Bacteria Modeling with SWAT for Assessment and Remediation Studies: A Review

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Abstract. *A module to simulate bacteria fate and transport in watersheds was first tested in SWAT 2000 and fully integrated into the SWAT2005 code. Since then, few investigators have utilized SWAT to model bacteria fate and transport in spite of bacteria being a major cause of streams impairment in the U.S. In this article, bacteria equations are briefly presented. Modeling applications, which range from 16 to 3,870 km^2, from Missouri, Kansas, and Georgia in the U.S. and from Brittany in France, are reviewed, highlighting the modeling successes and the challenges. In all cases, land use included agricultural and forested land with a mix of point and nonpoint sources. Nonpoint sources included indirect (manure deposited on land) and direct contributions from cattle or wildlife to the streams. In some cases, urban and residential contributions were included. Strategies to represent the different sources, calibration methods, and goodness of fit were compared. Changes to the model's code that were necessary to handle contributions from urban areas were reviewed. Overall, SWAT reasonably simulated the range and frequencies of bacteria concentrations. In all cases, direct bacteria inputs into streams appeared to have a major impact on the model results. This review also indicates that the model processes that simulate the release and transport of bacteria in surface runoff may need to be revisited. This improvement could enable SWAT to be more reliable for predicting bacteria concentrations and evaluating the impact of different management scenarios on bacteria contributions to surface water resources.*

Keywords. *Bacteria, Bacteria fate and transport,* E. coli*, Fecal coliform, Modeling, Watershed.*

By the frequency of being the cause of water quality impairment, bacteria rank first and third among all pollutants in rivers and estuaries, respectively, in the U.S. (USEPA, 2009). This latest list of impaired waters also lists bacteria as the second most frequent cause of impairment in coastal and Great Lakes shorelines. Pathogen contamination in streams, lakes, and reservoirs is known to occur from variety of sources, including animal manure application, effluents from municipal wastewater treatment plants (WWTP), septic tanks, land application of sewage and sludge, pets, and wildlife.

An important feature of pathogenic microorganisms that distinguishes them from other waterborne contaminants is the difficulty of collection and enumeration. While enumeration of fecal coliform by the membrane filtration procedure is a common and relatively economical procedure (Rippey et al., 1987), the cost of monitoring pathogenic bacteria or protozoa oocysts in natural water is one to three orders of magnitudes more as compared with inorganic and organic contaminants (Pachepsky et al., 2006). In addition, the cost of bacterial source tracking to determine sources is beyond what most communities and agencies can afford. Thus, modeling capability has become an important management tool for estimating the contribution from each source, their combined impact, and the effectiveness of potential mitigation strategies. Early modeling efforts resulted in deterministic relationships that provided crude estimates of bacterial concentrations in runoff (Khaleel et al., 1979; Springer et al., 1983). Moore et al. (1989, 1983) proposed a "mass balance" approach and developed an event-based compartmental model (MWASTE) that describes bacterial movement from land-applied animal wastes through the various collection, storage, treatment, and land-spreading components of the manure management systems, and ultimately into runoff. Walker et al. (1990) developed a comprehensive, proba–bilistic-based model (COLI) to evaluate best manure management practices (BMPs). COLI, however, has not been adequately validated. Neither MWASTE nor COLI can be used to characterize the temporal variability of the populations under the variable climate inputs, management practices, and soil conditions.

Geographic Information Systems enabled watershed modeling at larger scales, taking into account the diversity of physical characteristics and anthropogenic sources that exist within these watersheds. Fraser et al. (1998) developed the GIS-based SED-MOD model that uses the spatial variations in loading rates to describe the amount of coliforms reaching streams as a function of delivery ratio (a weighted function, based on distance to stream and several other overland flow parameters). More recently, Tian et al. (2002) and Dorner et al. (2006) included microbial fate and movement equations into the GIS-based WAMstream and WATFLOOD hydrologic models. Their approach was to consider pathogen detachment and transport with runoff analogous to soil particles detachment and transport.

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To address the need for realistic simulations of the wide variety of management practices and pathogen sources in watersheds, equations were introduced in the Soil Water Assessment Tool (SWAT; Neitsch et al., 2005) to simulate the deposition, fate, and transport of bacteria. The equations, developed by Sadeghi and Arnold (2002), were based on previous modeling work and field studies conducted in Virginia during which fecal coliform and *E. coli* soil concentrations had been measured every 10 days for 150 days after dairy or beef manure application on pasture and corn plots. In general, the equations produced results that mimicked the observed trends. They were first successfully tested at the watershed level in the Shoal Creek watershed in Missouri (Baffaut and Benson, 2003).

Since then, the model has been applied in other watersheds, for various sources of contamination, and by different modelers in locations including Missouri (Baffaut and Benson, 2009; Baffaut, 2006), Kansas (Parajuli et al., 2006, 2009), Georgia (Chin et al., 2009), and Brittany, France (Bougeard et al., 2008). The goal of this review is to learn from past model applications and experiences gained to understand the research and model development needs that would hopefully lead to better bacteria source characterization and better simulation of bacteria fate and movement in the environment. Our objectives are to present and synthesize the equations used for bacteria fate and transport in SWAT, present and synthesize a set of SWAT applications for bacteria fate and transport, identify changes to the model that needed to be made, highlight strategies to represent and quantify bacteria loadings on the landscape, review calibration methods and goodness of fit, and identify future research needs.

Bacteria Fate and Transport Equations

The SWAT pathogen fate and transport component was first developed based on a two-population assumption, a mix of persistent and less-persistent strains of bacteria. This approach was followed to specifically reflect the two-stage kinetic decay normally observed in field studies. Alternatively, these two populations can be used to simulate two different bacteria. With consideration of this assumption, bacteria fate and movement is simulated by deposition of manure from grazing animals or fertilizer applications, adsorption to soil, decay, infiltration, incorporation through tillage, extraction by runoff, and transport by stream flow. Additional inputs to streams include legal or illicit connections, failing or poorly operating septic systems, and urban runoff.

The two main subsystems relevant to bacteria processes are the 10 mm surface soil layer and the streams. For each of these systems, mass balance theory is used to account for the bacteria loadings at the end of any given day. In the 10 mm surface soil layer, the inputs and outputs of bacteria can be represented by the following equation:

$$\Delta_{Bact} = Surface_{Loading} - Decay_{Solution} - Decay_{Adsorbed} - Mixed_{Bact} - Bact_{Surf} - Bact_{perc} - Bact_{sed} \quad (1)$$

where Δ_{Bact} is the change of bacteria loading in the 10 mm surface soil layer from one day to the next; $Surface_{Loading}$ is the total bacteria loading deposited on that day on the soil surface; $Decay_{Solution}$ and $Decay_{Adsorbed}$ are the amounts of bacteria in soil solution and adsorbed to soil particles that decayed on that day; $Mixed_{Bact}$ is the amount of bacteria redistributed to lower soil layers by tillage; and $Bact_{Surf}$, $Bact_{erc}$, and $Bact_{Sed}$ are the amounts of bacteria transported by runoff, percolation, and with moving sediment on that day. In addition, the surface loading is partitioned between bacteria in soil solution and bacteria adsorbed to soil particles, but that process does not modify the loading.

In the streams, the bacteria mass balance is represented by the following equation:

$$\Delta_{Stream-bact} = Bact_{Surf} + Bact_{Sed} + Direct\_inputs - Decay_{Stream} - Bact_{Flow} \quad (2)$$

where $\Delta_{Stream-bact}$ is the change of bacteria loading in a stream reach over one day; $Bact_{Surf}$ and $Bact_{Sed}$ are the loadings of bacteria in solution and adsorbed to soil particles transported by surface runoff; *Direct_inputs* are the bacteria loadings directly discharged into the streams by WWTP, wildlife, and other licit and illicit connections; $Decay_{Stream}$ is the amount of bacteria decayed during that day; and $Bact_{Flow}$ is the amount of bacteria transported out of the reach by streamflow.

The following describes the equations used in the model with a special emphasis on available or lacking data sources for estimating input parameter values and the effect that increasing or decreasing a parameter will have on the results.

Deposition of Bacteria From Grazing or Fertilizer Applications

Bacteria can be applied to the landscape by manure application or grazing operations, or to the streams by direct discharges. The bacteria loadings are specified by the concentrations of colonies forming units (cfu) of each pathogen population in the manure or direct discharge. The deposited amount is directly proportional to the amount deposited. Bacteria applied to the soil surface are then subjected to adsorption, decay, incorporation into the soil profile, and transport by runoff and soil particles. Bacteria directly added to streams are subject to only decay.

Multiple data sources exist for *E. coli* or fecal coliform concentrations in specific manures: Walker et al. (1990) for beef, Reddy et al. (1981) for livestock species and wildlife, Moore et al. (1989) for livestock, and Hartel et al. (2000) for broiler litter. However, these sources might be outdated and location-specific given the high dependency between bacterial production, genetics, and diet. A major data source is the ASAE (now ASABE) standards, which are regularly updated and include mean values and standard deviations of fecal coliform and streptococcus bacteria production for beef, dairy, swine, sheep, horses, layer hens, and ducks (*ASAE Standards*, 2003). These tables highlight the large variability of daily bacteria production, as the standard deviations are often very close and sometimes larger than the mean values. Attempts to characterize manure production from dietary models resulted in new values (*ASAE Standards*, 2005); however bacteria amounts were not included in this revision. The bacteria source load calculator (Center for TMDL and Watershed Studies, 2007) provides useful data and references on daily production of manure and bacteria concentrations for several wildlife species.

Adsorption to Soil

Adsorption to soil particles is the process used to simulate retention of bacteria by soil particles. It results in less bacteria in soil solution and available for transport by runoff. Bacteria deposited on the ground surface by grazing or manure applications are partitioned between soluble and adsorbed phases. The bacterial partition coefficient (KdDB) in the SWAT model controls how much of the active colony forming units contained in deposited bacteria (*Active_bacteria*) are in soil solution (*Bacteria_solution*) based on the following equation:

$$\mathrm{KdDB} = \frac{Bacteria\_solution}{Active\_bacteria} \quad (3)$$

where *Active_bacteria* is calculated as a function of the total bacteria content in the manure and the fraction of active colony forming units (BACT_SWF). Because of lack of information for each type of animal manure, if no value assigned to this parameter, the SWAT model sets BACT_SWF to 0.15. However, it could have a range of 0 to 0.50, depending on the type of animal manure.

The SWAT model considers that the bacterial partition coefficient is specific to each manure type and is independent of soil properties or land use. Only bacteria in soil solution are assumed to be available for extraction and transport by runoff; however, bacteria adsorbed to soil particles can also move with runoff when there is soil erosion. No data have been found to determine the value of this parameter for different types of manure. Given this lack of data, one could use this parameter during calibration. Its value directly affects transported bacteria loads by modifying how much is available to runoff.

Decay

Chick's law first-order decay equation is used to simulate decay of bacteria. Decay rates can be defined for each phase of the bacteria but are assumed to be independent of the source of the bacteria. Thus, decay rates are specified for each bacteria population, for the solution and the adsorbed phases, for different locations in the landscape: canopy, soil, streams, ponds, and reservoirs. In each phase and landscape location, bacteria decay is exponentially derived with time as:

$$bacteria(t) = bacteria(t-1) * \exp(-K) \quad (4)$$

where $bacteria(t)$ is the bacteria count of a bacteria population in one phase at one location on day t, and K is the decay rate (d^{-1}). This rate is calculated as a function of the soil or water temperature (T) and the decay rate at 20°C with the equation proposed by Mancini (1978):

$$K(T) = K(20)\theta^{(T-20)} \quad (5)$$

where θ is the temperature adjustment factor. Both θ and $K(20)$ are user-specified, and more data are available for these parameters than for any other bacteria-related parameter. Reddy et al. (1981) conducted an extensive review of published values of fecal and streptococci decay rates in soils and proposed equations to adjust these rates according to soil pH, soil moisture, soil temperature, and method of application. Hartel et al. (2000) presented data on fecal coliform decay in stacked broiler litter and on how temperature affected that decay. Litter moisture content was not shown to affect the decay rate in that case. In SWAT, $K(20)$ is specified for each type of bacteria (persistent or less persistent), each phase (adsorbed or in soil solution), and each location in the landscape (soil, stream, ponds, reservoirs). In each study, the authors defined only a subset of these decay rates: persistent bacteria in the stream (WDPRCH), persistent bacteria in soil solution (WDPQ), and persistent bacteria adsorbed to soil particles (WDPS).

Incorporation through Tillage

When manure is mixed with the topsoil by a tillage operation, bacteria incorporated within the tillage depth are calculated using equation 6, which is similar to incorporation of residues, nutrients, and pesticides:

$$bacteria = bacteria * (1 - emix) \quad (6)$$

where *bacteria* represent persistent or less persistent bacteria in soil solution or adsorbed to soil particles, and *emix* is the mixing efficiency of the tillage operation implemented. That characteristic is a property associated with the tillage implement selected, not a bacteria-specific input parameter. Once the bacteria have been incorporated into the second soil layer, they are no longer available for transport by surface runoff or by sediment.

Extraction by Runoff

The SWAT approach to simulate bacteria transport with surface runoff and percolate is similar to the approach used to simulate soluble phosphorus movement. Those equations, in turn, were based on pesticide equations proposed by Leonard and Wauchope (Pierson et al., 2001; Knisel, 1980) to partition the compound between the soluble and sediment phases.

Transport of bacteria from the soil surface layer (top 10 mm) due to runoff is a function of both runoff volume and soil/bacteria interaction (eq. 7). This equation is derived from the assumption that bacteria are mostly associated with sediment in the top soil layer. The strength of this association is embedded in the bacteria-soil partitioning coefficient (BactKdQ):

$$bacteria_{surf} = \frac{bacteria_{solution} * Q_{surf}}{\rho_b * depth * \mathrm{BactKdQ}} \quad (7)$$

where $bacteria_{surf}$ is the amount of bacteria transported by runoff (cfu m^{-2}), $bacteria_{solution}$ is the amount of bacteria in soil solution in the top 10 mm (cfu m^{-2}), Q_{surf} is the volume of surface runoff (mm), ρ_β is the bulk density (Mg m^{-3}), *depth* is the thickness of the surface soil layer (10 mm), and BactKdQ is the bacteria-soil partitioning coefficient (m^3 Mg^{-1}). This user-specified coefficient is the ratio of the bacteria concentration in the top soil layer to that in the surface soil water. It is assumed to be independent of the type of bacteria simulated in the model, the land use and land cover, or the soil type. Little data exist for determining its precise value, and it is often used as a calibration parameter. No indication is given regarding the range of values this parameter can take for bacteria. However, the stronger the bacteria associate with sediment, the higher the value of BactKdQ. For phosphorus, the default value is reported as 175 in SWAT (Neitsch et al., 2004), 175 in the Erosion Productivity Impact Calculator (EPIC) (Williams, 1995), and 100 in the Agricultural Policy Extender (APEX) model (Williams et al., 2008) with a range of 100 to 200 (Steglich and Williams, 2008).

Thus, a value between 100 and 200 is a logical start for the calibration of bacteria movement.

Experimental work by Soupir et al. (2006) provided some insight into the proportions of planktonic and attached *E. coli* in surface runoff from vegetated pastures and bare plots. The results indicated low and higher amounts of attached bacteria in well managed pastures and bare plots, respectively. However, higher erosion rates from bare plots may impact the attachment ratio calculated, and the results cannot be used directly to estimate the bacteria-soil partitioning coefficient used in equation 7.

Infiltration

Movement of bacteria in the soil matrix has mostly been assessed in relation to the contamination potential of subsurface and groundwater resources (McMurry et al., 1998; Gannon et al., 1991). However, leaching of bacteria in SWAT is simulated only from the surface layer to the second soil layer, primarily to remove bacteria from potential transport by surface runoff or soil movement. Once the bacteria reach the second layer they are no longer available for surface transport.

Transport of bacteria from the upper soil layer to the second soil layer is determined using equation 8:

$$bacteria_{perc} = \frac{bacteria_{solution} * W_{perc}}{10 * \rho_b * depth * \text{Bactmix}} \quad (8)$$

where $bacteria_{perc}$ is the amount of bacteria transported from the first to the second layer (cfu m^{-2}), $bacteria_{solution}$ is the amount of bacteria in the top 10 mm (cfu m^{-2}), w_{perc} is the volume of percolate from the top 10 mm to the second soil layer (mm), ρ_b is the bulk density (Mg m^{-3}), *depth* is the thickness of the surface soil layer (10 mm), and Bactmix is the bacteria percolation coefficient (10 m^3 Mg^{-1}), which is the ratio of the bacteria concentration in the surface 10 mm of soil to the bacteria concentration in solution in the percolate. Again, there are few guidelines on the values of this last parameter. The default value is 10 with a range from 7.0 to 20.0, which are the values used for percolation of soluble phosphorus. Given the lack of information specific to bacteria percolation, these same default values were adopted.

The procedure used here is also similar to calculating percolation of soluble phosphorus from the first to second soil layer. Further percolation of bacteria through the soil profile and to the aquifer is currently not simulated.

Transport by Sediment

The movement of bacteria adsorbed to soil particles is based, in SWAT, on the concept of the enrichment ratio. The amount of bacteria transported with sediment is calculated as a function of the concentration of bacteria attached to sediment in the soil, the sediment yield, and the enrichment ratio for bacteria. This ratio is calculated as a power function of the sediment concentration in surface runoff. The SWAT user's manual (Neitsch et al., 2004) details all these equations; since no input parameter is user-specified, the information is not repeated herein.

Direct Inputs to the Stream

Direct inputs to the streams include pathogen discharges from permitted facilities such as wastewater treatment plants as well as inputs from grazing livestock or wildlife and illicit connections. All direct inputs to the streams are described in SWAT as point sources, and the model allows for one point source per subbasin. Thus, all point sources in each subbasin need to be aggregated and characterized by a single discharge (volume per day, month or year) and an associated bacteria concentration. While permitted facilities are known and monitored, illicit discharges are by definition not inventoried or known. Direct bacteria loadings to the streams from livestock or wildlife are also difficult to estimate because they are a function of animal density, habitat, watering points, diet, and weather.

Transport by Stream Flow

Once in the stream, bacteria in solution and adsorbed to sediment are treated the same and together. Bacteria are subject to advection by the moving water in the streams and are considered at this point a dissolved pollutant. As mentioned earlier, first-order decay adjusted by water temperature is applied to each of two types of bacteria. Similarly, first-order decay occurs in ponds and reservoirs with specific decay rates for each bacteria population and water body.

Description of SWAT Bacteria Applications

Studies of watershed-scale bacteria transport were conducted in Missouri, Kansas, Georgia, and France. The general characteristics of each watershed are described in table 1 with additional general information provided below.

Missouri Studies

Several studies were conducted in southwest Missouri, where poultry and cattle operations are important economic activities. These agricultural operations, along with urban centers, residential housing, and tourism, contribute to elevated surface loadings of bacteria in the landscape and direct discharges in the streams. The high rock content of the soils and the karst topography features of the region impede the filtering and self-treatment capacity of these soils, leading to high bacteria counts in streams and lakes. Two watersheds were studied: the Little Sac watershed (Baffaut, 2006) and the James River basin (Baffaut and Benson, 2009). Nonpoint sources included grazing cattle, failing septic tanks, poultry litter applications, and wildlife. Point sources included bacteria contained in WWTP discharges and in spring flow. In the Little Sac, 30 years of continuous flow were available at one station and one year of weekly (March-October) or monthly (November-February) *E. coli* concentrations at two stations. In addition, bacterial source tracking was performed to estimate the contributions of each bacteria source. In the James River basin, more than 30 years of continuous flow were available at five stations in the watershed. Monthly *E. coli* concentrations were measured for seven years at four stations.

Kansas Studies

Three watersheds in the Upper Wakarusa watershed in northeast Kansas were studied for bacteria transport: the Rock Creek watershed, the Auburn watershed, and the Deer Creek watershed. Sources included livestock (cattle), humans (failing septic tanks), and wildlife. Information about

Table 1. General characteristics of the watersheds featured in each study.

		Little Sac, Missouri	James River, Missouri	Upper Wakarusa, Kansas	Little River, Georgia	Mignonne River, Brittany, France
Area (km^2)		644	3,600	51-152	17	68
Nonpoint sources		Cattle, septic systems, wildlife	Cattle, poultry, septic systems, wildlife	Cattle, septic systems, wildlife	Wildlife	Dairy manure
Point sources		WWTP, springs	WWTP, springs	Cattle, septic systems, wildlife	WWTP	Wildlife
No. of flow gauges		1	5	0	1	1
No. of water quality monitoring sites		2	4	3	4	1
Land use (%)	Row crops	0	0	23-39	45	45
	Pasture	67	63	51-70	25	--
	Wood land	30	30	6-9	20	55
	Urban	3	7	--	10	--
Soils		Silt loams	Gravelly silt loams	Silty clay loams	Clay loams	Sandy loams

this work was obtained from Parajuli et al. (2006, 2009). Direct discharges of feces and associated bacteria into the streams were assumed to be 10% of the loadings deposited on the land. Monitoring data included two years of weekly (April-September) or monthly (October-March) fecal coliform concentrations at the outlet of each watershed. Flow at the time of sampling was estimated using the Manning's equation. Bacterial source tracking using antibiotic resistance was performed in the three watersheds.

Brittany Study

The study concerns a small coastal watershed in Brittany, France, which was heavily impacted by runoff from dairy operations and point discharges from urban centers. Information about this work was obtained from Bougeard et al. (2008) and from personal e-mail communications with M. Bougeard (scientist with Idhesa, Plouzané, France, May through June 2009). Sources of bacteria in the watershed included applications of dairy manure on crop fields and point discharges from wastewater treatment plants. The stream discharged into an estuary used for shellfish harvest. Monitoring data included one year of weekly flow and *E. coli* concentrations at four points in the watersheds, with additional *E. coli* concentration values available at one of them. Continuous flow data were available at one of the four points. Additionally, shellfish *E. coli* concentration data collected from 1991 to 2007 were available and used as a surrogate for *E. coli* concentrations in the waters of the estuary.

Georgia Study

The study concerns a 16.7 km^2 subcatchment of Little River watershed in south central Georgia. Results and information about this study were obtained from Chin et al. (2009). Soils are sandy and underlain by limestone at a depth of 2 m. The watershed is characterized by row crop agriculture (45% of watershed) and forested areas (55% of watershed) used for recreational hunting. Wildlife is the primary source of bacteria loadings on the landscape as well as through direct inputs into the streams. However, no attempt was made to identify and quantify the source of the stream bacteria loadings. Bacteria direct inputs into the streams and application rates on the landscape were considered calibration parameters of the model. Continuous flow data were available for seven years during which 53 instantaneous samples were collected at the outlet of the watershed and analyzed for fecal coliform.

Strategies to Represent and Quantify Bacteria Loadings

In Missouri, Kansas, and Brittany, bacteria loadings were estimated based on the land use of the watershed along with agricultural statistics. Agricultural activities were inventoried from local knowledge and quantified from county-based agricultural statistics or surveys. In Missouri and Kansas, the National Agricultural Survey Statistics were used as a mean to estimate cattle and poultry numbers, poultry litter application rates, grazed areas, and grazing densities. Final loadings were estimated from the number of animals and published manure bacteria content. Permitted facilities were defined by either the permitted flow or, when available, actual average or measured daily flow discharge obtained from the facilities or the state information database. In Brittany, bacteria loadings were estimated from livestock numbers estimated from farm surveys and aerial photos (cattle, hogs, and poultry), watershed population, and published manure bacteria content. Data were available to quantify the discharges from wastewater treatment plants and their bacteria concentration.

In contrast, in the Georgia study, bacteria surface loadings and in-stream inputs were considered unknown parameters of the model and adjusted during calibration. There was no attempt to quantify these loadings by other means. This methodology was likely justified because the main source of bacteria in that watershed came from wildlife, which is not well quantified anywhere. While game or endangered species are monitored, other wildlife population estimates are often derived from secondary sources of information, such as road or hunting kills, and there is no standardized and agreed upon method to quantify them.

Changes to the Code

All of these studies were performed with SWAT2005. Some additional changes were incorporated into the model to accommodate urban areas and karst features in the Little Sac

and James River basin studies in Missouri. For urban areas, the model was modified to account for the high bacteria concentrations of urban surface runoff. Set concentrations for urban surface runoff were defined: 549 colonies per 100 mL for the Little Sac study (the average value measured in this region) (Baffaut, 2006) and 5000 colonies per 100 mL for the James River study, considered to better represent runoff from impervious areas (Baffaut and Benson, 2009).

Karst hydrology was an important factor in these two studies as well. The problem was handled in two different ways. In the Little Sac study, high infiltration rates were specified for the channels of streams classified as losing streams. In addition, springs were defined by point sources. Since these springs were sometimes contaminated with bacteria (Baffaut, 2006), an average concentration was derived from available measurements and specified in the point source definition. In the James River study, losing streams were defined in the same way. For sinkholes and springs, a modification of the code was introduced to allow rapid vertical infiltration of water through sinkholes to the shallow aquifer. Return flow was then calculated by the model as a function of the water depth in the shallow aquifer. No springs were defined, but increased return flow resulted from the additional rapid infiltration. These changes resulted in a modified partition of surface and groundwater flow and improved simulation results during droughts (Baffaut and Benson, 2009). Bacteria fate and movement equations were not modified and, to our knowledge, the SWAT code was also not modified for the Kansas, Georgia, and Brittany studies.

Calibration Methods and Goodness of Fit

Flow Calibration

In Missouri, flow calibration was achieved manually using the r^2 value and the Nash-Sutcliffe efficiencies for daily flow values. One gauge was available on the Little Sac River, and five gauges were available for the James River basin. The length of the flow records available for calibration and validation was 30 years in both cases.

In Kansas, flow was manually calibrated at the outlet of one of the watersheds: Rock Creek watershed. Since only three years of data were available, the model was verified using data from the two other watersheds instead of validating over a different time period.

In Brittany, flow autocalibration based on the shuffled complex evolution algorithm was performed at one gauge using four years of daily data. Three years of daily flow data were available for the validation of the model. In addition, simulated flow values at the outlet of two other subbasins were compared to measurements made over six months on a weekly basis.

In Georgia, flow autocalibration was based on a maximum likelihood method (Chin et al., 2009) for three years of daily data. The model was not validated in the bacteria study. However, other studies for which a SWAT model has been calibrated and validated for the Little River watershed or some of its subwatersheds suggest that the authors had a good understanding of the model behavior in that watershed (Feyereisen et al., 2007; Van Liew et al., 2007).

Bacteria Calibration Based on Concentration Frequency Curves

Frequency curves of fecal coliform bacteria concentration values were the calibration basis in the Missouri and Brittany studies. Concentration frequency curves of measured and simulated values were developed for each sampling point using all the data available during the calibration period. The prediction efficiency (PE), i.e., the coefficient of determination (r^2) between the curves from measured and simulated values, was the goodness of fit indicator. True r^2 values and Nash-Sutcliffe efficiencies (NSE) were also calculated. The following parameters were adjusted to obtain the highest prediction efficiencies: the bacteria-soil partitioning coefficient (BactKdQ), the bacterial partition coefficient (KdDB), the fraction of manure containing active colony forming units (BACT_SWF), spring bacteria concentrations, stream decay rate of bacteria (WDPRCH), as well as decay rates in soil solution and adsorbed to soil particles (WDPQ and WDPS).

Using this methodology, correct ranges and frequencies of concentration values were consistently reproduced. Of interest for land managers, this method ensures that the model can be utilized to compare the impact of different land management scenarios on the frequency of occurrence of fecal coliform concentrations or loadings.

Calibration Based on NSE and r^2 Values of Concentrations

In the Kansas study, the Nash-Sutcliffe efficiency and the r^2 values were used to manually adjust the bacteria parameters of the model; BactKdQ and the temperature adjustment factor for bacteria die-off (θ) were the only parameters adjusted during bacteria calibration. Final values were equal to initial default values, i.e., the default values were those producing the best results.

In the Georgia study, the landscape and stream inputs were also adjusted during the calibration. In total, six bacteria parameters were identified as sensitive and selected for calibration: BactKdQ, the bacteria percolation coefficient (Bactmix), the daily stream inputs, the bacteria application rate on agricultural and forest land, the rate of bacteria decay in the stream (WDPRCH), and the decay rate in soil solution (WDPQ).

Results

Table 2 presents the final input parameters and variables for the five SWAT applications in the U.S. and France. Surface loadings for the Missouri and Kansas studies were not homogeneous throughout the watershed, and an average value was calculated to compare with values obtained for the other watersheds. Similarly, in the Brittany study, the value in table 2 represents an average value calculated by considering the total amount spread on all cropland between January 15 and June 30. In fact, a specific schedule of applications on each crop field was specified to represent the true manure management.

Overall, surface loadings were comparable between the five watersheds, as they differed by two orders of magnitude at the most. Considering the differences in location and agricultural practices, and the variability and uncertainty in bacteria concentrations in animal feces, these differences are remarkably small. The differences that appear can be ex-

Table 2. Comparison of input parameter values for five studies in the U.S. and France.

	Unit	Little Sac, Missouri	James River, Missouri	Rock Creek, Kansas	Little River, Georgia	Mignonne River, Brittany, France
Area	km^2	644	3,600	75	17	68
BactKdQ	$m^3\ Mg^{-1}$	75	90	175	0.53	90
KdDb	--	0.9	0.9	0.9	*0.9*[a]	*0.9*
θ	--	1.07	1.07	1.07	*1.07*	1.07
Bactmix	$10\ m^3\ Mg^{-1}$	10.0	10.0	10.0	5.60	10.0
SWF	--	0.55	1.00	0.15	0.15	1.00
WDPRCH	d^{-1}	1.05	1.05	2.01	2.33	0.35
WDPQ	d^{-1}	0.32	0.11	0.40	0.00	2.01
WDPS	d^{-1}	0.032	0.010	0.040	N/A[b]	0.023
Direct stream input	$\times 10^6$ cfu $ha^{-1}\ d^{-1}$	2.3×10^{-1}	7.2×10^{-1}	3.7×10^3	2.1×10^1	1.0×10^2
Surface loadings	$\times 10^6$ cfu $ha^{-1}\ d^{-1}$	2.6×10^3	1.8×10^3	3.7×10^4	1.3×10^3	4.1×10^5

[a] Values in *italics* indicate that no information about these parameters was found and default values were assumed.
[b] N/A = value not available.

plained by the differences in sources. The smallest surface loadings were obtained by calibration in Georgia where they are due to wildlife grazing. While those were only slightly smaller than the values estimated for the Missouri studies (cattle grazing, septic systems, and some poultry litter applications), loadings used in the Kansas studies (pasture cattle grazing, wildlife, and septic systems) were slightly more than one order of magnitude larger. The higher surface loading value used in Brittany reflects the higher concentrations of bacteria in dairy manure.

Some direct stream inputs of bacteria were specified for all the watersheds. In Missouri, they were estimated from monitoring of WWTP and springs. In Kansas, direct stream inputs were assumed to be 10% of the surface bacteria loadings. In Georgia, they were part of the calibrated inputs; in Brittany, they were estimated from populations served by the wastewater treatment plants. To facilitate comparison between the watersheds and compare surface loadings with stream direct inputs, average total daily stream inputs were divided by the watershed area to obtain a stream direct input density. Overall, direct stream inputs were small in comparison to what was spread or deposited on the land. For all the watersheds except in Kansas, the stream direct input density was two to four orders of magnitude smaller than the surface loadings. However, organisms deposited on the land decay during dry weather without contaminating the water, while those deposited directly in the streams contribute to the problem right away. All investigators pointed to the importance and the sensitivity of these direct stream inputs.

There were larger differences in direct stream inputs than in surface loadings among the five watersheds. Direct stream inputs were smallest for the Missouri studies, in spite of the presence of WWTP in these two watersheds. Treatment plants that discharge in losing streams are required to disinfect the effluent before release. In addition, direct wildlife contributions to the streams were not considered in these two studies. The largest stream direct inputs were obtained for the Kansas study, where they were one order of magnitude larger than in Brittany (WWTP) and two orders of magnitude larger than in Georgia (wildlife).

The stream decay rate of fecal coliform bacteria was different in all cases but reflected the climatic conditions in each area. In the cooler spring-fed waters of Little Sac and the James River, the decay rate was lower ($1.05\ d^{-1}$). The value in Kansas corresponds to a faster decay in warmer, non-springfed waters ($2.01\ d^{-1}$). In the Little River of Georgia, warmer temperatures could explain the higher stream decay rate ($2.33\ d^{-1}$). In Brittany, the cooler temperatures and higher cloud cover can explain the lower decay rate ($0.35\ d^{-1}$).

Similarly, the decay rates of bacteria in soil solution were different for all the watersheds and ranged from $0.0\ d^{-1}$ in Georgia to $2.01\ d^{-1}$ in Brittany. Except in Georgia, this parameter was first estimated from published literature and then adjusted during manual calibration. In Georgia, the parameter was determined by autocalibration. These different rates may reflect different types of manure, soil types, land cover, and climate.

Finally, the automatic calibration algorithm utilized in the Georgia study led to a much higher Nash-Sutcliffe efficiency but a very different value of the bacteria soil partitioning coefficient (BactKdQ). The BactKdQ of the Georgia study was very low compared to those used in Missouri, Kansas, and Brittany.

Table 3 compares the goodness of fit criteria for fecal coliform or *E. coli* concentrations between the different applications. The Little Sac watershed was not included in table 3 because the goodness of fit between the concentration frequency curves was assessed only visually. Sample sizes indicate

Table 3. Comparison of calibration and validation goodness of fit criteria for four groups of studies in the U.S. and France.

	Missouri		Kansas			Georgia	Brittany, France	
	James River	James River	Rock Creek	Deer Creek	Auburn	Little River Subcatchment K	Point 1	Points 2-4
NSE flow	0.33-0.56	0.24-0.56	0.83	0.82	0.76	0.65	0.80	
Run type[a]	Cal	Val	Cal	Ver	Ver	Cal	Cal	Ver
Sample size	30-43	18-33	60	60	60	53	49	36-39
NSE	-6.0-0.11	0.0-0.21	0.20	0.31	-2.2	0.73	-1.0	N/A
r^2	0.0-0.24	0.0-0.26	0.42	0.41	0.36	N/A	0.0	N/A
PE	0.65-0.88	0.33-0.99				N/A	0.99	0.96-0.99

[a] Cal = calibration, Val = validation, and Ver = verification.

that, in each case, the calibration and validation of the model was performed with data sets ranging from 18 to 60 data points.

Whenever calculated, prediction efficiencies were all greater than 0.65, except in one case in the James River basin where it was 0.33. Nash-Sutcliffe efficiencies and coefficients of determination ranged from low (negative to 0.2) to moderate (02 to 0.4), except in the case of the Georgia study where a Nash-Sutcliffe efficiency greater than 0.7 was obtained. These results indicate that the frequencies and ranges of bacteria concentrations can be simulated, but the correspondence between calculated daily concentrations and the concentrations measured in the grab samples is variable, and sometimes poor.

DISCUSSION

The five studies presented in this article all pointed to the importance of direct stream inputs. However, the sensitivity of the model results and of the goodness of fit to this type of input could be an artifact of the data sets used in these studies. In all watersheds but in Kansas, flow information was available on a continuous basis and aggregated on a daily basis for comparison with SWAT output. On the other hand, all bacteria data sets consisted of grab samples collected at best on a weekly basis. No watershed had access to a refrigerated autosampler and to a sample collection protocol that would have allowed the systematic collection and analysis of storm water samples, including samples collected during the rising stage of the hydrograph. Analysis of the Little Sac flow and water quality data showed that 24% of the samples were collected during storm flow conditions, or nine samples out of 38. It is probable that only a fraction of these were collected during the rising phase or peak stage of the hydrograph. We expect similar conditions in the Kansas and Georgia studies given that the sampling operating procedures were similar. The Brittany data set may have contained more events because rain events are more frequent in Brittany than in Missouri or Kansas. Thus, base flow conditions were over-represented relative to storm events in these data sets, and none of these watersheds had sufficient bacteria data to adequately calibrate the model over the full range of flow conditions. During base flow conditions, direct stream inputs, i.e., discharges from wastewater treatment plants, cattle and wildlife direct deposits into the streams, and spring contributions, are the only source of bacteria. Consequently, it is logical that the goodness of fit of these models would be more sensitive to these inputs.

In all studies, only one type of bacteria, persistent or less persistent, was considered. None of the studies discussed the possibility of using two types of bacteria to represent either two groups of bacteria present in the watershed or a two-stage decay mechanism for the bacteria under study. Making use of this assumption would require additional information, including the partition of the initial bacteria population into persistent and less persistent groups and the definition of decay rates for each group. Finding data to parameterize the bacteria equations using only one group is sufficiently challenging that a lower number of parameters may be preferable at this point.

To further test the model at the watershed scale, sampling protocols need to be designed to characterize bacteria concentrations during storm events. This presents some challenge because of the requirement of analyzing the samples within 4 to 6 h after collection, according to standard operating procedures. However, from a study by Pope et al. (2003) conducted at different sites, in varying conditions, and with various analysis methods, *E. coli* densities measured in samples held for longer than 8 h at temperatures greater than 0°C but below 10°C were, in general, not significantly different from those measured within 8 h of the collection time. Thus, upon further verification, it could be possible to relax the 4 to 6 h time constraint to facilitate sample collection during storm events.

The automatic calibration of the bacteria parameters led to widely different values of the bacteria soil partitioning coefficient (BactKdQ), which is the ratio of the bacteria concentration in the surface soil layer to that in surface runoff. This parameter affects how much bacteria will move with runoff given the runoff depth and the amount of bacteria present in soil solution. For example, a value of 0.53 implies that for all but the smallest events, all of the bacteria in soil solution will be transported. A value of 175 implies that only the largest events will carry away all of the bacteria, and smaller events will transport only part of what is available. Additionally, a value less than one is questionable since it implies that the runoff is richer in bacteria than the soil water in the surface layer. In their sensitivity analysis, Parajuli et al. (2009) reported that this parameter had an effect on the Nash-Sutcliffe efficiency (to measure the goodness of fit) only when less than 100. While leading to encouraging results in terms of goodness of fit, these low values of the bacteria soil partitioning coefficient raise questions regarding the validity of the assumptions used to simulate the transport of bacteria by runoff. On the other hand, the poor results obtained with parameter values in the expected range lead to questions as well. These discrepancies indicate a need for additional field research to improve our knowledge of the transport and decay processes and to determine the parameterization of the equations that represent them. A few studies have attempted to assess the partitioning of bacteria between dissolved and adsorbed phases during runoff transport. However, they are sometimes contradictory with some concluding that bacteria primarily attached to sediment particles (Ling et al., 2002; Henry, 2004) while others (Muirhead et al., 2005, 2006; Soupir et al., 2006) demonstrated a preference for the dissolved phase. Thus, additional work is needed in this area.

CONCLUSION

The objectives of this review were to synthesize the methodology and results from five SWAT studies to simulate fecal coliform and *E. coli* transport from the agricultural landscape and out of the watershed. Model predictions for bacteria were variable. In general, SWAT adequately simulated the range and frequencies of bacteria concentrations. However, the goodness of fit ranged from poor to good. Bacteria surface loadings were part of the calibration parameters of the model for one study. In the other studies, surface loadings and direct stream inputs were estimated based on the livestock and human populations in the watershed and agricultural management practices. Surface loadings were similar within two orders of magnitude between the five watersheds, a relative small value given the geographic and land use differences.

Stream direct inputs were more variable: five orders of magnitude between the smallest and highest stream direct input densities, which we defined as the daily bacteria stream input per unit area of the watershed. In all studies, stream direct inputs were identified as having a major influence on the model results and goodness of fit. However, monitoring protocols that favored base flow conditions, which are impacted only by direct stream inputs, could explain these results.

A review of available sources to estimate decay rates of fecal coliform and *E. coli* from various manures in different environments showed a significant amount of data to help in the estimation of these parameters. Values used in this study could be explained by climatic differences among the locations.

The lack of guidance on values for key parameters such as the bacterial partition coefficient or the bacteria-soil partitioning coefficient suggests that additional research is needed in this area. Additionally, the calibration efforts conducted in the Georgia study led to values outside of the expected range. In others, the goodness of fit for bacteria concentrations was poor to moderate. These results indicate that the equations that simulate the release and transport of bacteria in surface runoff may need to be revisited and tested. This could enable the SWAT model to be more useful for the prediction of bacteria concentrations and allow water resource managers to evaluate the impact of different management scenarios beyond the magnitude, range, and frequencies of bacteria concentrations.

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