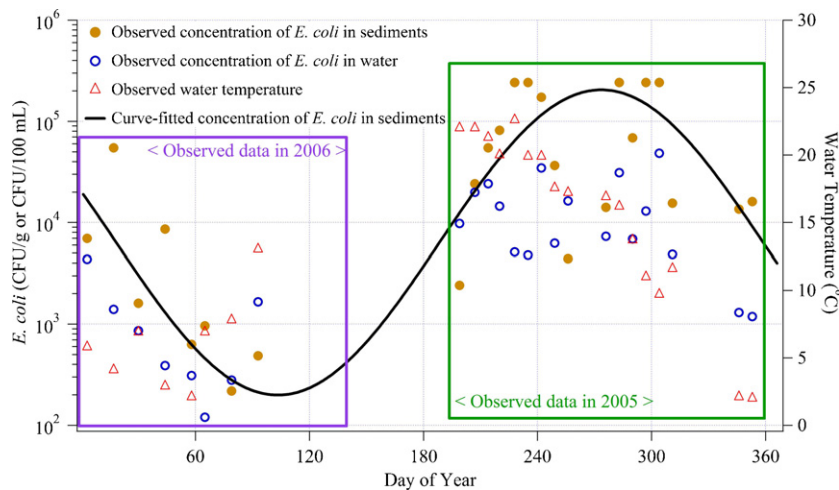


Fig. 2. *E. coli* concentrations in stream water and streambed sediments, corresponding stream water temperature, and curve-fitted daily *E. coli* concentration in streambed sediments in Little Cove Creek watershed between 2005 and 2006.

based on random sampling such as Monte Carlo sampling but uses a stratified sampling approach to avoid a significant computational cost due to a large number of input parameters (McKay, 1988). OAT design (Morris, 1991), which modifies only one input parameter between two successive runs of the model, was an example of an integration of a local into a global sensitivity method. In LH-OAT sampling, N ranges of each parameter were uniformly distributed by LH sampling, and then random values of the parameters were generated within each range. Each of the N random combinations of the parameters becomes the initial points for an OAT design. A partial effect S_{ij} (%) for each parameter e_i around each LH point j was defined by (van Griensven et al., 2006):

$$S_{ij} = \left| \frac{100 \cdot \left(\frac{M(e_1, \dots, e_i(1+f), \dots, e_p) - M(e_1, \dots, e_i, \dots, e_p)}{[M(e_1, \dots, e_i(1+f), \dots, e_p) + M(e_1, \dots, e_i, \dots, e_p)]/2} \right)}{f} \right| \quad (9)$$

where $M(\cdot)$ refer to the model functions, f is the fraction by which the parameter e_i is changed (a predefined constant), and P is the number of input parameters. Therefore, the LH-OAT method requires a total of $N \cdot (P+1)$ runs as a robust and efficient analysis. The global measures of sensitivities (S) of each parameter were calculated by averaging these partial effects S_{ij} , and the parameters were finally ranked according to the relative sensitivity in each N random combination.

For the calibration, SWAT employed the Shuffled Complex Evolution method developed at the University of Arizona (SCE-UA) which was known as a global calibration method and was an efficient calibration technique for calibrating watershed models. The details of the method are given by Duan et al. (1994). The criterion of the calibration is Nash and Sutcliffe (1970) model efficiency (E):

$$E = 1 - \frac{\sum (O_i - P_i)^2}{\sum (O_i - \bar{O})^2} \quad (10)$$

where O_i are the daily observed data, P_i are the daily simulated data, and \bar{O} is the average of O_i .

Some of SWAT parameters, in particular, the parameters indicated with "*" in Table 2, are spatially explicit (i.e. vary among individual HRU). For these parameters, relative changes (%) from default values were used in the sensitivity analysis and the calibration.

2.7. Model setup

2.7.1. Input data and parameters

Two-year daily rainfall data were used for the weather input of SWAT, and one-year daily streamflow data were used for the calibration of SWAT hydrologic parameters. The observed *E. coli* concentration in Little Cove Creek was used for the calibration of SWAT bacterial parameters.

Grazing operation in the pasture was assumed to be the only bacterial source of surface runoff in this study. Based on the field observations, the dominant livestock within the watershed was assumed to be dairy cows and annual grazing operation schedule was set as 210 days from April 1st. American Society of Agricultural and Biological Engineers (ASABE, 2005) reported that typical total manure excreted from lactating cow was 68 kg/day/animal and manure moisture content was 87%. Using the stocking rate of 2.5 animals/ha obtained from interviews, the manure (dry weight) application rate was computed as 22.1 kg/ha/day. ASABE (2003) also reported that the colony number of fecal coliform bacteria in the fresh manure from 1000 kg animal mass of dairy cow per day was 16×10^{10} CFU with high variation (standard deviation = 28×10^{10} CFU). Based on the ASABE Standards (ASABE, 2003, 2005), *E. coli* concentration in manure was set as 4×10^7 CFU/g dry manure in this study. *E. coli* die-offs in surface runoff and stream water at 20 °C were 0.659 day^{-1} and 0.990 day^{-1} , respectively, as reported in Crane and Moore's (1986) review of bacterial die-off. Observed rather than predicted dynamics of the *E. coli* concentrations in the streambed sediments was used in all subbasins.

2.7.2. Layout of simulations

The modified SWAT model was run for 2007 and 2008. The year 2007 was regarded as the pre-run period and only results for the year 2008 were used for the sensitivity analysis and calibration. The sensitivity analyses and calibrations were conducted separately for hydrologic parameters and bacterial parameters.

The sensitivity analysis and calibration of hydrologic parameters with respect to daily streamflow at each stream monitoring site were conducted using the module of SWAT2005 which was described in Section 2.5. The sensitivity analysis included 27 hydrologic parameters which are listed in Table 1 with definitions. The number of intervals in the LH (N) was 10 and the parameter change in the OAT (f) was set at 0.05. The sensitivity analysis was followed by the calibration for the parameters highly ranked by the sensitivity.

Table 2

Twenty-seven hydrologic parameters for the sensitivity analysis with their ranges (from min to max), sensitivity rank, and sensitivity value, and the calibrated values of nine parameters.

Parameter	Min	Max	Rank	S ^b	Value ^c	Definition	Process
CN2 ^{a,*}	–70	50	1	1.970	–57	Initial SCS runoff curve number for moisture condition II	Runoff
SMFMX	0	10	2	0.370	6.87	Melt factor for snow on June 21 (mm H ₂ O/°C-day)	Snow
SOL_K [*]	–50	50	3	0.328	–34	Saturated hydraulic conductivity (mm/hr)	Soil
ALPHA_BF	0	1	4	0.321	1	Baseflow alpha factor – baseflow recession constant	Groundwater
SLOPE [*]	–50	50	5	0.295	–	[HRU.SLP] Average slope steepness (m/m)	Geomorphology
ESCO	0	1	6	0.237	1	Soil evaporation compensation factor	Evaporation
TIMP	0.01	1	7	0.221	1	Snow pack temperature lag factor	Snow
SOL_Z [*]	–50	50	8	0.205	–	Depth from soil surface to bottom of layer (mm)	Soil
SOLAWC [*]	–50	50	9	0.166	48	Available water capacity of the soil layer (mm H ₂ O/mm soil)	Soil
SMTMP	0	5	10	0.123	0.69	Snow melt base temperature (°C)	Snow
CANMX	0	15	11	0.120	11.36	Maximum canopy storage (mm H ₂ O)	Runoff
CH_K2	0	150	12	0.046	–	[CH_K(2)] Effective hydraulic conductivity in main channel alluvium (mm/hr)	Channel
SMFMN	0	10	13	0.043	–	Melt factor for snow on December 21 (mm H ₂ O/°C-day)	Snow
SFTMP	0	5	14	0.019	–	Snowfall temperature (°C)	Snow
EPCO [*]	–50	50	15	0.009	–	Plant uptake compensation factor	Evaporation
SOL_ALB	0	1	16	0.007	–	Moist soil albedo	Evaporation
CH_N [*]	–20	20	17	0.004	–	Manning's "n" value	Channel
SURLAG	0	10	18	0.004	–	Surface runoff lag coefficient	Runoff
SLSUBBSN [*]	–50	50	19	0.001	–	Average slope length (m)	Geomorphology
GWQMN	0	5,000	20	0.000	–	Threshold depth of water in the shallow aquifer for return flow (mm H ₂ O)	Soil
GW_REVAP	0.02	0.2	28	0.000	–	Groundwater "revap" coefficient	Groundwater
REVAPMN	0	500	28	0.000	–	Threshold depth of water in the shallow aquifer for percolation to the deep aquifer (mm H ₂ O)	Groundwater
TLAPS [*]	–50	50	28	0.000	–	Temperature lapse rate (°C/km)	Geomorphology
GW_DELAY	0	100	28	0.000	–	Groundwater delay time (days)	Groundwater
RCHRG_DP	0	1	28	0.000	–	Deep aquifer percolation fraction	Groundwater
BLAI [*]	–50	50	28	0.000	–	Maximum potential leaf area index	Crop
BIOMIX	0	1	28	0.000	–	Biological mixing efficiency	Soil

* Parameters are varied by relative change (percentage) maintaining spatial relationship.

^a Parameters shadowed are calibrated.

^b Global measure of sensitivity.

^c Calibrated values.

The sensitivity analysis of bacteria-related parameters (21 parameters listed in Table 2 with definitions) was also conducted using the LH-OAT method. Since no sensitivity analysis of bacteria-related parameters could be done with existing SWAT modules, the LH-OAT method was coded in MATLAB which was also used as the shell for multiple LH-OAT runs¹. Since the modified bacterial module of SWAT used sediment resuspension and deposition data, sediment-related parameters were included in the sensitivity analysis. The parameter change for OAT (f) was 0.1, and the number of intervals in LH (N) was 100, and thus the total number of model runs was 2200 ($= 100 \times (21 + 1)$). In order to distinguish the contributions of *E. coli* from surface runoff and streambed release, the sensitivity analysis was conducted for the bacterial parameters with respect to in-stream *E. coli* concentrations for two cases: (a) considering and (b) NOT considering streambed *E. coli* release.

To calibrate modified SWAT model with respect to bacterial parameters, combinations of highly ranked sensitive bacterial parameters were randomly sampled within the LH ranges (5000 LH grid intervals) of each parameter. The predicted logarithms *E. coli* concentrations at each monitoring site were compared with the logarithms of observed ones for each run, and the performance was evaluated in terms of *E. coli*. These 5000 runs have also been used to generate the probability distribution functions of (a) the total annual mass of sediments (= resuspended – deposited), (b) the total annual number of *E. coli* originated from surface runoff, and (c) the total annual number of *E. coli* released from streambed.

3. Results and discussion

3.1. Sensitivity analysis and calibration of hydrologic parameters

Table 2 shows the 27 hydrologic parameters with their ranges (from min to max: parameters indicated with "*" were varied by relative change (%) of default values maintaining spatial relationship) for the sensitivity analysis and the sensitivity rank results. The runoff curve number (CN2) was the most sensitive parameter ($S = 1.97$) followed by the group of nine parameters with much smaller sensitivity (from 0.1 to 0.4). This group included snowmelt related parameters (SMFMX, TIMP, and SMTMP), base/lateral flow parameters (SOL_K, ALPHA_BF, and SOLAWC), watershed morphology parameters (SLOPE and SOL_Z), and evapotranspiration parameter (ESCO) (Table 2). The sensitivity ranking of hydrologic parameters in this study was in agreement with the sensitivity ranking obtained for other SWAT sensitivity studies. The CN2 was usually ranked as the first or the second, and the ESCO and the SOLAWC were usually ranked as the top five most sensitive parameters (Arnold and Allen, 1996; Spruill et al., 2000; White and Chaubey, 2005; Holvoet et al., 2005; van Griensven et al., 2006). The relative importance of lateral flow and snowmelt in the Little Cove Creek watershed caused high sensitivity ranks of the corresponding parameters.

The highly ranked ($S > 0.1$) hydrologic parameters, except watershed morphology parameters, such as SLOPE and SOL_Z, were calibrated using daily streamflows at all three stream monitoring sites. Calibration results for the remaining nine hydrologic parameters are shown in Table 2. The median CN2 value across the watershed was 34 with the maximum of 38 and the minimum of 24. Values of CN2 at pastures were 34 which indicated that more

¹ The code is available from the corresponding author upon request.

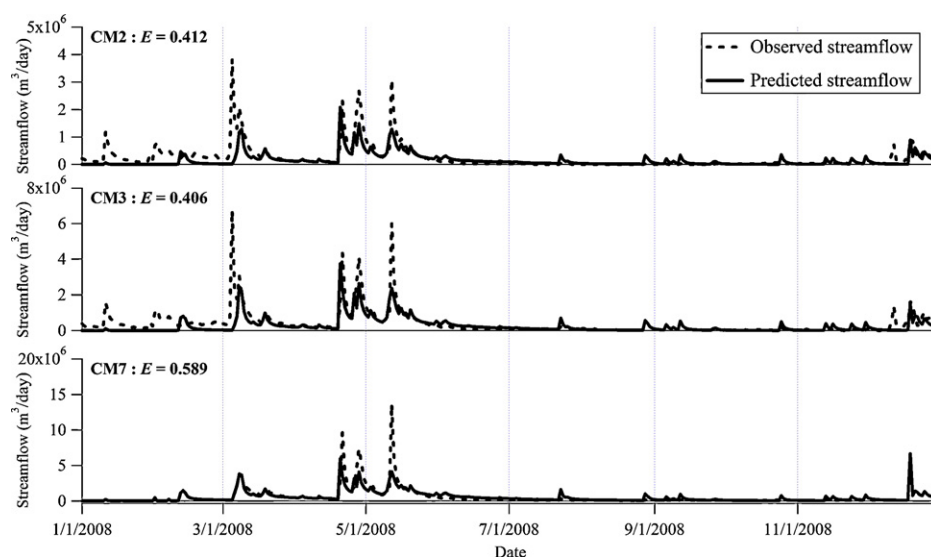


Fig. 3. Temporal variations of observed and predicted daily streamflows at three stream monitoring sites. E is the Nash-Sutcliffe model efficiency statistic.

than 75% of pastures were not heavily grazed and soil above a depth of 100 cm was highly permeable (Neitsch et al., 2005). CN2 values in forests varied from 26 to 36 which indicated that the forest litters and brushes almost adequately cover the highly permeable soil (Neitsch et al., 2005). The calibrated soil hydraulic conductivity in forests (median SOL_K = 67 mm/h) was greater than that in pastures (median SOL_K = 22 mm/h). The high values of ALPHA_BF (=1) indicated that the base or groundwater flow rapidly responds to changes in recharge (Neitsch et al., 2005). Due to the rapid response of baseflow, sharp increases and decreases in simulated streamflow were expected. The available water capacity of soil (SOLAWC) was relatively high with median value of 0.21 mm H₂O/mm soil layer compared to the default median soil texture value of 0.14 mm H₂O/mm soil layer. The high values SOLAWC implied the potential of substantial retention of precipitation in soil with corresponding decrease of recharge and lateral flow. Overall, the calibrated parameter set characterized soils in Little Cove Creek watershed as highly permeable and able to store substantial amounts of water.

The SWAT performance with the calibration of hydrologic parameters with the temporal variations of observed and predicted daily streamflows at each stream monitoring site for the year 2008 is shown in Fig. 3. High streamflow was observed in the spring season, while summer and fall seasons were relatively dry. Values of the E statistic were larger than the threshold value of 0.4 which suggested to assess the performance of hydrologic modeling in small-scale watersheds using SWAT2005 by Green and van Griensven (2008). SWAT2005 was not really able to simulate the high peaks of streamflow. This SWAT feature has also been observed in other SWAT modeling works (e.g. Kirsch et al., 2002; Chu et al., 2004). Generally, the peak of streamflow occurs within hours (Atkinson et al., 2003) which were shorter than the daily time step of SWAT model. The SWAT's inability to simulate the peak streamflow in short high-flow events was probably due to the daily time step.

3.2. Performance of the modified bacteria module in SWAT

3.2.1. Sensitivity analysis

Table 3 shows 21 bacteria- and sediment-related parameters with their ranges (from min to max) for the sensitivity analysis and the sensitivity ranks in terms of *E. coli* concentration in stream water in simulations with and without streambed *E. coli* release. When only surface runoff was considered as the *E. coli*

source, the parameters related to the grazing operation (BIO_MIN and PHU_PLT) and available *E. coli* fractions in manure (BACT_SWF and BACT_KDDDB) were most sensitive because those parameters controlled the bacterial input on the surface available for runoff transport. On the other hand, the parameters related on sediment resuspension/deposition were much less sensitive to the *E. coli* concentration. When streambed *E. coli* release was considered, however, the results were reversed. The most sensitive parameters were the parameters related on sediment routing in stream (SPEXP, PRF, and SPCON) and sediment erosion in streambed (CH_COV and CH_EROD). Percentage of clay in sediments (CLAY) which was a determinant parameter of *E. coli* partitioning and deposition was ranked low (rank 21). Partitioning coefficient of *E. coli* to the suspended sediments (K_p) was the only function of CLAY in Eq. (7). Since the mass of suspended sediments in water ($M_{S,W}$ in ton) were relatively small (0–3 orders of magnitude different) compared with the volume of stream water (Q in m³), K_p was not an influential parameter to *E. coli* deposition ($M_{B,dep}$) anymore in Eq. (6).

3.2.2. Calibration results

Based on the sensitivity analysis, 10 bacteria- and sediment-related parameters (five parameters with the highest ranks in simulations with and without the streambed *E. coli* release) were selected to be calibrated and the calibrated values are shown in Table 3. Other parameters were set at default values of SWAT or at mean values of the parameter ranges as listed in Table 3. Although sediment-related parameters were calibrated indirectly, i.e. using bacteria concentration rather than sediment content data, values of calibrated parameters compared favorably with SWAT calibration results from other works. For example, peak rate adjustment factor for sediment routing (PRF), linear parameter for calculating the channel sediment routing (SPCON), and exponent for calculating the channel sediment routing (SPEXP) were respectively 0.61 and 0.20, 0.0023 and 0.0031, and 1.06 and 1.5 for the Little Cove mountain watershed (Table 3) and the comparable Big Creek watershed studied by Muleta and Nicklow (2005). The bacteria partition coefficient in surface runoff (BACTKDQ) and the temperature adjustment factor (TBACT) were the same as in the works of Parajuli et al. (2009) where they were obtained by manual calibration, and in the work of Coffey et al. (2010). The only substantial difference between the Parajuli et al. (2009) and this work was in values of the parameter BACTKDDDB which partitions deposited bacteria between soil solution and soil solids. Parajuli et al. (2009) used the value of this

Table 3

Twenty-one bacteria- and sediment-related parameters for the sensitivity analysis with their ranges (from min to max) and sensitivity ranks in terms of in-stream *E. coli* concentrations with and without streambed *E. coli* release, and the calibrated values of 10 parameters.

Parameter	Min	Max	Sensitivity rank		Value	Definition
			Streambed <i>E. coli</i> release			
			Included	Not included		
ADJ PKR	0	1	10	12	1	Peak rate adjustment factor for sediment routing in the subbasin (tributary channels)
BACT SWF	0	1	3	14	0.97	Fraction of manure applied to land areas that has active colony forming units
BACTKDDB	0	1	4	16	0.36	Bacteria partition coefficient in manure
BACTKDQ	150	200	8	17	175	Bacteria soil partitioning coefficient (m³/Mg)
BACTMIX	7	20	14	19	10	Bacteria percolation coefficient (m³/Mg)
BIOMIX	0	1	7	8	0.2	Biological mixing efficiency
BIO_EAT	10	100	12	13	70	Dry weight of biomass consumed daily ((kg/ha)/day)
BIO_INIT	100	500	11	11	300	Initial dry weight biomass (kg/ha)
BIO_MIN	50	300	1	7	56	Minimum plant biomass for grazing (kg/ha)
BIO_TRMP	10	100	13	18	70	Dry weight of biomass trampled daily ((kg/ha)/day)
CH_COV	0	1	16	5	0.43	Channel cover factor
CH_EROD	0	1	17	4	0.01	Channel erodibility factor
CLAY	10	30	21	21	20	Percentage of clay in sediments (%)
FILTERW	0	2	5	15	1.50	Width of edge-of-field filter strip (m)
LAI_INIT	0	1	6	9	0.5	Initial leaf area index
PHU_PLT	1,000	2,000	2	6	1,880	Total number of heat units or growing degree days needed to bring plant to maturity (days)
PRF	0	1	18	2	0.61	Peak rate adjustment factor for sediment routing in the main channel
SPCON	1E-04	0.01	19	3	0.0023	Linear parameter for calculating the channel sediment routing
SPEXP	1.0	1.5	20	1	1.06	Exponent parameter for calculating the channel sediment routing
USLE_P	0.1	1.0	9	10	0.5	USLE equation support practice factor
WOF_P	0	1	15	20	0.5	Wash-off fraction for bacteria

Parameters shadowed are calibrated.

parameter of 0.9 whereas calibration in this work led to the value of 0.36. These differences may reflect the differences in soil structure (Guber et al., 2009).

Although a single set of parameters was finally selected as the result of calibrations (Table 3), we decided to summarize the results of all 5000 model runs generated in Latin Hypercube-based calibration with parameter values in reasonable ranges at first. The summary was done in form of cumulative probability distribution functions of total annual mass of sediments (= resuspended – deposited) and total annual number of *E. coli* generated across the watershed for 2008 (Fig. 4). The net total mass of resuspended sediments was positive, i.e. the resuspension exceeded deposition, in 75% of simulations for 2008 (Fig. 4a). When more sediment was deposited than resuspended, differences between deposited and resuspended amounts were relatively small. The

small probabilities of sediment deposition compared with sediments resuspension were consistent with small probabilities of *E. coli* deposition and probably resulted in the low sensitivity of parameter CLAY, which was related on the *E. coli* partitioning to the suspended sediments (Table 3). The average values of logarithms of total *E. coli* counts from surface runoff and streambed release for 2008 were 12.7 and 14.9, respectively, and the standard errors of each were 0.007 and 0.013, respectively (Fig. 4b). The average number of *E. coli* released from the streambed was about two orders of magnitude greater than that the input from surface runoff for 2008. The higher variability of *E. coli* from streambed release than that from surface runoff was consistent with the results of sensitivity analysis in which the parameters related on sediment routing and streambed sediments erosion were most sensitive (Table 3). The summary in Fig. 4b indicated that streambed *E. coli* dominated

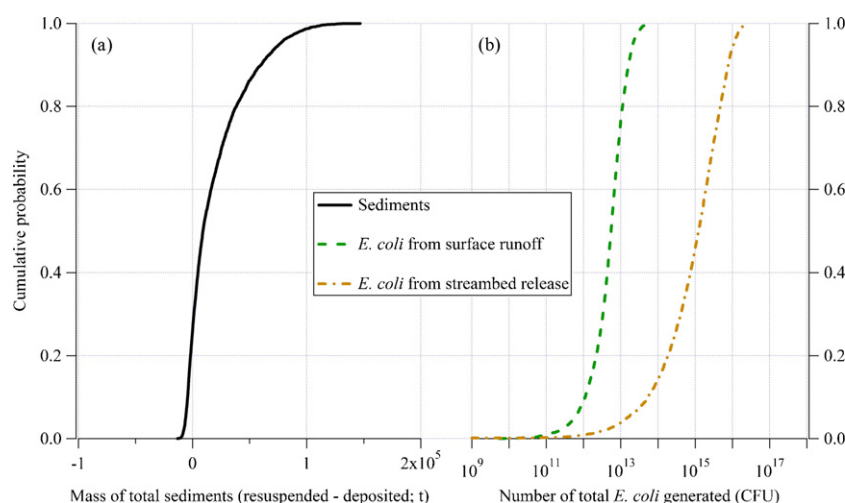


Fig. 4. Cumulative probability distribution functions of total net mass of sediments (= resuspended sediments – deposited sediments) and total number of *E. coli* generated from surface runoff and streambed release throughout the watershed for the year 2008.

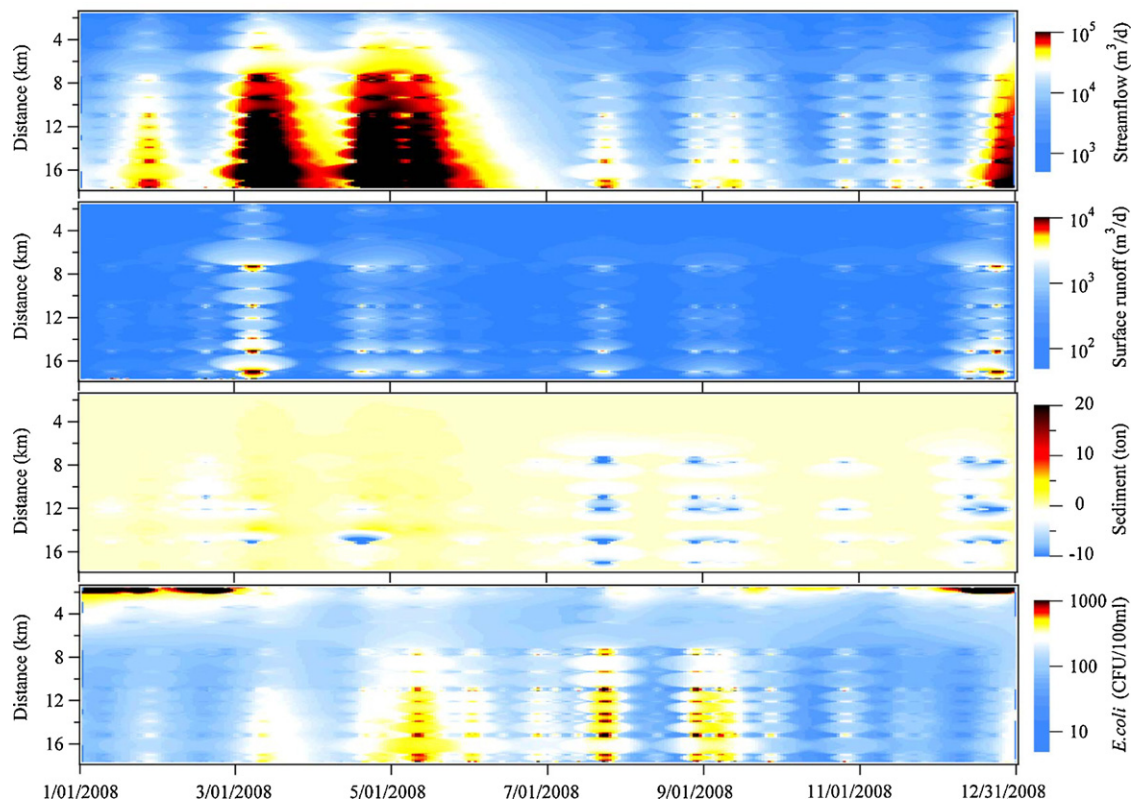


Fig. 5. Spatial and temporal variations of streamflow, surface runoff, sediment resuspension(+)/deposition(–), and in-stream *E. coli* concentration from simulations with the calibrated model for the year 2008.

the microbiological budget of the stream water for practically all combinations of parameters taken within plausible ranges.

Spatial and temporal variations of streamflow, surface runoff, sediment resuspension/deposition, and *E. coli* concentration for the calibrated model results are depicted in Fig. 5. Streamflow in the winter and spring seasons was high while summer and fall seasons were relatively dry. Although surface runoff in the wet season was higher than in the dry season, the overall contribution of surface runoff to streamflow was not large. Baseflow contributed to the streamflow more than surface runoff. This was due to the high permeability of soils across the Little Cove Creek watershed as found in hydrologic calibration (Table 2). Net sediment resuspension occurred more often than deposition, especially in upstream. Sediment deposition usually coincided with the occasional surface runoff events downstream indicating that sediment input was caused by surface runoff. Sediment resuspension events occurred often and involved mostly only moderate amounts of sediment, whereas sediment deposition events were infrequent but intensive. The overall amount of deposited sediments was larger than suspended sediments by 2678 ton in 2008. *E. coli* concentration was generally affected by the combination of streamflow conditions and presence of surface runoff. High *E. coli* concentrations upstream in winter were caused by low streamflow. The surface runoff as the source of *E. coli* into the stream increased *E. coli* concentration. The high contributions of baseflow to the stream, which was *E. coli*-free, diluted stream water with respect to *E. coli*.

Observed and predicted *E. coli* concentrations in the simulations with and without streambed *E. coli* release at each stream monitoring site are plotted in Fig. 6. When streambed *E. coli* release was not considered, the simulated *E. coli* concentration had scattered spikes during the grazing season (from April to October). This could also be explained by the rare substantial surface runoff events (Fig. 5).

Outside the grazing season (from November to March), no *E. coli* influx to the stream water was predicted although more surface runoff was predicted (Fig. 5). When streambed *E. coli* release was considered in the modified SWAT model, the simulated presence of *E. coli* in stream water became persistent, and the *E. coli* coming from surface runoff resulted in peaks of *E. coli* in stream water. This was consistent with the results of Vidon et al.'s (2008) recent research on the correlation between hydrological variables and *E. coli* concentration in stream water. The authors suggested that turbidity, which was related on the sediment resuspension, might be the best indicator of *E. coli* at low streamflow while *E. coli* concentration in stream water might be dominated by surface runoff at high streamflow.

Comparison of observed and predicted *E. coli* concentrations for the same days (Fig. 7) shows more clearly the difference in performance of SWAT model with and without streambed *E. coli* release. Simulations without accounting for streambed *E. coli* release result in predicted concentrations that are substantially lower than observed ones for all but one observation date.

The calibration performance measures of the modified SWAT model were relatively low; *E* values at CM2, CM3, and CM7 were –0.2, –0.7, and 0.2, respectively, although they were improved substantially compared with the original model that did not account for the streambed *E. coli* release (Fig. 6). The *E. coli* concentrations in the dry season were mostly underestimated at each monitoring site even when the streambed *E. coli* release was accounted for (Fig. 6). In summer compared to winter, for instance, accesses of wildlife, livestock, and human activity to the stream become more frequent and thus the disturbance of streambed with *E. coli* release to the stream water increases. The relatively low accuracy of the model can be partly attributed to the uncertainty of *E. coli* concentrations in streambed sediments and to possible inputs from

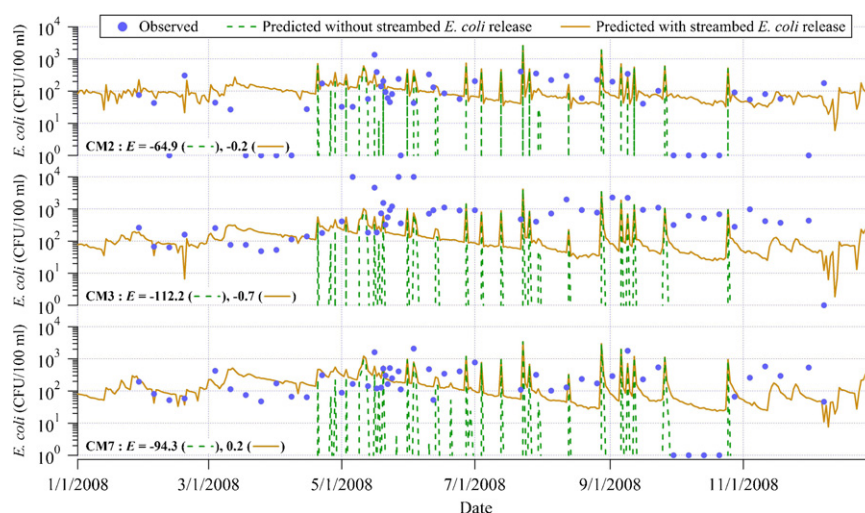


Fig. 6. Temporal variations of in-stream *E. coli* concentrations predicted and observed at three stream monitoring sites for the year 2008. Predicted results are shown for from the calibrated model considering with and without streambed *E. coli* release. *E* (Nash–Sutcliffe model efficiency statistic) values are for each predicted result.

wildlife. Besides, the same regression equation [8] to estimate temporal variation in streambed *E. coli* concentrations was used across the watershed, and the accuracy of this equation was relatively low ($R^2 = 0.66$ in Fig. 2).

E. coli input from wildlife was not considered in this study. It can be divided into indirect (via surface runoff) and direct (deposition in streams) inputs (Benham et al., 2006). If the indirect input from wildlife was considered, the surface runoff-related peaks of *E. coli* in Fig. 6 may be higher or parameters related to surface runoff and grazing operation may be changed. However, the die-off during long periods between surface runoff will still be causing concentrations in the stream that were negligible compared with measured. Furthermore, smaller CN2 values and higher hydraulic conductivity in forest soil reduced the effects of indirect deposits of wildlife on the water quality of runoff. However, if the persistent direct deposition from wildlife would be considered, the concentrations of *E. coli* might become higher and thus the gap between the observed and the predicted *E. coli* in a dry season would be expected to decrease thus improving the model performance. The uncertainty is common in estimates of wildlife inputs to the water

quality of rural creeks (Parajuli et al., 2009). Without analyzing the sediments, wildlife is usually assumed to be the source of *E. coli* in water in forested watersheds (e.g., Fisher et al., 2000). The wildlife inputs may account for 15–30% of total land-deposited bacteria, according to estimates of Parajuli (2007) for the watershed with landuse comparable with the watershed of this study. Developing parameters and functions to include the behavioral and physiological patterns of wildlife into SWAT model presents an interesting avenue of research.

The simulations did not include the *E. coli* inputs from residential sources. In the studied watershed, household sources generate substantially smaller amount of fecal coliforms than livestock. For 168 households generating on average 1 m^3 effluent per septic system (U.S. EPA, 2001), about 10% septic system failure rate (<http://www.epa.gov/reg3wapd/septic/>), and a typical concentration of fecal coliforms in human waste of $6 \times 10^6 \text{ CFU } 100 \text{ mL}^{-1}$, the total daily generated amount of coliforms is about 100 times less than the daily amount from livestock. Parajuli (2007) studied the Rock Creek watershed with the landuse similar to the one in this work and 20% septic system failure rate and found that the probability to find fecal coliforms from household sources in the creek was about 4%. This author was able to see some sensitivity of the SWAT predictions to household sources for a comparable rural watershed only if he assumed the direct input of bacteria to the creek. Most of houses are farther than 0.3 km from the creek in this study, and the direct input of fecal coliforms from human sources to the creek does not seem to be significant, although cannot be excluded completely.

We have observed persistently high concentrations of *E. coli* in sediments in summer (Fig. 2). It is not clear whether high concentrations of *E. coli* in sediments are caused by the ability of *E. coli* population to persist in stream sediments or by intermittent additions of bacteria from wildlife sources. *E. coli* can and do grow in streambeds that are hospitable environments for these organisms. Such growth has demonstrated (e.g. Desmarais et al., 2002; Solo-Gabriele et al., 2000). Haller et al. (2009) and Poté et al. (2009) reported the higher growth of *E. coli* in sediments with high level of organic matter and nutrients. Quite different *E. coli* survival times have been observed when the die-off of *E. coli* was monitored in sediments. For example, van Donsel and Geldreich (1971) reported a 90% die-off of fecal coliforms in 7 days in various sediments whereas the 85 days period was required for the 90% die-off of fecal coliforms in the study of Davies et al. (1995). Mechanisms of *E. coli* survival in sediments are not understood yet, and sediment properties seem

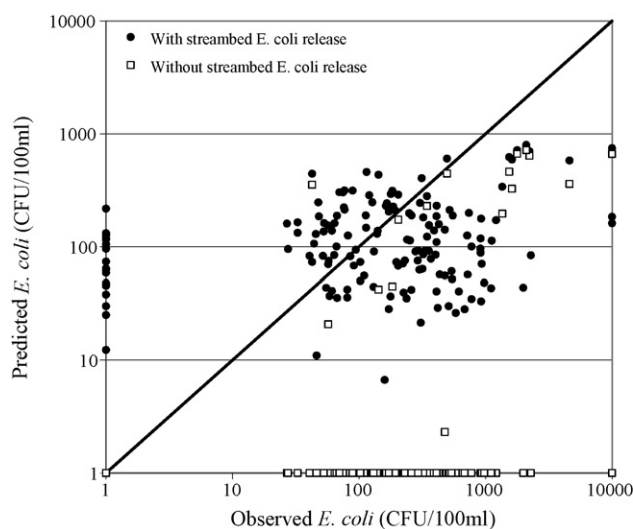


Fig. 7. The 1:1 plot of observed and predicted daily *E. coli* concentrations in stream water from the calibrated model considering with and without streambed *E. coli* release throughout the watershed for the year 2008.

to control both *E. coli* survival rates and sensitivity of those rates to temperature (e.g., Garzio-Hadzick et al., in press). *E. coli* populations adapt to the sediment environments and, for example, Smallbeck and Bromel (1975) showed that *E. coli* survival in sediment after re-inoculation was much better than after the first inoculation.

Small probabilities of *E. coli* deposition that we have inferred do not contradict to persistently high *E. coli* concentrations in sediments. *E. coli* concentrations in stream sediments decline with depth. Garzio-Hadzick et al. (in press) observed the half order of magnitude decrease in concentrations in a rural creek in Maryland. Concentrations of fecal coliforms in the top 2 cm of sediments were significantly ($p < 0.001$) higher than in the 2–10 cm layer in the study in Australia (Ferguson et al., 1996). Haller et al. (2009) observed the fast, about one order of magnitude per cm, decrease of *E. coli* concentrations with depth within first 5 cm of sediment in Lake Geneva. As the sediment and bacteria are scoured, smaller populations of *E. coli* from deeper sediment layers gain access to nutrients and have the opportunity to grow. Evanson and Ambrose (2006) observed a substantial increase of *E. coli* concentrations in water and sediment during two consecutive rainfalls after a long drought but no increase after the third rainfall. They concluded that after the flush of *E. coli* from the surface layers during the first two rain events there was insufficient time for *E. coli* regrowth, resulting in subsequent low level flushes during later periods of rainfall.

Overall, current understanding of *E. coli* population dynamics in sediments is expanding but still is not sufficient to develop a model (Pachepsky and Shelton, in press). This is the reason why the observed rather than simulated concentrations of *E. coli* in sediment were used as the inputs for the streambed bacteria release algorithms in this work. We note that the first model that included both growth and die-off of *E. coli* in stream sediments was proposed by Rehmann and Soupir (2009). Testing of this model may help to advance modeling dynamics of bacteria populations within streambeds which is necessary development to advance modeling of microbiological water quality of streams.

One concern of using measured *E. coli* concentrations in sediment as the input for resuspension–deposition model is that if the new independent bacteria source is introduced then this source rather than the land deposition can be made responsible for all changes in microbial population. That was not the case in our work. The in-stream bacteria source affected concentrations of bacteria during the whole period of observations whereas while the landuse bacteria source contributed to the peaks of bacteria concentration during grazing period. Therefore, other model user will have pathogen fate and transport sensitive to landuse provided the landuse at realistic parameter values is able to provide the substantial bacteria contribution bacteria to the stream during rainfall events.

The site-specific magnitude of streambed *E. coli* effect on the stream water quality would depend on the concentration of *E. coli* in streambed sediments. Reported *E. coli* or fecal coliform concentrations in streambed sediments in the literature range from 0 to 10^5 CFU 100 mL⁻¹ (Crabill et al., 1999) and variations within 2–4 orders of magnitude in the same streambed is not uncommon (e.g., Cinotto, 2005; He et al., 2007). Such variability may be the reason for the fact that several successful in-stream bacteria SWAT simulations have been done without taking into account the streambed bacteria release (e.g., Parajuli et al., 2009; Baffaut and Benson, 2003; Coffey et al., 2010). No substantial effect of streambed bacteria release should be expected if the streambed concentrations are small. Information about the streambed bacteria concentration has not been collected so far in amounts sufficient to understand the reasons of the differences between streams. Results of this work indicate that streambed pathogen and indicator microorganism concentrations should be determined where modeling is used to assist in watershed or stream management decisions.

4. Conclusions

SWAT, as a tool for modeling fate and transport of *E. coli* at the watershed scale, was modified in this study by including streambed *E. coli* release with resuspended sediments and *E. coli* deposition with sediments. The modified SWAT was applied to reproduce the monitoring dataset on streamflow and *E. coli* in the Little Cove Creek watershed, southern Pennsylvania, for 2008. *E. coli* in sediment was estimated from monitoring data rather than simulated. The soils in the watershed were pervious, and thus the surface runoff was only moderately contributing to the streamflow, but it carried large numbers of *E. coli* to the stream. On the other hand, sediment resuspension contributed to the persistent concentration of *E. coli* in the stream water. The high scattered peaks of *E. coli* in the stream water originated from both surface runoff and sediment resuspension while the persistent *E. coli* in stream water could be attributed to the release of *E. coli* from the streambed.

Overall, the SWAT model modified with the streambed *E. coli* release and deposition module showed better performance in predicting *E. coli* concentration in stream water as compared to the original SWAT model. Although the uncertainty of *E. coli* in streambed sediments and from wildlife probably hampered the performance of the modified SWAT model, this study qualitatively confirmed the significance of *E. coli* release from streambed and deposition for the SWAT microbial water quality simulations.

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