Sensitivity of fecal coliform bacteria transport to climate change in an agricultural watershed
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ABSTRACT
Climate change is expected to have impacts on our surface water resources, especially on the deterioration of surface water quality. The objectives of this study were to develop a calibrated and validated watershed model for daily streamflow and daily fecal coliform bacteria (FCB) concentrations using the Soil and Water Assessment Tool (SWAT) for the Big Sunflower River Watershed (BSRW) and to assess the sensitivity of FCB concentrations to changes in precipitation, temperature, and CO2 concentrations. The model demonstrated reasonable performances in simulating daily streamflow ($R^2 = 0.64–0.77$, $NSE = 0.57–0.75$) and FCB concentrations ($R^2 = 0.56–0.60$, $NSE = 0.23–0.40$) as compared to the previous literature. The one-at-a-time sensitivity analyses showed that average FCB concentrations were sensitive to changes in rainfall, temperature, and CO2 concentrations. Increased rainfall caused greater wash-off of FCB colonies from soil surfaces, while increased temperatures caused a decrease in surface water bacteria concentrations due to increased bacteria die-off rates. The CO2 concentration parameter was determined as the least sensitive parameter in this study.

Key words | climate change, fecal coliform bacteria, hydrology, water quality, watershed modeling

INTRODUCTION
Deterioration of surface water quality in the USA is a growing concern and a major health issue. According to section 303(d) of the Environmental Protection Agency’s (EPA) Clean Water Act, pathogens, specifically fecal coliform and Escherichia coli (E. coli), are the largest cause of water quality impairment in the USA (EPA 2015). Pathogen contamination currently impairs over 257,495 km of rivers and streams within the USA (EPA 2015). Bacteria pollution in surface water can lead to serious health risks and illnesses such as typhoid fever, diarrhea, hepatitis, and cholera, among others (Pruß 1997; Leclerc et al. 2002; Parajuli et al. 2009; Thilakaratne et al. 2018). Sources of bacteria in surface water are mainly from manure applications, grazing operations, waste water treatment plants (WWTPs), failing septic systems, and wildlife (Parajuli et al. 2009). Most of these sources are prevalent in agriculturally dominated watersheds that contain large populations of livestock and rural households that rely on septic systems for waste disposal (Jayakody et al. 2014).

Bacteria transport and survival rates are dependent on the physical, chemical, and hydrological conditions in the watershed. For example, bacteria survival has been shown to be dependent on soil characteristics such as soil water content, porosity, nutrient availability, and soil texture (Ranjard & Richaume 2001; Holden & Fierer 2005). Suspended sediment particles in storm water runoff can also affect the survival and transport of bacteria by providing an attachment source for bacteria (Schillinger & Gannon 1985; Davies et al. 1995; Russo et al. 2011). Studies in New Zealand have demonstrated that bacteria concentrations in surface water drastically increase as a result of flooding in the watershed (Nagels et al. 2002; Muirhead et al. 2004). Scientists and researchers in the past have also demonstrated that concentrations of bacteria in surface water are...
controlled by the climate conditions of the watershed. A one plot-scale study in Virginia found that rainfall events following manure applications resulted in bacteria concentrations in surface water that were up to four orders of magnitude higher than established water quality standards for the basin (Mishra et al. 2008). Mallin et al. (2009) reported that fecal coliform bacteria (FCB) concentration was significantly higher during rainfall events compared with periods with no rainfall. On the other hand, bacteria populations in surface water have been shown to decrease or be susceptible to inactivation in the presence of increasing temperatures (Schijven & de Roda Husman 2005; Cho et al. 2010; Blaustein et al. 2013).

Because bacteria survival in natural surface waters is dependent on climatic conditions, it is important to understand how the potential impacts of future climate change can affect the fate and transport of bacteria within a given watershed. The Intergovernmental Panel on Climate Change (IPCC) predicts that global mean surface temperatures are expected to increase by 2.6–4.8 °C by the years 2081–2100 (IPCC 2013). General circulation model (GCM) results indicate that the magnitude and frequency of extreme rainfall events will most likely increase (IPCC 2013). Also, the instances and duration of drought are expected to increase in many areas around the world by the end of the 21st century (IPCC 2013).

Past researchers have recommended using a watershed modeling approach along with downscaled climate models to assess the impacts of climate change on bacteria fate and transport (Coffey et al. 2009). So far, little research has been conducted in the Big Sunflower River Watershed (BSRW) to investigate the possible impacts of future climate change on FCB concentrations in surface waters using a watershed modeling approach (Fonseca et al. 2014; Jayakody et al. 2014). However, before attempting to quantify the impacts of climate change, it is imperative to understand the sensitivity of FCB survival and transport to changes in each individual climate parameter such as increasing temperatures, changing rainfall patterns, and CO2 concentrations within a watershed. Model parameterized in this watershed can be used in any other watersheds with similar characteristics. Identification of bacteria sources within the BSRW is a unique study and a new research. However, the model needs to be calibrated and validated for conditions of the watershed as they are unique and heterogeneous by nature. Bacteria source characterization for each watershed and developing methods to input in the model are essential for bacteria modeling at the watershed scale. Methods and source characterization from one watershed to another watershed can be transferred as long as they are applicable. Therefore, the objectives of this study were (1) to develop a calibrated and validated watershed model for streamflow and FCB concentrations using the Soil and Water Assessment Tool (SWAT) and (2) to assess the sensitivity of FCB concentrations to changes in precipitation, temperature, and CO2 concentrations in an agricultural watershed.

MATERIALS AND METHODS

The SWAT model was developed for the BSRW located in the state of Mississippi. The sources of FCB incorporated in the model were WWTP discharge, poultry litter, beef cattle manure, hog manure, and failing septic systems. Observed data for streamflow and FCB concentrations were used to calibrate and validate the model using an auto-calibration technique. One-at-a-time sensitivity analyses were conducted to assess the sensitivity of FCB transport to climate changes using Latin Hypercube sampling.

Study area

The BSRW is part of the Mississippi River Alluvial Plain that covers an area of 10,488 km² and is located just east of the Mississippi River (Figure 1). The watershed consists of areas from 10 counties: Bolivar, Coahoma, Humphreys, Issaquena, Leflore, Sharkey, Sunflower, Tallahatchie, Washington, and Yazoo. The watershed contains over 80% of row crops, which mainly include soybean, corn, cotton, and rice. Most of the BSRW soils contain high clay and silt content, and over 90% of the soils are classified as National Resource Conservation Service (NRCS) hydrologic soil groups C and D, which have high runoff potential. The BSRW has very little topographic relief with an average slope of approximately 0.25 m/km (Coupe et al. 2012). Most of the precipitation in the watershed occurs during the winter and spring seasons, and the maximum temperatures can reach over 34 °C during July and August. The Big Sunflower River is listed as
one of the water bodies in Mississippi that is impaired due to FCB (MDEQ 2010). According to the Total Maximum Daily Load (TMDL) report published by the Mississippi Department of Environmental Quality (MDEQ), the sources of FCB pollution in the BSRW include livestock, wildlife, failing septic systems, and waste water discharge (MDEQ 2010). The MDEQ recommends that policy actions should be taken to reduce bacteria concentrations in the Big Sunflower River such as requiring NPDES permits to include fecal coliform limits and standards for disinfection (MDEQ 2010).

SWAT model description

The SWAT model is a semi-distributed watershed scale that quantifies the impacts of climate change and management practices on water quantity and quality in large complex watersheds at daily, monthly, and annual time scales (Arnold et al. 1998; Neitsch et al. 2011). The hydrological processes that can be modeled in SWAT include precipitation, surface runoff, streamflow, soil storage, evapotranspiration, infiltration, subsurface flow, and groundwater flow (Neitsch et al. 2011). The pollutants that can be modeled in SWAT are sediment, nitrogen, phosphorus, pesticide, and bacteria. In addition, SWAT allows the user to model climate change by adjusting climate parameters such as precipitation, temperature, solar radiation, relative humidity, and CO₂ levels. The SWAT model uses a digital elevation model (DEM) to delineate a watershed into sub-basins, which are then further divided into hydrological response units (HRUs) that contain a unique combination of land use, soil, and slope (Neitsch et al. 2011). For this study, ArcSWAT2012, which is the ArcGIS extension version of SWAT, was used to process the spatial input data and develop the model, and the SWAT executable revision 635 was used to generate the model results. The bacteria sub-model in SWAT can model fecal bacteria populations as either persistent or less persistent, which have different growth rates and die-off rates (Neitsch et al. 2011). Bacteria populations modeled in SWAT using Chick’s law can exist on plant foliage, by attachment to soil particles, or dissolved in soil water storage (Neitsch et al. 2011).

Watershed model inputs

A 10 m × 10 m DEM grid was obtained from the National Elevation Dataset (NED) from USGS to delineate the watershed into 32 sub-basins. The land use data was obtained from the USDA National Agricultural Statistics Service (NASS), which consisted of a cropland data layer with over 40 different land cover classes (USDA-NASS 2011). The soils data were obtained from the Soil Survey Geographic (SSURGO) database, which consisted of a raster image with multiple soil layers (USDA 2005). The sub-basins were then divided into multiple HRUs as a function of the land use types, soils, and slope classes. Daily precipitation and temperature data from 1 January 1996 to 31 December 2010 from 11 weather stations were obtained from the USDA climate database. These climate data were obtained from the Cooperative Observer Network and the Weather Bureau Army Navy Stations from the National Oceanic and Atmospheric Administration (NOAA). In addition to precipitation and temperature inputs, daily solar radiation and relative humidity data from one weather...
station at the Delta Research and Extension Center were incorporated in the model. The sources of FCB incorporated in the model include WWTP discharge, poultry litter applications, beef cattle manure, hog manure, and failing septic systems. WWTP discharge was modeled by obtaining discharge data from the EPA's Discharge Monitoring Report (DMR) pollutant loading tool. A total of 38 facilities that have discharge and pollutant data in the DMR database were included in the model (Figure 1). The discharge amounts and FCB loads between the years 2007 and 2010 were averaged for each facility. The average flows and average bacteria loads from the facilities were averaged across each sub-basin.

Poultry, beef cattle, and hog populations at the county level were obtained from the USDA-NASS census of agriculture for the years 2002 and 2007 (USDA 2007). The amount of manure deposited by each animal type and the FCB levels were estimated using the American Society of Agricultural Engineering standards (ASAE 2003). The FCB concentrations used in this study for poultry, beef cattle, and swine manures are 5.83 × 10^6, 1.17 × 10^6, and 2.14 × 10^6 colony forming units per gram (cfu/g), respectively (ASAE 2003). To model the bacteria pollution emanating from failing septic systems in the watershed, the number of septic systems for each county was obtained from the Mississippi Department of Health (MSDH 2014). Assuming the septic systems are evenly distributed throughout each county on the range, pasture, forested, and crop land uses, and it was estimated that there are a total of 9,375 septic systems in the BSRW. Because there are no reports documenting septic system failures in the BSRW, this study assumed a failure rate of 40%, which is similar to failure rate values used in other studies (Coffey et al. 2009; Jayakody et al. 2014). Based on the population data provided by the MSDH, there are approximately three persons using each septic system in the counties located in the BSRW (MSDH 2014). For this study, it was assumed that each person using these failing septic systems produces 150 g of feces and a sewage effluent of 0.32 m^3/day (Reddy et al. 1981; Parajuli et al. 2009).

Model calibration and validation procedures

After the SWAT model set-up, the model was calibrated and validated for streamflow and FCB concentrations. Observed daily streamflow data were obtained from 1996 to 2003 at the Merigold, Sunflower, and Leland USGS gauge stations (Figure 1). Observed streamflow data is scarce between January 1996 and October 2002 at the Sunflower USGS gauge station and some streamflow data is not available for the years 1996 and 1998 at the Leland USGS gauge station. Observed daily FCB concentrations from 1996 to 2000 at the Sunflower gauge station was obtained from the MDEQ TMDL report for the Big Sunflower River published in 2002 (MDEQ 2002). Additional observed bacteria concentration data from 2001 to 2003 at the Sunflower gauge station was obtained from the Yazoo Mississippi Delta (YMD) joint water management district. The observed FCB data from MDEQ and YMD district were combined for a total of 65 observed data points to be used for the calibration process. It is important to mention that while the observed streamflow data for the Sunflower gauge station is limited, every observed bacteria concentration data point coincided with an observed streamflow data point.

An auto-calibration procedure called Sequential Uncertainty Fitting version 2 (SUFI-2) was used in the SWAT Calibration and Uncertainty Programs (SWAT-CUP) (Abbaspour 2013). The SUFI-2 algorithm optimizes the objective function by taking sources of uncertainty into account through the computation of p-factors and r-factors. The p-factor represents the percentage of the observed data in the 95% prediction uncertainty (95PPU) obtained through Latin Hypercube sampling. The r-factor is the average thickness of the 9kPU band divided by the standard deviation of the observed data. SUFI-2 allows the user to optimize the objective function by updating the input parameter ranges to smaller ranges than the previous iterations that are centered on the best simulation (Abbaspour 2013). The model was first calibrated for streamflow by adjusting 12 different hydrological parameters that affect the surface water transport, soil water storage, evapotranspiration, and groundwater. The model was then calibrated for FCB concentrations by adjusting 11 more input parameters associated with bacteria growth and die-off, soil particle attachment, and bacteria transport in surface water. The performance of the model was evaluated using the coefficient of determination (R^2) and the Nash–Sutcliffe Efficiency (NSE) index (Nash & Sutcliffe 1970), which quantify the correlation between the observed and simulated values.
Climate change sensitivity analysis

Latin Hypercube sampling was employed in this study to generate input values for potential climate change because of its widespread use in hydrological modeling studies involving sensitivity and uncertainty analyses (Yang et al. 2008; Ficklin et al. 2012; Woznicki & Nejadhashemi 2014). Latin Hypercube sampling is a type of stratified sampling that generates a random value in each segment for a particular probability distribution. The user can define the input parameter range and segments from which the samples are drawn. For this study, Latin Hypercube sampling was applied to three climatic inputs to generate input values for the sensitivity analysis: precipitation, temperature, and CO2 concentration. The input ranges used in Latin Hypercube sampling for the climate variables were based on the end of the century projections from GCM results reported in the IPCC 5th assessment report (IPCC 2013).

The one-at-a-time sensitivity analyses were conducted in this study to assess the sensitivity of bacteria concentrations to climate change parameters. A one-at-a-time sensitivity analysis allows the user to assess the sensitivity of the output to changes in an input variable if all of the other parameters are kept constant (Abbaspour 2013). It is important to note that while the one-at-a-time analysis can provide the sensitivities of each of the climate inputs, but it cannot provide information regarding the sensitivity of an input variable while other input variables are changing. Therefore, the sensitivity of one parameter depends on the values of other input parameters. For this study, 50 samples were generated for each of the three climatic inputs for the one-at-a-time sensitivity analysis: rainfall ±20%, temperature from 0 to 5 °C, and CO2 concentration from 350 to 1,000 ppm.

RESULTS AND DISCUSSION

Streamflow calibration and validation

The model showed good to very good performance in simulating daily streamflow with the highest $R^2$ value of 0.77 and NSE index of 0.75 at the Leland gauge station, which is the most downstream gauge station (Table 1). The model was able to capture some of the peak flow events at all three gauge stations, but most of the simulated peak flows usually underestimated the observed peak stream flows (Figure 2). Even with the small amount of available observed streamflow data, the simulated vs. observed streamflow values at the Sunflower gauge station yielded good model performance statistics with $R^2$ values of 0.70 and 0.67 and NSE values of 0.68 and 0.67 during calibration and validation (Figure 2 and Table 1). The model generally showed relatively low uncertainty for the daily streamflow prediction, which is indicated by the calculated p-factors (0.75–0.80) and r-factors (1.15–1.17) generated from the SUFI-2 auto-calibration program (Table 1). These uncertainty measures indicate that 75–80% of the observed streamflow values were captured by the 95PPU, and the r-factors of 1.15–1.17 describe the thickness of the 95PPU band divided by the standard deviation of the measured streamflow (Abbaspour 2013).

The final calibrated values for the hydrological parameters are listed in Table 2. Out of the 12 hydrological parameters, the Manning’s roughness coefficient (CH_N2), SCS curve number (CN2), and the surface runoff lag coefficient (SURLAG) were the most sensitive parameters at the 0.05 level of significance (Table 2). The SUFI-2 auto-calibration program yielded a value of 0.26 for CH_N2 for the BSRW, which indicates that the watershed’s main channels are lined with dense brush and weeds. While the CN2 parameter was sensitive to streamflow, the final value was only –1.10% from the default curve number values from the SWAT land use database. The final SURLAG value of 1.23 indicates a fast response time for the overland flow to reach the main channels in the BSRW. The final values for these parameters are similar to the values used in another watershed modeling study conducted in the same watershed (Parajuli et al. 2013).

The groundwater parameters were also incorporated in the auto-calibration. However, as indicated by the low t-values and high p-values from the sensitivity analysis, the

<table>
<thead>
<tr>
<th>Station</th>
<th>Calibration</th>
<th>Validation</th>
<th>Uncertainty</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$R^2$</td>
<td>NSE</td>
<td>$R^2$</td>
</tr>
<tr>
<td>Merigold</td>
<td>0.638</td>
<td>0.572</td>
<td>0.643</td>
</tr>
<tr>
<td>Sunflower</td>
<td>0.696</td>
<td>0.673</td>
<td>0.683</td>
</tr>
<tr>
<td>Leland</td>
<td>0.769</td>
<td>0.748</td>
<td>0.665</td>
</tr>
</tbody>
</table>
groundwater parameters did not significantly impact streamflow in the model (Table 2). The final calibrated values of the input parameters are similar to the parameter values used in past watershed modeling studies using SWAT (Gassman et al. 2010; Douglas-Mankin et al. 2010; Tuppad et al. 2011).

**Bacteria calibration and validation**

The model simulated FCB concentrations reasonably well when compared with observed bacteria (Figure 3). The model performed slightly better at modeling bacteria concentrations during the validation period (1 January 2000–31 December 2003) than the calibration period (1 January 1996–31 December 1999) (Figure 3). The model usually underestimated bacteria concentrations for both low and high streamflow events. However, the model did show an acceptable correlation between observed and simulated FCB concentrations during the calibration and validation periods ($R^2 = 0.56–0.60$). While the NSE values from the bacteria model are low (NSE = 0.23–0.40), the model is still

![Figure 2](http://iwaponline.com/jwcc/article-pdf/11/4/1250/829566/jwc0111250.pdf)
considered acceptable to conduct sensitivity analysis (Parajuli et al. 2009). Also, other bacteria modeling studies using SWAT have reported low NSE values as well (Baffaut & Sadeghi 2010). Twelve bacteria parameters were adjusted via the SUFI-2 auto-calibration program for 2000 simulations (Table 3). Among the parameters, the most sensitive at the 0.05 level of significance are the bacteria soil partitioning coefficient (BACTKDQ), which describes the ratio of the concentration of solution bacteria at the soil surface to the concentration of solution bacteria in surface runoff, the fraction of manure applied to land areas that have active colony forming units (BACT_SWF), and the bacteria partition coefficient for human feces (BACTKDDB(55)).

From the sensitivity analysis results, the BACTKDQ, BACT_SWF, and BACTKDDB(55) parameters had p-values of <0.01 and t-statistics of 4.51, -3.03, and 0.93, respectively. The final calibrated value for BACTKDQ is 87.88, which is similar to BACTKDQ values used in other SWAT bacteria modeling studies (Baffaut & Sadeghi 2010). The final BACT_SWF value of 0.27 indicates that most of the manure applied in the watershed contains bacteria that is not readily active. The final value for BACTKDDB(55) is 0.93, which indicates that most of the bacteria is primarily found in solution as opposed to being sorbed to soil particles (Neitsch et al. 2011).

The BACTKDQ and BACT_SWF parameters were found to be sensitive likely due to the bacteria sources being represented in the model as fertilizer applications, which applies the manure directly onto the soil surface. The BACTKDQ parameter allows the ratio of bacteria solution in the soil surface to the bacteria solution in surface runoff to be adjusted directly. The BACTKDDB parameters for layer and beef cattle manure were also found to be moderately sensitive in the model. The sensitivity of the BACTKDDB parameters indicates that the partitioning of the bacteria colonies between soil particles and surface water was an important process in modeling the transport of bacteria within the BSRW. The final values for the other bacteria input parameters are listed in Table 3.

### One-at-a-time sensitivity analysis

The daily FCB concentrations from 1 January 1996 to 31 December 2003 were averaged for each simulation generated from the one-at-a-time sensitivity analyses. The average bacteria concentrations for each one-at-a-time
sensitivity analysis were analyzed by comparing it to the Latin hypercube samples of each climate parameter. The sensitivity of the resulting average FCB concentrations to changes in rainfall is displayed in Figure 4. Generally, increasing rainfall caused the average bacteria concentrations to increase, whereas decreasing rainfall caused the average bacteria concentrations to decrease (Figure 4). The baseline average bacteria concentration of 258 cfu/100 ml increased to 277 cfu/100 ml as a result of +20% rainfall and decreased to 238 cfu/100 ml as a result of −20% rainfall. The average bacteria concentrations appear to have a linear relationship with changing rainfall rates in the BSRW. Overall, increasing or decreasing rainfall has the same effect on the change in the magnitude of average bacteria concentrations (Figure 4). From these results, it is evident that increasing rainfall causes greater wash-off of bacteria from the soil surface, which leads to more bacteria being transported to rivers and streams. These results are in
agreement with past bacteria modeling studies in other watersheds, where the peak bacteria concentrations tend to coincide with peak stream flows (Cho et al. 2010; Jayakody et al. 2014). It is possible that increased rainfall magnitudes could decrease bacteria concentration due to increased dilution. However, for this study, the increased wash-off of FCB colonies from soil surfaces resulted in higher bacteria concentrations in surface waters. Conversely, when rainfall decreases, there was less wash-off of FCB, which results in lower bacteria concentrations in surface waters. More rainfall also leads to increased stream flows, which could lead to higher microbial transport by attachment to suspended sediment particles (Wilkes et al. 2011).

The sensitivity of average FCB concentrations to increases in temperature is displayed in Figure 5. In-stream bacteria concentration was found to be very sensitive and inversely related to temperature in the BSRW model. As air temperature increased to 5 °C, average bacteria concentration from 1996 to 2003 decreased by 30% from the baseline condition (Figure 5). The baseline average bacteria concentration of 258.0 cfu/100 ml decreased to 220.4, 191.8, and 180.4 cfu/100 ml as a result of increasing air temperature by 2 °C, 4 °C, and 5 °C, respectively. From Figure 5, it appears that the watershed’s air temperature and bacteria concentration are linearly related. Based on these results, the decreasing bacteria concentrations is most likely caused by the increases in die-off rates and inactivation of bacteria growth in manure applications and in surface waters. Increasing air temperatures essentially created an environment for the watershed that is not

Table 3 | Bacteria parameters, range, final value, \( t \)-statistic, and \( p \)-value used in auto-calibration

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Parameter definition</th>
<th>Range</th>
<th>Final</th>
<th>( t )-statistic</th>
<th>( p )-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BACTKDQ</td>
<td>Bacteria soil partitioning coefficient (m(^2)/Mg)</td>
<td>0–500</td>
<td>87.88</td>
<td>4.51</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>BACT_SWF</td>
<td>Fraction of manure applied to land areas that have active colony forming units</td>
<td>0–1</td>
<td>0.27</td>
<td>-3.03</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>BACTKDDB(55)</td>
<td>Bacteria partition coefficient (human feces)</td>
<td>0–1</td>
<td>0.93</td>
<td>-3.01</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>BACTKDDB(51)</td>
<td>Bacteria partition coefficient (layer manure)</td>
<td>0–1</td>
<td>0.45</td>
<td>1.71</td>
<td>0.09</td>
</tr>
<tr>
<td>BACTKDDB(45)</td>
<td>Bacteria partition coefficient (beef manure)</td>
<td>0–1</td>
<td>0.22</td>
<td>1.06</td>
<td>0.29</td>
</tr>
<tr>
<td>THBACT</td>
<td>Temperature adjustment factor for bacteria die-off/growth</td>
<td>1–10</td>
<td>1.10</td>
<td>-0.69</td>
<td>0.49</td>
</tr>
<tr>
<td>WOF_LP</td>
<td>Wash-off fraction for less persistent bacteria</td>
<td>0–1</td>
<td>0.75</td>
<td>-0.44</td>
<td>0.66</td>
</tr>
<tr>
<td>BACTMINLP</td>
<td>Minimum daily bacteria loss for less persistent bacteria (cfu/m(^2))</td>
<td>0–1</td>
<td>0.80</td>
<td>0.39</td>
<td>0.69</td>
</tr>
<tr>
<td>BACTKDDB(47)</td>
<td>Bacteria partition coefficient (swine manure)</td>
<td>0–1</td>
<td>0.74</td>
<td>-0.29</td>
<td>0.76</td>
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<tr>
<td>BACTMX</td>
<td>Bacteria percolation coefficient (10 m(^2)/Mg)</td>
<td>7–20</td>
<td>7.20</td>
<td>0.16</td>
<td>0.87</td>
</tr>
<tr>
<td>WDLPRCH</td>
<td>Die-off factor for less persistent bacteria in streams at 20 °C (1/day)</td>
<td>0–1</td>
<td>0.38</td>
<td>0.08</td>
<td>0.93</td>
</tr>
<tr>
<td>WDLPS</td>
<td>Die-off factor for less persistent bacteria adsorbed to soil particles at 20 °C (1/day)</td>
<td>0–1</td>
<td>0.52</td>
<td>-0.02</td>
<td>0.98</td>
</tr>
</tbody>
</table>

Figure 4 | Sensitivity of average FCB concentrations to changing rainfall.

Figure 5 | Sensitivity of average FCB concentrations to increasing temperature.
conducive for the growth of FCB in manure and septic effluent. This is in agreement with Chick’s law first-order decay equation, which stipulates that increasing temperature should cause the die-off of bacteria to increase. It is possible that increased temperatures could also lead to drier and hardened soil surfaces that allow for less infiltration and more runoff, which results in higher wash-off of bacteria colonies into rivers and streams (Jayakody et al. 2014). However, as mentioned previously, most of the soils in the watershed fall in the soil hydrologic group categories of C and D, which indicate that most of the soils have low infiltration and high runoff potential, to begin with. Therefore, in this study, increasing air temperatures even slightly seemed to directly cause a decrease in simulated average bacteria concentration. For example, decreasing air temperature by just 0.5 °C resulted in a 5% decrease in average bacteria concentration in the watershed (Figure 5). Overall, these results indicate that the die-off rates of FCB are directly related to even small increases in temperatures in the BSRW.

The sensitivity of average FCB concentrations to increases in CO2 concentrations is displayed in Figure 6. Based on the model simulations, bacteria concentrations were not that sensitive to changes in CO2 compared changes in rainfall and temperature. As CO2 concentration in the watershed increased from the baseline of 330–800 ppm, average FCB concentration did not significantly change (Figure 6). However, as CO2 concentration increased above 800 ppm, the average bacteria concentration decreased drastically (Figure 6). Compared with the baseline climate condition, average FCB concentration decreased by 4.7% when CO2 concentration increased to 1000 ppm. The narrow CO2 concentration range of 800–1000 ppm caused a noticeable decrease in bacteria concentration due to a number of possible watershed responses. For example, increasing CO2 levels can exacerbate the greenhouse effect, which can lead to temperature increases. The increase in temperature can increase the inactivation of bacteria and pathogens in surface water (Hofstra 2011). To our knowledge, there is currently no research that has been conducted that investigates the direct impact of changing CO2 concentration on bacteria transport in a watershed. Such an investigation would be interesting because it would provide new insight into the relationship and interaction of CO2 and bacteria survival in surface waters.

It is important to note that the one-at-a-time sensitivity analyses result depend on the bacteria parameters set in the calibrated model. The bacteria parameters, which affect processes in the model such as bacteria wash-off, die-off rates, and bacteria percolation, can influence the sensitivity of bacteria concentrations to climate changes. For example, the BACTKDQ parameter was set to 87.88 in the calibrated model, which indicates that surface runoff will only partially interact with the solution bacteria at the soil surface. Had a higher value been chosen for the BACTKDQ parameter, rainfall would most likely have been a more sensitive parameter in the global sensitivity analysis due to more interaction between surface runoff and bacteria concentration at the soil surface. Another parameter that could influence the climate change sensitivity analysis results is the THBACT parameter. Altering the THBACT value changes the sensitivity of bacteria die-off and growth to changes in temperature. The results of this study would be very different if the sensitivity analyses were conducted in another watershed because the bacteria parameters for the calibrated model would have different values. Essentially, the climate sensitivity results found in this study are only applicable to the BSRW and do not necessarily reflect how bacteria concentrations in other watersheds would respond under these same climate changes. Future studies that use the SWAT model to assess the sensitivity of bacteria transport to climate change should also consider incorporating the SWAT bacteria parameters in the climate change sensitivity analysis. Incorporating the bacteria parameters could lead to more comprehensive sensitivity analysis and demonstrate the interaction of the SWAT bacteria
parameters and the climate change parameters on bacteria fate and transport.

The purpose of this study was to see how the individual potential climate change parameters can affect bacteria concentrations in surface waters. It is suggested that before implementing future climate change scenarios, more modeling and field-based studies should be conducted to investigate how each of the individual climate changes reacts with bacteria concentrations. Such studies will provide valuable information for future modelers looking to apply down-scaled climate models to assess the impacts of climate change on bacteria fate and transport.

**CONCLUSION**

This study assessed the sensitivity of FCB concentrations to changes in precipitation, temperature, and CO2 concentrations in an agricultural watershed. The model was calibrated and validated for streamflow and FCB concentrations using SWAT. The model demonstrated good to very good performance in simulating daily streamflow ($R^2 = 0.64–0.77$, NSE = 0.57–0.75) and fair performance in simulating FCB concentrations ($R^2 = 0.56–0.60$, NSE = 0.23–0.40). The bacteria parameters that were found to be the most sensitive in the model were BACTKDO, BACT_SWF, and BACKTKDDB. The one-at-a-time and global sensitivity analyses showed that average FCB concentrations were sensitive to changes in rainfall, temperature, and CO2 concentrations. Increased rainfall caused greater wash-off of FCB colonies from soil surfaces, which resulted in higher bacteria concentrations in surface waters. Conversely, when rainfall decreased, there was less wash-off of FCB, which resulted in lower bacteria concentrations in surface waters. When the temperature in the watershed was increased even slightly, bacteria concentration decreased due to higher bacteria die-off rates. Increasing CO2 concentration from the baseline condition to 800 ppm did not cause any significant changes in FCB concentration, but when CO2 reached over 800 ppm, average bacteria concentration decreased only by 4.7%.

The results of this study point to a need for more watershed modeling and field-based research that fully investigates the impact of each individual climate parameter on bacteria concentrations in surface water. More specifically, future research should focus on thoroughly understanding bacteria transport processes and mechanisms that are directly affected by changes in climate. Such studies would help inform and guide watershed managers and policy makers who are tasked with setting water quality standards. These standards should be set while taking potential climate changes into account, especially when it comes to addressing uncertainty in water quality modeling results.

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