

MODELING FECAL BACTERIA IN A SUBURBAN WATERSHED IMPACTED BY SEPTIC SYSTEMS

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Abstract. Watershed scale models such as the soil and water assessment tool (SWAT) are promising tools for studying the impacts of septic systems on water quality and quantity. In this study, SWAT was used to assess the influence of septic systems on bacterial loads in a suburban watershed. The model was first calibrated and validated for flow in the Big Haynes Creek watershed located in Gwinnett County, GA.

The model performed satisfactorily for flow predictions at the watershed level with Nash Sutcliffe Efficiency (NSE) values of 0.67 and 0.70 for calibration and validation periods, respectively. Flow predictions in the study area shows that on average septic systems contributed approximately 6% to the total water yield annually. This observation is significant and contradicts suggestions that septic systems are 100% consumptive use.

Although NSE values for bacterial predictions were low in this study, the results in general compares with previous SWAT bacterial studies and reflects the uncertainties involved in bacterial modeling at the watershed scale. Model results suggest that failing septic systems were not a significant source of fecal bacteria in streams.

In contrast, bacterial output was sensitive to instream deposition from livestock including cattle in the watershed. Further assessment of alternative pathways for effluent transport from failing septic systems into streams is necessary to fully understand septic influence at the watershed level.

BACKGROUND

Recent studies by the present authors suggest the impact of septic systems on microbial water quality of streams (Sowah et al., 2014; Sowah et al., 2016). These studies show that FIB loads in streams can be partly explained by the density of septic systems and the average distance of septic systems to streams in the watersheds. Understanding septic system impacts at the watershed level would require multiple approaches including watershed scale modeling. Watershed scale models such as SWAT have showed promise as a predictive tool for studying the impacts of septic systems on water quality and quantity (Oliver et al., 2014b; McCray et al., 2009).

The goal of this study was to evaluate the water quality impact of septic systems on bacterial loads using the SWAT watershed scale model.

METHODS

Study Area

The study area was the Big Haynes Creek watershed located in Gwinnett County, Georgia, USA (Fig. 1). The watershed, which has a USGS gage station at the outlet, is 44.77 km² in area and falls within the Altamaha River Basin in the Southern Piedmont physiographic region. The predominant land use in the Big Haynes Creek watershed is residential (approximately 65% of the watershed area). Other significant land uses include forest (25%), pasture/hay (8.7%) and septic systems (0.9%) based on an assumed septic drainfield area of 100 m².

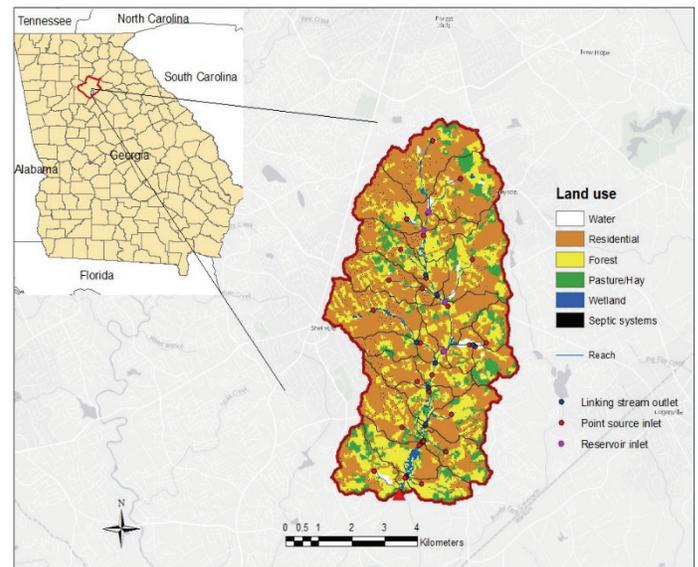


Figure 1. Map of study area showing land use distribution

SWAT model set-up

The SWAT model is a continuous-time, semi-distributed model and is interfaced with ArcGIS which provides capability to represent spatial data on land use,

topography, climate and hydrology (Arnold et al., 2012). The SWAT model was selected for this study due to the incorporated septic system subroutine which allows the modeling of septic influence at the watershed level. Major model components relevant to flow and bacteria include weather, hydrology, soil properties, agricultural operations, stream/pond/reservoir routing and septic systems (Gassman et al., 2007; Neitsch et al., 2011).

The model works by dividing the watershed into sub-basins which are further divided into hydrologic response units (HRUs) (Coffey et al., 2010). These HRUs are unique combinations of soil, land use and slope within the sub-basins and have no spatial context.

Watershed Delineation and HRU Definition

A 10 m digital elevation model (DEM) of the area was used to delineate the Big Haynes Creek watershed and estimate watershed characteristics such as slope, topography and flow direction. A threshold of 2% of the watershed area was used as a threshold to initiate a perennial stream to define the stream network and sub-basins in the watershed. The watershed was then delineated using the outlet at the USGS gage station (USGS 02207385 Big Haynes Creek at Lenora Road, Nr Snellville, GA). A total of 32 sub-basins were created with the watershed delineation tool in SWAT.

Bacteria Source Characterization

The main sources of fecal bacteria in the watershed include manure from grazing beef cattle, confined dairy cows and wildlife, instream deposition from livestock and runoff from failing septic systems.

Livestock and Wildlife

The amount of manure produced by cattle in the watershed was estimated from the stock density of animals in the watershed. A total of 184 cattle (122 beef cows and 62 dairy cows) were estimated for the watershed based on a stock density of 0.47 cows ha⁻¹ in Gwinnett County as reported by the Department of Agriculture (USDA Census, 2002). Due to inadequate data on wildlife populations in the watershed, only the effect of white-tailed deer was simulated in this study. A density of 0.14 deer per ha was used in the watershed (GDNR, 2007). Manure production rates and fecal bacterial loads are presented in Table 1.

Grazing operations were assumed to continue year round for beef cows and deer, and between the months of April and November for dairy cows. Manure accumulation from dairy cows during the winter was applied as a fertilizer to pasture/hay land use areas once a month from April to November.

Septic system loading

A total of 4,068 septic systems were located in the Big Haynes Creek watershed. Because the septic system algorithm in SWAT does not currently quantify bacterial loads from failing septic systems, effluent from failing systems

was land applied to septic HRU's as a continuous fertilization operation. The number of failing septic systems was estimated to be 43 septic units in the entire watershed based on septic systems located on poorly drained soils (hydrologic group D soils). It was assumed that septic systems on this soil type were prone to failure due to the low infiltration and high runoff potential of these soils. Table 1 details effluent and bacterial loading rates from failing septic systems.

Sensitivity analysis and calibration

The SWAT-Cup SUFI-2 calibration and uncertainty analysis program (Abbaspour, 2007) was used to calibrate and validate the SWAT model. The SWAT model was first calibrated for flow using 22 flow parameters identified from the literature and using expert judgment.

During the calibration process, global sensitivity analysis was performed to determine sensitive parameters to focus calibration efforts. The flow model for Big Haynes Creek was calibrated for the period 1998 – 2007 and validated for the period 2008 – 2013 with a warm-up of 4 years. The model was then calibrated and validated for bacteria by running simulations with bacteria parameters (Table 2). The bacteria sub-model was calibrated and validated in years 2003 and 2004 respectively for fecal coliform concentration (CFU 100 ml⁻¹) at the Big Haynes Creek outlet.

. Model evaluation

Model performance was evaluated using the recommendations from Moriasi et al. (2015). A combination of Nash-Sutcliffe efficiency (NSE) coefficient, coefficient of determination (R²) and percent bias (PBIAS) were used to assess model performance.

Table 1. Manure application rates for animals and failing septic systems

Source	Type of application	Manure input	Fecal coliform load (CFU/g)
Cattle	Grazing (kg dry wt. ha ⁻¹ day ⁻¹)	1.74	3.2 x 10 ⁶
	Fertilizer application (kg ha ⁻¹)	129	3.2 x 10 ⁶
	Instream deposition (CFU 100 ml ⁻¹)		1.6 x 10 ⁸
Deer	Grazing (kg dry wt. ha ⁻¹ day ⁻¹)	0.031	2.2 x 10 ⁵
Failing septic systems	Continuous application (kg ha ⁻¹)	31	1 x 10 ⁷

Table 2. List of bacteria parameters calibrated

Parameter	Min	Max	Criteria	Fitted value	Definition
BACT_SWF	0	1	v	0.93	Fraction of manure with active colony forming units
BACTKDQ	100	250	v	176	Bacteria soil partition coefficient.
BACTMX	8	19	v	16	Bacteria percolation coefficient in manure
WOF_P	0	1	v	0.44	Wash-off fraction for bacteria
THBACT	0.5	8	v	1.13	Temperature adjustment factor for bacteria die-off
WDPS	0	1	v	0.22	Die-off factor for bacteria adsorbed to soil
WDPRCH	0	1	v	0.34	Die-off factor for bacteria in streams at 20°C
BACTMINP	0	1	v	0.4	Minimum daily bacteria loss
BACTKDDB	0	1	v	0.96	Bacteria partition coefficient
BIO_MIN	-0.2	2	r	0.3	Minimum plant biomass for grazing
BIO_JNIT	-0.2	2	r	1.54	Initial dry weight biomass

v = replace existing value; r = an existing parameter value is multiplied by (1+ a given value)

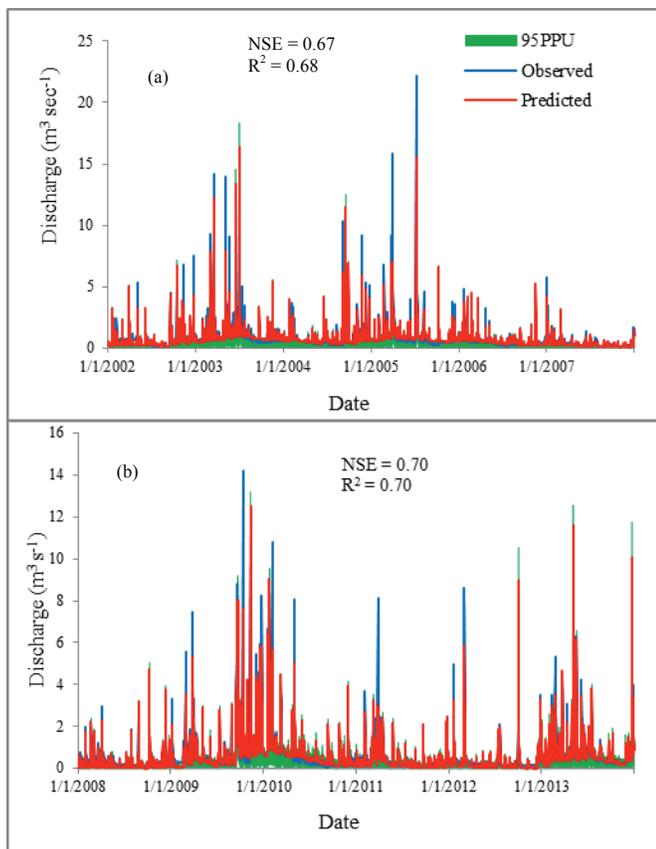


Fig. 2 Flow model calibration (a) and validation (b) at watershed outlet

The NSE index indicates how well the plot of observed versus simulated data fits a 1:1 line. Values of NSE ranges between $-\infty$ and 1.0 with $NSE = 1$ indicative of a perfect fit between predicted and measured values (Moriassi et al. 2007). The R^2 statistic describes the proportion of the measured data variance explained by the model and ranges from 0 to 1 with 1 indicating perfect model fit (Moriassi et al., 2007).

Another important performance metric is the PBIAS which measures the tendency of the simulated data to be larger or smaller than the observed values. The NSE, R^2 and PBIAS are widely used in hydrology and water quality modeling with extensive information on reported values for comparison (Moriassi et al., 2007). According to Moriassi et al. (2015), model predictions are satisfactory when daily $NSE > 0.50$, $R^2 > 0.60$ and $PBIAS \leq \pm 15\%$ for flow predictions. Similar performance criteria for bacterial modeling have not been described and as such model accuracy for bacterial predictions in this study was assessed relative to previous studies.

RESULTS AND DISCUSSION

Flow calibration and validation

After sensitivity analysis to determine important flow parameters to focus calibration efforts, the model was calibrated for flow using USGS flow data at the watershed outlet. In general, flow predictions at the outlet of Big Haynes Creek watershed was satisfactory based on performance criteria recommended by Moriassi et al. (2015). In this study, flow calibration on a daily time-step at the outlet of Big Haynes Creek resulted in NSE, R^2 and PBIAS of 0.67, 0.68 and 5.9% respectively (Fig. 2a). Model performance was slightly better during the validation period with NSE, R^2 and PBIAS of 0.70, 0.70 and 8.6% (Fig. 2b).

The flow model performance exceeded results reported by Oliver et al. (2014a) who modeled flow in the same watershed using shorter calibration and validation time intervals. It was estimated that septic systems contributed $\sim 6\%$ of the total water yield at the watershed outlet. This result compares with previous studies (Oliver et al., 2014a; Landers and Ankcorn, 2008) that all support a consumptive use less than 100%. This observation is also significant, especially during dry or drought conditions where the inflow from septic systems can be a significant source of recharge into the streams.

Bacteria sub-model

The results from sensitivity analysis showed that the temperature adjustment factor for bacteria die-off (THBACT), die-off factor for less persistent bacteria in streams at 20°C (WDPRCH) and instream deposition from livestock were the most sensitive bacteria parameters in the watershed. The observed effect of direct deposition by cattle into streams shows the impact these animals can have on water quality if given free access into water bodies. Even a small number of cows with direct access to water bodies can have profound effects on downstream water quality as observed in this study. Parameters relevant to overland transport of bacteria, including BACTKDQ (bacteria partition coefficient in surface runoff),

Manure_KG (amount of manure applied to soil) and septic effluent applied to the drainfield area, appears to

have little influence on bacterial output. Similar studies in the literature found THBACT to be one of the most sensitive parameters that affect bacterial fate and transport at the watershed level (Parajuli et al., 2009a; Niazi et al., 2015; Coffey et al., 2010).

Model predictions of bacterial concentrations ranged from 35 – 330 CFU 100 ml⁻¹ at the outlet of the watershed and were within the observed ranges (Fig. 3). On average, the model under-predicted bacterial concentrations by 6% for the calibration period and over-predicted concentrations by 5.4% for the validation timeframe. In general, both the predicted and observed bacterial concentrations did not follow the trend in discharge at the watershed outlet.

This suggests that runoff from land areas was not a significant source of fecal bacteria – contradicting the general trend reported in previous studies that shows increasing fecal bacterial loading from stormwater runoff. This finding could be partly due to uncertainties in livestock numbers and timing of manure applications in the watershed.

Comparison of the predicted and observed bacterial concentrations showed poor agreement, with low NSE estimates for both the calibration (NSE = -0.06) and validation (NSE = -0.16) periods. Although, the NSE estimates were low in this study, the PBIAS estimates were within the acceptable evaluation criteria recommended for modeling water quality parameters such as nitrogen and phosphorus (Moriassi et al., 2015).

CONCLUSIONS

This study demonstrated the influence of septic systems on watershed hydrology through effluent inflow into streams. Model results showed that, on average, septic systems contributed ~ 6% to total water yield in the study area. This observation is significant and challenges assumptions that septic systems are 100% consumptive use. Model results suggest that failing septic systems were not a significant source of fecal bacteria in streams when effluent was applied as a fertilizer operation in SWAT.

Other potential pathways for septic effluent transport into streams, such as through groundwater recharge and illicit connections need to be evaluated to fully understand septic influence at the watershed level. Finally, we recommend improvements in SWAT septic biozone module to include processes that directly account for bacterial transport from failing septic systems into streams.

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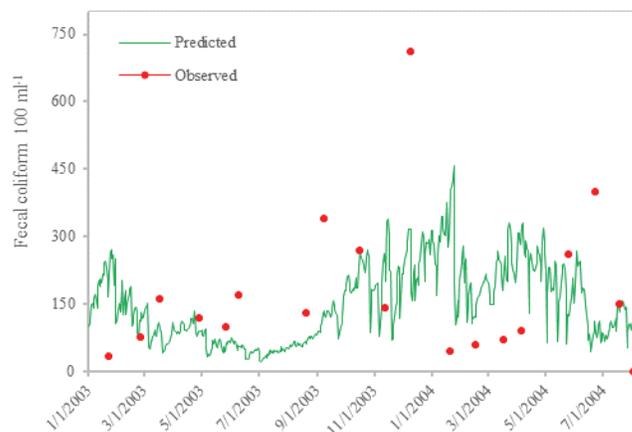


Figure 3. Comparison of predicted and observed bacterial concentrations at the watershed outlet

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