SWAT BACTERIA SUB-MODEL EVALUATION AND APPLICATION

by

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BS, Tribhuvan University, Nepal, 1998
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AN ABSTRACT OF A DISSERTATION

submitted in partial fulfillment of the requirements for the degree

DOCTOR OF PHILOSOPHY

Department of Biological and Agricultural Engineering
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Manhattan, Kansas
2007

Abstract

The overall goal of this study was to evaluate and apply the Soil and Water Assessment Tool (SWAT) model for fecal bacteria modeling. Methods were developed to characterize fecal coliform bacteria (FCB) from livestock, human, and wildlife sources to use as input in the model. Model sensitivity to predict FCB concentration was evaluated for the model parameters and input parameters using both SWAT 2000 and 2005 versions. Sensitivity of input parameters generally, ranked as Bacteria concentration ≥ TBACT > Wildlife source loads > Livestock stocking rate ≥ Livestock manure production rate > BACTKDQ for SWAT 2000 whereas it was ranked as BACTKDQ > TBACT > Bacteria concentration > WDLPQ > WDLPS for SWAT 2005. Sensitivity of model and input parameters were found changed from SWAT 2000.

The SWAT (2005) model was calibrated and validated for daily flow, sediment, and fecal bacteria concentration using one year of measured data (January to December, 2004). The SWAT model predicted results with poor to very good agreement when compared with measured data with coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E) range of 0.10 to 0.89 for daily flows, sediment, total phosphorus, total nitrogen and total FCB concentration. More extensive in-stream data are needed for more comprehensive model assessment. The SWAT model (2005) was evaluated for source-specific FCB modeling using three years (2004-2006) of observed modified deterministic probability of bacteria source tracking (BST) data. The FCB sources were modeled with three combinations (livestock and human, livestock and wildlife, wildlife and human) and each single source to evaluate the source-specific FCB concentrations. The SWAT model determined poor to good agreement for the combined source of FCB (R^2, E range from -2.92 to 0.71) but determined generally decreased agreement for each single source of bacteria (R^2, E range from -5.03 to 0.39) potentially due to BST uncertainty, spatial variability and source characterization.

The SWAT model identified critical sub-watersheds in the watershed where implementing vegetative filter strips (VFS) could be most effective to abate fecal bacteria pollution. The targeting method of VFS application to the watershed sub-basins was found to be more effective in reducing both FCB (60% vs. 42%) and sediment yield (63% vs. 33%) as compared to a random approach.

The FCB source characterization methods for modeling developed in this study are general and have the potential to be extended to other watersheds. The results of this study demonstrate that the SWAT model can be used to characterize the distribution of bacteria sources within a bacteria-impaired watershed and assist with developing total maximum daily loads (TMDLs) and watershed restoration strategies.

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CHAPTER 1 - OVERVIEW

1.1 Introduction

Water is basic to life and health. Over 1 billion people worldwide have no access to safe drinking water. Waterborne diseases cause about 6, 000 deaths everyday in the world (WHO, 2004). The United States is fortunate to have one of the best supplies of drinking water in the world. Although tap water that meets federal and state standards generally is safe to drink, threats to drinking water quality in the United States still exist. Outbreaks of drinking water-associated illness demonstrate that people cannot take their drinking water for granted. Though widespread waterborne pathogen outbreaks typically are rare, they do occur and have the potential to impact a large number of people.

Since 1971, the U. S. Environmental Protection Agency (EPA), Centers for Disease Control and Prevention (CDC) and Council of State and Territorial Epidemiologists have collaborated to collect information about the causes of waterborne disease outbreaks (WBDOs). For an event to be defined as a WBDO, two or more persons must have experienced a similar illness (Blackburn et al., 2004). M. Craun et al. (2006) reported that during 1920 to 2002, at least 1,870 outbreaks (an average of 23 year^{-1}), 883,806 illnesses (an average of 10, 648 cases year^{-1}) and 1,165 deaths (an average of 14 deaths year^{-1}) were associated with drinking water. In the most recent 12-year period (1991-2002), 207 WBDOs and 433,947 illnesses were reported. Illnesses in 67 of the WBDOs were severe enough for 4,901 persons to be admitted to the hospital; 4,400 of the hospital admissions occurred during the Milwaukee WBDO in 1993. Most WBDOs that reported hospitalizations were from a bacterial source. The vast majority of pathogenic contamination events are small, generally isolated, and un-reported (The Groundwater Foundation, 2007).

Fecal pathogen contamination of surface waters can result in illness and death, and it accounts for a majority of the assessed water-quality impairments in the U. S. (US EPA, 2005a). Fecal coliform bacteria often are used as indicators of the potential presence of fecal pathogens. Infectious waterborne diseases usually are caused by exposure to enteric pathogens that are transmitted by the “fecal–oral” pathway. Occasionally, the pathogens may be in urine (e.g., Leptospira). Waterborne pathogens are excreted by infected persons and in many instances, by wild or domestic animals. Of the waterborne outbreaks reported during 1971-2002, 54% had an unknown etiology. The remaining 46% were due to bacteria, parasites, and viruses (G. Craun, et al., 2006). G. Craun et al. (2006) examined those outbreaks and found that illness associated with drinking water outbreaks included gastroenteritis, typhoid fever, hepatitis, and cholera. Illness associated with recreational water outbreaks included aforementioned illnesses associated with drinking water, but also dermatitis, primary amebic meningoencephalitis, leptospirosis, ottis externa, and pharyngitis (Wang, 2003). Fecal pathogens were identified as the etiologic agents responsible for most of those WBDOs. During 1991-2002, WBDOs were caused by a number of fecal-origin pathogens, including Giardia, Cryptosporidium, norovious, *Escherichia coli* O157:H7, Campylobacter, and Legionella.

Fecal pathogens excreted by humans, domestic animals, and wildlife can enter natural water resources with storm-water runoff. Curriero et al. (2001) found that more than half of the WBDOs in the United States in the past 50 years were proceeded by heavy rainfall. Rose et al. (2001) concluded that an increase in the frequency and severity of extreme precipitation events would increase the risk of contamination events, which, in turn, would increase the risk of water-borne illnesses. Although several factors affected this result, critical element included the increased transport of disease-causing organisms during extreme precipitation events. Casman et al. (2001) and Kistemann et al. (2002) found that extreme precipitation events increase the loading of contaminants to waterways that could increase the risk of illness associated with fecal pathogens. An excessive quantity of fecal bacteria in surface water increases the risk of bacteria−induced illness to humans (Frenzel and Couvillion, 2002). Payment et al. (2000) found that the occurrence of pathogenic microorganisms (human enteric virus, Cryptosporidium, and Giardia) in the Saint Lawrence River in Canada was significantly correlated with bacterial indicators (total coliform, fecal coliform, and Clostridium perfringens). A fecal coliform concentration of 200 colony−forming units (cfu) per 100 mL of water was established as a water quality standard by the Federal Water Pollution Control Administration of the Department of the Interior in 1968 (US EPA, 1986). In order to protect water quality in the nation, extensive efforts are being undertaken based on the foundation of the 1972 Clean Water Act.

In the United States, 39% of the assessed stream miles are impaired due to one or more causes, and 35% of the assessed impaired stream miles are impaired by pathogens (USEPA, 2000). In Kansas, 55% of the assessed stream miles are impaired due to one or more causes with 22% of the assessed stream miles impaired by pathogens (KDHE, 2004). Similarly, 45% of the assessed lake acres in the nation are impaired due to one or more causes, and 23% of the assessed lake acres are impaired by pathogens. In Kansas, 72% of lake acres are impaired due to one or more causes with 53% of the assessed lake acres being impaired by pathogens.

Water pollution derives from point and non-point sources. A Total Maximum Daily Load (TMDL) is defined by the U. S. EPA as the calculated maximum amount of a pollutant that a waterbody can receive and still meet applicable state water quality standards. The TMDL allocates this maximum amount to the pollutant’s sources (Muñoz−Carpena et al, 2006). A TMDL comprises the sum of loads from point and nonpoint sources plus a margin of safety. The U.S. Congress mandated the TMDL program in Section 303(d) of the original Clean Water Act of 1972 and charged the USEPA and the states to focus on controlling point sources through National Pollutant Discharge Elimination System (NPDES) permits. The validity of the TMDL process was reaffirmed in 2001 after the U. S. Congress requested a committee to assess the scientific basis of reducing water pollution.

The objective of a TMDL is to allocate loads among different pollutant sources so that the appropriate corrective actions can be taken to meet water quality standards (USEPA, 1991). Under the current demands of the nation’s TMDL program, a large number of watershed-scale modeling projects are being conducted in the attempt to identify and quantify pollutant sources so that the pollution from those sources may be reduced to improve water quality. Much of the modeling is directed toward TMDL development for waters impaired due to excessive levels of bacteria (Kim et al., 2007).

The TMDL program is a watershed management process that integrates watershed planning and remediation with water quality assessment and protection (Benham et al., 2006). For the USEPA to approve a TMDL, all major point and non-point sources of the offending pollutant(s) must be identified and quantified. Developing a TMDL involves a study that quantifies the pollutant contribution from each source (or source category in the case of non-point source pollution) and determines the pollutant reduction from each source required to meet applicable state water-quality standards. The point and non-point components of TMDL loads can be evaluated via monitoring and computer modeling. Although monitoring is potentially the most desirable method, its use is limited due to high cost and extreme spatial and temporal ecosystem variability. Mathematical models, in combination with field monitoring data, can potentially save time, reduce cost, and minimize the need for experimentally evaluating management alternatives.

Hydrologic and water quality models are often used to identify and quantify pollutant sources so that the pollution from those sources may be reduced in order to improve water quality and meet applicable state water quality standards. Watershed modeling is also directed toward TMDL development for waters impaired due to excessive levels of bacteria. In watershed modeling, the watershed and water bodies are first assessed to identify the level of impairment and then prioritized for water quality improvement through implementing Best Management Practices (BMPs). Kansas has established bacterial TMDLs for 13 of 20 reservoirs. Ten of these 13 reservoirs are on the high priority list. Clinton Lake reservoir, to which the Upper Wakarusa River watershed drains, is one of them.

A model user should fully understand the background, potentials, and limitations of a model before using it. Example field applications, sensitivity analyses, calibration and validation, and full documentation of a model is essential for using the model in the watershed modeling context. Rigorous education and training with model applications and demonstrations are needed for users to understand the potentials, limitations, and appropriate applications of a model. Modeling of hydrology, sediment and nutrients has advanced tremendously, but it has not always been consistent with the needs of the water quality goals program. Numerous useful models are available today with various capabilities, many of which are applicable or adaptable to water quality goal development and implementation. However, benefits to the water quality goal program will only accrue when future advances, made by making the best use of existing models and enhancing the existing models or supplemental components, are undertaken with consideration of their application for water quality goal development and implementation (Borah et al., 2006).

During the last two decades, computer simulation models for water quality have been developed to simulate numerous components of pollution from watersheds. These components include surface runoff, sediment, nutrients, and pesticides. However, little has been done to address fate and transport of pathogens from watersheds. Most frequently, fecal bacteria is assumed to be associated with surface water flow. Flow-associated constituents are assumed to accumulate on the land surface until the occurrence of a rainfall event (Paul et al., 2004). The following six models have been developed but have not proven to be the best solution for modeling bacterial fate and transport to the streams: Agricultural Runoff Management (ARM) II, (Overcash et al., 1983); UTAH State (Springer et al., 1983); MWASTE (Moore et al., 1989); COLI (Walker et al., 1990); Hydrologic Simulation Program Fortran (HSPF), (Bicknell et al., 1997); and Spatially Explicit Delivery Model (SEDMOND), Fraser et al., 1998).

In 2000, a microbial sub-model was developed and added to the Soil and Water Assessment Tool (SWAT) to address fate and transport of both more persistent and less persistent fecal bacteria (Neitsch et al., 2002; Sadeghi and Arnold, 2002). Currently for hydrologic simulations, a significant amount of research is being done using the SWAT model because it appears to be the most inclusive of the numerous variables needed to make accurate predictions of hydrologic systems. A microbial sub-model considers sources of bacteria and their fate and transport (Sadeghi, and Arnold, 2002) and it has been in a continual development process since that time. The most recent update was released in 2005 (Neitsch et al., 2005).

The SWAT water quality model has been applied and validated for runoff, sediment yield, and nutrient losses from watersheds at different geographic locations, conditions, and management practices (Saleh et al., 1999; Spruill et al., 2000; Santhi et al., 2001; Kirsch et al., 2002; Van Liew et al., 2003; White et al., 2004; Qi and Grunwald, 2005; White and Chaubey, 2005; Wang et al., 2006; Jha et al., 2007; Gassman et al., 2007). However, a limited amount of research has been performed using the SWAT microbial sub-model in predicting fecal bacteria transport.

Baffaut and Benson (2003) studied bacteria TMDLs for the Shoal Creek watershed in southwest Missouri using the SWAT microbial sub-model (2000). They presented reasonable results and recommendations using this model. The SWAT model was applied to the watershed and calibrated using crop yield, flow, and water quality data. The model represented the variations of fecal coliform measured in the stream in the correct range of values and frequencies. The watershed scale testing validated mostly the fate and transport equations used by the model for dissolved bacteria. Further calibration and validation of the model in different watersheds was recommended. The SWAT model sensitivity was not tested. Although Baffaut and Benson tested the model considering different management practices, the model was not tested to model single or combination of source-specific fecal bacteria. Since bacteria source tracking methods are effective tools for determining the origin of fecal contamination in water bodies, they can be used to design best management practices to reduce fecal bacteria loading. Modeling single or combinations of the source-specific fecal bacteria can demonstrate the SWAT model as more useful tool for source-tracking.

Benham et al. (2006) pointed out that substantial additional research is needed to improve the methods and models used to develop bacteria impairment TMDLs. Regardless of the tool or method used to develop these TMDLs, accurate characterization of bacteria sources and load quantification is needed. Improved source characterization needs to include better estimates of animal populations, fecal production, and indicator-bacteria density. Model accuracy is dependent on the development of accurate input parameters.

1.2 Objectives of the study

The overall goal of this study was to evaluate and apply the SWAT microbial sub-model for fecal bacteria modeling using new methods. To understand the methods that can be used in fecal bacteria modeling and demonstrate the use of the model for various management conditions, the following objectives were set.

1) Determine sensitivity of model parameters and input parameters using the SWAT microbial sub-model (2000) at the watershed scale. (a) Characterize fecal bacteria

source loads (livestock, human, wildlife), (b) determine sensitivity to bacteria parameters, (c) determine sensitivity to livestock source parameters, (d) sensitivity to human source parameters, and (e) sensitivity to wildlife source parameters.

2) Determine sensitivity of model parameters and input parameter using the SWAT microbial sub-model (2005). (a) Characterize fecal bacteria source loads (livestock, human, wildlife), (b) determine sensitivity to model parameters, and (c) determine sensitivity to input parameter.

3) Calibrate and validate SWAT for flow, sediment, nutrients, and fecal bacteria for agricultural watersheds. (a) Select calibration parameters and calibration procedure, (b) characterize fecal bacteria source loads (livestock, human, wildlife), and (c) calibrate and validate model using preliminary one year (2004) of measured data.

4) Demonstrate modeling source-specific fecal bacteria using SWAT. (a) Calibrate and validate the model using three years (2004-2006) of measured hydrologic and water quality data, and (b) utilize observed modified deterministic probability of source-specific bacteria source tracking data.

5) Identify BMP targeting areas to abate fecal bacteria pollution using SWAT. (a) Utilize results from previously calibrated and validated model to estimate total fecal bacteria concentration contribution from each sub-watershed, (b) rank sub-watersheds according to fecal bacteria concentration, and (c) apply and evaluate effectiveness of different filter strip lengths.

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CHAPTER 2 - FECAL BACTERIA MODELING USING SWAT 2000 MODEL: SOURCE CHARACTERIZATION METHODS AND SENSITIVITY ANALYSIS

Abstract

The Soil and Water Assessment Tool (SWAT) version 2000 includes a microbial sub-model to simulate fecal bacteria transport from human, agricultural, and wildlife sources at the watershed scale. The objectives of this study were to demonstrate methods to characterize bacteria source loads and to assess the model sensitivity to input parameters and bacteria source application methods. The model was applied to Rock Creek watershed (77 km^2) in northeastern Kansas. Methods were developed to use commonly available data to describe model inputs of watershed sources of livestock, septic and wildlife manure.

Uncalibrated SWAT model-simulated flow was validated for a period from Jan. 1 to Dec. 31, 2004, with coefficient of determination (R^2) = 0.74 and Nash-Sutcliffe Efficiency Index (E) = 0.63. Although the model over-predicted average bacteria concentration by 158% when compared with measured bacteria concentration values for nine runoff events, the model response still showed good correlation in regard to source load characterization. The model predicted geometric mean value of fecal bacteria concentration was evaluated using the relative sensitivity index (S). The temperature adjustment factor (TBACT) showed low to high sensitivity (S from 0.47 to 3.18) depending upon percentage change in input parameter. The bacteria partition coefficient in surface runoff (BACTKDQ) showed an inverse relationship and low sensitivity ($S < 0.5$). The fecal bacteria concentration in manure had no to moderate sensitivity (S from 0.02 to 1.09) depending upon percentage change in input parameter. The direct point load applications of septic effluent or wildlife manure had moderate sensitivity (S from 0.5 to 1.0). Livestock manure production rate, animal stocking rate, and land application of septic effluent to land methods had no sensitivity (S from 0.04 to 0.05). Sensitivity of input parameters generally, ranked as Bacteria concentration ≥ TBACT >> Livestock stocking rate ≥ Livestock manure production rate > BACTKDQ. The model was relatively insensitive to changes in parameters related to land-application methods. Results suggest that SWAT bacteria modeling will require accurate input data that allocate sources that are directly input, deposited, or discharged to a stream vs. those that are land applied to upland areas.

2.1 Introduction

Fecal coliform bacteria often are present in surface water at concentrations that indicate the potential to cause severe illnesses in humans (Craun and Frost, 2002). Fecal bacteria sources include land application of manures, grazing operations, winter feeding operations, failing septic systems, and wildlife (Zeckoski et al., 2005). Water movement and sediment erosion increase the chance of bacteria reaching surface water systems especially during high intensity rainfall events. Watershed models can be a useful tool to use to help evaluate pollution from fecal bacteria.

In recent years, the U.S. Environmental Protection Agency (EPA) has increasingly emphasized the importance of incorporating variability and uncertainty into the modeling process (USEPA, 1997). In watershed-level assessment and management activities there are uncertainties - the only thing we are sure of is that we are “in doubt” (Hession et al., 1996a; 1996b).

Uncertainties may be classified into three categories: the inherent variability in natural processes, model uncertainty, and parameter uncertainty (Haan, 1989). The inherent variability in the natural processes is the unexplained random variability of the natural environment (Haan, 1989). This inherent variability in natural processes can be either variability in space (spatial variability) and/or variability in time (temporal variability). Spatial and temporal variability can be generally observed with environmental factors such as rainfall, temperature, and stream flow. Model uncertainty results from faulty conceptualizations of the world (Suter et al., 1987), such as: (1) using a small number of variables to represent a large number of complex phenomena, (2) choosing incorrect functional forms for interactions among variables, and (3) parameter uncertainty results when model parameters inaccurately represent the true value. Parameter uncertainty can be assessed by quantifying the sensitivity model response to parameter changes made of model response either independently (Tiscareno-Lopez et al., 1993, 1994) or dependently (Silberbush and Barber, 1983). The range of the perturbation may be a specific percentage (Barnes and Young, 1994) or determined from experimental measurements (Fontaine et al., 1992; Gwo et al., 1996).

The most common form of sensitivity analysis is independent parameter perturbation (IPP) in which model parameters are varied individually by a fixed percentage around a base value (Ferreira et al., 1995). An example of this approach is with first-order analysis (Haan and Zhang, 1996), which is most applicable to linear systems. Model output responses to parameter perturbation may be quantified by percentage change of selected output variables and relative change of output versus input (Larocque and Banton, 1994). The overall model response may be obtained by measuring the average response of selected output variables (Nearing et al., 1989).

Model sensitivity can be evaluated quantitatively using local or global analysis (Soutter and Musky, 1999). Local techniques represent one-at-a-time parameter change from the base value, whereas global sensitivity analysis techniques include random parameter changes over their actual ranges, which generate input and output distributions that can be statistically analyzed (Soutter and Musy, 1999). Despite the benefit of evaluating an entire input-parameter space, global methods can be cumbersome and daunting when models are complex and contain numerous inputs, and extensive computational effort often is required. In these cases, single-variable analysis is often preferred (Graff et al., 2005). The response of the output to variations in input can be quantified using relative sensitivity for a given perturbation (Graff et al., 2005).

The Soil and Water Assessment Tool (SWAT) is a watershed scale process-based model developed by USDA Agricultural Research Service (ARS) (Arnold et al., 1998). The bacteria transport routine was added to the SWAT model in 2000 (Sadeghi and Arnold, 2002; Neitsch et al., 2002), which allowed it to be used as a tool for addressing microbial contamination of water caused by point and non-point sources. However, sensitivity analysis of the SWAT model focusing on the bacteria transport sub-model is needed to allow it to be used and parameterized appropriately. Sensitivity analysis of the SWAT microbial sub-model of SWAT has not been assessed. It is therefore important to know the influence of the model coefficients and input parameters on model response.

2.2 Objectives

The objectives of this study were to (a) demonstrate methods to characterize model inputs of bacteria source loads and to (b) assess the model sensitivity to input parameters and bacteria source application methods.

2.3 Materials and Methods

2.3.1 Watershed Stream Description

The study focused on the 77 km^2 Rock Creek watershed (Fig. 2.1), located in Douglas County, KS. The watershed area primarily grassland (52%), cropland (33%), and woodland (14%) with predominately silty-clay textured soils (STATSGO MUID: 20142 and 20151). The pastures included native prairie, smooth brome, and tall fescue grasses. Average slope in the watershed sub-basins ranged from 3.8% to 6.3%. Parameters for each hydrologic response unit (HRU) in each watershed were defined on the basis of soil, land use, and topographic characteristics of the watershed as described in the SWAT documentation version 2000 (Neitsch et al., 2002).

Stream flow and bacteria data were collected at the Rock Creek watershed outlet to validate model results. Grab samples (about 250 ml) were collected from the mid-point of the flowing stream at the watershed outlet. Samples were placed immediately into an ice chest and transferred to a laboratory refrigerator within two to four hours of collection. Bacteria enumeration procedures were started within 24 hours. A serial dilution method (Clesceri et al., 1998) was applied to enumerate fecal coliform bacteria colonies. Bacterial samples typically required four serial dilutions to obtain reasonable bacteria colony counts.

Flow at the time of sample collection was calculated using Manning's equation, as outlined by Ward and Elliot (1995). Flow depth, cross-sectional area, and channel slope were measured, and the channel roughness factor was estimated based on channel roughness characteristics and degree of meandering (Cowan, 1956). The calculated flow was validated based on ratio of the watershed area using data from the U. S. Geological Survey (USGS) Richland gage station. The calculated flow showed very good correlation (>90%) with the weighted area flow. This study used data collected from January to December 2004.

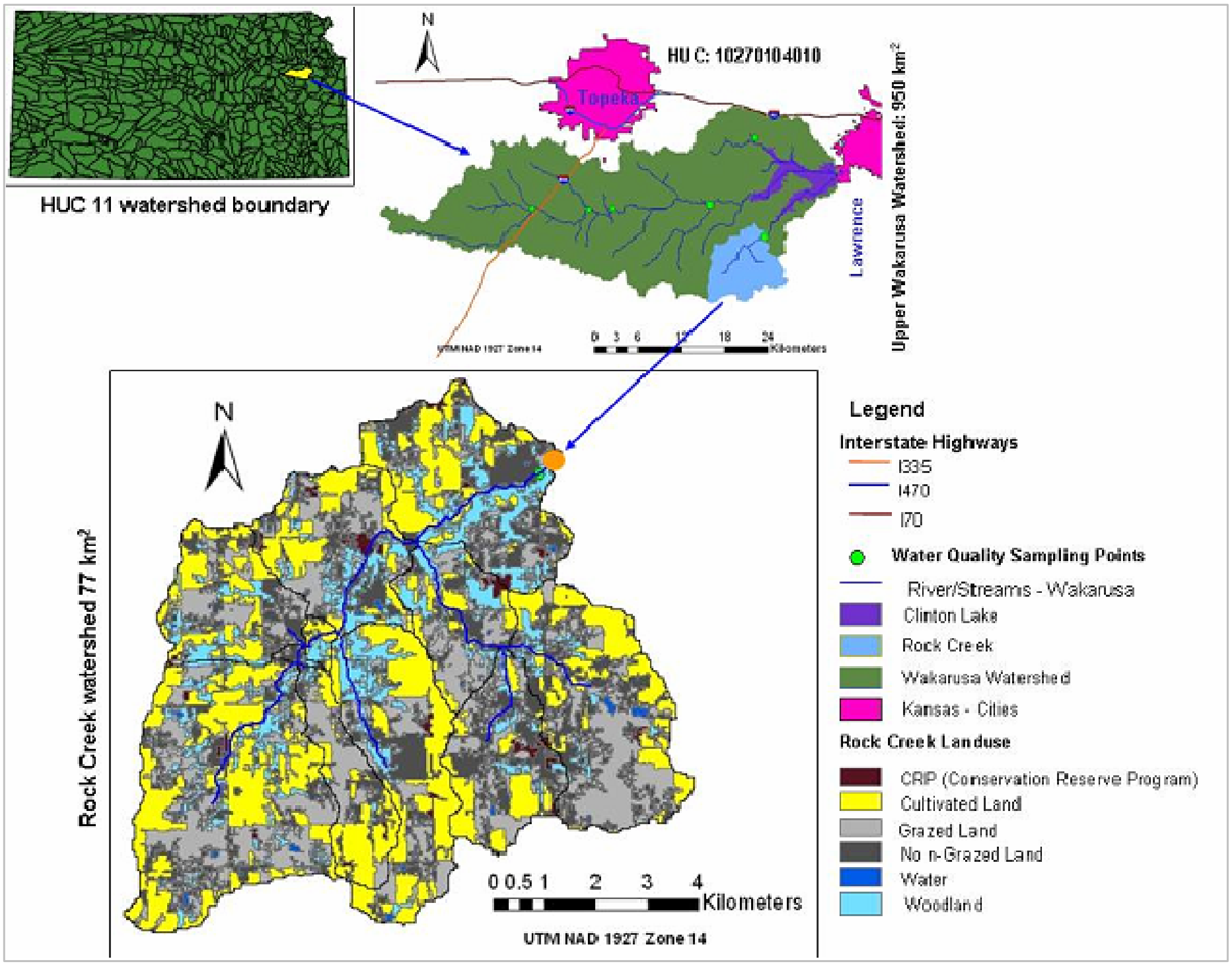

Figure 2.1. Location map of the Rock Creek Watershed in NE Kansas

2.3.2 SWAT Model

The SWAT watershed-scale model (Arnold et al., 1998; Neitsch et al., 2002) processes continuously on a daily time step. It simulates hydrological processes, sediment yield, nutrient loss, and pesticide losses into surface/groundwater. A USGS 30m x 30m resolution digital elevation model (DEM) was used to delineate the watershed boundaries and topography (USGS, 1999). State Soil Geographic Database (STATSGO) was utilized to create a soil database (USDA, 1994). The gap analysis program (GAP) landcover data of 2001 that depicts twenty general landcover classes by Kansas Applied Remote Sensing (KARS, 2001) was used. Wardlow and Egbert (2003) evaluated GAP (2001) and National Land Cover Data NLCD (1992) landuse data for the State of Kansas. The Kansas GAP provided better discrimination of most land-cover classes as compared to NLCD. Accuracy assessment found an overall accuracy of 87 percent for GAP and 81 percent for NLCD, and GAP had higher accuracies for most individual land-coverclasses. The Kansas GAP and NLCD land-cover products were found to be comparable in terms of characterizing broad scale land-cover patterns, but the Kansas GAP land-cover map appears to be more appropriate for localized applications that require detailed and accurate land-cover information.

The GAP land-use classes were reclassified into eight classes based on field-verified land use conditions (Mankin and Koelliker, 2001; Mankin et al., 2003). The weighted land-use, soil types, pasture operation, cropping patterns, and tillage systems for the watershed were used to execute the model.

The SWAT model version 2000 (Neitsch et al., 2002) parameters affecting runoff and erosion processes, such as curve number II, USLE P factor, minimum plant biomass for grazing, and initial residue cover in the ground, were selected to be consistent with SWAT documentation and other published studies (Baffaut and Benson, 2003; Crane et al., 1980; and Reddy et al., 1981) without further calibration.

The microbial survival and transport sub-model added to the SWAT version 2000 (Sadeghi and Arnold, 2002; Neitsch et al., 2002) uses the first-order decay equation as revised by Moore et al. (1989) to model fecal bacteria die-off and re-growth (Eq. 2.1).

$$C_t = C_o \times e^{-k_{20} t \theta^{(T-20)}} \tag{2.1}$$

where

C_t = bacteria concentration at time t, count/100ml

C_o = initial bacteria concentration, count/100ml

k_{20} = first-order die-off rate at 20°C, day^{-1}

t = exposure time, days

θ = temperature adjustment factor (TBACT in SWAT)

T = temperature, ^{0}C

The SWAT water quality model has been applied and validated for runoff, sediment yield, and nutrient losses from watersheds at different geographic locations, conditions, and management practices (Saleh et al., 1999; Spruill et al., 2000; Santhi et al., 2001; Kirsch et al., 2002; White and Chaubey, 2005; Jha et al., 2007; Gassman et al., 2007). Limited research has been performed for the SWAT/Microbial model in predicting bacteria movement. Baffaut and Benson (2003) studied bacteria loads for the Shoal Creek watershed in southwest Missouri using the SWAT/Microbial sub-model 2000 version. They calibrated model using daily flow, weekly fecal coliform bacteria concentration collected from water-quality grab samples, and annual hay yield reported to USDA. A frequency analysis method was used to compare measured vs. predicted data for daily flow and fecal coliform bacteria concentration. Daily flow was reported to be reasonable except for over-predictions of high daily flows. They compared 18 months of weekly measured fecal coliform bacteria concentration data with model-predicted fecal coliform bacteria concentration data using average plus or minus one standard deviation. The model-predicted bacteria concentration validated up to 70% using the frequency curve.

Several authors previously have completed sensitivity and output-uncertainty analysis for SWAT model (Lenhart et al., 2002; Eckhardt et al., 2002; Sohrabi et al., 2002; Benaman and Shoemaker, 2004; Huisman et al., 2004; Feyereisen et al., 2005). However, sensitivity analysis of the SWAT bacteria sub-model has not been completed.

2.3.3 Model Parameters Evaluated

The two key user-defined model parameters used in this study were BACTKDQ and TBACT. The bacteria partition coefficient in surface runoff (BACTKDQ; 0-500 m^3 Mg^{-1} or mL g^{-1} range, base = 175 m^3 Mg^{-1}) represents the ratio of sorbed (cfu m^{-3}) to solution-phase (cfu Mg^{-1}) bacteria, where increasing BACTKDQ indicates greater proportion of sorbed bacteria. The temperature adjustment factor (TBACT; 0 to optional, base = 1.07) impacted the bacteria concentration prediction by an exponential first-order-decay relationship (Eq. 2.1). Other important user-defined model inputs relate to manure characteristics, livestock management practices, septic-system loads and method of delivery to the environment, and wildlife populations and distributions within the watershed. Methods for quantifying each of these parameters will be discussed in the following section.

2.3.4 Fecal Bacterial Source Characterization

2.3.4.1 Livestock

Manure applied due to grazing, feeding operations, and winter feeding areas were major bacterial sources in this study. Livestock population at the county and watershed level was estimated using agricultural census/GIS layers data (USDA, 2006). The county animal census population was equally distributed on a total land-area basis to determine the fraction of total livestock in the study watershed. The USDA data were compared with data from the Kansas Department of Agriculture (KDA, 2004a). The in feedlot AUs within the watershed were estimated using active feedlot data (both federally permitted feedlots > 1000 AUs and state registered feedlots > 300 AUs) from the

Kansas Department of Health and Environment (KDHE) (Jepson, 2005). Permitted and registered livestock were subtracted from the total number of AUs in the watershed to estimate the net grazed livestock population. The field reported stocking rate of 3 ha per cow and calf pair (KDA, 2004b) was used as the baseline value, but can vary due to pasture management activities, animal growth and animal sales in the watershed. Animal stocking rates in the pastureland were also validated using county-wide livestock population data (KDA, 2004a). Animals in the pasturelands could be brought from feedlots, barnyards and leasing agreements for grazing during the warm season (generally from April to September). However, the stocking rate of the animals in the pastureland was assumed to be constant throughout the grazing season and at a decreased level during the winter period.

The Rock Creek watershed was estimated to be populated with 558 beef AUs in the pastureland (based on stocking rate), 104 beef AUs in the feedlots, and 223 beef AUs in the winter feeding areas (40% of 558), which was modeled in this study to represent the current scenario of the watershed. Manure production by beef cattle was estimated based on standard production rates (ASAE, 2000), of 26.36 kg of wet manure per day per 1000-kg animal unit (AU). The actual manure production by each animal unit may vary depending on dietary habit of the animal, reflected in a reported standard deviation of 17 kg day^{-1} for manure estimation (ASAE, 2000). Fecal coliform bacteria concentration in manure was estimated based on ASAE (2000), which reported 13x10^{10} cfu day^{-1} AU^{-1} wet-weight-basis bacteria concentration from the beef manure with a 12 x10^{10} cfu day^{-1} AU^{-1} standard deviation. The bacteria concentration was converted into model-input units of colonies forming units (cfu) per gram of dry-weight manure using standard mean manure moisture content (86% moisture; ASAE, 2000).

The pastureland was simulated under two major grass-type management conditions, which represent the typical field conditions. The two major grass types in the watershed include grazed (80%, typically native prairie) and non-grazed (20%, typically smooth brome and tall fescue). The native prairie grass typically is not fertilized, but tall fescue is fertilized with 70-15-0 (NPK) (Boyer, 2005). It was estimated that about 1.81 kg ha^{-1} day^{-1} dry weight of manure is applied in the pasturelands due to grazing operation during the growing season. This estimation is based on the ASAE (2000) standards that include: (a) a beef AU produces 26.4 kg of wet weight manure per day, (b) the moisture content of wet manure is 0.139, and (c) cattle are grazed for 153 days in the pastureland. It is possible that the actual animal density varies in the watershed every day because of animal growth and the pattern of incoming and outgoing animals. It was assumed that about 20% of the air-dry biomass is trampled every day, and about 341 kg of air-dry forage is required for an AU for 30 days (Paul and Watson, 1994). Grazing starts about a month earlier in tall fescue grasslands than in native prairie grass. All of the native prairie is grazed whereas only 80% of the tall fescue is grazed; the remaining tall fescue is un-grazed and used for haying or the Conservation Reserve Program (CRP). About 3.7 Mg ha^{-1} of hay is harvested annually from the un-grazed area, whereas biomass is not removed from the CRP land (Boyer, 2005). Cattle density in the pastureland was estimated as 3 ha per cow-calf pair based on the bluestem pasture guidelines for grazing (KDA, 2004b). Since cattle do not graze pastureland from October to March, no biomass uptake from the pastureland occurred, with no grass trampling and no manure deposition on the soil during this period.

All source loads due to livestock in confined animal feedlots were modeled to be land-applied as grazing operations in pasturelands of the sub-watershed where the active permitted feedlots were located. The winter feeding areas were modeled assuming that all livestock were confined within 40% of the grazed land of the watershed based on observed animal congregating behavior. Animals in feedlots and winter feeding areas contributed fecal bacteria for 212 days during the dormant season of the year (generally October to March). It was estimated that about 4.52 kg ha^{-1} day^{-1} dry weight of cattle manure (2.5 times greater than regular pastureland operation) was applied in the respective pasturelands of the sub-watersheds due to winter feeding operations.

2.3.4.2 Human

Digital orthophoto quarter quadrangles (DOQQ) of the watershed from 2002 were digitized depending on the physical context, roads, and type of houses to represent each septic system in the watershed. Each rural house was assumed to have one septic system, resulting in a total of 107 septic systems in the watershed. About 20% of the estimated septic systems (or 43 septic systems) were assumed failing in the watershed (KDHE, 2000). Each septic system was assumed to be used by three persons in the household that can contribute about 0.32 m^3 of sewage effluent per household per day (US EPA, 2001). The failing septic systems in the watershed were modeled using two techniques: effluent was either land-applied or input as a direct-daily point load to the outlet of the each sub-basin. The fecal bacteria concentration in failing septic system effluent was taken as 6.3×10^6 cfu 100 mL^{-1} (Overcash and Davidson, 1980).

2.3.4.3 Wildlife

No comprehensive wildlife inventory was available for the Rock Creek watershed. The wildlife population density was estimated based on the information received from the Kansas Department of Wildlife and Parks (KDWP). The 2002 summer road-kill indices survey data (Peek,

2005) for Kansas were used to estimate small-mammal populations in the watershed. The information include various wild-animal species: raccoon, opossum, striped skunk, coyote, badger, bobcat, red fox, gray fox, swift fox, beaver, mink, muskrat, river otter, spotted skunk, weasel, armadillo, woodchuck and porcupine. The population of raccoon, opossum, striped skunk, and coyote constituted about 81% of the total small mammals in Kansas. Population of the predominate large mammal (white-tailed deer) in the watershed was estimated based on expert opinion from the KDWP big-game coordinator (Lloyd, 2006). Similar data were collected for the predominate indigeneous avian species (turkey) from the KDWP small-game coordinator (Pitman, 2006).

In order to estimate the animal units of each wildlife species in the watershed, the population data were first distributed over the potential habitat for each species. Small mammals and turkey population data were counted from a road survey. Most of the small mammals were counted dead at the road shoulder. The sight distances of 5 m for small mammals and 50 m for turkey from each side of the road were assumed, and the population density of each species was estimated as number of animals per unit area, using total length of the road driven during survey. For deer, the number of deer harvested in northeastern Kansas was estimated and equally distributed in the total land area of northeastern Kansas to get the deer population density. Animal weights were estimated based on the information received from “mammals of Kansas” (Timm et al., 2007) and personal communication (Pitman, 2006). The population in 1,000-kg AUs of about 60 turkey AUs, 24 deer AUs, and 7 small mammal AUs were estimated to represent the current scenario of the Rock Creek watershed. All the wildlife-generated manure was applied into the woodland to be considered as baseline scenario. Other scenarios applied all or part of the wildlife loads to cropland. Corn and soybeans were major warm-season crops, and winter wheat was a primary cool-season crop grown in three year’s rotation in the watershed (Boyer, 2005). The warm season crop was planted on May 1 and harvested on October 1. The cool-season crop was planted on October 20 and harvested on July 30. The crop residue is left on the cropland between the crop periods. These dates represent the typical planting and harvesting dates in the watersheds. The conservation tillage system is the most widely adopted system for corn/soybean/wheat in the watershed. The croplands of the watershed were simulated with a 5-m wide filter strip at the edge of HRUs.

2.3.5 Weather and Hydrologic Data

Daily precipitation data for the watershed were used from Overbrook weather station located about 4.8 km south of the watershed. The 2004 annual rainfall for Overbrook was about 1,126 mm (Fig. 2.2). Data from the Silver Lake weather station, which is located about 22.5 km south were used for the daily temperature, daily solar radiation, daily wind speed, and daily relative humidity data. The missing watershed data were adjusted using the SWAT weather generator. The SWAT model uses data from the Ottawa weather station (Franklin County), which is located about 23 km southeast.

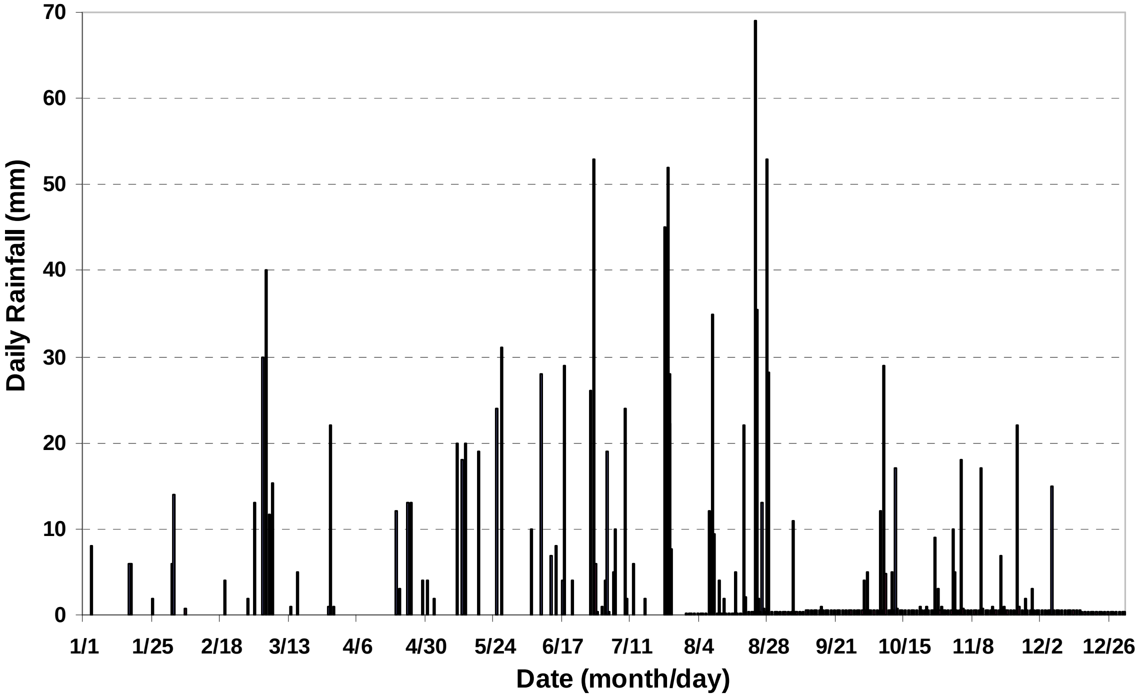

Figure 2.2 Distribution of daily rainfall data for Overbrook weather station, 2004

2.3.6 Statistical Analysis Methods

The SWAT model predicted nine daily mean flow events, which were compared with field-measured daily flow data. The statistical parameter used to evaluate measured vs. predicted daily mean flow were coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E). The R^2 values indicate how consistently measured vs. predicted values follow a best fit line and can range from zero (no correlation) to 1.0 (perfect correlation). The E indicates how consistently measured values (range $-\infty$ to 1.0) match predicted values, with 1.0 representing a perfect model (Nash and Sutcliffe, 1970). As similar to Moriasi et al. (2007) the model efficiencies were classified as excellent ($E \geq 0.90$), very good (E = 0.75 to 0.89), good (E = 0.50 to 0.74), fair (E = 0.25 to 0.49), poor (0 to 0.24), and unsatisfactory (< 0).

2.3.7.1 Sensitivity Indices

The relative sensitivity index (S) was used to test the model sensitivity for each model parameter or input parameter (Nearing et al., 1989). The S represents a ratio of maximum differences output values to input values, with each normalized to average values (Eq. 2.2).

$$S = [(O_2 - O_1)/(O_{avg}]/[(I_2 - I_1)/I_{avg})] \qquad (2.2)$$

where,

S = the relative sensitivity index

I_1, I_2 = smallest and greatest input values tested for a given parameter

Iavg = average of I_1 and I_2

O_1, O_2 = model output values corresponding to I_1 and I_2

O_{avg} = average of O_1 and O_2

An index of 0 indicates the output does not respond to changes in the input. An index of 1 indicates that the normalized output range is directly proportional to the normalized input range. A negative value indicates that an increase in input value caused a decrease in output value. A greater absolute value of the index indicates a greater impact of an input parameter on a particular output (Walker et al., 2000). Similar to Zerihun et al. (1996), we used four sensitivity classes: $\pm 0 < S \leq \pm 0.10$ was no sensitivity, $\pm 0.10 < S \leq \pm 0.50$ was low sensitivity, $\pm 0.50 < S \leq \pm 1.00$ was moderate sensitivity, and $S > \pm 1.00$ was high sensitivity.

Using the results of 42 model runs of different scenarios, the sensitivity index (Eq. 2.2) was computed for each combination of input and output for a given combination of model parameters and input parameters (Table 2.1). The model parameters studied were temperature adjustment factor (TBACT) and bacteria partition coefficient in surface runoff (BACTKDQ). The input parameters included manure production rate, bacteria concentration in manure, stocking rate of animals, land application and point load application of septic effluent, and land-use location of wildlife defecation. The model was simulated using percentage change in the input of parameters from their base values (Table 2.1). The die-off factor for fecal bacteria in solution was 0.40 day^{-1}, based on a three-day half-life, whereas die-off factor for bacteria adsorbed to soil particles was 0.040 day^{-1}, based on 1/10th of solution factor (Baffaut and Benson, 2003). The bacteria partition coefficient in fertilizer/manure was 0.90, assuming 90% of bacteria was in solution (Soupir et al., 2006). The model-predicted daily fecal bacteria concentration for 2004 was converted into geometric mean (GM) values for the annual period to calculate sensitivity for the model. A geometric mean is defined as a mean of the number of values (n) that is computed by taking the nth root of the product of the n terms.

Table 2.1. Relative Sensitivity Index and Percentage Changes in Input and Output

	Input		Output		
Parameters	**Value**	**% change**	**Value***	**% change**	**S index**
TBACT	0.96	-10	568	-5	0.47
(factor)	1.02	-5	565	-5	1.07
	1.07	0	596	0	0.00
	1.12	5	668	12	2.30
	1.18	10	809	36	3.18
BACTKDQ	0.00	-100	713	0	0.00
(m^3 Mg^{-1})	0.95	-99	974	37	-0.16
	8.75	-95	1026	44	-0.20
	17.50	-90	1077	51	-0.25
	43.75	-75	1029	44	-0.30
	87.50	-50	876	23	-0.31
	175.00	0	713	0	0.00
	262.50	50	635	-11	-0.29
	350.00	100	588	-18	-0.29
	500.00	186	541	-24	-0.28
Bacteria Concentration	3.55E+06	-90	20404	4434	-1.17
(cfu g^{-1})	1.78E+07	-50	1360	202	-1.51
	2.66E+07	-25	1436	219	-3.66
	3.55E+07	0	450	0	0.00
	5.33E+07	50	1652	267	2.86
	7.10E+07	100	1789	298	1.79
	3.55E+08	900	1510	236	0.66
	99999999	181	545	21	0.20
	100000000	181	368	-18	-0.21
Livestock Manure Production	18.45	-25	509	-13	0.39
(kg day^{-1}AU^{-1})	23.73	-10	559	-4	0.41
	26.36	0	583	0	0.00
	29.00	10	607	4	0.42
	34.27	25	655	12	0.44
Livestock Stocking Rate	1.52	-50	420	-22	0.38
(ha^{-1} cow-calf-pair)	2.28	-25	483	-11	0.40
	3.04	0	542	0	0.00
	3.80	25	597	10	0.44
	4.56	50	651	20	0.46
Septic Effluent					
Land-applied	2.81	-50	734	3	0.04
(kg ha^{-1} month^{-1})	4.22	-25	745	1	0.04
	5.63	0	754	0	0.00
	7.04	25	761	-1	0.04
	8.45	50	767	-2	0.04
	11.26	100	776	-3	0.04
Point load	305.15	-50	7242	38	0.71
(cfu 100mL^{-1} day^{-1})	457.72	-25	9510	19	0.72
	610.29	0	11707	0	0.00
	762.86	25	13799	-18	0.74
	915.44	50	15859	-35	0.75
	1220.58	100	19645	-68	0.76
Wildlife Source Loads					
All cropland	3.39	-50	34	29	0.50
(kg ha^{-1} month^{-1})	5.09	-25	41	14	0.53
	6.78	0	47	0	0.00
	8.48	25	54	-13	0.54
	10.17	50	59	-25	0.56
	13.56	100	71	-49	0.59
All woodland	8.00	-50	552	46	0.90
(kg ha^{-1} month^{-1})	12.01	-25	791	23	0.90
	16.01	0	1025	0	0.00
	20.01	25	1256	-23	0.91
	24.00	50	1495	-46	0.93
	32.02	100	1975	-93	0.95
Cropland/woodland equal	2.39	-50	342	44	0.84
(kg ha^{-1} month^{-1})	3.58	-25	474	22	0.86
	4.77	0	608	0	0.00
	5.96	25	740	-22	0.88
	7.15	50	870	-43	0.89
	9.54	100	1146	-89	0.92

* cfu 100 mL^{-1}

2.4 Results and Discussion

2.4.1 Flow Validation

The un-calibrated baseline SWAT model, using ground-truthed land-use conditions and other parameters to define current conditions, produced good agreement for simulation of daily mean flow from the watershed. The SWAT model predicted the daily average flow rate of the watershed with good correlation ($R^2 = 0.74$, $E = 0.63$) between measured and predicted values (Fig. 2.3). The field measured data for nine rainfall-runoff events were available to compare with the SWAT-model-predicted data. The SWAT model under-predicted during five daily flow events due to either low rainfall events (from 0 to 26 mm) or low/no prior day rainfall condition (from 0 to 26 mm). Model over-predicted flow during one storm event when there was 35 mm rainfall and 12 mm prior day rainfall. The observed good correlation of the un-calibrated model suggests that the SWAT hydrologic model was reasonably robust and model input data affecting hydrologic processes were of reasonable accuracy. This confirmation of reasonable flow results provided confidence that the sensitivity analysis was being conducted with minimal bias from the flow-prediction algorithms of the model.

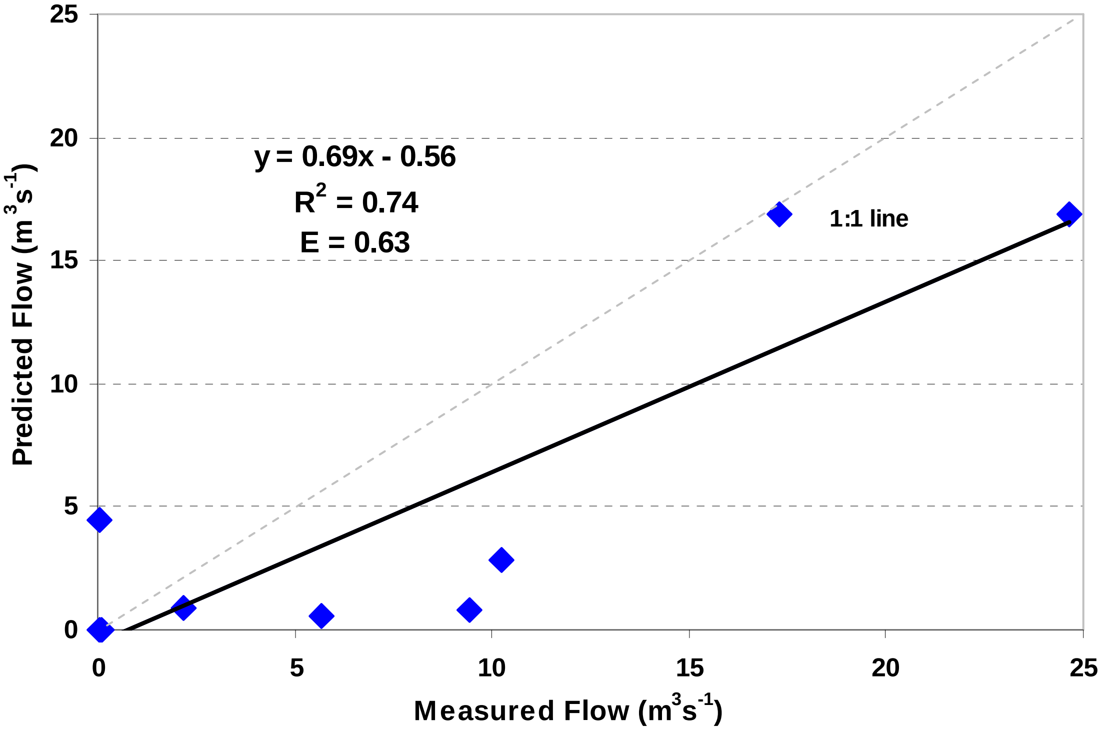

Figure 2.3. Daily measured vs. daily predicted mean flow for 2004

2.4.2 Bacteria Load Validation

The un-calibrated baseline SWAT model, using livestock, septic and wildlife loadings to represent current conditions, over-predicted average daily fecal coliform bacteria concentration by 158% and gave a fair correlation of measured vs. predicted data with $R^2 = 0.40$ (Fig. 2.4). The model under-predicted bacteria during a single no-flow event. Although the model over-predicted bacteria concentration during all of the runoff events, the slope of predicted vs. measured regression was 1.24, which was considered to be similar enough to 1.00 to allow sensitivity analysis. Further calibration of the model was not attempted before sensitivity analysis was conducted.

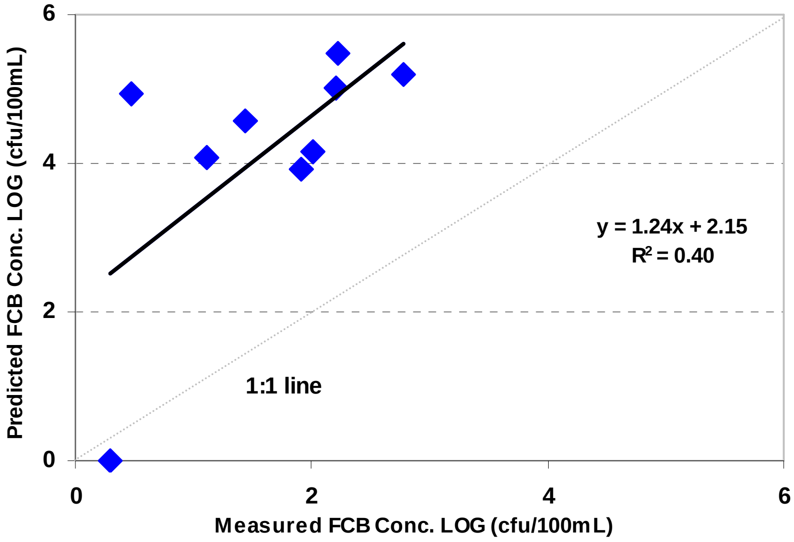

Figure 2.4. Measured fecal coliform bacteria (FCB) concentration model response

2.4.3 Model Sensitivity to Bacteria Parameters

The model parameters and input parameters used in the study ranged from no relative sensitivity (S = 0) to high relative sensitivity (S = 3.18). The TBACT model parameter response followed a second-order polynomial relationship ($R^2 = 0.99$) with bacteria prediction (Fig. 2.5). The higher values of TBACT resulted in higher values of bacteria-concentration prediction, reflecting lower bacteria-concentration removal efficiency, because TBACT is a negative exponential function in the first-order decay bacteria equation (Eq. 2.1).

Average bacteria concentration varied by 36% over the range recommended by SWAT (Neitsch et al., 2002), from 0.96 to 1.18 (Fig. 2.6). This study showed high model sensitivity, mostly in the upper range of the TBACT parameter. The model prediction showed a low relative sensitivity index of 0.47 at -10% input change (TBACT = 0.96) and a high relative sensitivity index of 3.18 at +10% input change (TBACT = 1.18) (Fig. 2.6). These results demonstrate that it is important for the model user to accurately define TBACT, particularly in the mid to upper range (high sensitivity above TBACT = 1.02) of recommended values.

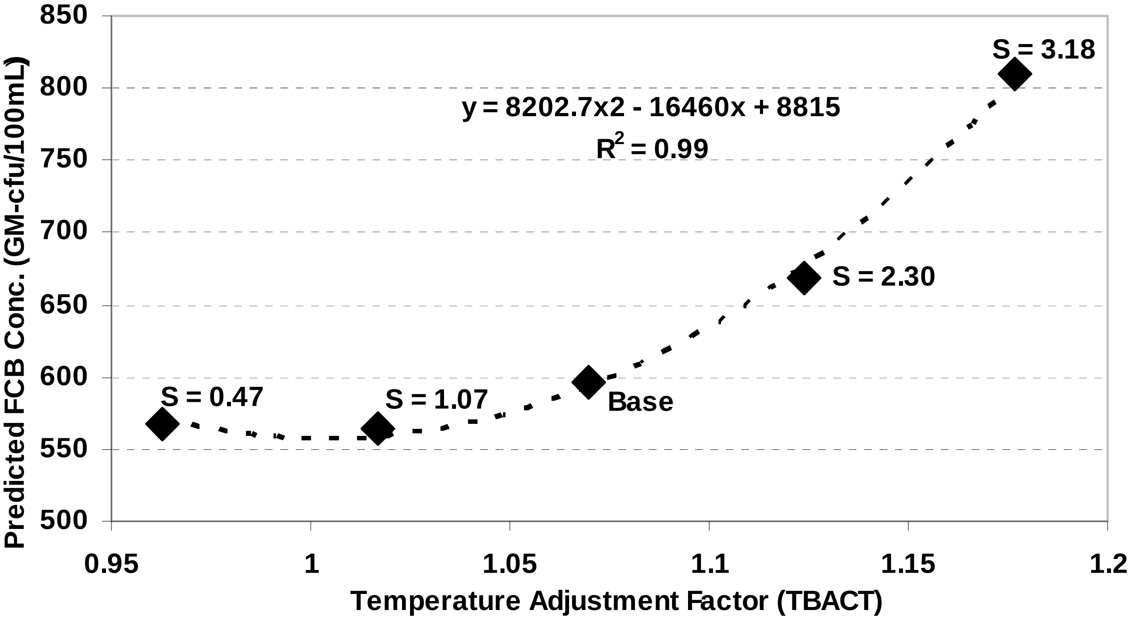

Figure 2.5. Second-order polynomial response of annual geometric mean FCB concentration prediction to temperature adjustment factor (TBACT)

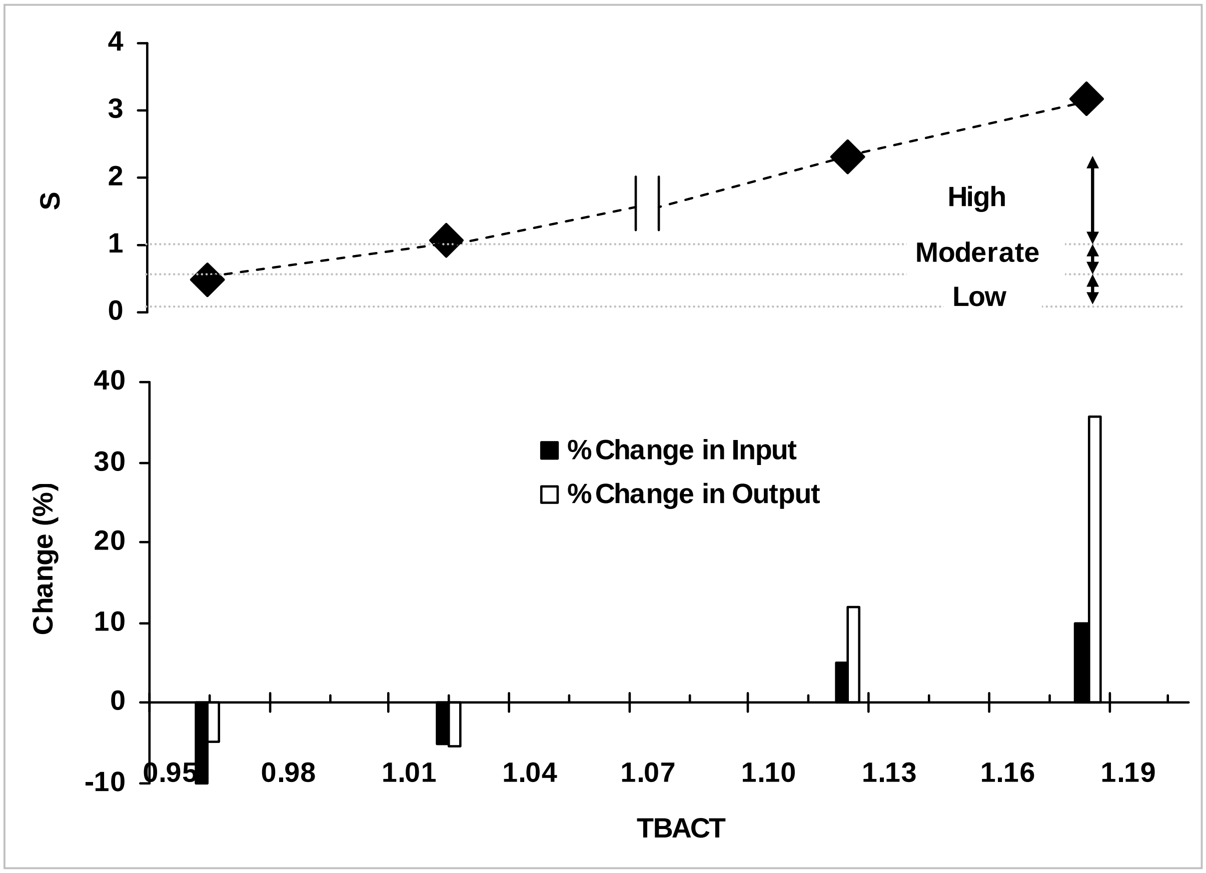

Figure 2.6. Temperature adjustment factor (TBACT) relative sensitivity index (S) response

The model generally responded with an inverse relationship between BACTKDQ value and predicted surface-water bacteria concentration over most of the parameter range. Lower values of BACTKDQ generally decreased removal efficiency of bacteria and increased predicted bacteria concentration. With lower BACTKDQ, a greater fraction of bacteria were in solution phase. In SWAT, bacteria in solution phase are suspended and transported in surface runoff directly, whereas bacteria in solid phase are suspended and transported with eroded sediment particles. Rainfall events that generate runoff but do not have adequate energy to generate soil erosion will transport solution-phase bacteria but not solid-phase bacteria. (/Prem: What is the minimum size rainfall event that generates runoff and what is the minimum size rainfall event that generates erosion?/). The modeled increase in surface-water bacteria concentration occurred despite having 10 times greater bacterial die-off rate in solution-phase compared to solid-phase. Together, these results suggest that die-off processes play a less important role in bacteria removal during storm events than processes involved in suspending and transporting bacteria.

The model prediction showed low sensitivity, with the greatest relative sensitivity of only -0.31 at -50% input change (Fig. 2.7). The -100% input change (BACTKDQ of 0) resulted in S = 0, which indicates that the model essentially used the base value (BACTKDQ of 175) as a default (Fig. 2.7). Relative sensitivity increased (more negative) as BACTKDQ increased from 0 to 44, but remained nearly constant with further increases up to 500 (Fig. 2.7).

Henry and Dillaha (2004) defined BACTKDQ using a linear regression between attached and planktonic concentration of bacteria. They found significantly higher correlation when they used BACTKDQ of 595 m^3 Mg^{-1} instead of using 315 m^3 Mg^{-1}. They cautioned against directly applying BACTKDQ results from this controlled-environment study to water quality modeling studies. Mankin et al., (2007) found BACTKDQ of 106 m^3 Mg^{-1} for silt loam soil over a wide range of bacterial concentrations (5.3×10^3 to 8.4×10^7 cfu g^{-1}). This study found SWAT to be insensitive to changes in BACTKDQ over the range of values greater than 29 m^3 Mg^{-1} (Fig. 2.7). Although BACTKDQ may vary by characteristics of the runoff event or spatially within the watershed, the low sensitivity of SWAT to changes in BACTKDQ indicate that the user should seek only to represent the average condition for the watershed.

The bacteria decay rate on land or in water varies diurnally and seasonally with temperatures as modeled using TBACT in Eq. 2.1. Also, TBACT itself may vary due to change in the ambient temperature. Wang et al. (2004) calculated the TBACT factor in excreted manure as 1.026 for temperatures between 4°C and 27°C and 1.034 for temperatures between 27°C and 41°C, all within the range of 1.07 ± 0.05 (Reddy et al., 1981; Crane and Moore, 1986) in the temperature range at which most biological reactions occur. Howell et al., (1996) found fecal bacteria mortality to become increasingly nonlinear as temperature increased. These results suggest that future versions of SWAT might be improved by adding capability to input TBACT nonlinearity with temperature.

SWAT applies equation 2.1 and TBACT on a daily basis according to daily average temperature in the watershed. When daily average temperature approaches 20^0C, the TBACT parameter has less impact on dieoff-rate (Eq. 2.1). Generally, the temperatures were greater than 20^0C (average temperature about 21.5^0C) during April to September and probably below 20^0C during the rest of the year.

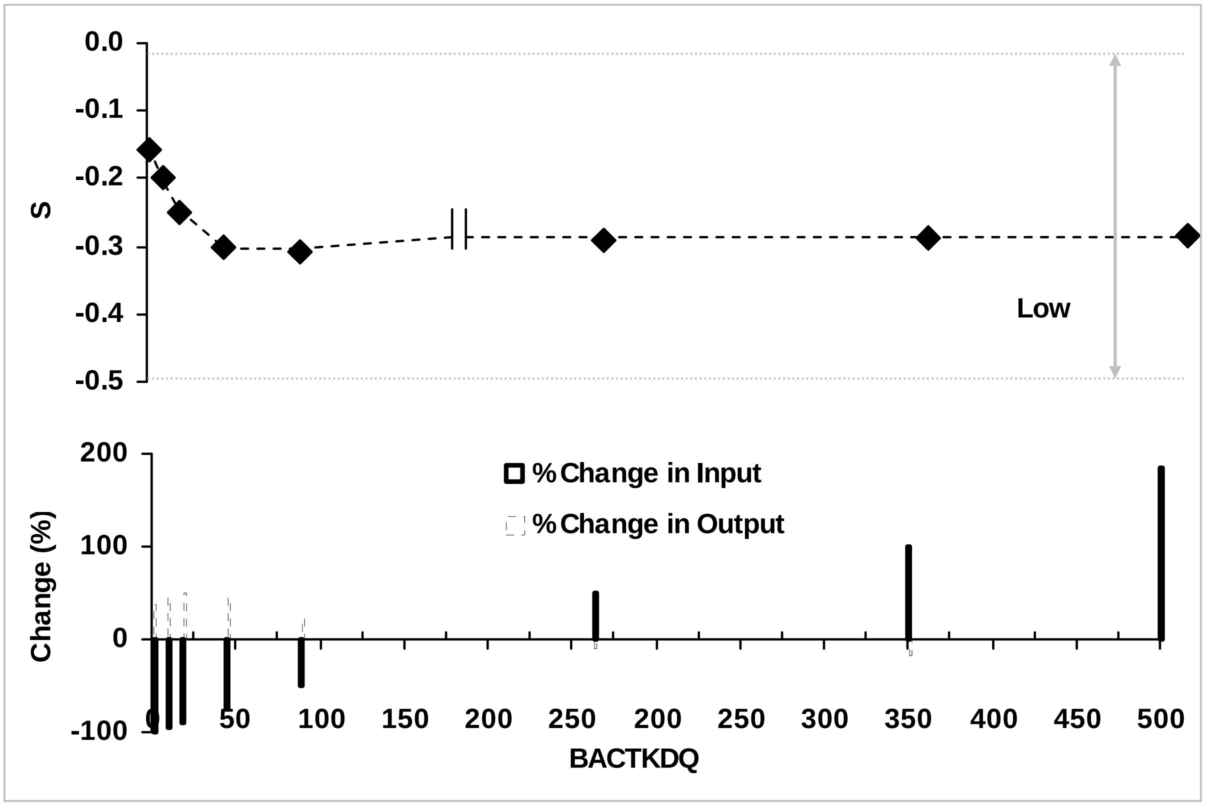

Figure 2.7. Bacteria partition coefficient in surface runoff (BACTKDQ) relative sensitivity index (S) response

2.4.4 Model Sensitivity to Livestock Source Parameters

Increasing livestock manure production rate increased bacteria concentration prediction but with only about 40% relative sensitivity (Fig. 2.8). The model sensitivity increased very slightly (from 0.39 to 0.44) through a reasonable range of manure input variation (-25% to +25%) indicating a slight increase in delivery efficiency as the amount of applied manure increased. The livestock stocking rate (ha^{-1} cow-calf pair) in the watershed responded similar results as manure production rate from the watershed. Although stocking rate is analogous to manure production rate, increasing livestock stocking rate increases trampling impact and delivery rate of bacteria to the watershed outlet thus slightly increase in the relative sensitivity. The model sensitivity due to stocking rate increased very slightly (from 0.38 to 0.46) through a reasonable range of manure input variation (-50% to +50%). Both the magnitude and change in relative sensitivity over the range of manure production rate and livestock stocking rate studied indicate a reasonable model response.

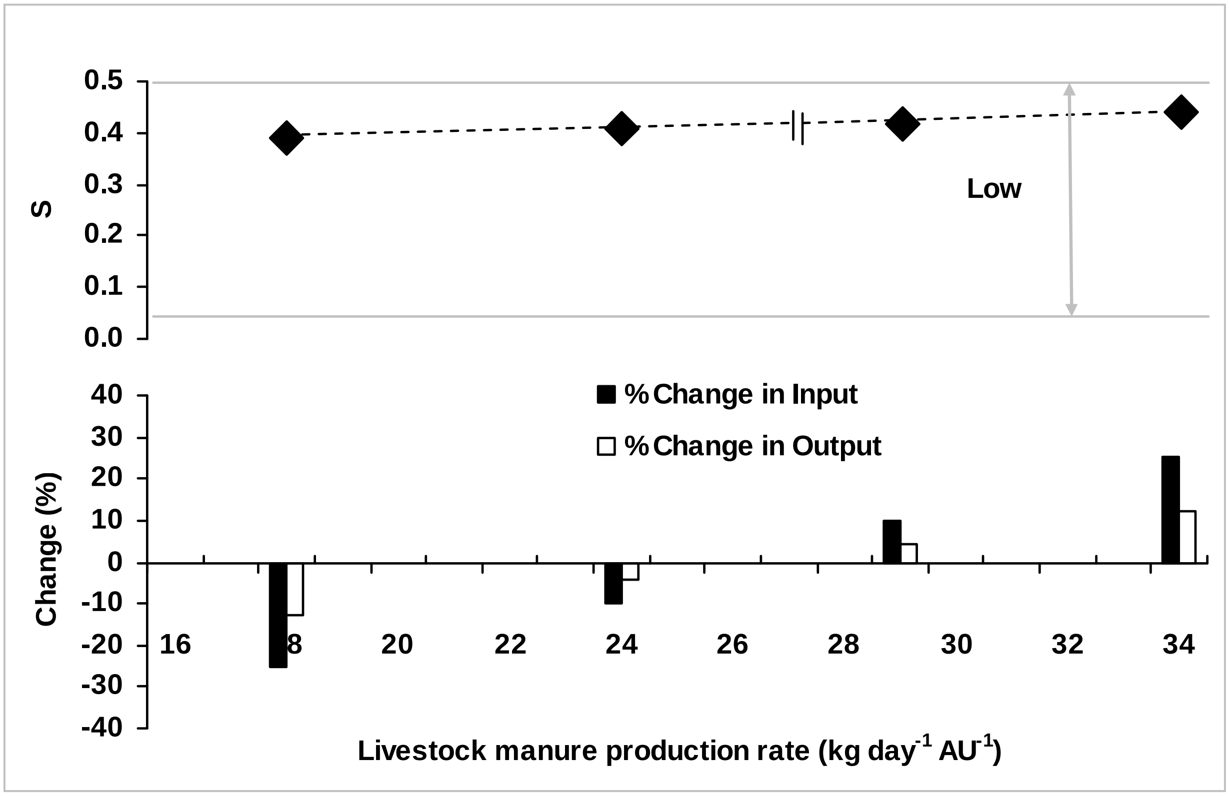

Figure 2.8. Livestock manure production rate relative sensitivity response

Bacteria concentration input in the model (cfu g^{-1}) is generally an eight digit integer values. Small percentage change in bacteria concentration results into difference of large number in the input change, however this study determined small change in the model output. Since relative sensitivity is estimated based on the change in input vs. change in output, the sensitivity of the change in bacteria concentration is expected to be high.

Bacteria concentrations in livestock manure responded generally high model sensitivity over the range of concentrations from -90% to +100% of the baseline (3.6×10^6 cfu g^{-1} to 7.1×10^7 cfu g^{-1}) amount (Fig. 2.9). However, the model showed moderate sensitivity (0.66) at +900% input change (3.6×10^8 cfu g^{-1}) but low sensitivity (0.20) at +181% input change (1.0×10^8 cfu g^{-1}).

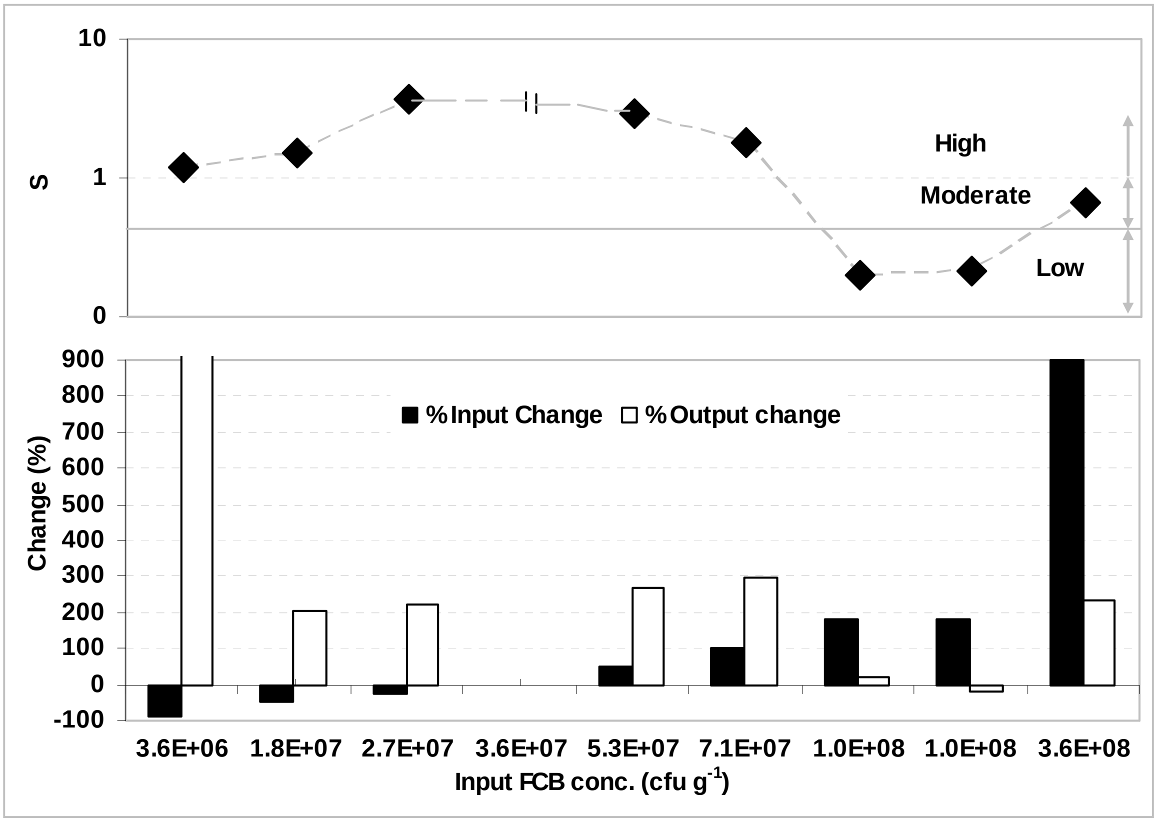

Figure 2.9. Bacteria source concentration relative sensitivity response

The manure production and characterization data were used from ASAE, 2000 standard which uses mean values that varied with a standard deviations of 17. The actual values may vary due to differences in animal diet, age, usage, productivity and management. No site specific data were available to be considered in lieu of the mean values. The manure production values used in this study covers a reasonable range of manure production. The high amount of manure application on the land such as bio-solids in a limited land area is out of the scope of this study. The level of sensitivity changes based on manure application rate. For example, ten percent increase in the manure production rate increase the sensitivity up to about 50% from the base whereas one hundred percent increase will increase sensitivity up to 87% from the base. These results are based on a separate SWAT model runs.

The animal stocking rate may also vary daily due to change in the seasons, growth of animals, and conditions of the pastureland. However, stocking rate mainly impacts the total manure production from the watershed which did not show much support in the high sensitivity mode of the model. However, increased stocking rate, manure production, length of grazing period, average manure loading rate are the potential source factors to serve as a non-point source pollution (Sweeten and Rendell, 1978; Thelin and Gerald, 1983).

The fecal coliform bacteria concentration estimation values were varied with a standard deviation of 12 (ASAE, 2000). Bacteria concentration was stored in the model in floating-point 8.3 format (eight integers followed by three decimals: xxxxxxxx.xxx). When nine integer digit bacteria concentration values were input, model determined lower sensitivity predicting lower number of stream bacteria concentration than eight digit input values. If seven digit values were input, the model showed sensitive behavior, predicting even higher number stream bacteria concentrations than eight digit input values.

2.4.5 Model Sensitivity to Human Source Parameters

The septic system effluent was modeled in two ways to identify the impact on bacteria concentration at the outlet of the watershed. The land-applied method of septic effluent generally showed a linear relationship between septic load and bacteria prediction (Fig. 2.10a). The model prediction resulted in a no relative sensitivity (<0.05) over the -50% to +50% range of effluent land application rates. The point load input method of septic effluent also generally resulted in a linear relationship (Fig 2.10b). The model prediction resulted in a moderate sensitivity with relative sensitivity of 0.70 at -50% (305 cfu100 mL^{-1}) and 0.75 at +50% (915 cfu 100 mL^{-1}).

The land-applied method was not sensitive because of having overland flow process in the model, which allows septic effluent sorption, decay and gasification. Soil is the main treatment unit for the onsite septic effluent disposal. Soil filters the septic effluent, removing fine particles, bacteria, and nutrients. The direct point load method proved more sensitive than the land-applied method because of having only channel flow process which allowed relatively less degradation and absorption fields as compared to overland flow process. The point load represents failing septic conditions in which septic effluent runs down to the stream from its location. The delivery efficiency increases due to limited absorption fields in the point load application method. Rice et al. (2003) evaluated the lateral extent of fecal bacteria at the soil surface from failing onsite waste water system in eight Kansas counties. The soil samples were analyzed monthly for fecal coliforms at distances up to 200 m from failing systems. Fecal bacteria at the soil surface did not consistently extend beyond 80 m from the discharge of failing systems. The higher soil moisture conditions of soil encourage fecal coliform survival and mobility during rainfall events but in most cases 100 m distance was the distance of maximum transport.

Modeling either land-applied or point load septic systems is based on the field condition of the watershed. The percentage failing rate of point load septic systems is more important than land-applied septic systems which is supported by the result of this study. Therefore, the reason for comparing these effluent application processes was to help in watershed management and modeling decisions.

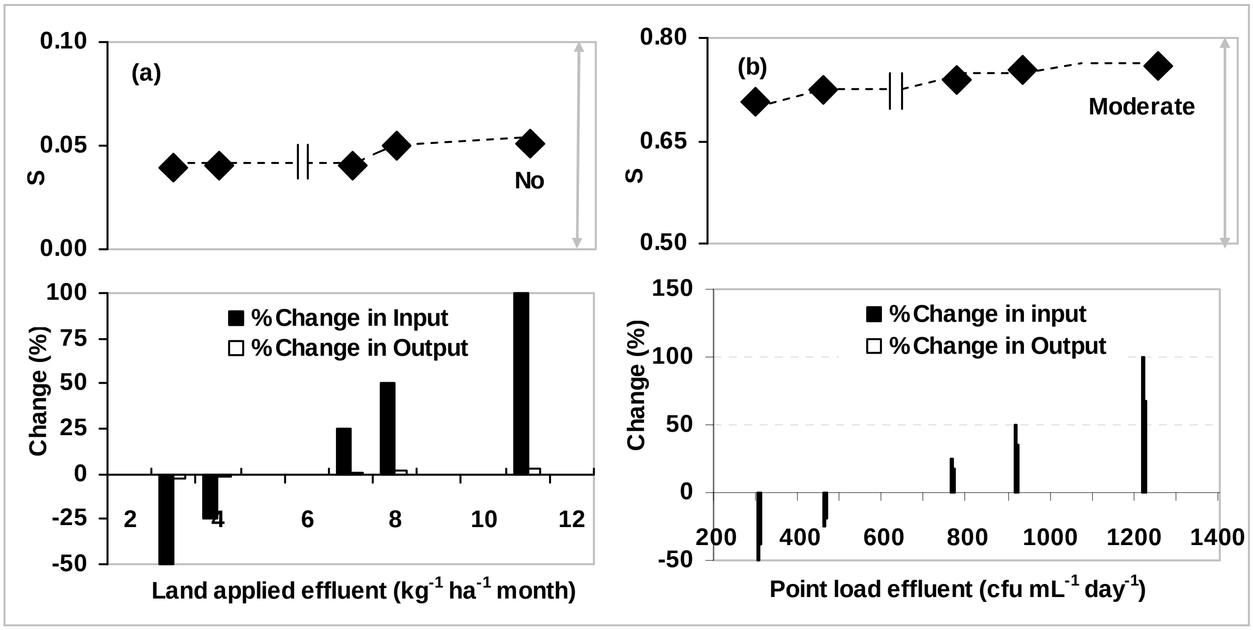

Figure 2.10. Septic source load application methods relative sensitivity response for (a) land-applied and (b) point load

2.4.6 Model Sensitivity to Wildlife Source Parameters

The wildlife source loads portion in this study modeled three types of wild animals: large mammals, small mammals, and birds. The habitat for these animals was mostly woodlands and croplands, though the proportion of bacterial loads in each land use type was unknown. In this study, the sensitivity of the model was tested applying all wildlife source loads in woodland, all wildlife source loads in cropland, and all wildlife source loads applied equally to cropland and woodland. The model responded reasonably between application of wildlife source loads and bacteria prediction. Although, model determined moderate sensitivity for all three cases, sensitivity was found increased in the woodland and combined cropland and woodland areas as compare to cropland area only. The model prediction identified a moderate sensitivity with relative sensitivity of 0.53 for cropland case at ±50% input change. Increased sensitivity of 0.93 was found at ±50% input change for the woodland case. The case of equal cropland and woodland (Fig. 2.11) resulted in a relative sensitivity of 0.89 at ±50% input change.

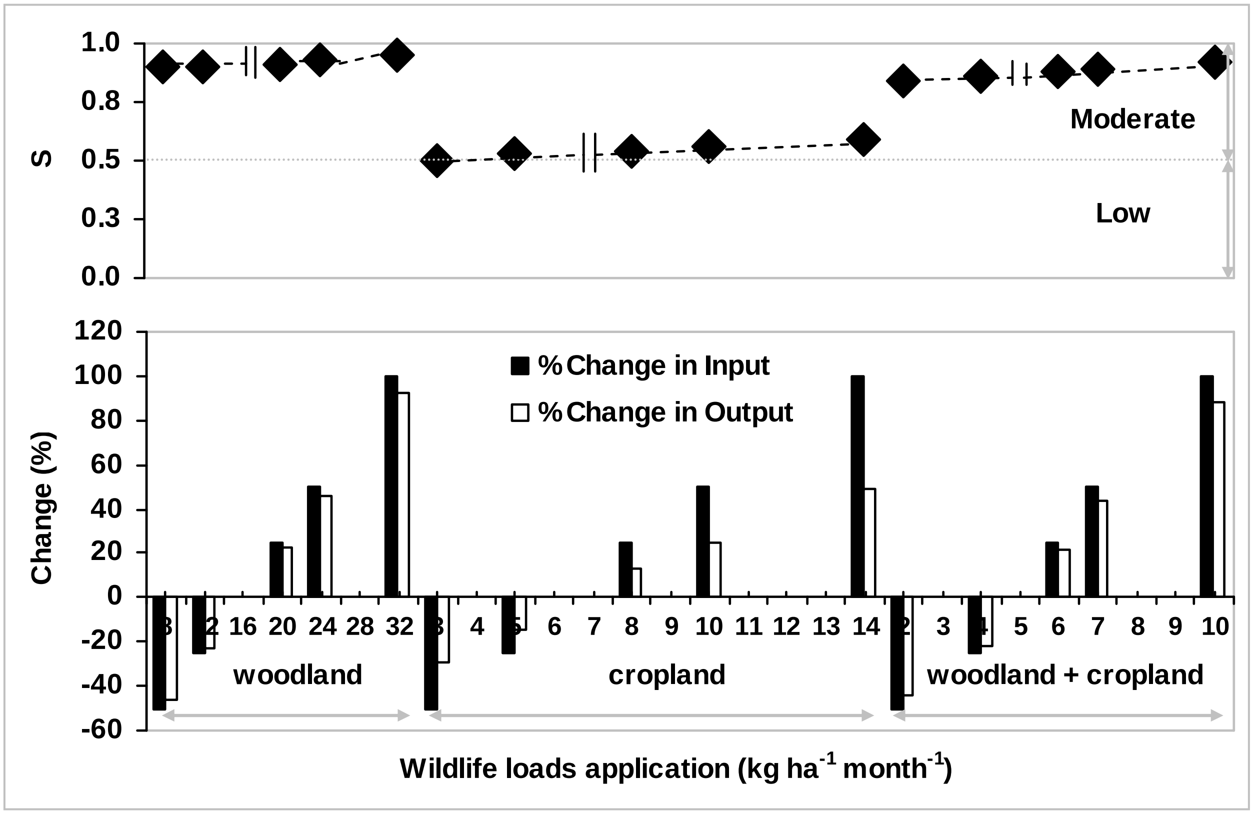

Figure 2.11. Wildlife source load application methods relative sensitivity response

This study did not consider bacteria source loads due to migratory birds in the watershed. The Kansas wildlife (animals or birds) live weight and bacteria concentration were taken from published literatures, but it may not be truly representative of the watershed. However, the best available data for wildlife were utilized for this study. The decrease in the total land area where wildlife source load was applied made a difference in the relative sensitivity. The cropland area in the watershed consists of 33% of the watershed area, but woodland area only makes up 14% of the total watershed area. Since the estimated wildlife source loads remain constant and only application area was varied, there was more sensitivity of the model when applying wildlife source loads into woodland areas than cropland areas. Un-calibrated model used a similar curve numbers for the woodland and cropland in the watershed. Cropland areas of the watershed were simulated under conservation tillage systems two times a year, (April 10 and September 20) but it had no effect in bacteria transport when compared with no-till system using SWAT. Because wildlife bacteria source loads were considered continuously applied (365 days) throughout the year in the model. Applying two times tillage had no contribution in order to transport bacteria because there was no same day and five previous day's rainfall in the watershed when checked with rainfall data. Most of the rainfall events in the watershed were occurred during April to September after the first tillage and before the second tillage. Therefore, tillage had no effect in the modeling results. The SWAT model really did good job in determining the tillage effect in bacteria transport. The use of filter strip (5 m) in the HRUs decreased the bacteria transport to the stream from the cropland areas. Therefore, more flow and bacteria delivery rate from the woodland area was expected.

2.5 Conclusions

This study demonstrated methods to characterize bacteria source loads and to assess the model sensitivity to model parameters, input parameters and bacteria source application methods. The potential bacteria source loads, such as livestock, failing septic systems, and wildlife, were characterized for the watershed.

Un-calibrated model results for in-stream fecal bacteria concentrations compared fair agreement with measured data, providing general confirmation of source-load characterization methods. Further detailed calibration with more extensive in-stream data are needed for more comprehensive model assessment. Model use to predict fecal bacteria concentration at the watershed scale requires knowledge of both bacteria source application methods and model sensitivity in selection of bacteria model and source-load input parameter values. The result of this study can help in selection of more realistic model parameters to simulate watershed management scenarios.

Sensitivity of input parameters generally, ranked as Bacteria concentration ≥ TBACT > Wildlife source loads > Livestock stocking rate ≥ Livestock manure production rate > BACTKDQ. The model was relatively insensitive to changes in parameters related to land-application methods. Results suggest that SWAT bacteria modeling will require accurate input data that allocate sources that are directly input, deposited, or discharged to a stream vs. those that are land applied to upland areas.

Bacteria concentration was stored in the model in floating-point 8.3 format (eight integers followed by three decimals: xxxxxxxx.xxx). When nine-integer-digit bacteria concentration values were input the model responded with lower sensitivity and by predicting lower stream bacteria concentration than eight-digit input values. This format problem should be solved when update SWAT model.

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CHAPTER 3 - FECAL BACTERIA SOURCE CHARACTERIZATION AND SENSITIVITY ANALYSIS OF SWAT 2005

Abstract

The sensitivity of the Soil and Water Assessment Tool (2005) and its input parameters that impact the prediction of fecal coliform bacteria concentrations were evaluated. The model was applied at Rock creek watershed (77 km^2), Kansas. Methods were developed to use commonly available data to describe model inputs of watershed sources of livestock, septic and wildlife loads. The flow and bacteria loads were validated reasonably for the watershed. The runoff events of the simulated period geometric mean value of the fecal coliform bacteria concentration were evaluated using a relative sensitivity index (S).

The four model parameters and one input parameter were tested using Latin Hypercube Sampling (LHS) and independent parameter perturbation (IPP) methods. The bacteria partition coefficient in surface runoff (BACTKDQ) showed an inverse relationship and no to very high sensitivity (S up to 8.69). The temperature adjustment factor (TBACT) showed no to high sensitivity (S up to 3.25), less persistent bacteria die-off factor in solution (WDLPQ) showed no to moderate sensitivity (S up to 0.72), and less persistent bacteria die-off factor in sorbed (WDLPS) showed no to low sensitivity (S up to 0.42). The fecal coliform bacteria concentration in manure had no to moderate sensitivity (S up to 1.05).

Sensitivity of model and input parameters generally, ranked as BACTKDQ > TBACT > Bacteria concentration > WDLPQ > WDLPS. Sensitivity of model and input parameters were found changed from SWAT 2000. Bacteria concentration was stored in the model in floating-point 8.3 format (eight integers followed by three decimals: xxxxxxxx.xxx). When nine-integer-digit bacteria concentration values were input the model responded with lower sensitivity and by predicting lower stream bacteria concentration than eight-digit input values.

This study suggested to revise SWAT model to address format problem with bacteria concentration, which is not addressed by SWAT 2005. Also, this study suggested to provide default WDLPQ and WDLPS values in the SWAT model from natural life perspectives.

3.1 Introduction

Pathogen contamination from fecal bacteria is one of the causes of surface water-quality impairment which often results from non-point source pollution. The fecal bacteria often are present in surface water at concentrations that indicate the potential to cause severe illnesses in humans (Craun and Frost, 2002). Fecal bacteria sources include land application of manures, grazing operations, winter feeding operations, failing septic systems, and wildlife (Zeckoski et al., 2005). Surface water movement and sediment erosion increase the chance of bacteria reaching surface water systems especially during high intensity rainfall events. The current water quality assessment techniques generally include two methods (a) water quality field monitoring and (b) computer/mathematical modeling. Field monitoring method is most appropriate and reliable method to support in water quality assessment. However, it is expensive due to high costs and tremendous spatial and temporal ecosystem variability. Therefore, computer/mathematical models provide an alternative to monitoring that can save time, reduce cost, and minimize the need for testing management alternatives (Shirmohammadi et al., 2006). Models can be used to assess water quality goals on large watersheds. However, the sensitivity of mathematical model simulation results is a concern.

In recent years, the U.S. Environmental Protection Agency (EPA) has increasingly emphasized the importance of incorporating variability and uncertainty into the modeling process (USEPA, 1997). It identified probability analysis techniques like Monte Carlo analysis, as useful tools for adequately quantifying variability and uncertainty (Chang, 1999). In watershed-level assessment and management activities there are uncertainties, and the only thing we are sure of is that we are “in doubt” (Hession et al., 1996a; 1996b). There are many uncertainties inherent in watershed modeling, including monitoring/measurement error, model error, model input parameter errors, spatial variability, errors in spatial data layers within a geographic information system (GIS), the effects of aggregation of spatial data when modeling watersheds, and temporal variability. These different errors or uncertainties can be additive. Uncertainties may be classified into three categories: the inherent variability in natural processes, model uncertainty, and parameter uncertainty (Haan, 1989). The inherent variability in the natural processes is the unexplained random variability of the natural environment (Haan, 1989). This inherent variability in natural processes can be either variability in space (spatial variability) and/or variability in time (temporal variability). Spatial and temporal variability can be generally observed with environmental factors such as rainfall, temperature, and stream flow.

The model uncertainty results from faulty conceptualizations of the world (Suter et al., 1987), such as: (1) using a small number of variables to represent a large number of complex phenomena, (2) choosing incorrect functional forms for interactions among variables, and (3) setting inappropriate boundaries for components of the world to be included in the model. The parameter uncertainty is resulted when model parameters are allowed to vary around their base values independently (Tiscareno-Lopez et al., 1993, 1994) or dependently (Silberbush and Barber, 1983). The range of the perturbation may be a specific percentage (Barnes and Young, 1994) or determined from experimental measurements (Fontaine et al., 1992; Gwo et al., 1996).

The most common form of sensitivity analysis is independent parameter perturbations (IPP) in which parameters are varied individually by a fixed percentage around a base value (Ferreira et al., 1995). An example of this approach is with first-order analysis (Haan and Zhang, 1996), which is most applicable to linear systems. Model output responses to parameter perturbation may be quantified by percentage change of selected output variables and relative change of output versus input (Larocque and Banton, 1994).

The overall model response may be obtained by measuring the average response of selected output variables (Nearing et al.,1989). Model sensitivity can be evaluated quantitatively using either local or global analysis (Soutter and Musy, 1999). Local techniques represent one-at-a-time parameter change from the base value, whereas global sensitivity analysis techniques include random parameters changes over their actual ranges, which generate input and output distributions that can be statistically analyzed (Soutter and Musky, 1999). Latin Hypercube Sampling-One variable At a Time (LHS) is a modified Monte Carlo simulation method that integrates local and global sensitivity of model parameters (Griensven, 2005).

Despite the benefit of evaluating an entire input-parameter space, global methods can be cumbersome and daunting when models are complex and contain numerous inputs, and extensive computational effort often is required. In these cases, single-variable analysis is often preferred (Graff et al., 2005). Independent Parameter Perturbation (IPP) from the LHS-Mean values for each model input parameter may help to compare local and global method responses. The response of the output to variations in input can be quantified using relative sensitivity for a given perturbation (Graff et al., 2005). The relative sensitivity of the model parameters may be obtained by measuring the relative response of each input vs. output variables (James and Burges, 1982; Nearing et al., 1989; White and Chaubey, 2005; Jesiek and Wolfe, 2005).

The Soil and Water Assessment Tool (SWAT) is a watershed scale process-based model developed by USDA Agricultural Research Service (ARS) (Arnold et al., 1998). The bacteria transport routines were added to the SWAT model in 2000 (Neitsch et al., 2002). The bacteria routines were improved (Sadeghi and Arnold, 2002) and the SWAT model was modified in 2005 (Neitsch et al., 2005), which allowed it to be used as a tool for addressing microbial contamination of water caused by point and non-point sources. However, sensitivity analysis of the SWAT 2005 version of the model focusing on bacteria transport part is needed to allow it to be used and parameterized appropriately. Sensitivity analysis of the microbial sub-model of SWAT (2005) has not been assessed. It is therefore important to know the influence of the model parameters and input parameter on model response.

3.2 Objectives

The objectives of this study were to (a) demonstrate methods to characterize bacteria source loads and to (b) assess the model sensitivity to model parameters, and input parameter using SWAT 2005.

3.3 Materials and Methods

3.3.1 Watershed Stream Description

The study was done in the 77 km^2 Rock Creek watershed (Fig. 3.1), located in Douglas County, KS. The study-area land uses were primarily grassland (52%), cropland (33%), and woodland (14%) with predominately silty-clay textured soils (SSURGO: KS0457302, KS0457325, KS0458962). The pastures were native prairie, smooth brome, and tall fescue grasses. Average slope in the watershed sub-basins ranged from 3.8% to 6.3%.

Grab samples (about 250 ml) were collected from the mid point of the flowing stream at the watershed outlet. Samples were placed immediately into an ice chest and transferred to a laboratory refrigerator within two to four hours of collection. Bacteria enumeration procedures were started within 24 hours.

A serial dilution method (Clesceri et al.,1998) was applied to enumerate fecal coliform bacteria colonies. Bacterial samples typically required four serial dilutions to obtain reasonable bacteria colony counts. Flow at the time of sample collection was calculated using Manning’s equation, as outlined by Ward and Elliot (1995). Flow depth, cross-sectional area, and channel slope were measured, and the channel roughness factor was estimated based on channel roughness characteristics and degree of meandering (Cowan, 1956). The calculated flow was validated based on ratio of the watershed area using data from the USGS Richland gage station data. The calculated flow data showed very good correlation (>90%) with the weighted area flow data. This study used the data collected from January to December 2004.

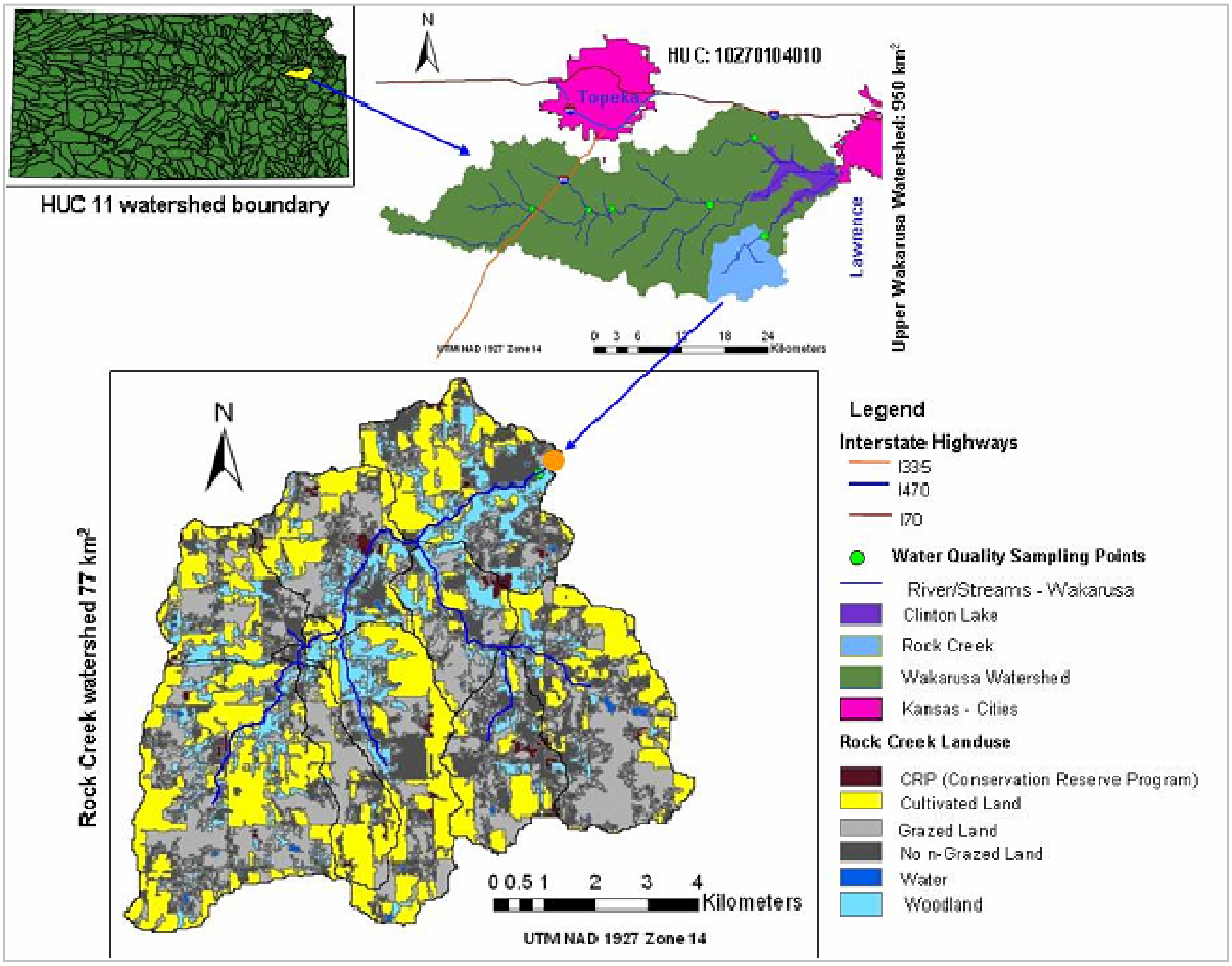

Figure 3.1. Location map of the Rock Creek Watershed in NE Kansas

3.3.2 SWAT model

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

The SWAT model utilizes geospatially referenced data to satisfy the necessary input parameters. A United State Geological Survey (USGS, 1999) 7.5-minute digital elevation data was used to delineate the watershed boundaries and topography. Soil Survey Geographic Database

(SSURGO) was utilized to create a soil database (USDA, 2005). The Gap Analysis Program (GAP) land cover data of 2001 that depicts twenty general land cover classes by Kansas Applied Remote Sensing (KARS, 2001) was used. Wardlow and Egbert (2003) evaluated GAP (2001) and National Land Cover Data NLCD (1992) landuse data for the State of Kansas. The Kansas GAP provided better discrimination of most land-cover classes as compared to NLCD. Accuracy assessment found an overall accuracy of 87 percent for GAP and 81 percent for NLCD, and GAP had higher accuracies for most individual land-coverclasses. The Kansas GAP and NLCD land-cover products were found to be comparable in terms of characterizing broad scale land-cover patterns, but the Kansas GAP land-cover map appears to be more appropriate for localized applications that require detailed and accurate land-cover information.

The landuse classes were re-classified into eight classes (grazedland, non-grazedland/hay, cropland, woodland, Conservation Reserve Program, water, urban areas and quarry) based on field-verified landuse conditions (Mankin and Koelliker, 2001; Mankin et al., 2003). Parameters for each Hydrologic Response Unit (HRU) in each watershed were defined on the basis of soil, landuse, and topographic characteristics of the watershed as described in the SWAT documentation version 2005 (Neitsch et al., 2005).

The microbial component of the SWAT simulates the fate and transport of bacterial organisms. The microbial sub-model uses the first-order decay equation as applied by Moore et al. (1989), to model fecal bacteria die-off and re-growth (Eq. 3.1).

$$C_t = C_o \times e^{-K_{20}\, t\, \theta^{(T-20)}} \tag{3.1}$$

where

C_t = bacteria concentration at time t, count/100ml

C_o = initial bacteria concentration, count/100ml

K_{20} = first-order die-off rate at 20 ^{0}C, day^{-1}

t = exposure time, days

θ = temperature adjustment factor (TBACT in SWAT)

T = temperature, ^{0}C

The less persistent fecal bacteria in manure/fertilizer were added with a different bacteria partition coefficient (0 to 1). The bacteria partition coefficient (BACTKDDB) in the fertilizer database separates bacteria concentration in sorbed and solution phases. As the bacteria partition coefficient approaches zero, bacterium is primarily sorbed to the soil particles and as it approaches to one bacterium is primarily in solution. The die-off rate of bacteria in the solution and sorbed phases impact the bacteria concentration. The BACTKDDB value used was 0.9 (Soupir et al., 2006).

The SWAT water quality model has been applied and validated for runoff, sediment yield, and nutrient losses from watersheds at different geographic locations, conditions, and management practices (Saleh et al., 1999; Spruill et al., 2000; Santhi et al., 2001; Kirsch et al., 2002; White and Chaubey, 2005; Jha et al., 2007; Gassman et al., 2007). Limited research has been performed for the SWAT bacteria part of the model in predicting bacteria movement. Baffaut and Benson (2003) studied bacteria TMDLs (Total Maximum Daily Load) for the Shoal Creek watershed in southwest Missouri using the SWAT model (2000). They calibrated model using daily flow, weekly fecal coliform bacteria concentration collected from water quality grab samples, and annual hay yield reported to USDA (United States Department of Agriculture). A frequency curve analysis method was used to compare measured vs. predicted data for daily flow and fecal coliform bacteria concentration. Daily flow curve was reported reasonable except over-predictions of peak flow. The SWAT model predicted values were compared with 18 months of weekly measured fecal coliform bacteria concentration data using average plus or minus one standard deviation. The model predicted bacteria concentration validated up to 70% using the frequency curve.

Several authors have previously completed sensitivity and output-uncertainty analyses for SWAT model (Lenhart et al., 2002; Eckhardt et al., 2002; Sohrabi et al., 2002; Benaman and Shoemaker, 2004; Huisman et al., 2004; Feyereisen et al., 2005) but only one (Parajuli et al., 2006) study has been done for SWAT (2000) microbial sub-model sensitivity analysis. Parajuli et al. (2006) reported low ($S < \pm 0.50$) to high ($S > \pm 1.00$) relative sensitivity for TBACT factor; low ($S < \pm 0.50$) relative sensitivity for BACTKDQ factor; low ($S < \pm 0.50$) relative sensitivity for: manure production rate, livestock stocking rate, land application method of septic effluent, moderate ($\pm 0.50 < S > \pm 1.00$) to relative sensitivity for point load application method of septic effluent; low to moderate relative sensitivity for applying wildlife bacteria source loads in the cropland, woodland, and cropland and woodland; and high ($S > \pm 1.00$) relative sensitivity for bacteria concentration in livestock manure. However, sensitivity analysis of the SWAT (2005) bacteria part of the model has not been assessed.

3.3.3 Model and Input Sensitive Parameters

The bacteria partition coefficient in surface runoff (BACTKDQ) separate bacteria between sorbed and solution phases in surface runoff. The temperature adjustment factor (TBACT) impacts the bacteria concentration prediction by an exponential first-order-decay relationship. In order to determine sensitivity of model parameters and input parameter in the SWAT/Microbial sub-model (2005) at the watershed scale, first the SWAT/Microbial sub-model (2005) was applied to satisfy daily flow from the Rock Creek watershed. Four key model parameters were tested for sensitivity: (a) bacteria partition coefficient in surface runoff (BACTKDQ); (b) temperature adjustment factor (TBACT); (c) less persistent bacteria die-off factor in solution (WDLPQ); and (d) less persistent bacteria die-off factor in sorbed (WDLPS). Only one input parameter which is bacteria concentration in manure was tested for sensitivity. Parajuli et al. (2006) found low to moderate relative sensitivity for other input parameters such as manure production, stocking rate, land application and direct input of septic effluent, wildlife source loads applied into cropland/woodland. The lower and upper ranges of each parameter were set as: (a) BACTKDQ (0 - 500), (SWAT, 2005); (b) TBACT (0.80 - 1.20) (Moore et al., 1989; Walker et al., 1990); (c) WDLPQ (0.40 - 0.693) (McFeters and Stuart, 1972; Baffaut and Benson, 2003); (d) WDLPS (0.04 - 0.069) (Baffaut and Benson, 2003). Assuming 3 days half-life, the bacteria die-off factor of 0.40 was used for bacteria in soil solution and a factor of 0.04 was used for sorbed bacteria assuming $1/10^{th}$ of the die-off in solution (Baffaut and Benson, 2003). Bacteria concentration in manure was used as 1.3×10^{10} to 1.2×10^{12}, based on the ±1 standard deviation range cited for beef livestock manure (ASAE, 2000). The model predicted daily fecal bacteria concentration for 2004 were converted into geometric mean (GM) values to calculate sensitivity for the model. A geometric mean is defined as a mean of number of values (n) that is computed by taking the n^{th} root of the product of the n terms. The model predicted outputs and calculated sensitivity index values were log-transformed.

3.3.4 Fecal Bacterial Source Characterization

3.3.4.1 Livestock

Manure applied due to grazing, feeding operations, and winter feeding areas were major bacterial sources in this study. Livestock population at the county and watershed level was estimated using agricultural census/GIS layers data (USDA, 2006). The county animal census population was equally distributed per total land-area basis to determine the fraction of total livestock in the study watershed. The USDA data were compared with Kansas Department of Agriculture farm facts data from the Kansas Department of Agriculture (KDA, 2004a). The AUs in feedlots within the watershed were estimated using active feedlot data (both federally permitted feedlots >1000 AUs and state registered feedlots > 300 AUs) from the Kansas Department of Health and Environment (KDHE) (Jepson, 2005). Permitted and registered livestock were subtracted from the total number of animals in the watershed to estimate the net grazed livestock population. Animal stocking rates in the pastureland was also validated using county-wide livestock population data (KDA, 2004b). Animals in the pasturelands could be brought from feedlots, barnyards and leasing agreements for grazing during the warm season (generally from April to September). However, the stocking rate of the animals in the pastureland was assumed to be maintained.

The Rock Creek watershed was estimated to be populated in 1000-kg animal units of 558 beef animal units (AU) in the pastureland (based on stocking rate), 104 beef AUs in the feedlots, and 223 beef AUs in the winter feeding areas (40% of 558), which was modeled in this study to represent the current scenario of the watershed. Manure production (26.4 kg day $^{-1}$ AU^{-1}) and fecal coliform bacteria concentration (13x10^{10} cfu day^{-1} AU^{-1}) for each beef animal were estimated based standard production rates (ASAE, 2000). The bacteria concentration was converted into model-input units of colonies forming units (cfu) per gram of dry-weight manure using standard mean manure moisture content (86% moisture; ASAE, 2000).

3.3.4.2 Human

Digital Orthophoto Quarter Quadrangles (DOQQ) (State of Kansas, 2002) of the watershed from 2002 was digitized depending on the physical context, roads, and type of houses to represent each septic system in the watershed. Each rural house was assumed to have one septic system, resulting in a total of 107 septic systems in the watershed. About 20% of the estimated septic systems (22 septic systems) were assumed failing in the watershed (KDHE, 2000). Each septic system was assumed to be used by three persons in the household that can contribute about 0.32 m^3 of sewage effluent per day (US EPA, 2001). The failing septic system in the watershed was modeled using land application method. Parajuli, et al. 2006 found higher model sensitivity when applying septic effluent as direct point-load method than land application method. The fecal bacteria concentration in failing septic system was taken as 6.3x10^6 cfu 100 mL^{-1} (Overcash and Davidson, 1980).

3.3.4.3 Wildlife

No comprehensive wildlife inventory was available for the Rock Creek watershed. The wildlife population density was estimated based on the information received from the Kansas Department of Wildlife and Parks (KDWP). The 2002 summer road-kill indices survey data (Peek, 2005) for Kansas were used to estimate small-mammal populations in the watershed. The information include various wild-animal species: raccoon, opossum, striped skunk, coyote, badger, bobcat, red fox, gray fox, swift fox, beaver, mink, muskrat, river otter, spotted skunk, weasel, armadillo, woodchuck and percupine. The population of raccoon, opossum, striped skunk, and coyote constituted about 81% of the total small mammals in Kansas. Population of the predominate large mammal (white-tailed deer) in the watershed was estimated based on expert opinion from the KDWP big-game coordinator (Lloyd, 2006). Similar data were collected for the predominate indigenous avian species (turkey) from the KDWP small-game coordinator (Pitman, 2006).

In order to estimate the animal units of each wildlife species in the watershed, the population data were first distributed over the potential habitat for each species. Small mammals and turkey population data were counted from a road survey. Most of the small mammals were counted dead at the road shoulder. The sight distances of 5 m for small mammals and 50 m for turkey from each side of the road were assumed, and the population density of each species was estimated as number of animal per unit area using total length of the road driven during survey. For deer, the number of deer harvested in northeastern Kansas was estimated and equally distributed in the total land area of northeastern Kansas to get the deer density. The population in 1000-kg animal units of about 60 turkeys, 24 deers, and 7 small mammals were estimated for the Rock Creek watershed to model in this study that represents the current scenario of the watershed. Animal weights were estimated based on the information received from “mammals of Kansas” (Timm et al., 2007) and personal communication (Pitman, 2006).

3.3.5 Management Scenarios

3.3.5.1 Pastureland

The pastureland was simulated under two major grass-type management conditions, which represent the typical field conditions. The two major grass types in the watershed include grazed (80%, typically native prairie) and non-grazed (20%, typically smooth brome and tall fescue). The native prairie grass is typically not fertilized, but tall fescue is fertilized with 70-15-0 (NPK) (Boyer, 2005). It was estimated that about 1.81 kg ha^{-1} day $^{-1}$ dry weight of manure is applied in the pasturelands due to grazing operation during the growing season. This estimation is based on the ASAE (2000) standards that include: (a) a beef AU produces 26.4 kg of wet weight manure per day, (b) the moisture content of wet manure is 0.139, and (c) cattle are grazed for 153 days in the pastureland. It is possible that the actual animal density varies in the watershed every day because of animal growth and the pattern of incoming and outgoing animals.

It was assumed that about 20% of the air-dry biomass is trampled every day, and about 341 kg of air-dry forage is required for an AU for 30 days (Paul and Watson, 1994). Grazing starts about a month earlier in tall fescue grasslands than in native prairie grass. All of the native prairie is grazed whereas only 80% of the tall fescue is grazed; the remaining tall fescue is un-grazed and used for haying and the Conservation Reserve Program (CRP). About 3.7 Mg ha^{-1} of hay is harvested annually from the un-grazed area, whereas biomass is not removed from the CRP land (Boyer, 2005). Cattle density in the pastureland was estimated as 3 ha per cow-calf pair based on the bluestem pasture guidelines for grazing (KDA, 2004b). Since cattle do not graze pastureland from October to March, no biomass uptake from the pastureland occurred, with no grass trampling and no manure deposition on the soil during this period.

All the source loads due to livestock in the confined animal feedlots were assumed to be applied as grazing operation in the pasturelands of the sub-watershed of the watershed where the active permitted feedlots were located. The winter feeding areas were modeled with the assumption that the estimated total number of AUs were confined within 40% of the grazed land of the watershed. Animals in feedlots and winter feeding areas contributed fecal bacteria for 212 days during the dormant season of the year (generally October to March). It was estimated that about 4.52 kg ha^{-1} day $^{-1}$ dry weight of cattle manure (2.5 times greater than regular pastureland operation) was applied in the respective pasturelands of the sub-watersheds of the watersheds due to winter feeding operations. There is only one permitted feedlot located in the watershed at Overbrook with 288 AUs that produces about 29.4 kg ha^{-1} of solid manure to be applied in the pastureland as an additional bacterial source.

3.3.5.2 Cropland and woodland

Corn and soybeans were major warm-season crops, and winter wheat was a primary cool-season crop grown in three year's rotation in the watershed (Boyer, 2005). The warm season crop was planted on May 1 and harvested on October 1. The cool-season crop was planted on October 20 and harvested on July 30. The crop residue is left on the cropland between the crop periods. These dates represent the typical planting and harvesting dates in the watersheds. The conservation tillage system is the most widely adopted system for corn/soybean/wheat in the watershed. All the wildlife-generated manure was applied into the woodland to be considered as baseline. The croplands of the watershed were simulated with providing 5 m filter strip length at the edge of HRUs which represents the field conditions.

3.3.6 Weather and Hydrologic Data

Daily precipitation data for the watershed were used from Overbrook weather station located about 4.8 km south of the watershed. The 2004 annual rainfall for Overbrook was about 1,126 mm (Fig. 3.2). Data from the Silver Lake weather station, which is located about 22.5 km south from the nearest point of the watershed, were used for the daily temperature, daily solar radiation, daily wind speed, and daily relative humidity data. The missing watershed data were adjusted using the SWAT weather generator. The SWAT model uses data from the Ottawa weather station (Franklin County), which is located about 23 km southeast from the nearest point of the Rock Creek watershed.

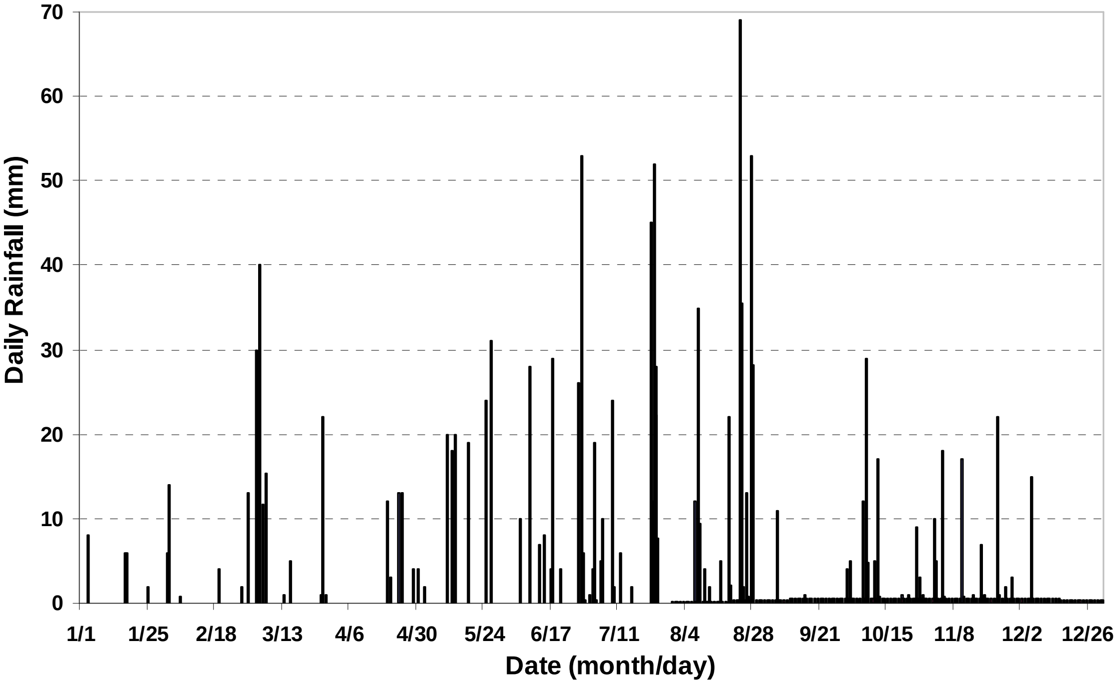

Figure 3.2 Distribution of daily rainfall data for Overbrook weather station, 2004

3.3.7 Statistical Analysis Methods

The SWAT model was validated using monitored flow and FCB concentrations from nine daily events. The statistical parameter used to evaluate measured vs. predicted daily mean flow includes coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E). The R^2 value indicates how consistently measured vs. predicted values follow a best fit line. If the R^2 value is less than or very close to zero, the model prediction is considered unacceptable or poor. If the value is 1.0, then the model prediction is perfect (Santhi et al., 2001). The E indicates how consistently measured values (range - ∞ to 1.0) match predicted values (Nash and Sutcliffe, 1970). As similar to Moriasi et al. (2007) the model efficiencies were classified as excellent ($E \geq 0.90$), very good (E = 0.75 to 0.89), good (E = 0.50 to 0.74), fair (E = 0.25 to 0.49), poor (0 to 0.24), and unsatisfactory (< 0).

3.3.7.1 LHS Sensitivity

The LHS-OAT (One-At-a-Time) method uses a stratified sampling method, in which the range of each model input parameter is divided into n intervals of equal probability, 1/n. Then, one sample is randomly generated within each interval, resulting in a total of n non-overlapping samples for each input parameter. In this study, each of the model input parameters was divided into 20 intervals of equal probability, for each of the 4 bacteria related model input parameters. In the OAT method, only one factor varies at a time while other factors are fixed. The change in model output can then be unambiguously attributed to such a change in the factor. The LHS method (Griensven, 2005) was applied to analyze sensitivity of parameter change for 100 model runs (Table 3.1) for Rock Creek watershed. A total of 103 model runs were used in the LHS analysis, including the 100 randomly generated parameter sets, two additional runs (simulation 101 and 102 in Table 3.1) to refine model sensitivity and the baseline parameter set.

A relative sensitivity index, defined as the ratio between the relative normalized changes in output to the normalized change in related input, was calculated to facilitate a direct comparison and to avoid difficulties concerning the different orders of magnitude in input parameters (Brunner et al., 2004). The modified version of relative sensitivity (S), equation (3.2) was used to consider the absolute change in model output and related input and their partial effects due to parameters change (Table 3.2) (Wang et al., 2005).

$$S = \frac{(O_2 - O_1)}{(O_2 + O_1)} * \frac{I}{\Delta I} \qquad (3.2)$$

where

S = relative sensitivity index

O_1, O_2 = model output values corresponding to I and ΔI in the LHS sample

I and ΔI = base and changed input parameter in the LHS sample

Using results from 103 model runs, the relative sensitivity index as defined by equation (3.2) was computed for each combination of input and output for a given combination of model parameters and input parameters. The total sensitivity for each parameter is calculated using equation 3.3.

$$S_{,Total} = \frac{\Sigma S}{N} \qquad (3.3)$$

where

$S_{,Total}$ = total relative sensitivity index of the entire LHS samples parameter

ΣS = summation of relative sensitivities of all LHS samples

N = number of samples

Table 3.1. Model Generated LHS-OAT Sample Parameters and Outputs Used in the Sensitivity Study

Simulation	BACTKDQ[1]	TBACT[2]	WDLPQ[3]	WDLPS[4]	Output (cfu/100mL)[5]	Simulation	BACTKDQ[1]	TBACT[2]	WDLPQ[3]	WDLPS[4]	Output (cfu/100mL)[5]
Base	175.000	1.070	0.400	0.040	30	52	237.930	1.152	0.588	0.049	23
1	3.289	0.931	0.637	0.046	55	53	237.930	1.152	0.588	0.047	24
2	28.289	0.931	0.637	0.046	25	54	212.930	1.152	0.588	0.047	24
3	28.289	0.931	0.623	0.046	25	55	212.930	1.132	0.588	0.047	25
4	28.289	0.931	0.623	0.045	25	56	151.190	0.819	0.471	0.057	10
5	28.289	0.911	0.623	0.045	23	57	151.190	0.819	0.471	0.058	10
6	378.280	1.019	0.558	0.040	29	58	151.190	0.819	0.485	0.058	10
7	378.280	1.019	0.543	0.040	29	59	151.190	0.839	0.485	0.058	12
8	353.280	1.019	0.543	0.040	29	60	126.190	0.839	0.485	0.058	12
9	353.280	1.019	0.543	0.042	28	61	56.233	1.136	0.618	0.047	27
10	353.280	0.999	0.543	0.042	28	62	56.233	1.136	0.603	0.047	27
11	364.180	1.103	0.568	0.060	22	63	56.233	1.156	0.603	0.047	26
12	364.180	1.103	0.583	0.060	22	64	56.233	1.156	0.603	0.046	27
13	364.180	1.083	0.583	0.060	23	65	31.233	1.156	0.603	0.046	29
14	364.180	1.083	0.583	0.061	23	66	451.080	0.958	0.542	0.056	21
15	389.180	1.083	0.583	0.061	23	67	426.080	0.958	0.542	0.056	21
16	421.940	0.971	0.503	0.062	20	68	426.080	0.958	0.527	0.056	21
17	421.940	0.971	0.503	0.060	21	69	426.080	0.978	0.527	0.056	22
18	421.940	0.951	0.503	0.060	19	70	426.080	0.978	0.527	0.057	22
19	446.940	0.951	0.503	0.060	19	71	439.210	1.033	0.424	0.066	22
20	446.940	0.951	0.488	0.060	19	72	439.210	1.053	0.424	0.066	22
21	97.868	0.884	0.413	0.065	15	73	464.210	1.053	0.424	0.066	22
22	97.868	0.884	0.428	0.065	15	74	464.210	1.053	0.424	0.065	22
23	97.868	0.864	0.428	0.065	13	75	464.210	1.053	0.439	0.065	22
24	97.868	0.864	0.428	0.066	13	76	284.410	0.843	0.585	0.045	13
25	72.868	0.864	0.428	0.066	14	77	284.410	0.843	0.571	0.045	13
26	346.340	0.998	0.456	0.043	27	78	284.410	0.823	0.571	0.045	12
27	346.340	0.998	0.442	0.043	27	79	284.410	0.823	0.571	0.046	11
28	346.340	0.998	0.442	0.045	27	80	259.410	0.823	0.571	0.046	11
29	371.340	0.998	0.442	0.045	27	81	194.280	1.058	0.442	0.069	22
30	371.340	0.978	0.442	0.045	25	82	219.280	1.058	0.442	0.069	22
31	301.970	0.879	0.519	0.061	14	83	219.280	1.058	0.427	0.069	22
32	301.970	0.879	0.505	0.061	14	84	219.280	1.058	0.427	0.067	22
33	276.970	0.879	0.505	0.061	14	85	219.280	1.078	0.427	0.067	22
34	276.970	0.859	0.505	0.061	13	86	26.084	0.914	0.486	0.042	25
35	276.970	0.859	0.505	0.062	13	87	26.084	0.934	0.486	0.042	28
36	217.170	1.097	0.687	0.051	25	88	26.084	0.934	0.501	0.042	28
37	217.170	1.097	0.687	0.053	24	89	51.084	0.934	0.501	0.042	25
38	217.170	1.077	0.687	0.053	25	90	51.084	0.934	0.501	0.040	26
39	192.170	1.077	0.687	0.053	25	91	274.620	0.827	0.504	0.058	10
40	192.170	1.077	0.673	0.053	25	92	299.620	0.827	0.504	0.058	10
41	122.850	1.075	0.653	0.065	23	93	299.620	0.827	0.519	0.058	10
42	122.850	1.055	0.653	0.065	23	94	299.620	0.827	0.519	0.056	10
43	122.850	1.055	0.668	0.065	23	95	299.620	0.847	0.519	0.056	12
44	97.853	1.055	0.668	0.065	23	96	129.980	1.190	0.669	0.052	21
45	97.853	1.055	0.668	0.067	23	97	129.980	1.170	0.669	0.052	22
46	483.650	1.177	0.626	0.054	21	98	154.980	1.170	0.669	0.052	22
47	483.650	1.197	0.626	0.054	20	99	154.980	1.170	0.669	0.053	22
48	483.650	1.197	0.612	0.054	20	100	154.980	1.170	0.654	0.053	22
49	458.650	1.197	0.612	0.054	20	101	1.500	1.070	0.400	0.040	103
50	458.650	1.197	0.612	0.053	20	102	0.970	1.070	0.400	0.040	136
51	237.930	1.152	0.603	0.049	23	Mean	249.136	1.002	0.544	0.054	16

[1] Bateria partition coefficient in surface runoff

[2] Temperature adjustment factor

[3] Less persistent bacteria die-off in solution

[4] Less persistent bacteria die-off in sorbed

[5] Geometric mean value of the fecal coliform bacteria concentration

Table 3.2. Relative partial effects of parameters around the latin hypercube

	Variable	BACTKDQ	TBACT	WDLPQ	WDLPS	Output	Relative partial effects (S_{ij})
LH1		x1	x2	x3	x4	y1	
	OAT1	x1+Δ	x2	x3	x4	y2	I(y2-y1)I/(y2+y1)*x1/IΔx1I
	OAT2	x1+Δ	x2+Δ	x3	x4	y3	I(y3-y2)I/(y3+y2)*x2/IΔx2I
	OAT3	x1+Δ	x2+Δ	x3+Δ	x4	y4	I(y4-y3)I/(y4+y3)*x3/IΔx3I
	OAT4	x1+Δ	x2+Δ	x3+Δ	x4+Δ	y5	I(y5-y4)I/(y5+y4)*x4/IΔx4I
LH2		xx1	xx2	xx3	xx4	y6	
	OAT1	xx1+Δ	xx2	xx3	xx4	y7	I(y7-y6)I/(y7+y6)*xx1/IΔxx1I
	OAT2	xx1+Δ	xx2+Δ	xx3	xx4	y8	I(y8-y7)I/(y8+y7)*xx2/IΔxx2I
	OAT3	xx1+Δ	Xx2+Δ	xx3+Δ	xx4	y9	I(y9-y8)I/(y9+y8)*xx3/IΔxx3I
	OAT4	xx1+Δ	Xx2+Δ	xx3+Δ	xx4+Δ	y10	I(y10-y9)I/(y10+y9)*xx4/IΔxx4I

3.3.7.2 IPP Sensitivity

The most common form of sensitivity analysis is independent parameter perturbation (IPP) in which parameters is varied individually by a fixed percentage around a base value (Ferreira et al., 1995). Model output responses to parameter perturbation may be quantified by percentage change of selected output variables and relative change of output versus input (Larocque and Banton, 1994). In order to compare IPP method with LHS method, the model was run an additional 53 times taking LHS mean value for each parameter separately and the percentage change from the LHS-Mean value (IPP) to see the model sensitivity (Table 3.3). For additional 53 runs samples, relative sensitivity index for each result was analyzed using equation 3.4 (James and Burges, 1982; Nearing et al., 1989; White and Chaubey, 2005; Jesiek and Wolfe, 2005):

$$S = \frac{(R - R_b)}{(P - P_b)} * \frac{P_b}{R_b} \tag{3.4}$$

where

S = relative sensitivity index

R = result (model output)

P = parameter (model input)

b = base scenario value

The relative sensitivity index (S) was used to test the model sensitivity for each model parameter or input parameter as described by equations 3.2 -3.4. The relative sensitivity classes were classified based on Table 3.4 (Zerihun et al., 1996; Walker et al., 2000; Graff et al., 2005).

An index of 0 indicates the output does not respond to changes in the input. An index of 1 indicates that the normalized output range is directly proportional to the normalized input range. A negative value indicates that an increase in input value caused a decrease in output value. A greater absolute value of the index indicates a greater impact of an input parameter on a particular output (Walker et al., 2000). Similar to Zerihun et al. (1996), this study used five sensitivity classes: ±0 < S ≤ ±0.10 was no sensitivity, ±0.10 < S ≤ ±0.50 was low sensitivity, ±0.50 < S ≤ ±2.00 was moderate sensitivity, ±2.00 < S ≤ ±5.00 was high sensitivity and S > ±5.00 was very high sensitivity.

Table 3.3. Sensitivity analysis of parameters using the mean of LHS-OAT samples as baseline

Parameters	% change from base	Input	Output (cfu/100mL)[5]	Parameters	% change from base	Input	Output (cfu/100mL)[5]
BACTKDQ[1]	0%	249.100	9	TBACT			
	5.0%	261.593	9		16.0%	1.163	10
	-5.0%	236.680	10		-16.0%	0.842	12
	12.5%	280.278	10		19.5%	1.198	10
	-12.5%	217.994	10		-19.5%	0.807	13
	25.0%	311.420	11	WDLPQ[3]	0.00%	0.544	11
	-25.0%	186.852	11		5.0%	0.571	11
	37.5%	342.563	11		-5.0%	0.517	12
	-37.5%	155.710	11		12.5%	0.612	11
	50.0%	373.705	11		-12.5%	0.476	12
	-50.0%	124.568	12		16.0%	0.680	11
	67.5%	417.303	13		-16.0%	0.408	13
	-67.5%	80.969	14		20.0%	0.631	11
	75.0%	435.989	16		-20.0%	0.457	12
	-75.0%	62.284	18		25.0%	0.653	11
	87.5%	467.131	21		-25.0%	0.435	12
	-87.5%	31.142	24	WDLPS[4]	0.0%	0.054	14
	-97.0%	7.474	32		5.0%	0.057	14
	-99.5%	1.246	57		-5.0%	0.052	14
	100.0%	498.273	107		12.5%	0.061	14
TBACT[2]	0.0%	1.002	11		-12.5%	0.048	14
	5.0%	1.052	11		15.0%	0.068	14
	-5.0%	0.952	11		-15.0%	0.041	14
	12.5%	1.128	11		24.0%	0.063	14
	-12.5%	0.877	12		-24.0%	0.046	14
	15.0%	1.153	11		26.0%	0.069	14
	-15.0%	0.852	12		-26.0%	0.040	14

[1] Bateria partition coefficient in surface runoff

[2] Temperature adjustment factor

[3] Less persistent bacteria die-off in solution

[4] Less persistent bacteria die-off in sorbed

[5] Geometric mean value of the fecal coliform bacteria concentration

Table 3.4. Relative Sensitivity (S) Classses (Zerihun et al., 1996)

Class	Symbol	S range
No Sensitivity	N	±0 < S ≤ ±0.10
Low Sensitivity	L	± 0.10 < S ≤ ±0.50
Moderate Sensitivity	M	±0.50 < S ≤ ±2.0
High Sensitivity	H	±2.00 < S ≤ ±5.00
Very High Sensitivity	VH	S > ±5.00

3.4 Results and Discussion

The model parameters and input parameter used in the study showed different degrees of relative sensitivity indexes (no to very high) when compared with model results using a relative sensitivity index (S). The fecal coliform bacteria concentration at the outlet of the watershed could be dependent upon several factors including the AUs in the pastureland, winter feeding areas, and confined feedlots; failing septic systems; wildlife; and daily rainfall amount that contributed to generate surface runoff. The SWAT model daily simulation covered one year period (January to December, 2004) in this study.

3.4.1 Flow Validation

The un-calibrated SWAT model (2005), using ground-truthed land use conditions and other parameters to define current conditions, produced fair agreement for simulation of daily mean flow from the watershed. The SWAT model predicted the daily average flow rate of the watershed with good correlation ($R^2 = 0.73$ and $E = 0.39$) between measured and predicted values (Fig. 3.3). The SWAT-model-predicted nine rainfall-runoff events were compared with the field measured data. The SWAT model under-predicted during five daily flow events due to either low rainfall events or low or no one day previous rainfall condition. The model over-predicted flow during one storm event when there was good amount of same day rainfall and one day previous rainfall. The observed reasonable correlation of un-calibrated model suggests that model input data affecting hydrologic processes were of reasonable accuracy. Baffaut and Benson, 2003 evaluated SWAT model for bacteria type of study in the Shoal Creek watershed in southwest Missouri. The calibrated SWAT model showed $R^2 = 0.40$ and $E = 0.21$ for daily flow whereas the model determined $R^2 = 0.61$ and $E = 0.54$ during model validation in their study.

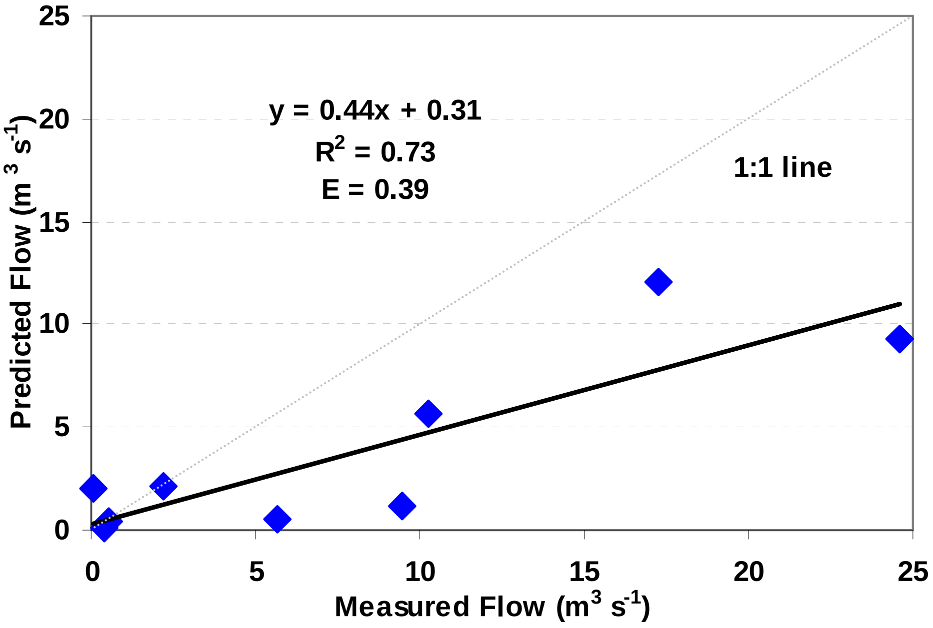

Figure 3.3. Measured daily flow model response

3.4.2 Bacteria Load Validation

The un-calibrated baseline SWAT (2005) model, using livestock, septic and wildlife loadings to represent current conditions under-predicted average daily fecal coliform bacteria concentration by 126% and gave unsatisfactory agreement but reasonable correlation of measured vs. predicted data with R^2 = 0.37 (Fig. 3.4). The model under-predicted bacteria during no or low-flow event. Although the model under-predicted bacteria concentration by average of one fold of log transformation during most of the runoff events, the slope of predicted vs. measured regression was 0.51, which was considered adequate to allow sensitivity analysis. Further calibration of the model was not attempted before sensitivity analysis was conducted because model still showed good relationship in regard to the source load characterization. The measured and model predicted values were varied by about a 0.8 of standard deviation. Generally, sensitive parameters identified during sensitivity analysis are used to calibrate and validate model. White and Chaubey (2005) studied sensitivity analysis of SWAT model. They identified sensitive parameters from sensitivity analysis then used those parameters for model calibration and validation for the Beaver Watershed located in northwestern Arkansas. Parameters identified by sensitivity analysis were modified during calibration.

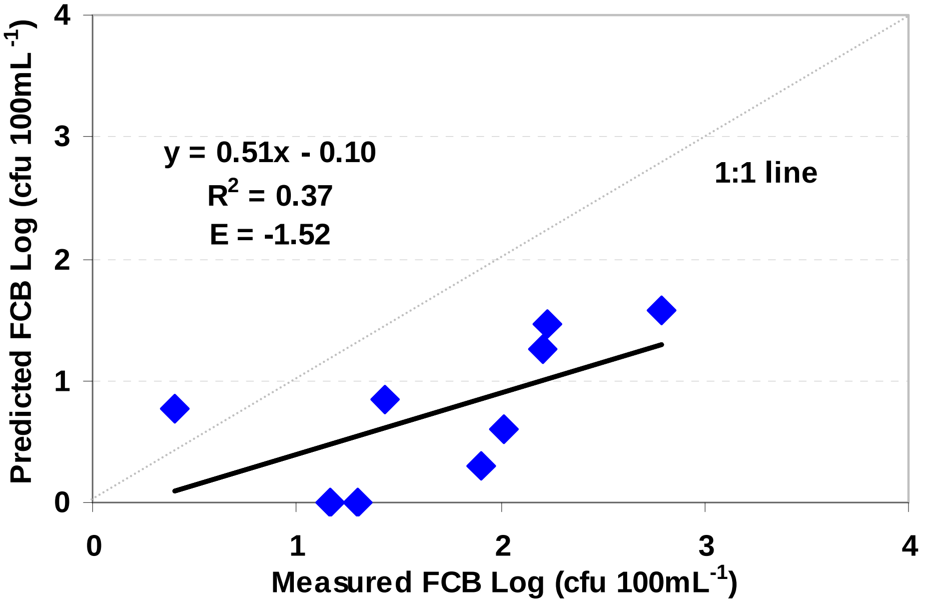

Figure 3.4. Measured fecal coliform bacteria (FCB) concentration model response

3.4.3 Model Parameters Sensitivity

When analyzed relative sensitivity of 103 model runs, the results showed varied sensitivity of each model runs for different parameters used in this study. One thing clearly noticed that because of the interaction between parameters used some data noise can be seen while using LHS method. For example, simulation 102 predicted significantly high model outputs (Table 3.1) than base simulation because of the major change in BACTKDQ factor values. The impact of TBACT, WDLPQ, and WDLPS factors had very less to do with. The BACTKDQ model parameter generally showed no sensitivity with a relative sensitivity index < 0.10 during LHS samples. However, the LHS samples randomly generated one hundred values only at the range from 28 to 483 for BACTKDQ parameter. When ran the model choosing lower BACTKDQ values resulted moderate to very high relative sensitivity (S > 5). Generally, increase in the percentage input vs. percentage output, increase the relative sensitivity. The LHS method of model simulations showed daunting and cumbersome performance in some areas. Although there was great increase in the percentage change in input (up to +155%), the percentage change in the output was relatively low (up to -55%). The low output was resulted due to a sudden change in the parameters in the LHS samples (Fig. 3.5). However, additional model runs using percentage change from the IPP method showed very good relationship between model prediction and change in the BACTKDQ factor values (Fig. 3.6). Actually, model showed a sensitivity of using lower values from the LHS-Mean value. The model sensitivity determined moderate to very high when used lower values of BACTKDQ.

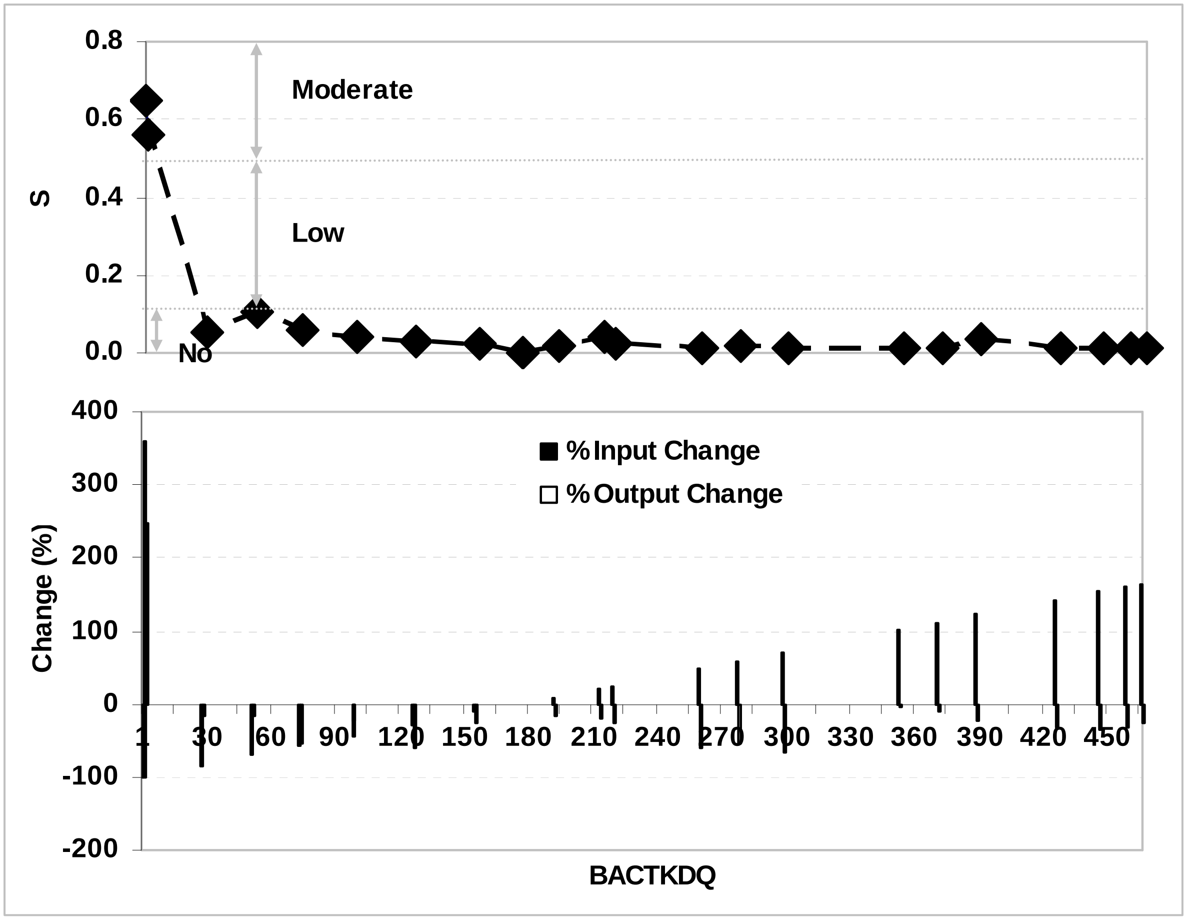

Figure 3.5. LHS method: bacteria partition coefficient in surface runoff (BACTKDQ) relative sensitivity index (S) response

The BACTKDQ factor is provided as an equilibrium constant in the SWAT model which shows inverse relationship between input values and model predictions. Model prediction shows power trend line relationship in the equation (Neitsch et al., 2005). But using LHS method samples model predicted data showed low power-trend line relationship ($R^2 = 0.23$) which means there was no specific rate of increase in bacteria prediction with the decrease in BACTKDQ factor values. However, additional runs from the IPP samples result showed very good correlation of power-trend line relationship ($R^2 = 0.97$) (Fig. 3.7). This result determines that local method is better than global method of sensitivity analysis. However, 103 model runs may not be enough for LHS method. More model runs such as 1000 may provide better correlation of power-trend line relationship for LHS method. The model sensitivity needs to improve especially for low BACTKDQ conditions which are less than 62. Parajuli et al. (2006) reported that using BACTKDQ below 44 might be sensitive for SWAT 2000 version of the model. They reported BACTKDQ factor had low sensitivity because the maximum change in % output using SWAT 2000 was estimated about 51% whereas this study using SWAT 2005 determined the maximum change in % output about 359% for LHS method and about 865% for the IPP method especially only at the extreme lower values of BACTKDQ.

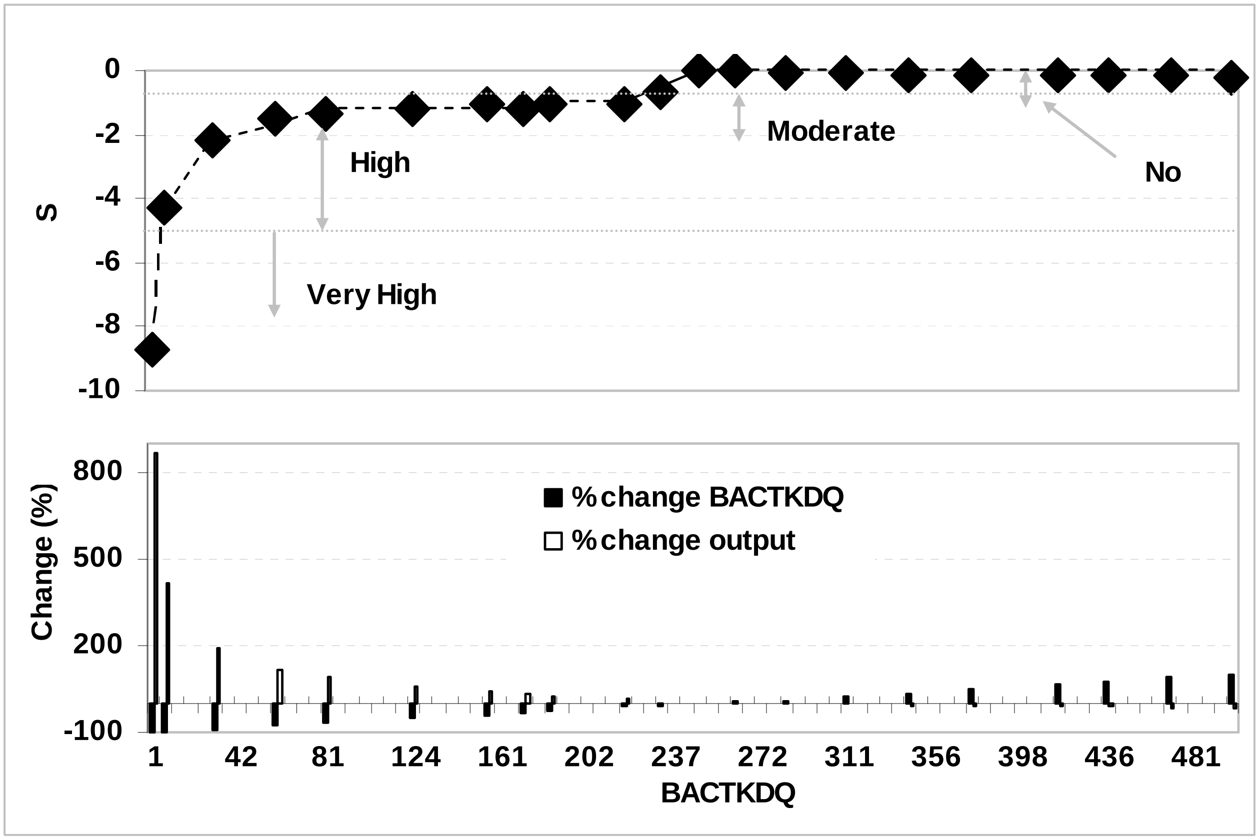

Figure 3.6. IPP method: bacteria partition coefficient in surface runoff (BACTKDQ) relative sensitivity index (S) response

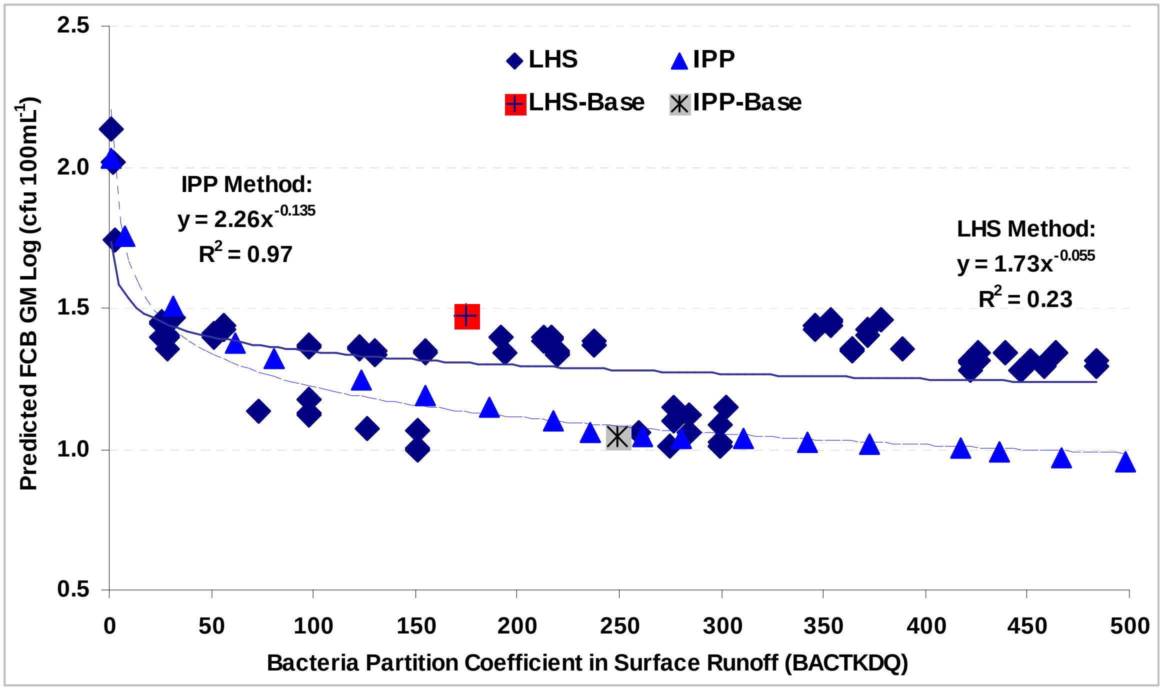

Figure 3.7. Power trend line showing correlation of LHS and IPP method model responses

The TBACT, model parameter showed no relative sensitivity to high relative sensitivity (S > 2.00) and very good relationship between relative sensitivity and % input parameter and % model output change both for LHS method (Fig. 3.8) and IPP method (Fig.3.9). The bacteria decay rate on land and in the water varies due to air or water temperatures. The TBACT may vary due to change in the daily ambient temperature. The selection of the right temperature adjustment factor is important which had low to moderate sensitivity especially either at the upper or lower range of TBACT values (example: >1.12 or <0.86). When used the TBACT factor below 0.86 in this study, model showed floating underflow error which means that model simulation exceeded range of values given in the model. The SWAT model needs to be re-compiled with larger range of values but the accuracy of the simulations was still valid (Sammons, 2007). Parajuli et al. (2006) reported that TBACT factor had low to high sensitivity using SWAT 2000 version of the model. They also reported that model sensitivity increases either at the extreme lower or upper range of TBACT values.

Wang et al. (2004) calculated the TBACT factor in excreted manure as 1.026 for temperatures between 4°C and 27°C and 1.034 for temperatures between 27°C and 41°C, all within the range (1.07 ±0.05) given by Reddy et al. (1981) in the temperature range at which most biological reactions occur. The calculated temperature range above is also supported by Crane and Moore (1986) and Reddy et al. (1981). Using a TBACT greater than 1.07 ±0.05 may be sensitive

(Reddy et al., 1981). Although these studies were done with in a lab environment, the result of this study generally supported them. SWAT applies equation 3.1 and TBACT on a daily basis according to daily average temperature in the watershed. When daily average temperature approaches near 20^0C, the TBACT parameter becomes less important parameter because it does not contribute for less or high bacteria concentration prediction. When daily average temperature approaches 20°C, the TBACT parameter has less impact on die-off rate (Eq. 3.1). Generally, the temperatures were greater than 20°C (average temperature about 21.5°C) during April to September and probably below 20°C during the rest of the year.

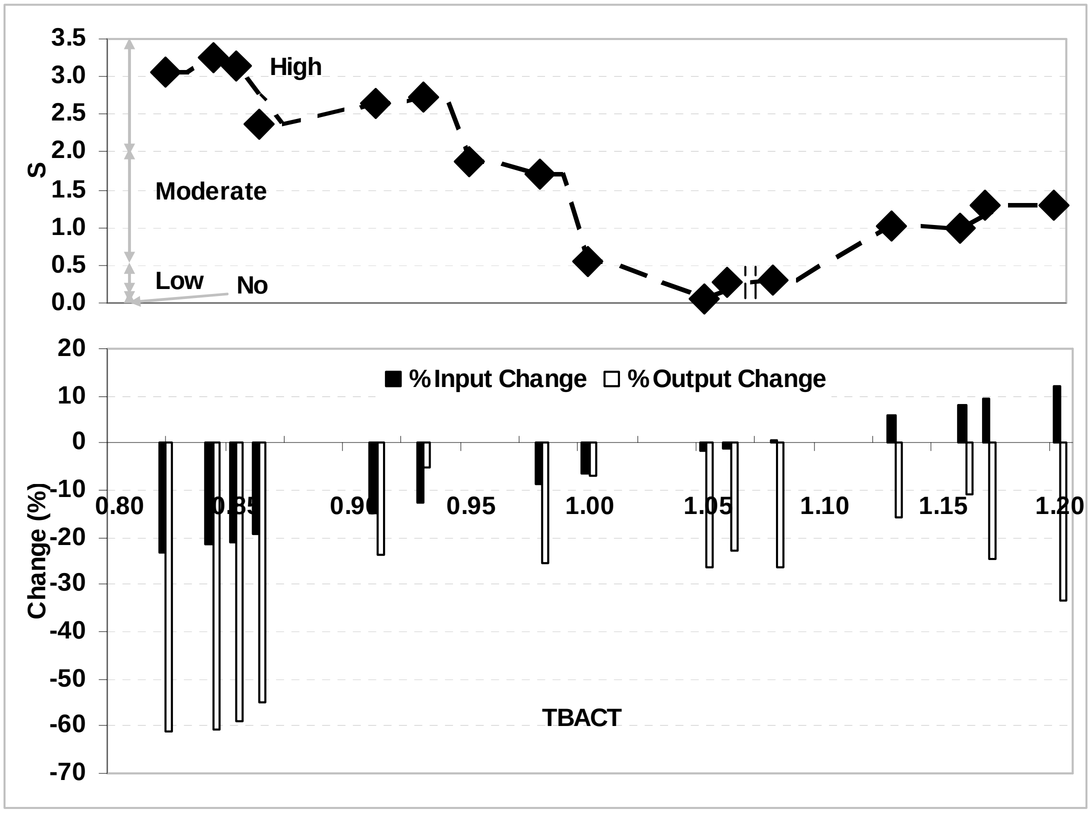

Figure 3.8. LHS method: temperature adjustment factor (TBACT) relative sensitivity index (S) response

The SWAT model TBACT default value of 1.07 or 1.07 ±0.05 is reasonable to use in the model but exceeding this range could be sensitive. Although the current model of SWAT uses only one TBACT value for the entire model simulation period (365 days in this study), it is generally reasonable to represent the average condition of the watershed.

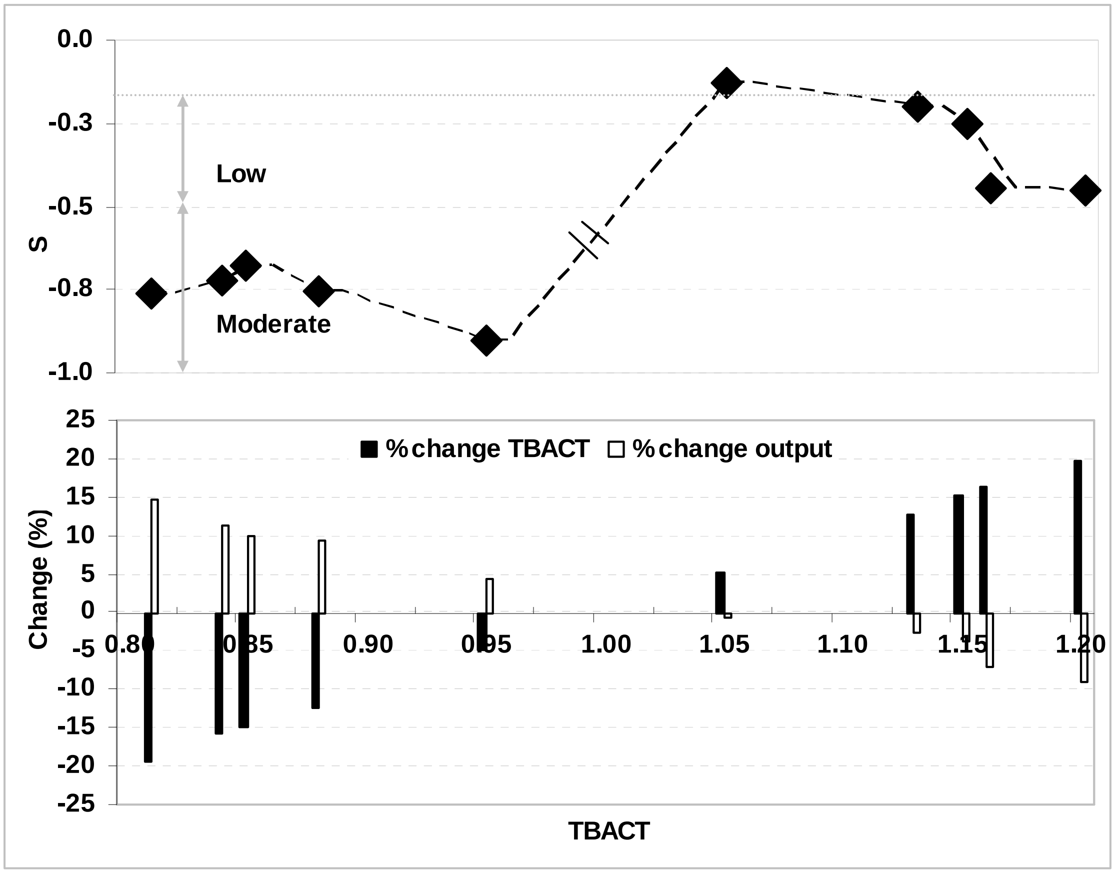

Figure 3.9. IPP method: temperature adjustment factor (TBACT) relative sensitivity index (S) response

Large difference between base condition model output and model predicted output due to change in input values made impact on relative sensitivity of WDLPQ and WDLPS parameters. These two parameters had low relative sensitivity in the model except for WDLPQ for IPP method model runs. The change in these two parameters had combined effect of TBACT factor and BACTKDQ. Generally, increase in the percentage input and percentage output had increased relative sensitivity. Although low sensitivity of the model simulations was determined for WDLPQ parameter (Fig. 3.10), additional simulations (11) from the IPP method showed moderate sensitivity (S up to 0.98) with respect to percentage change in the input/output (Fig. 3.11). The decrease in the input values contributed to higher relative sensitivity of WDLPQ parameter.

The WDLPS parameter was the least sensitive parameter in this study because 90% of the bacteria were (BACTKDDB = 0.9) assumed to be in the solution phase leaving only 10% of bacteria in sorbed phase. There was almost no difference in bacteria output (Fig. 3.12). The IPP method of simulations (13) of model determined almost no sensitivity (Fig. 3.13). The WDLPQ and WDLPS parameters given in the model had no recommendation of range of values. The effect of these parameters are associated with TBACT and BACTKDQ parameters, therefore WDLPQ and WDLPS had generally low sensitivity except the WDLPQ had moderate sensitivity when using IPP method. The greater % output change due to the change in WDLPQ parameter affected in the model sensitivity. This study used professional recommended values for WDLPQ and WDLPS. Change in BACTKDQ parameter superseded the effects of other parameters in this study (LHS).

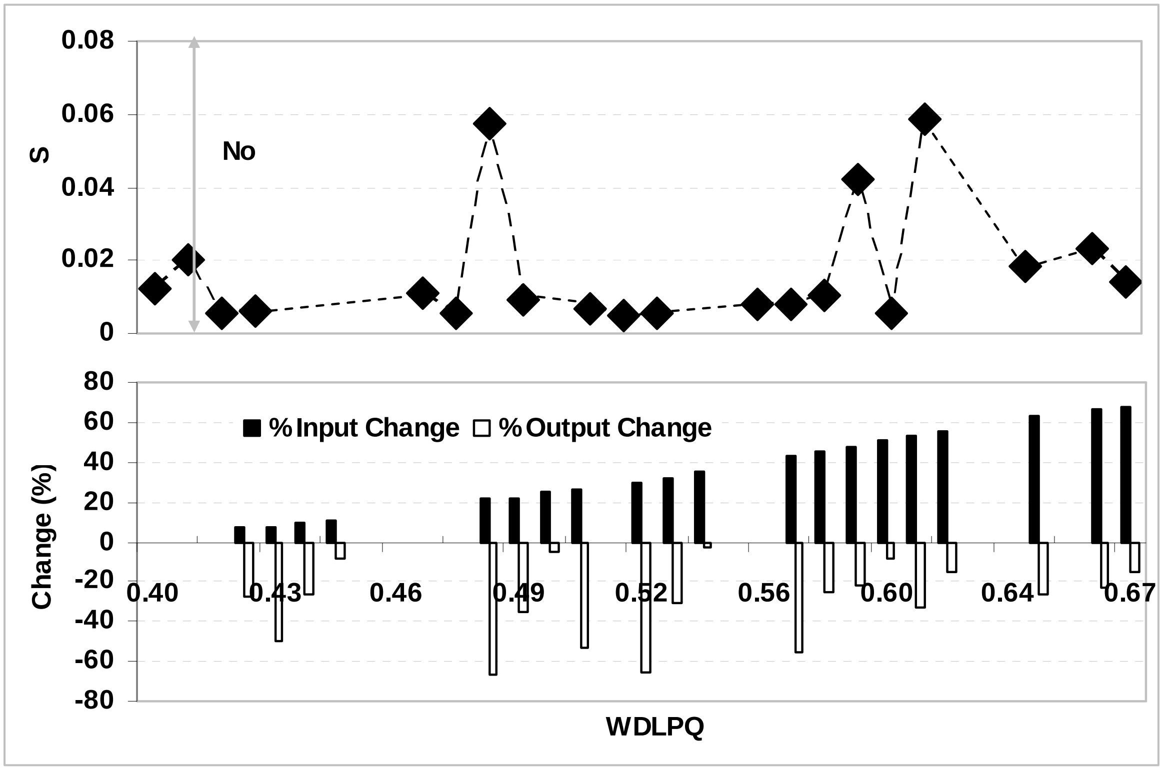

Figure 3.10. LHS method: less persistent bacteria die-off in solution (WDLPQ) relative sensitivity index (S) response

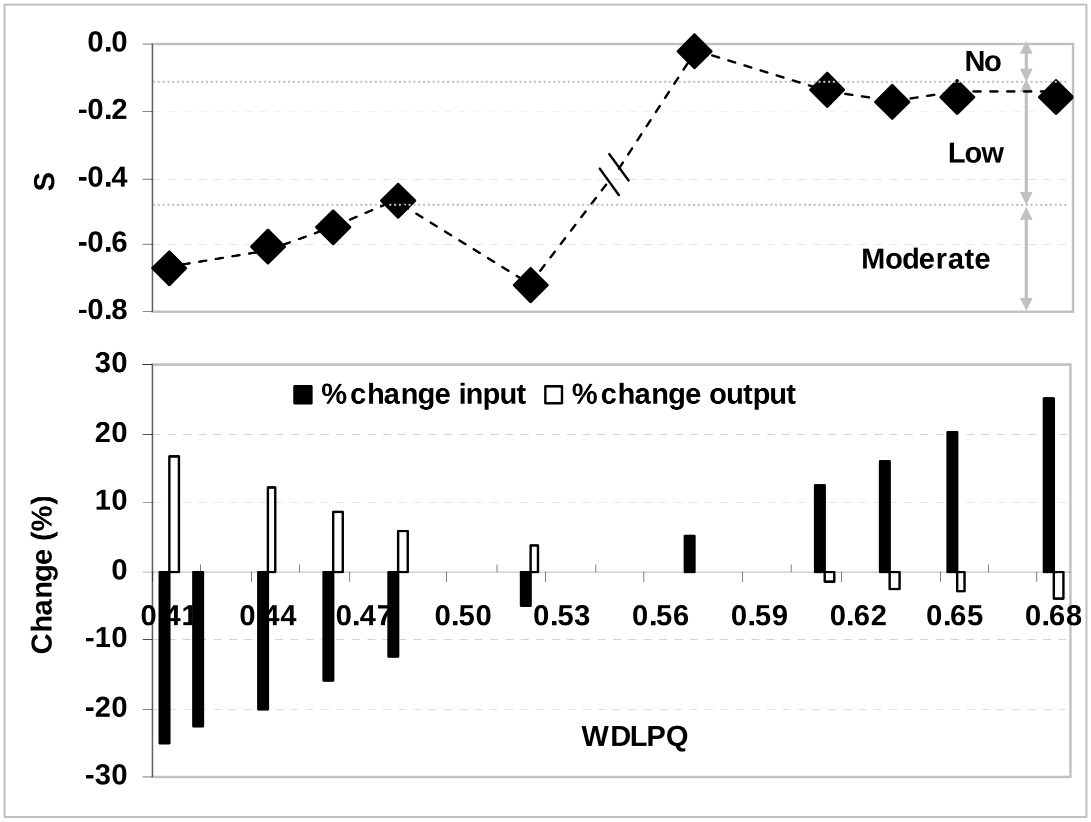

Figure 3.11. IPP method: less persistent bacteria die-off in solution (WDLPQ) relative sensitivity index (S) response

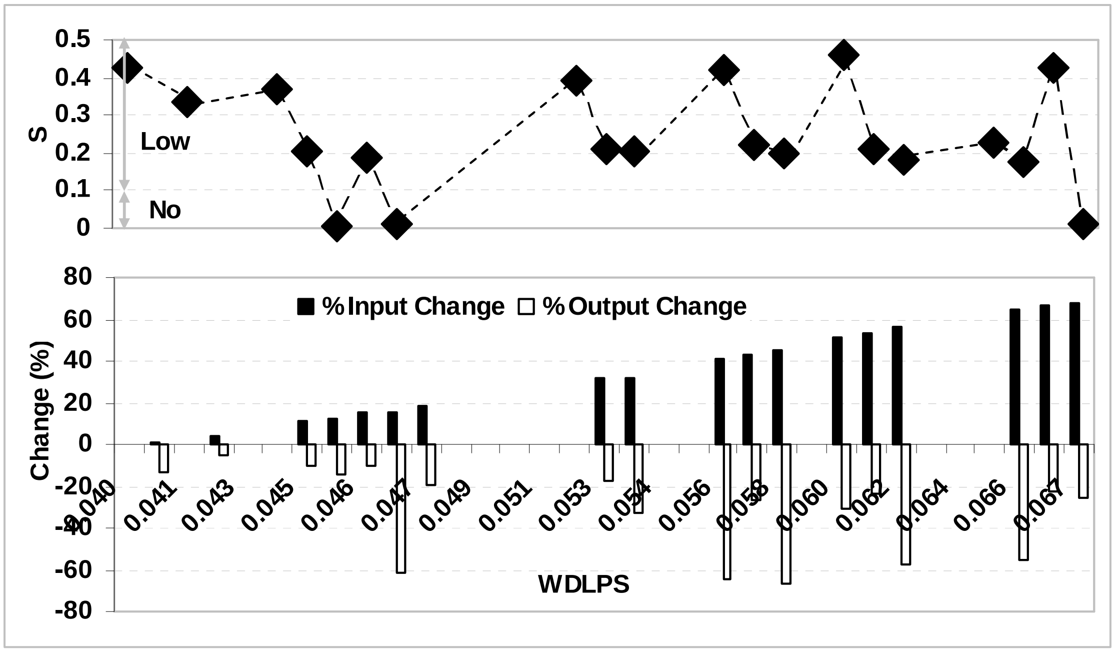

Figure 3.12. LHS method: less persistent bacteria die-off in sorbed (WDLPS) relative sensitivity index (S) response

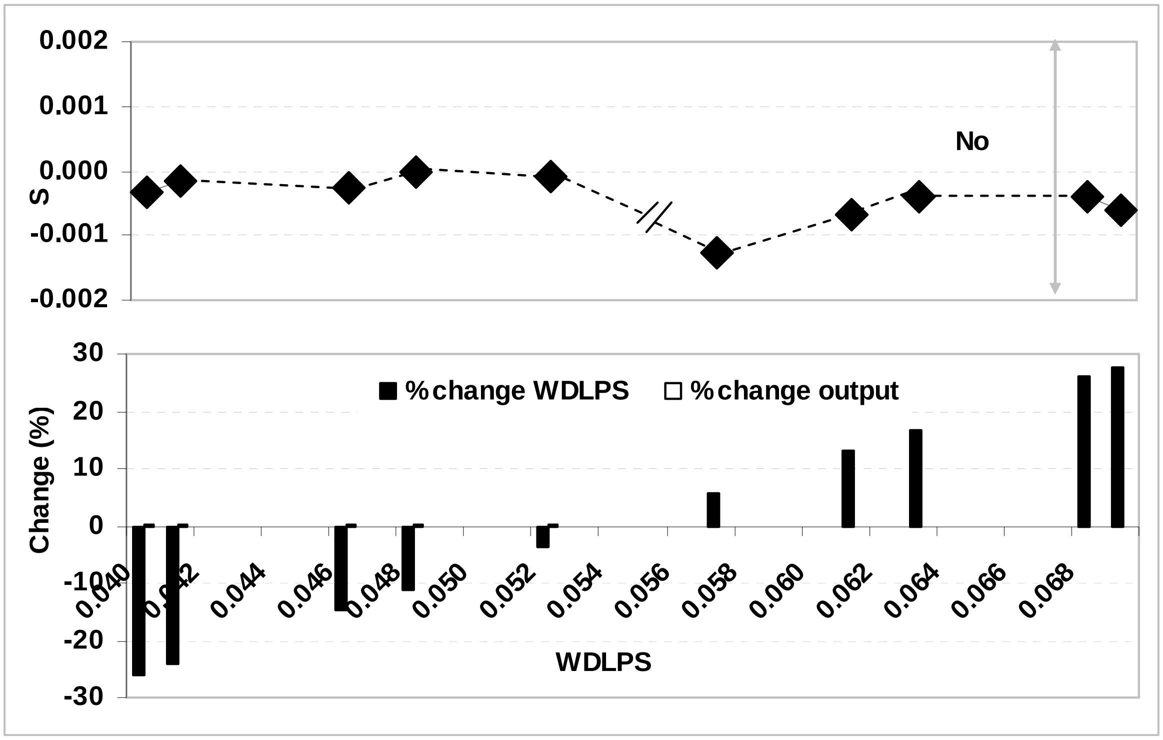

Figure 3.13. IPP method: less persistent bacteria die-off in sorbed (WDLPS) relative sensitivity index (S) response

3.4.4 Input Parameter Sensitivity

Bacteria concentrations in manure showed direct relationship between bacteria concentration and bacteria prediction except at low input values. A moderate sensitivity was determined with relative sensitivity of 1.05 at -25% (2.6x10^7 cfu g^{-1}) and 0.04 at +900% (3.5x10^8 cfu g^{-1}) (Fig. 3.14). Bacteria concentration was stored in the model in floating-point 8.3 format (eight integers followed by three decimals: xxxxxxxx.xxx). When nine integer digits bacteria concentration values were input, model determined lower sensitivity predicting lower number of stream bacteria concentration than eight digit input values. If seven digit values were input, the model showed higher sensitivity (S = 0.99) than eight digit input values (S = 0.84). If eight digit values were input (99,999,999), the model predicted about eight times more bacteria than nine digit values input (100,000,000) with lower sensitivity (last two data points in the right, Fig. 3.14). The SWAT model program may be recompiled to allow the model to adjust to 15.3 format (xxxxxxxxxxxx.xxx) in order to improve the current sensitivity problem due to bacteria concentration input. Parajuli et al. (2006) reported similar problems with the SWAT 2000 model.

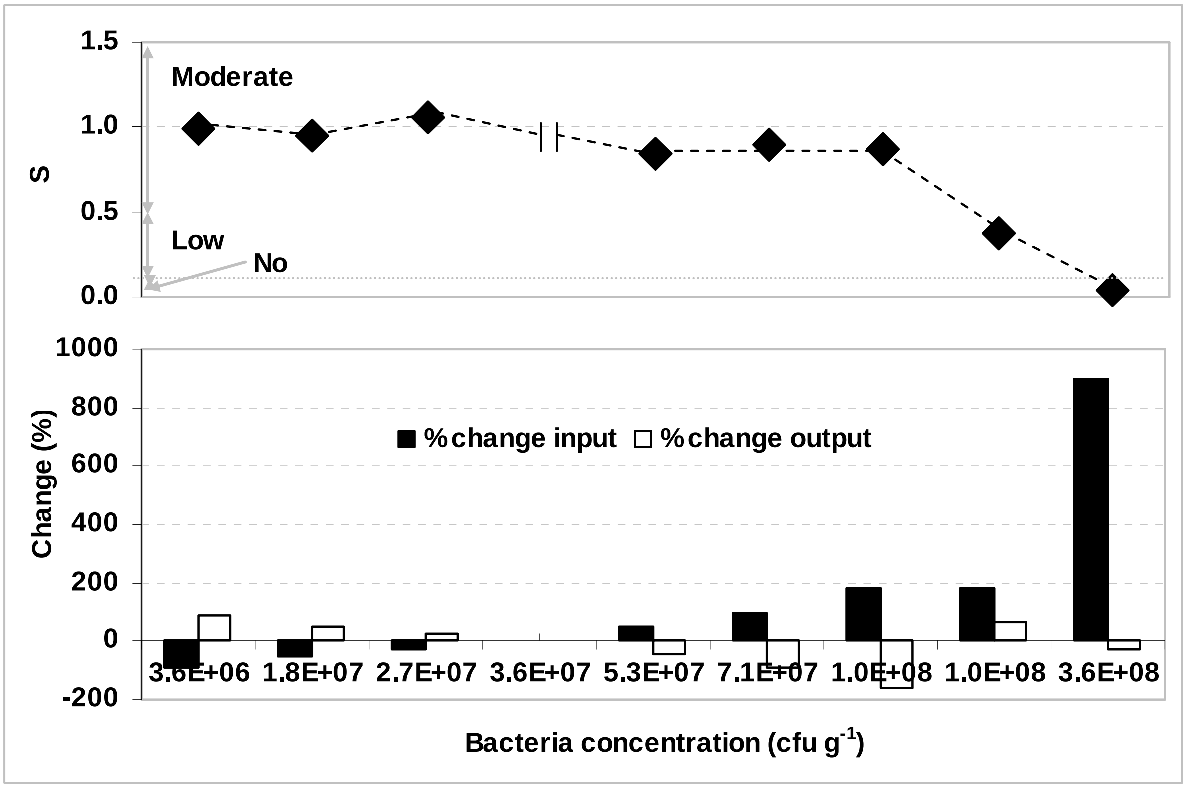

Figure 3.14. Bacteria concentration relative sensitivity index (S) response

The maximum relative sensitivity index absolute values calculated for each tested parameter during LHS and IPP simulations were summarized using equation 3.3 (Table 3.5). The BACTKD and bacteria concentration parameters had high sensitivity especially when used extreme range of lower values. Otherwise, generally low sensitivity was determined. The TBACT factor generally showed moderate sensitivity especially when using either extreme low or high range of values. The WDLPQ and WDLPS factors generally showed no sensitivity except the WDLPQ showed low moderate sensitivity when using low WDLPQ values during IPP method simulations.

Table 3.5. Relative Sensitivity (S) for Parameters Tested during LHS and IPP

Parameter	ISI using LHS	ISI using IPP
BACTKDQ	0.65(M)*	8.69(VH)*
TBACT	1.56(M)*	0.90(M)*
WDLPQ	0.02(N)*	0.72(M)*
WDLPS	0.20(L)*	0.001(N)*
Bacteria Concentration	-	1.39(M)*

M* = Moderate VH* = Very High N* = No
L* = Low

3.5 Conclusions

This study demonstrated methods to characterize bacteria source loads and to assess the model sensitivity to model parameters, and input parameter. It is essential to know the influence of the model parameter and input parameters to improve model accuracy. The result of this study can help in watershed management and modeling decisions choosing more realistic model parameters to the natural life-perspectives.

Un-calibrated model results for in-stream fecal bacteria concentrations compared unsatisfactory agreement but fair correlation with measured data, providing general confirmation of source-load characterization methods. Further detailed calibration with more extensive in-stream data are needed for more comprehensive model assessment. Model use to predict fecal bacteria concentration at the watershed scale requires knowledge of both bacteria source application methods and model sensitivity in selection of bacteria model and source-load input parameter values. The result of this study can help in selection of more realistic model parameters to simulate watershed management scenarios.

Sensitivity of model and input parameters generally, ranked as BACTKDQ > TBACT > Bacteria concentration > WDLPQ > WDLPS. Sensitivity of model and input parameters were found changed from SWAT 2000. Bacteria concentration was stored in the model in floating-point 8.3 format (eight integers followed by three decimals: xxxxxxxx.xxx). When nine-integer-digit bacteria concentration values were input the model responded with lower sensitivity and by predicting lower stream bacteria concentration than eight-digit input values.

This study suggested to revise SWAT model to address format problem with bacteria concentration, which is not addressed by SWAT 2005. Also, this study suggested to provide default WDLPQ and WDLPS values in the SWAT model from natural life perspectives.

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CHAPTER 4 - SWAT CALIBRATION AND VALIDATION FOR FLOW, SEDIMENT, NUTRIENTS, AND FECAL BACTERIA FOR AGRICULTURAL WATERSHEDS

Abstract

Fecal coliform bacteria (FCB) contamination is one of the causes of water-quality impairments in surface waters which often result from the non-point source pollution. The Soil and Water Assessment Tool (SWAT) model (2005) was used to simulate the daily flows, sediments, nutrient, and bacteria concentrations in two grazed sub-watersheds (Rock Creek and Deer Creek) of the Upper Wakarusa watershed in the north east Kansas. The watershed characteristics for bacterial source such as livestock, human, and wildlife were modeled together to evaluate the bacteria concentration at the outlet of the each watershed.

The objectives of this research was to develop bacteria source load characterization, calibration and validation of SWAT model (2005) using about one year (January to December, 2004) of measured data. The model was calibrated at Rock Creek sub-watershed (75 km^2) and validated at Deer Creek sub-watershed (51 km^2) of the Upper Wakarusa watershed in north east Kansas (950 km^2). The daily time scale model simulation results showed the good to very good agreement with coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E) range of 0.58 to 0.89 for flows, 0.54 to 0.77 for sediments, 0.55 to 0.78 for total phosphorus (TP). The model determined poor to fair agreement with R^2 and E values of 0.10 to 0.46 for total nitrogen (TN) and 0.14 to 0.46 for FCB concentrations during calibration and validation. The result of this research was successful to calibration and validation of the SWAT model (2005). Further detailed calibration with more extensive in-stream data are needed for more comprehensive model assessment.

4.1 Introduction

The majority of the Kansas population (over 70%) uses surface water for drinking water and other daily uses (KWO, 2004). Out of the 55% of the impaired stream miles and 72% of the impaired lake acreage, about 22% of the assessed stream miles and 53% of the lake acreage are bacteria impaired in Kansas (KDHE, 2004). As a result, the concentration of fecal coliform bacteria in the surface water has become an increasing concern. The concentration of fecal coliform bacteria in surface water has been an increasing concern because it indicates the potential to cause severe illnesses in humans (Craun and Frost, 2002). Concentrations of fecal coliform bacteria in surface water could be due to land application of livestock manures, grazing operations, winter feeding operations, failing septic systems, and wildlife. Water movement and sediment erosion increase the chance of bacteria reaching surface water systems especially during high intensity rainfall events like those found in eastern Kansas during the spring and summer.

Watershed models serve as a tool for linking pollutants to the receiving streams. Models are useful tools for organizing and interpreting research data. It also provides water quality predictions in a quick and economic way. Water quality models are used to assess water quality goal attainment. Models are important tools because they can be used to understand hydrologic processes, develop management practices, evaluate the risks and benefits of landuse over various period of time, and recommend the effectiveness of Best Management Practices (BMPs). Bacteria models could be one of the good tools to use that can help in evaluating watersheds.

Model development is a continuing process to capture the natural processes. The inherent variability in natural processes can be either variability in space (spatial variability) and/or variability in time (temporal variability). Spatial and temporal variability can be generally observed with environmental factors such as rainfall, temperature, and stream flow. The SWAT (2000) bacteria sub-model was calibrated and validated (Parajuli et al., 2005). However, numerous revisions to the SWAT 2005 model and bacteria sub-model require independent calibration and validation.

4.1.1 Flow, Sediment and Nutrient

Saleh et al. (1999) applied the SWAT (98.1 version) model in the Upper North Bosque River Watershed (UNBRW), an intensive dairy production region in north central Texas. The UNBRW covers about 93, 250 ha area with 94 dairies. They applied and tested SWAT model to estimate flow and sedimentation for the UNBRW stream system. The watershed is 98% rural with the primary land uses being rangeland (43%), forage fields (23%) and dairy waste application fields (7%). The SWAT model was simulated for the period 1993 -1995. The SWAT model reasonably predicted average monthly flow and sediment losses from the UNBRW with Nash-Sutcliffe model efficiency (E) of $\geq$ 0.82. Based on the E values the SWAT model was able to predict the average monthly flow and sediment.

Spruill et al. (2000) applied SWAT model in a small central Kentucky watershed. Streamflow data from 1996 were used to calibrate the model and streamflow data from 1995 were used for evaluation. The model adequately predicted the trends in daily streamflow during this period although E values were –0.04 for 1995 and 0.19 for 1996. The E values for monthly total flows were 0.58 for 1995 and 0.89 for 1996. The SWAT model was determined as an effective tool for describing monthly runoff from small watersheds in central Kentucky that have developed on karst hydrology.

Santhi et al. (2001) applied SWAT model in the Bosque River Watershed that had a drainage area of 4277 km^2, and has four tributaries: North Bosque River, Middle Bosque River, South Bosque River, and Hog Creek, that drain into Lake Waco. Land use in this watershed is mostly range and pasture with some cropland in the southern portion of the watershed. Measured water quality data were used for calibrating and validating the model for flow, sediment, and organic and mineral nitrogen and phosphorus on a monthly basis from 1993 through 1998. The water quality measurement data for Hico and Valley Mills were used for monthly model calibration (1993 to 1997) and monthly model validation (1998). The calibrated SWAT model showed E values of 0.72 to 0.86 for monthly flow, 0.69 to 0.80 for monthly sediment, -0.08 to 0.58 for monthly nitrogen, and 0.53 to 0.70 for monthly phosphorus when compared with the measured data. The validated model had Nash Sutcliffe efficiency of 0.62 to 0.87 for monthly flow, 0.23 to 0.70 for monthly sediment, 0.43 to 0.73 for monthly nitrogen, and 0.39 to 0.72 for monthly phosphorus when compared with the measured data.

Kirsch et al. (2002) utilized the SWAT model (98.1 version) to assess the effect of the Best Management Practices (BMPs) in the Rock River Basin (RRB) watershed (9708 km^2) which lies within the glaciated portion of south central and eastern Wisconsin. The major landuse in the watershed include: agriculture (62%), grassland (11%), and forest (10%). The SWAT model was calibrated and validated with the twenty-three USGS (United States Geological Survey) measured data in 1999 from the different monitoring sites. The beta version of the SWAT ArcView (AVSWAT) interface was used to delineate the watersheds. A 30-meter digital elevation model (DEM), State Soil Geographic Database (STATSGO) and different management scenarios were used. The dominant crop rotations used in the model include: corn-soybean, continuous corn, dairy rotation of corn and vegetable rotations. The calibrated SWAT model for Yahara and Mendota sub-watersheds from 1989 to 1995 in their study had E values of 0.61 for annual flow prediction, 0.75 for annual sediment prediction, and 0.07 for annual phosphorus prediction when compared with measured flow data.

When calibrated model validated at Jackson Creek sub-watershed the model prediction efficiency was decreased with the E value of 0.41 for annual runoff. The average sediment yield prediction from this sub-watershed was not found reasonable as they had relatively low samples. The average annual sediment yield prediction was 54% lower than the USGS measured data. The average annual phosphorus prediction was found 36% lower than USGS measured data. The SWAT model was calibrated with flows and then to sediment. The wet conditions of the watershed impact into the less efficiency in model prediction because the model adjustment was needed to decrease in surface flow. Additionally, adjustment in evapotranspiration (ET) equation was required to increase infiltration potential. In addition, the SWAT model was applied in the 12 river basins of the RRB, the annual flow rate prediction efficiency was varied from R^2 0.28 to 0.98 and E from 0.18 to 0.84. The model predictions largely depend upon each sub-watershed’s topography, crop and plant vegetation, management practices and soil characteristics.

Stewart et al. (2003) applied SWAT model at Upper North Bosque River (UNBR) watershed. The predominant landcover in the watershed is rangeland and major agricultural activity is dairy production. The SWAT model was used to simulate the monthly flows and phosphorus concentrations. 30m x 30m size Digital Elevation Data (DEM) was used to derive watershed topography. In order to match the SWAT model setup, Soil Survey Geographic (SSURGO) dataset of the watershed was manipulated to State Soil Geographic (STATSGO) soil input. The landuse data for the watershed was obtained from the National Land Cover Dataset (NLCD). The model was calibrated changing curve number and ESCO parameters. The SWAT model was calibrated with E = 0.81 for monthly flow and E = 0.53 for monthly sediment.

Van Liew et al. (2003) evaluated the performance of SWAT on eight nested watersheds within 610 km^2 Little Washita River Experimental Watershed (LWREW) and two adjacent watersheds, 80 km southwest of Oklahoma City. They used two sub-watersheds within LWREW to calibrate for a wetter than average period of record and then validated in six other sub-watersheds within LWREW and two other adjacent watersheds under varying climatic conditions. Elevation data obtained from USGS DEM, landuse from 1997 Landsat-5 TM image, and STATSGO soil were used as model inputs. Predominant landuse in LWREW was rangeland (66%), cropland (18%), and forest (9%). The SWAT model provided consistent results in estimating streamflow from this watershed.

The model showed decreased level of model performance when model was simulated for daily time step as compared to monthly simulation. The calibrated model showed E values of 0.66 to 0.76 for monthly flow simulation and 0.56 to 0.58 for daily flow simulation when compared with the measured data. The validated model determined E values of -1.05 to 0.85 for monthly flow simulation and -0.35 to 0.72 for daily flow simulation when compared with the measured data.

White et al. (2004) evaluated SWAT model in the War Eagle Creek Watershed in Northwest Arkansas. War Eagle Creek Watershed covers approximately 681 km^2 with land use distributions of forest (64%), pasture (36%), and urban and waters (1%). The SWAT model predicted monthly total phosphorus yields with a correlation coefficient (R^2) of 0.34 in their study.

Qi and Grunwald (2005) applied SWAT model in the Sandusky watershed located within the Great Lakes basin which drains into Lake Erie with a drainage area at Fremont of 3,240 km^2. The study was focused on four sub-watersheds: Honey Creek (388.2 km^2), Rock Creek (90.3 km^2), Tymochtee (607.4 km^2), and Bucyrus (223.8 km^2). The model was calibrated using USGS gauge station observed monthly surface flow data from 1998 to 1999 and validated using observed monthly surface flow data from 2000 to 2001. The E values were determined for each sub-watersheds ranging from 0.31 to 0.65 for monthly surface flow calibration whereas the model efficiencies were ranges from -0.04 to 0.75 for monthly surface flow validation in the sub-watersheds.

Wang et al. (2006) evaluated responses of SWAT model on the 433,497 ha Wild Rice River watershed, located in northwestern Minnesota. The land use within this watershed consists of agriculture (67%), forest (18%), pasture (7%), and wetland and/or open water (8%). The basic model inputs included the 30 m USGS National Elevation Dataset (NED), the EPA 1:250,000 scale LULC, and the USDA-NRCS (Natural Resources Conservation Service) State Soil Geographic database (STATSGO). The SWAT model was calibrated using curve number and esco parameters. The esco parameter was adjusted up to 0.7. The model was calibrated and validated using different period of two USGS gage station data for annual, monthly and daily flow. The calibrated SWAT model predicted mean flow with E values from 0.72 to 0.80 for annual flow, -1.16 to 0.98 for monthly flow, and 0.64 to 0.67 for daily flow when compared with the measured flow data. The validated SWAT model predicted mean flow with E values from 0.68 to 0.98 for annual flow, -12.64 to 0.92 for monthly flow, and 0.50 to 0.62 for daily flow when compared with the measured flow data.

In summary, the SWAT water quality model as described earlier has been applied, calibrated and validated for one or more parameters such as; runoff, sediment yield, and nutrient losses from watersheds at different geographic locations, conditions, and management practices (Saleh et al., 1999; Spruill et al., 2000; Santhi et al., 2001; Kirsch et al., 2002; Van Liew et al., 2003; White et al., 2004; Qi and Grunwald, 2005 ; White and Chaubey, 2005; Wang et al., 2006; Jha et al., 2007; Gassman et al., 2007). Limited research has been performed for the SWAT (2005) model for predicting bacteria movement.

Baffaut and Benson (2003) studied bacteria TMDLs (Total Maximum Daily Load) for the Shoal Creek watershed in southwest Missouri using SWAT (2000) model. The watershed was consisted of grassland (89%) and wooded areas (11%). The soils in the watershed were very high rock content of 30% or more in the surface. They calibrated model using daily flow, weekly water quality grab samples, and annual hay yield reported to USDA. A frequency analysis curve method was used to compare measured vs. predicted data for daily flow and fecal coliform bacteria concentration. Daily flow curve found reasonable except peak flow over-predictions. The karst topography feature existed in the watershed contributed in high surface runoff from the watershed. While comparing model predicted values with 18 months of weekly measured fecal coliform bacteria concentration data with average plus or minus one standard deviation, the bacteria concentration curve validated up to 70% of the frequency curve.

4.2 Objectives

The objectives of this research was to: (a) develop methods to quantify bacteria source input data and (b) calibrate and validate the SWAT (2005) using measured flow, sediment, and fecal coliform bacteria concentration data for 2004.

4.3 Materials and Methods

4.3.1 Watershed Stream Description

4.3.1.1 Rock Creek Watershed

The Rock creek watershed (Fig. 4.1) is located in Douglas and Osage Counties which consists of 75.41 km^2 with average elevation of 317 m. The study area has three major landuses including grassland (56%), cropland (37%), and woodland (6%). The silty-clay textured soils (SSURGO stmuid: KS0457302, KS0457325, KS0458962, KS1397302, and KS1398735) is a major predominant soil type in this watershed. The model was calibrated in Rock Creek watershed.

4.3.1.2. Deer Creek Watershed

The Deer Creek watershed (Fig. 4.1) is located in Douglas and Shawnee Counties which consists of 51.37 km^2 with average elevation of 311 m. The study area has three major landuses including grassland (51%), cropland (39%), and woodland (9%). The silty-clay textured soils (SSURGO stmuid: KS1777302, KS1777325, KS1774752, KS1773891, KS0457302, and KS0457657) is a major predominant soil type in this watershed. The model was validated in Deer Creek watershed.

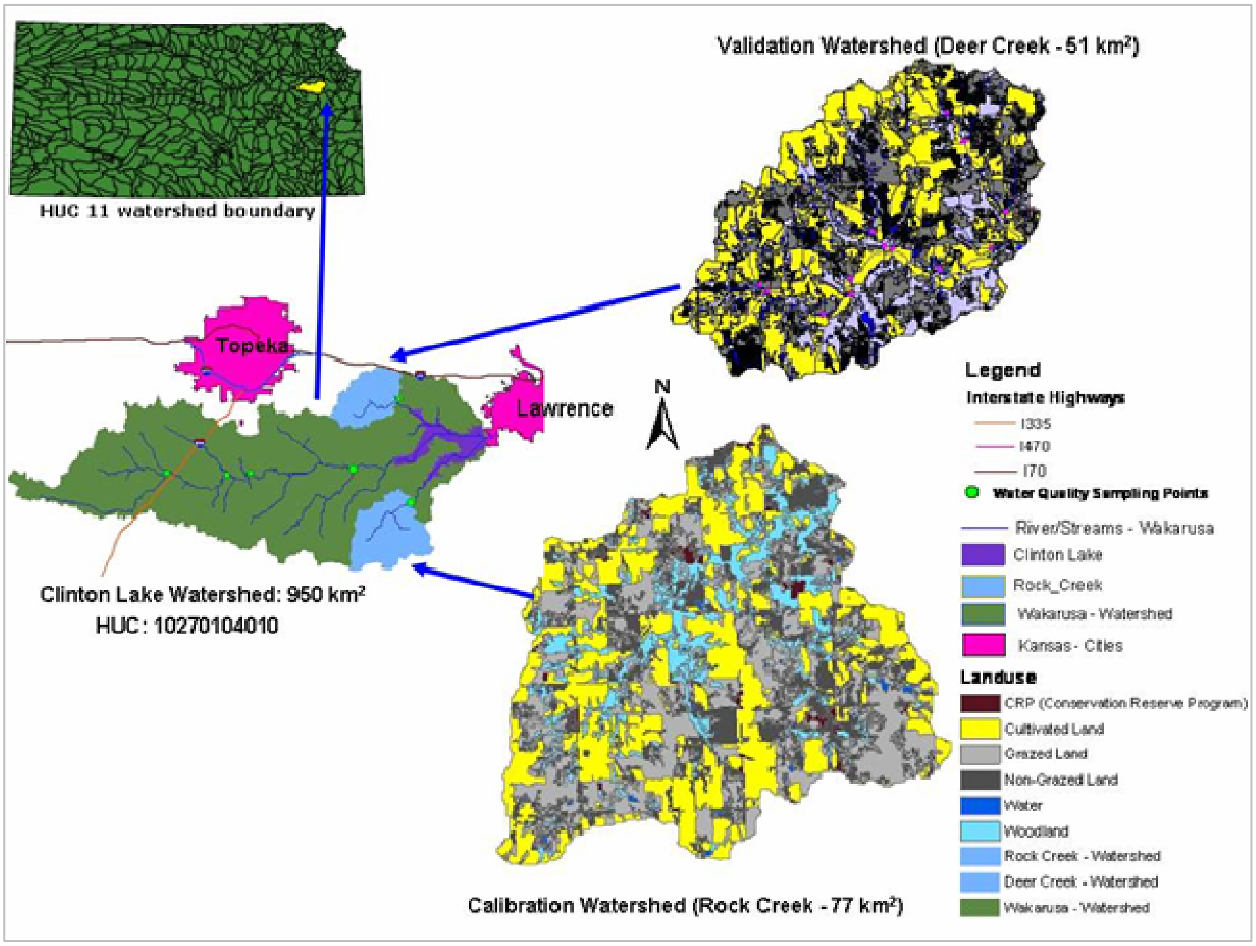

Figure 4.1. Location map of the Rock Creek Watershed in NE Kansas

4.3.1.3 Stream Description

Stream flow and bacteria data were collected at the outlet of the each watershed to validate model results. Grab samples (about 250 ml) were collected from the mid point of the flowing stream at each watershed outlet. Samples were placed immediately into an ice chest, and transferred to laboratory refrigerator within two to four hours of collection. Bacteria enumeration procedures were started with in 24 hours. Serial dilution method (Clesceri et al., 1998) was applied to enumerate fecal coliform bacteria colonies. Bacterial samples typically required four serial dilutions to obtain reasonable bacteria colony counts.

Flow was calculated at the time of sample collection using Manning's equation, as outlined by Ward and Elliot (1995). Flow depth, cross-sectional area, and channel slope were measured, and channel roughness factor was estimated based on the channel roughness characteristics, and degree of meandering (Cowan, 1956). The calculated flow was validated based on ratio of the watershed area using data from the USGS Richland gage station data. The calculated flow data showed very good correlation (>90%) with the weighted area flow data. This study used the data collected from January to December, 2004.

4.3.2 SWAT Microbial sub-model

The SWAT watershed scale model (Arnold et al., 1998; Neitsch et al., 2002) processes on a continuous daily time step. It simulates the hydrological processes, sediment yield, nutrient loss, and pesticide losses into surface and groundwater. Runoff volume is estimated from daily rainfall using the modified Soil Conservation Service (SCS) curve number method. Additionally, sediment yield is estimated using the Modified Universal Soil Loss Equation (MUSLE). The SWAT model utilizes lists of data to create layers of information to satisfy the necessary input parameters. United State Geological Survey (USGS, 1999) 7.5-minute elevation data was used to delineate the watershed boundaries and topography. Soil Survey Geographic Database (SSURGO) was utilized to create a soil database (USDA, 2005). The GAP land cover data of 2001 that depicts twenty general land cover classes for the state of Kansas (KARS, 2001) was used. Wardlow and Egbert (2003) evaluated GAP (2001) and National Land Cover Data NLCD (1992) landuse data for the State of Kansas. The Kansas GAP provided better discrimination of most land-cover classes as compared to NLCD. Accuracy assessment found an overall accuracy of 87 percent for GAP and 81 percent for NLCD, and GAP had higher accuracies for most individual land-coverclasses. The Kansas GAP and NLCD land-cover products were found to be comparable in terms of characterizing broad scale land-cover patterns, but the Kansas GAP land-cover map appears to be more appropriate for localized applications that require detailed and accurate land-cover information.

The landuse classes were reclassified into eight classes (grazedland, non-grazedland, cropland, woodland, CRP, water, urban areas and quarry) based on field-verified landuse conditions (Mankin and Koelliker, 2001; Mankin et al., 2003).

The microbial survival and transport part was added to the SWAT model in 2000 and modified in 2005. The SWAT model microbial component considers the fate and transport of organisms for bacterial concentration. The microbial sub-model uses Chick's Law, as revised by Moore et al. (1989), to model fecal bacteria die-off and re-growth. Chick's law, a first order decay equation, determines the quantity of bacteria that are removed or added by die-off and re-growth as described by Sadeghi and Arnold (2002) which is given by the equation (4.1),

$$C_t = C_o \times e^{-K_{20}\, t \theta^{(T-20)}} \tag{4.1}$$

where,

C_t = bacteria concentration at time t, count/100mL
C_o = initial bacteria concentration, count/100mL
K_{20} = first-order die-off rate at 20^0C, day^{-1}
t = exposure time, days
θ = temperature adjustment factor
T = temperature, ^{0}C

As described in the SWAT model (Neitsch et al., 2005), in the stream bacteria die-off is the only process modeled. SWAT calculates loading of pathogens and indicator bacteria for pathogens from land areas in the watershed. Due to the low mobility of bacteria in soil solution, surface runoff partially interacts with the bacteria present in the soil solution. The amount of bacteria transported in surface runoff is: bacteria transported in surface runoff and bacteria attached to soil particles that may be transported by surface runoff to the main channel.

The amount of bacteria transported in the surface runoff (cfu m^{-2}) is a function of amount of bacteria lost in soil solution, daily surface flow, bulk density of top 10mm soil layer, depth of the surface layer, and bacteria soil partitioning coefficient. The bacteria soil partitioning coefficient is the ratio of the bacteria concentration in the surface 10 mm soil solution to the concentration of bacteria in surface runoff. The amount of bacteria transported with sediment to the stream is calculated with a loading function developed and modified for nutrients. Once the bacteria load in surface runoff is determined, the amount of bacteria released to the main channel is calculated (cfu m^{-2}). The amount of bacteria in the reach or the outlet of the watershed is also calculated based on cfu m^{-2}. The calculated bacteria at the outlet of the watershed (cfu m^{-2}) are converted to cfu 100 mL^{-1} of bacteria using equation (4.2) (Sammons, 2007).

$$\frac{\#\, cfu}{m^2} * \frac{ha(da)}{m^3(flow)} * \frac{10{,}000\, m^2}{ha} * \frac{m^3}{10^6\, mL} = cfu100\, mL^{-1} \tag{4.2}$$

where,

cfu = colony forming units
ha = hectare
da = drainage area
mL = milliliter

4.3.3 Model Calibration Procedures

4.3.3.1 Calibration Parameters

Three widely used flow calibration parameter (Table 4.1) including curve number (CN), and soil evaporation compensation factor (ESCO), plant uptake compensation factor (EPCO) were selected based on professional judgments (Santhi et al., 2001; Saleh and Du, 2004; White and Chaubey, 2005; Choi et al., 2005). The SCS curve number or CN is a function of the soil's permeability, land use and antecedent soil water conditions. The esco is a soil evaporation compensation factor that allows model to modify depth distribution used to meet the soil evaporative demand to account for the effect of capillary action. As the value of esco is reduced, the model can extract more water from the lower levels to meet the evaporative demand. The epco is a plant uptake compensation factor that allows model to meet the potential water uptake by the plant. The epco approaches to 1.0, means the model allows more of the water uptake demand to be met by lower layers in the soil. As epco approaches 0.0, the model allows less variation from the original depth distribution to take place.

Two widely used sediment calibration factors including Universal Soil Loss Equation (USLE) crop cover management factor (C), and USLE support practice factor (P) were used (Table 4.1). The USLE cover and management factor, CUSLE, is defined as the ratio of soil loss from land cropped under specified conditions to the corresponding loss from clean-tilled, continuous fallow (Wischmeier and Smith, 1978). The support practice factor (P) is defined as the ratio of soil loss with a specific support practice to the corresponding loss with up-and-down slope culture. Support practices include contour tillage, stripcropping on the contour, and terrace systems. Stabilized waterways for the disposal of excess rainfall are a necessary part of each of these practices (Wischmeier and Smith, 1978).

No calibration parameters were used for phosphorus and nitrogen except turning on QUAL2E stream flow process for the model simulation and using organic nitrogen settling rate 0.10 day^{-1} (Bowie, et al., 1985). Experience showed that significant amount of phosphorus and nitrogen were decreased when applied stream flow process. Bacteria Partition Coefficient in Surface Runoff

(BACTKDQ) and Temperature Adjustment Factor (TBACT) model parameters were used for bacteria calibration. The less persistent fecal bacteria in manure/fertilizer were partitioned (0.90), 3 days half-life for bacteria die-off rate in solution, and 1/10 of the bacteria in solution die-off rate for bacteria die-off rate in sorbed conditions were used. The bacteria partition coefficient in the fertilizer database separates bacteria concentration in sorbed and solution phases. As the bacteria partition coefficient approaches to zero bacteria is primarily sorbed to the soil particles and as it approaches to one bacterium is primarily in solution (Soupir et al., 2006). Based on three days half-life, bacteria die-off rate in solution phase manure was estimated 0.40 day^{-1} and one tenth of this value 0.04 day^{-1} was used for bacteria adsorbed to soil particles (Baffaut and Benson, 2003).

Table 4.1. SWAT model parameters test and adjustment during calibration

Parameters	Default value	Test range value	Final value
Flow:			
Curve Number (CN)	73-83	73-83	77-79
Cropland	83	74-83	78
Pastureland	79	75-82	79
Woodland	73	73-80	77
Soil evaporation compensation factor (ESCO)	0.95	0.01 to 1.00	0.40
Sediment:			
USLE cover and management factor (C)	Crop varied	0 to 0.50	0.15
Bacteria:			
Bacteria Partition Coefficient in Surface Runoff (BACTKDQ)	175	1.75 to 262	175
Temperature Adjustment Factor (TBACT)	1.07	0.96 to 1.18	1.07

4.3.3.2 Calibration Procedure

Daily flow, sediment, total phosphorus, total nitrogen, and fecal coliform bacteria concentration data collected from the outlet of the each watershed from January through December 2004 were used to calibrate and validate the model. Model predictions were statistically evaluated with the coefficient of determination (R^2) and the Nash-Sutcliffe Efficiency Index (E) between measured values and model predicted values after each parameter run. The CN parameters were continuously modified within the range of values during the calibration phase to find the local maximum value that has maximum model efficiency. The curve number range of 77-79 (77 for woodland, 78 for cropland, and 79 for grassland) determined the maximum efficiency range to use in the model. The ESCO and EPCO parameters were tested changing values. Later in the calibration process, the EPCO parameter was found not sensitive, therefore EPCO was taken out from the flow calibration.

The ESCO parameter was tested in different range but come up with 0.40 values to apply in the model throughout the modeling process. Other studies reported ESCO 0.51 to 0.70 (Saleh and

Du, 2004; Choi et al., 2005; Wang X et al., 2006). Using middle range of ESCO probably means modeler allows less variability but more realistic representation of the natural life perspective for the soil layers depth distribution to meet the soil evaporative demand. The USLE (Universal Soil Loss Equation) cover and management factor was tested for corn and soybean crop over the range from 0.05 to 0.20. The C factor of 0.15 provided the best model efficiency in this study. The USLE practice factor was fixed to 0.10 which represents the current condition of the watersheds. The default bacteria parameters provided in model (BACTKDQ and TBACT) were found good during calibration. After calibration, the model input parameters were not changed during validation process.

4.3.4 Fecal Bacteria Sources

4.3.4.1 Livestock

Manure applied due to grazing, feeding operations, and winter feeding areas were major bacterial sources in this study. Livestock population at the county and watershed level was estimated using agricultural census/GIS layers data (USDA, 2006). The county animal census population was equally distributed per total land-area basis to determine the fraction of total livestock in the study watershed. The USDA data were compared with Kansas Department of Agriculture farm facts data from the Kansas Department of Agriculture (KDA, 2004a). The AUs in feedlots within the watershed were estimated using active feedlot data (both federally permitted feedlots >1000 AUs and state registered feedlots > 300 AUs) from the Kansas Department of Health and Environment (KDHE) (Jepson, 2005). Permitted and registered livestock were subtracted from the total number of animals in the watershed to estimate the net grazed livestock population. Animal stocking rates in the pastureland was also validated using county-wide livestock population data (KDA, 2004b). Animals in the pasturelands could be brought from feedlots, barnyards and leasing agreements for grazing during the warm season (generally from April to September). However, the stocking rate of the animals in the pastureland was assumed to be maintained.

The populations of all animals in the watersheds were estimated based on 1000-kg AUs. The Rock Creek watershed was populated with 558 beef animal units (AU) in the pastureland (based on stocking rate), 104 beef AUs in the feedlots, and 223 beef AUs in the winter feeding areas (40% of 558), which was modeled in this study to represent the current scenario of the watershed. Similarly, Deer Creek watershed was estimated with 311 beef AUs in the pastureland (based on stocking rate), 73 beef AUs in the feedlots, and 124 of the beef AUs in the winter feeding areas, which was modeled in this study to represent the current scenario of the watershed. About 8.5% of the livestock source loads were considered direct point loads in this study whereas 17% was considered for the sub-watershed where permitted feedlots were located. Manure production (26.4 kg day $^{-1}$ AU^{-1}) and fecal coliform bacteria concentration (13x10^{10} cfu day^{-1} AU^{-1}) for each beef animal were estimated based standard production rates (ASAE, 2000). The bacteria concentration was converted into model-input units of colonies forming units (cfu) per gram of dry-weight manure using standard mean manure moisture content (86% moisture; ASAE, 2000).

4.3.4.2 Human

Digital orthophoto quarter quadrangles (State of Kansas, 2002) of the watershed was digitized depending on the physical context, roads, and type of houses to represent each septic system in the watershed. Each rural house was assumed to have one septic system, resulting in a total of 107 septic systems for the Rock Creek watershed and 229 septic systems for the Deer Creek watershed. About 20% of the estimated septic systems were assumed failing in the watershed for modeling in this study. The number of failing septic systems may vary with in the watershed depending on the type of design, construction, and operation and maintenance (KDHE, 2000).

Each septic system was assumed to be used by three persons in the household that can contribute about 0.32 m^3 of sewage effluent per day (USEPA, 2001). The failing septic systems in the watershed were modeled using 90% land application method and 10% direct point load. Parajuli, et al. 2006 found higher model sensitivity when applying septic effluent as direct point load method than land application method. The fecal bacteria concentration in failing septic system was taken as 6.3x10^6 cfu 100 mL^{-1} (Overcash and Davidson, 1980).

4.3.4.3 Wildlife

No comprehensive wildlife inventory was available for the Rock Creek watershed. The wildlife population density was estimated based on the information received from the Kansas Department of Wildlife and Parks (KDWP). The 2002 summer road-kill indices survey data from KDWP furbearer biologist (Peek, 2005) for Kansas were used to estimate small-mammal populations in the watershed. The information include various wild-animal species: raccoon, opossum, striped skunk, coyote, badger, bobcat, red fox, gray fox, swift fox, beaver, mink, muskrat, river otter, spotted skunk, weasel, armadillo, woodchuck and percupine. The population of raccoon, opossum, striped skunk, and coyote constituted about 81% of the total small mammals in Kansas. Population of the predominate large mammal (white-tailed deer) in the watershed was estimated based on expert opinion from the KDWP big-game coordinator (Lloyd, 2006). Similar data were collected for the predominate indigenous avian species (turkey) from the KDWP small-game coordinator (Pitman, 2006); migratory birds (duck geese, sandhill crane) from the KDWP waterfowl research biologist (Kraft, 2006)

In order to estimate the animal units of each wildlife species in the watershed, the population data were first distributed over the potential habitat for each species. Small mammals and turkey population data were counted from a road survey. Most of the small mammals were counted dead at the road shoulder. The sight distances of 5 m for small mammals and 50 m for turkey from each side of the road were assumed, and the population density of each species was estimated as number of animal per unit area using total length of the road driven during survey. For deer, the number of deer harvested in northeastern Kansas was estimated and equally distributed in the total land area of northeastern Kansas to get the deer density. Migratory birds (duck, geese, and sandhill crane) are available in the watershed for about seven months of the year (Jan-March and Sept-Dec). The Kansas population of these wildlife species was equally distributed over the water surface area and wetland area to get their population density. The population density in the watershed was estimated based on the available water surface area.

The Rock Creek watershed was populated with 60 turkey AUs, 24 deer AUs, 7 small mammal AUs, and 36 migratory bird AUs which was modeled in this study to represent the current scenario of the watershed. Similarly, Deer Creek watershed was populated with 41 turkey AUs, 16 deer AUs, 5 small mammal AUs, and 27 migratory bird AUs which was modeled in this study to represent the current scenario of the watershed. About 10% of the wildlife source loads were considered direct point loads in this study. Animal weights were estimated based on the information received from “mammals of Kansas” (Timm et al., 2007) and personal communication (Pitman, 2006). It was estimated that about 0.80 kg ha^{-1} day^{-1} dry weight of total wildlife manure is applied in the different landuses of the watershed depending on the wildlife species, specific seasons, habitat and feeding areas (pastureland, woodland, cropland) which is a source of fecal coliform bacteria simulated in this study.

4.3.5 Management Scenarios

4.3.5.1 Pastureland

The pastureland was simulated under two major grass-type management conditions, which represent the typical field conditions. The two major grass types in the watershed include grazed

(80%, typically native prairie) and non-grazed (20%, typically smooth brome and tall fescue). The native prairie grass is typically not fertilized, but tall fescue is fertilized with 70-15-0 (NPK) (Boyer, 2005). It was estimated that about 1.81 kg ha^{-1} day $^{-1}$ dry weight of manure is applied in the pasturelands due to grazing operation during the growing season. This estimation is based on the ASAE (2000) standards that include: (a) a beef AU produces 26.4 kg of wet weight manure per day, (b) the moisture content of wet manure is 0.139, and (c) cattle are grazed for 153 days in the pastureland. It is possible that the actual animal density varies in the watershed every day because of animal growth and the pattern of incoming and outgoing animals.

It was assumed that about 20% of the air-dry biomass is trampled every day, and about 341 kg of air-dry forage is required for an AU for 30 days (Paul and Watson, 1994). Grazing starts about a month earlier in tall fescue grasslands than in native prairie grass. All of the native prairie is grazed whereas only 80% of the tall fescue is grazed; the remaining tall fescue is un-grazed and used for haying and the Conservation Reserve Program (CRP). About 3.7 Mg ha^{-1} of hay is harvested annually from the un-grazed area, whereas biomass is not removed from the CRP land (Boyer, 2005). Cattle density in the pastureland was estimated as 3 ha per cow-calf pair based on the bluestem pasture guidelines for grazing (KDA, 2004b). Since cattle do not graze pastureland from October to March, no biomass uptake from the pastureland occurred, with no grass trampling and no manure deposition on the soil during this period.

All the source loads due to livestock in the confined animal feedlots were assumed to be applied as grazing operation in the pasturelands of the sub-watershed of the watershed where the active permitted feedlots were located. The winter feeding areas were modeled with the assumption that the estimated total number of AUs were confined within 40% of the grazed land of the watershed. Animals in feedlots and winter feeding areas contributed fecal bacteria for 212 days during the dormant season of the year (generally October to March). It was estimated that about 4.52 kg ha^{-1} day $^{-1}$ dry weight of cattle manure (2.5 times greater than regular pastureland operation) was applied in the respective pasturelands of the sub-watersheds of the watersheds due to winter feeding operations.

4.3.5.2 Cropland and woodland

Corn and soybeans were major warm-season crops, and winter wheat was a primary cool-season crop grown in three year's rotation in the watershed (Boyer, 2005). The warm season crop was planted on May 1 and harvested on October 1. The cool-season crop was planted on October 20 and harvested on July 30. The crop residue is left on the cropland between the crop periods. These dates represent the typical planting and harvesting dates in the watersheds. The conservation tillage system is the most widely adopted system for corn/soybean/wheat in the watershed. This method applied in to both calibrated and validated watersheds.

4.3.6 Weather and Hydrologic Data

The daily precipitation data for the Rock Creek watershed was taken from Overbrook weather station located about 4.8 km south of the watershed. The 2004 annual rainfall data for Overbrook weather station was about 1126 mm (Fig. 4.2a). The daily precipitation data for the Deer Creek watershed was taken from Lecompton and Topeka weather stations. The Lecompton weather station is located about 6.5 km north-east whereas Topeka weather station about 12.2 km north-west from the respective watersheds. The 2004 annual rainfall data measured for Lecompton 1206 mm and for Topeka 1013 mm (Fig. 4.2b). Data from the Silver Lake weather station, which is located about 45 km west from Rock Creek watershed and about 32 km west from the Deer Creek watershed was used for the daily temperature, daily solar radiation, daily wind speed, and daily relative humidity. The missing data for the both watersheds were adjusted using SWAT database. The SWAT model uses data from the Ottawa weather station (Franklin County), which is located about 23 km south-east from the Rock Creek watershed and about 42 km south-east from the Deer Creek watershed.

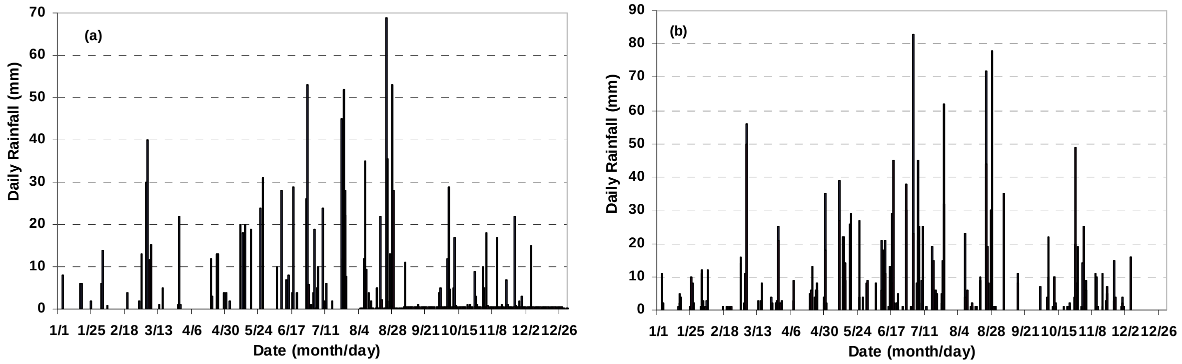

Figure 4.2 Distribution of daily rainfall for (a) Rock Creek, and (b) Deer Creek watersheds

4.3.7 Statistical Analysis

The SWAT model predicted nine daily mean flow events, sediment, total phosphorus, total nitrogen and fecal coliform bacteria concentration which were compared with field-measured data. The statistical parameter used to evaluate measured vs. predicted data includes coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E). The R^2 value indicates how consistently measured vs. predicted values follow a best fit line. The R^2 can range from zero (no correlation) or to

1.0 (perfect correlation) (Santhi et al., 2001). The E indicates how consistently measured values (range - ∞ to 1.0) match predicted values, with 1.0 representing a perfect model (Nash and Sutcliffe, 1970). As similar to Moriasi et al. (2007) the model efficiencies were classified as excellent ($E \geq 0.90$), very good (E = 0.75 to 0.89), good (E = 0.50 to 0.74), fair (E = 0.25 to 0.49), poor (0 to 0.24), and unsatisfactory (< 0).

4.4 Results and Discussion

4.4.1 Flow

Calibration of the SWAT model was needed since the model under-predicted mean daily flow with low model efficiency from the watershed. The calibrated SWAT model for Rock Creek watershed showed good to very good agreement for mean daily flow prediction ($R^2 = 0.85$ and $E = 0.58$) between mean daily measured and mean daily predicted flow values (Fig. 4.3a). The calibrated model, when applied to the Deer Creek watershed for validation, determined very good agreement for flow prediction ($R^2 = 0.87$ and $E = 0.89$) between mean daily measured and mean daily predicted flow values (Fig. 4.3b).

Van Liew et al (2003) applied SWAT model into Delaware Creek watershed in Oklahoma which has similar landuse conditions as Rock Creek and Deer Creek watersheds found a R^2 of 0.68 and an E of 0.84 for mean monthly flow prediction. Spruill et al. (2000) applied SWAT model in a small central Kentucky watershed. The SWAT model adequately predicted the trends in daily streamflow during their simulation period although E values were determined from –0.04 to 0.19. However, the E values for monthly total flows were determined from 0.58 to 0.89. The SWAT model was determined an effective tool for describing monthly runoff from small watersheds in central Kentucky that have developed on karst hydrology.

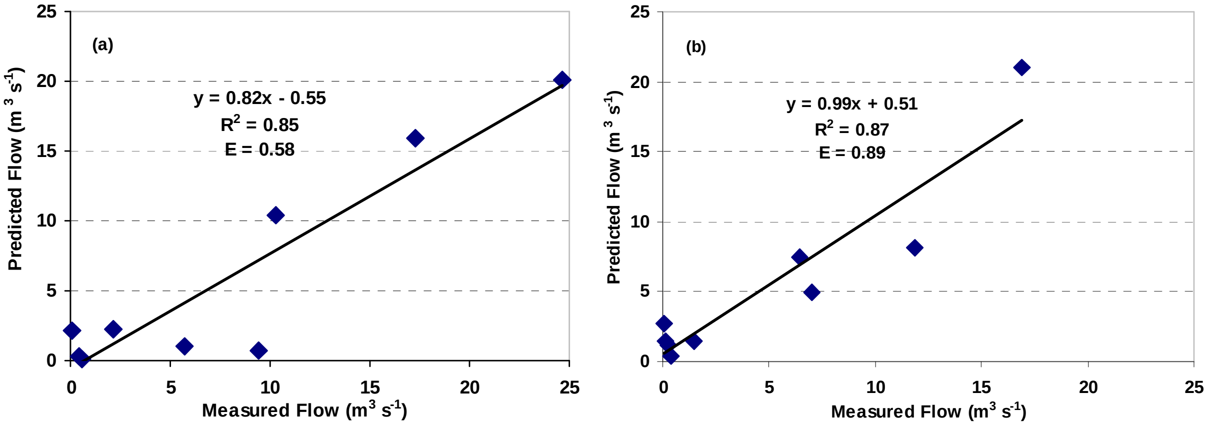

Figure 4.3. Measured daily flow model response for (a) Rock Creek, and (b) Deer Creek watersheds

4.4.2 Sediment

Calibration of the SWAT model was needed since the model over-predicted mean daily sediment yield from the watershed. The calibrated SWAT model for Rock Creek watershed reasonably predicted mean daily sediment yield of the watershed with good agreement (R^2 = 0.54 and E = 0.64) between mean daily measured and mean daily predicted sediment yield values (Fig. 4.4a). The calibrated model, when applied to the Deer Creek watershed for validation, performed very good agreement (R^2 = 0.76 and E = 0.77) to predict sediment yield between mean daily measured and mean daily predicted sediment yield values (Fig. 4.4b).

Santhi et al. (2001) calibrated and validated SWAT model in the Bosque River watershed, TX. The calibrated SWAT model showed E values of 0.69 to 0.80 for monthly sediment in their study. However, the validated model had E values of 0.23 to 0.70 for monthly sediment prediction when compared with the measured data in their study. Kirsch et al. (2002) calibrated SWAT model in the Rock River Basin watershed, WI. The calibrated SWAT model for Yahara and Mendota sub-watersheds in the Rock River Basin had Nash Sutcliffe efficiency of 0.75 for annual sediment prediction when compared with measured sediment data. They did not have enough sediment data for the model validation.

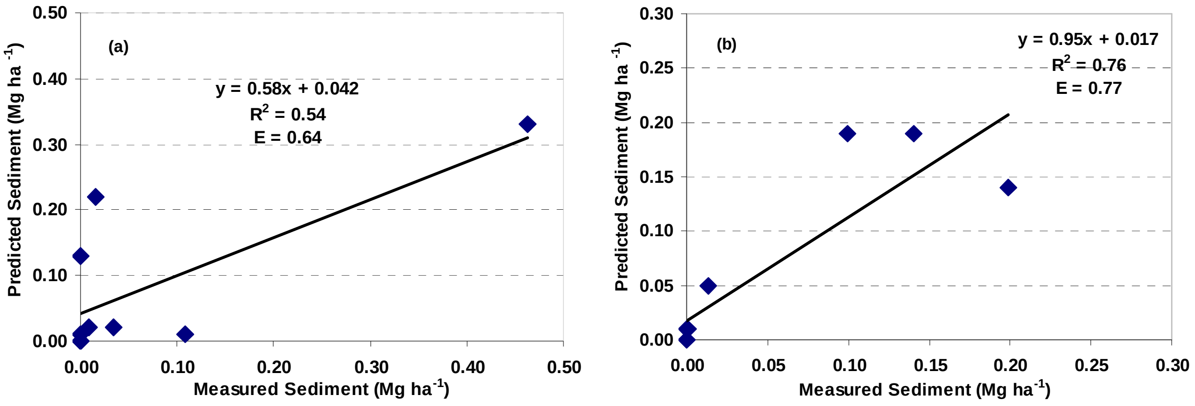

Figure 4.4. Measured daily sediment model response for (a) Rock Creek, and (b) Deer Creek watersheds

4.4.3 Nutrients

The SWAT model showed good agreement for mean daily total phosphorus prediction from the Rock Creek watershed (R^2 = 0.78 and E = 0.67) when compared between mean daily measured and mean daily predicted total phosphorus loss values (Fig. 4.5a). The SWAT model, when applied to the Deer Creek watershed for validation, predicted total phosphorus with good agreement (R^2 = 0.55 and E = 0.59) (Fig. 4.5b). The SWAT model predicted mean daily total nitrogen from the Rock Creek watershed with a poor agreement but reasonable correlation (R^2 = 0.43 and E = 0.19) (Fig. 4.6a). The SWAT model, when applied to the Deer Creek watershed for validation, predicted total nitrogen with a poor agreement but reasonable correlation (R^2 = 0.46 and E = 0.10) between mean daily measured and mean daily predicted phosphorus loss values (Fig. 4.6b).

Santhi et al. (2001) calibrated and validated SWAT model in the Bosque River watershed, TX. The calibrated SWAT model showed E values of -0.08 to 0.58 for monthly nitrogen, and 0.53 to 0.70 for monthly phosphorus when compared with the measured data. The validated model had E values of 0.43 to 0.73 for nitrogen, and 0.39 to 0.72 for phosphorus when compared with the measured data. White et al. (2004) evaluated SWAT model in the War Eagle Creek Watershed in Northwest Arkansas. The SWAT model predicted monthly total phosphorus yields with a correlation coefficient (R^2) of 0.34 in their study.

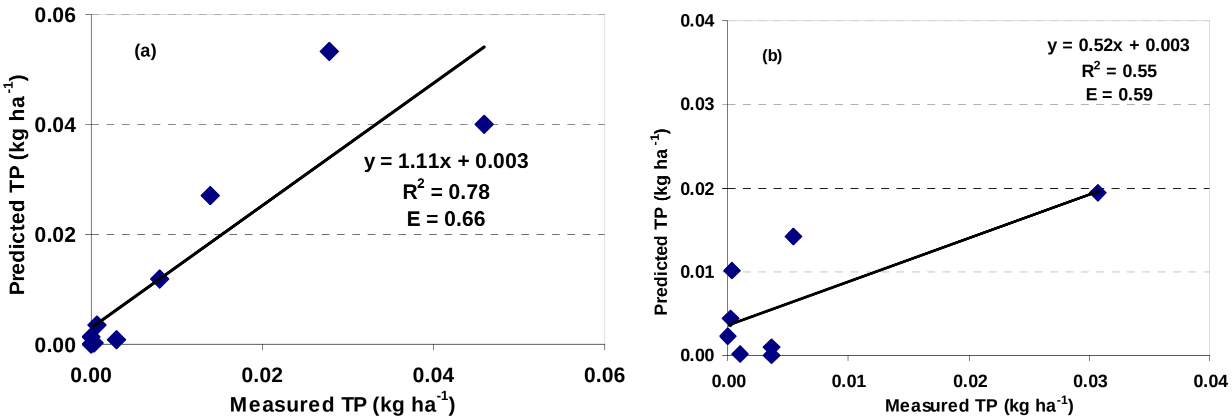

Figure 4.5. Measured daily total phosphorus (TP) model response for (a) Rock Creek, and (b) Deer Creek watersheds

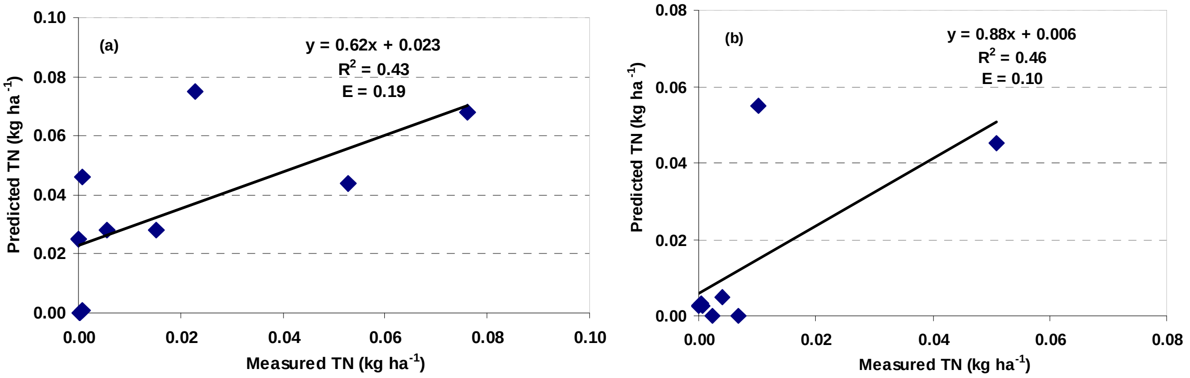

Figure 4.6. Measured daily total nitrogen (TN) model response for (a) Rock Creek, and (b) Deer Creek watersheds

4.4.4 Fecal Coliform Bacteria

The equation 4.2 converts cfu m^{-2} of bacteria in to cfu 100 mL^{-1} in the SWAT model. When bacteria source load (cfu m^{-2}) and the drainage area are fixed for a period of simulation, only variable that may change day to day is flow. When a high flow condition is observed the model tends to predict low bacteria concentration. However, due to high runoff more bacteria in solution and sorbed conditions tend to be transported to the outlet of the watershed. The equation 4.2 seems good for moderate flow condition. For very low flow condition model would predict high concentration of bacteria but measured data from the agricultural watersheds (this study) showed low bacteria concentration. Therefore, the actual number of bacteria concentration prediction in the model assumed flow based. The total number of model predicted bacteria for the entire simulation period which has flow values (> 0) were divided by the total flow of the simulation period to estimate bacteria concentration in cfu 100 mL^{-1} per m^3 s^{-1} of flow. Then model predicted each daily flow (m^3 s^{-1}) was multiplied by bacteria concentration (cfu 100 mL^{-1} per m^3 s^{-1} of flow) to estimate flow based bacteria concentration (cfu 100 mL^{-1}). Then the model predicted flow based bacteria concentration was log transformed.

The calibrated SWAT model for Rock Creek watershed determined poor agreement but reasonable correlation ($R^2 = 0.36$ and $E = 0.21$) between daily measured and daily mean predicted fecal coliform bacteria concentration (Fig. 4.7a). The calibrated model when applied to Deer Creek watershed for validation again showed poor agreement but reasonable correlation ($R^2 = 0.46$ and $E = 0.14$) between daily measured and mean daily predicted fecal bacteria concentration (Fig. 4.7b).

In a similar type of study, Baffaut and Benson (2003) used frequency analysis method to test the model simulated results using average plus or minus one standard deviation. The model simulated results were validated for up to 70% of the frequency curve.

The bacteria source input loads: % direct point loads, AUs in the feedlot, AUs in winter feeding area, stocking rate of cattle on the pastureland, numbers of failing septic systems, wildlife AUs, and flow calibration parameters made difference in the model prediction of fecal coliform bacteria concentration at the outlet of the each watershed. The fecal coliform bacteria transport was also dependent on rainfall time after grazing operation starts in the pastureland. It is obvious that surface runoff during grazing periods will have higher chance of fecal bacteria concentration reaching the outlet of the watershed as opposed to runoff outside the grazing period. Three different sources of bacteria (livestock, human, and wildlife) were modeled together in this study.

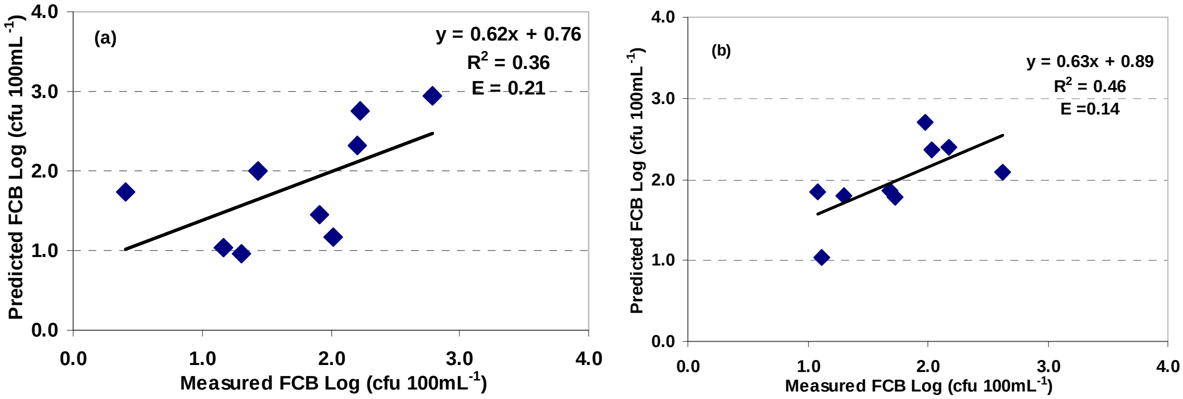

Figure 4.7. Measured fecal coliform bacteria (FCB) concentration model response for (a) Rock Creek, and (b) Deer Creek watersheds

4.5 Conclusions

This study calibrated and validated SWAT (2005) model for daily flow, sediment, nutrients, and fecal coliform bacteria concentration prediction at the watershed scale. The calibrated model results for daily flow, sediment, nutrients, and in-stream fecal bacteria concentrations compared reasonably with one year of measured data, providing confirmation of source-load characterization methods. Further detailed calibration with more extensive in-stream data are needed for more comprehensive model assessment.

The SWAT (2005) responded reasonably in predicting fecal coliform bacteria concentrations in this study. However, the model should be adjusted to address flow based bacteria concentration prediction. The bacteria transport part of the model needs especial attention to create input parameters while modeling bacteria. Further detailed calibration with more extensive in-stream data are needed for more comprehensive model assessment.

Acknowledgements

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CHAPTER 5 - SOURCE SPECIFIC FECAL BACTERIA MODELING USING SWAT MODEL

Abstract

Fecal bacteria can result in illness and death, but often the sources of contamination in water cannot be determined. Bacteria source tracking can identify non-point sources of fecal bacteria such as livestock, human and wildlife. The Soil and Water Assessment Tool (SWAT) microbial sub-model 2005, was used to evaluate source-specific fecal bacteria using three years (2004-2006) of observed modified deterministic probability of bacteria source tracking data and measured hydrologic and water quality data.

The watershed characteristics for fecal bacterial source, such as livestock, human, and wildlife, were first modeled together then with three separate combinations of source-specific bacteria concentration including livestock and human, livestock and wildlife, human and wildlife. The SWAT model was calibrated at Rock Creek sub-watershed and verified first at Deer Creek and Auburn sub-watersheds then at whole Upper Wakarusa watershed for predicting daily flow, sediment, nutrients, total fecal bacteria, and source-specific fecal bacteria. The model results showed good to very good agreement for each of the tested pollutants indicating parameters with a coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E) range from 0.52 to 0.84 for daily flow and from 0.50 to 0.87 for sediment; poor to very good agreement with R^2 and E range from 0.14 to 0.85 for total phosphorus; unsatisfactory to very good agreement with R^2 and E range from -3.55 to 0.79 for total nitrogen; unsatisfactory to good agreement with R^2 and E range from -2.2 to 0.52 for total fecal bacteria and determined generally decreased agreement for each single source of bacteria (R^2, E range from -5.03 to 0.39) potentially due to BST uncertainty and spatial variability.

5.1 Introduction

Water quality deterioration associated with point and non-point source (NPS) pollution has been a great concern for several decades. To date, about 65,000 types of impairments have been reported by the U. S. Environmental Protection Agency (US EPA, 2006) as violating different water quality standards such as drinking, swimming, fishing, etc. The top three common causes of waterbody impairments of the 303(d) listed waterbody segments after mercury include pathogens (13.2%), sediment (10.59%), and nutrients (8.76%) based on the total listed segments. These are responsible for about 21,000 impaired waters listed so far, for which about 11,114 Total Maximum Daily Load (TMDLs) have been approved. A total of 8,522 stream segments have been reported with bacteria impairments, each requiring development and implementation of a TMDL to meet the water-quality standard for bacteria in their respective states (US EPA, 2005a). The number of impaired waters, however, is expected to increase substantially as additional monitoring is performed and new and revised water quality standards are adopted.

The TMDL program, which is mandated by the Clean Water Act (33 U.S.C. §§ 1251-1387), is a watershed management process that integrates watershed planning and remediation with water quality assessment and protection (Benham et al., 2006). For the U. S. EPA to approve a TMDL, all major point and non-point sources of the offending pollutant(s) must be identified and quantified. Developing a TMDL involves a study that quantifies the pollutant contribution from each source (or source category, in the case of non-point source pollution) and determines the pollutant reduction from each source required to meet applicable state water-quality standards. Hydrologic and water-quality models are often used to identify and quantify pollutant sources so that the pollution from those sources may be reduced in order to improve water-quality standards. The watershed modeling is also directed toward Total Maximum Daily Loads (TMDL) development for waters impaired due to excessive levels of bacteria. In watershed modeling, watershed and water bodies are first assessed to identify the level of impairment and then prioritized for water quality improvement through Best Management Practices (BMPs) implementation.

A review of available information indicates that agriculture is the major contributor of NPS pollution to both the surface and groundwater (US EPA, 1994). Studies showed that livestock in agriculture is one of the major sources of bacterial pollution, although there are other environmental sources of pathogenic organisms, including humans, and wildlife.

In 2002, there were approximately 6.3 million cattle in Kansas with approximately 2.6 million in feedlots (KSA, 2004). It has been estimated that a 1000-pound cow can produce an average of 11.5 tons of manure a year at 88% water (Davis et al., 2004). Manure produced by livestock during grazing may be applied in the grazing land area, which creates a potential fecal bacteria source to runoff into a surface water system (Stoddard et al., 1998). Kansas supports a total of 6 million grazing animal-unit months, principally on Flint Hills tallgrass prairie, and the State is second only to Texas in total livestock production on native rangelands (Hickman et al., 2004).

Often the source of fecal contamination in water cannot be determined. Non-point sources, such as livestock, human and wildlife are possible sources of fecal contamination. In addition, the contribution of bacterial pollution "stored" in sediments and re-suspended during storm events is unknown. In order to adequately assess human health risks and develop watershed management plans, it is necessary to know the sources of fecal contamination.

Bacteria source tracking (BST) can identify bacteria source. Much of the impetus for developing and applying source tracking techniques came from the U.S. Environmental Protection Agency and its implementation of the TMDL concept. Since source tracking methods are effective tools for determining origins of fecal contamination of water bodies, they can be used to direct the types of best management practices needed to reduce fecal loading. Grazing operation, winter feeding, failing septic systems and wildlife fecal bacteria source loads increase the chance of fecal bacteria reaching surface water. Evaluation of the effectiveness of Best Management Practices (BMPs) is needed to address the problems. Bacteria models could be a useful tool for evaluating watersheds. However, no studies have been published using BST data in conjunction with a watershed model to calibrate the model or test model results.

5.1.1 Fecal Coliform Bacteria Sources

A fecal coliform bacterium is a facultative, anaerobic, gram negative, non-spore forming, and rod-shaped bacteria. Fecal pathogen contamination of surface waters can result in illness and death and accounts for a majority of the assessed water-quality impairments in the U.S. (US EPA, 2005a). Fecal coliform bacteria are often used as indicators of the potential presence of fecal pathogens. Waterborne disease outbreaks are defined by the Centers for Disease Control and Prevention (CDC) as incidences in which two or more than two persons have experienced an illness after ingesting drinking water or after recreational contact with water where epidemiologic evidence implicates water as the probable source of the illness. Between 1971 and 2000, there were 1,010 reported waterborne disease outbreaks, corresponding to 594,340 cases of illness (Wang, 2003). A majority of outbreaks (513; 51%) and cases of illness (505,189; 85%) were caused by pathogenic bacteria, viruses, or protozoa. Fecal bacteria excreted by humans, domestic animals, and wildlife can enter natural water sources with stormwater runoff, from inadequate sanitary facilities, and through direct deposition. Curriero et al. (2001) found that more than half the waterborne disease outbreaks in the U.S. in the past 50 years were preceded by heavy rainfall. Therefore, the concentration of fecal bacteria in the surface water have become an increasing concern because it indicates the potential to cause severe illnesses in humans, such as typhoid fever, hepatitis, cholera, dermatitis, and leptospirosis (Craun and Frost, 2002).

Large quantities of fecal coliform bacteria can be deposited with manure from heavy grazing, effluent disposal due to failing septic systems, direct deposition of manure in the stream or near the stream due to livestock access to the stream, or wildlife. The risk associated with surface water contamination by manure is, in part, a function of manure volume, site topography, hydrology, and proximity to surface waters. Continuous application of manure on the land, high rates of septic effluent disposal, particularly where application rates exceed soil assimilative capacity, increase the risks for surface and groundwater contamination. These risks may be offset by low rainfall, dryness, minimal land slope, relative isolation of the animal population, and methods of applying manure. Pathogens applied or deposited onto soil surfaces may infiltrate into the soil profile or, alternatively, may runoff to surface waters. Knowledge of redistribution and persistence of fecal coliform on agricultural land is, therefore, important in the assessment of any potential contamination of runoff emanating from these areas.

An on-site system is commonly used to treat household wastewater for houses not connected to public sewer systems. On-site systems disperse wastewater into the soil where physical, chemical and biological treatment processes remove pathogens and many of the potential chemical pollutants in sewage effluent. The high cost of centralized sewer systems and continuing urbanization/sub-urbanization are the two major reasons behind the popularity of on-site systems. The number of on-site systems is increasing every year. In the United States, 25% of the total housing units and 33% of all new development use on-site systems (U.S. EPA, 2005a).

People living in rural non-farm residences depend almost exclusively upon individual on-site systems for treatment of household wastewaters. Even within suburban and developing urban fringes, on-site systems are used extensively. On-site system densities also can be quite high in urban developing areas (Pradhan, 2004). Watershed-based bacteria models could be used to evaluate fecal bacteria sources. Parajuli et al. (2006) calibrated and validated the SWAT (2005) model, but they recommend that the model still needs to be verified for longer climatic period, different land use distributions, different watershed sizes, and using source-specific fecal bacteria data for comparison.

The majority of the Kansas population (over 70%) uses surface water for drinking water and other daily uses (KWO, 2004). Twenty two percent of the assessed stream miles in Kansas are impaired from fecal bacteria (KDHE, 2004a). Concentrations of fecal coliform bacteria in surface water could be due to land application of livestock manures, grazing operations, winter feeding operations, failing septic systems, and wildlife. Water movement and sediment erosion increase the chance of fecal bacteria reaching surface water systems, especially during high intensity rainfall events like those found in eastern Kansas during the spring and summer. Watershed-based bacteria models could be used to evaluate sources. The Soil and Water Assessment Tools (SWAT) microbial sub-model 2005 version is a useful tool for bacteria modeling, but it needs to be calibrated and verified.

The SWAT water quality model has been applied, calibrated and validated for one or more parameters such as runoff, sediment yield, and nutrient losses from watersheds at different geographic locations, conditions, and management practices (Saleh et al., 1999; Spruill et al., 2000; Santhi et al., 2001; Kirsch et al., 2002; Van Liew et al., 2003; White et al., 2004; Qi and Grunwald, 2005; White and Chaubey, 2005; Wang et al., 2006; Jha et al., 2007; Gassman et al., 2007). Limited research has been performed using the SWAT (2005) model for predicting bacteria movement.

Baffaut and Benson (2003) studied bacteria TMDLs (Total Maximum Daily Load) for the Shoal Creek watershed in southwest Missouri using SWAT (2000) model. The watershed was consisted of grassland (89%) and wooded areas (11%). The soils in the watershed were very high rock content of 30% or more in the surface. They calibrated model using daily flow, weekly water quality grab samples, and annual hay yield reported to USDA. A frequency analysis curve method was used to compare measured vs. predicted data for daily flow and fecal coliform bacteria concentration. Daily flow curve found reasonable results except for peak-flow over-predictions. The karst topography feature in the watershed contributed to high surface runoff from the watershed. While comparing model predicted values with eighteen months of weekly measured fecal coliform bacteria concentration data with average plus or minus one standard deviation, the bacteria concentration curve validated up to a 70% of the frequency curve.

Parajuli et al. (2006) calibrated (Rock Creek) and validated (Deer Creek) the SWAT model using one year (2004) of measured daily flow, total suspended solids, nutrients, and total fecal coliform bacteria concentration data. The land use patterns of these two sub-watersheds were homogeneous grassland and cropland. Additional data for these watersheds were utilized in this study and the model is further verified at Auburn watershed and whole Upper Wakarusa watershed.

5.2 Objectives

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

5.3 Materials and Methods

5.3.1 Watershed Stream Monitoring

5.3.1.1 Rock Creek Watershed

The Rock Creek watershed (Fig. 5.1) is located in Douglas and Osage Counties with an area of 75.41 km^2 in three major landuses: grassland (56%), cropland (37%), and woodland (6%). The silty-clay textured soils (SSURGO stmuid: KS0457302, KS0457325, KS0458962, KS1397302, and KS1398735) are the predominant soil types in this watershed. The model was calibrated in Rock Creek watershed.

5.3.1.2. Deer Creek Watershed

The Deer Creek watershed (Fig. 5.1) is located in Douglas and Shawnee Counties with an area 51.37 km^2 in three major landuses: grassland (51%), cropland (39%), and woodland (9%). The silty-clay textured soils (SSURGO stmuid: KS1777302, KS1777325, KS1774752, KS1773891, KS0457302, and KS0457657) are the predominant soil types in this watershed. The model was validated in Deer Creek watershed.

5.3.1.3. Auburn Watershed

The Auburn watershed (Fig. 5.1) is located in Shawnee and Wabaunsee Counties with an area of 152.42 km^2 in three major landuses: grassland (69 %), cropland (23%), and woodland (7%). The silty-clay textured soils (SSSURGO stmuid: KS1777302, KS1977302, and KS1774752) are the major predominant soil types in this watershed. The model was verified at Auburn watershed.

5.3.1.4. Upper Wakarusa Watershed

The Upper Wakarusa watershed (Fig. 5.1) is located in Douglas, Shawnee, Osage and Wabaunsee Counties with an area of 950 km^2 in three major landuses: grassland (57%), cropland

(28%), and woodland (9%). The silty-clay textured soils (SSSURGO stmuid: KS1777302, KS1977302, KS 0457302, KS 0457325, KS 1773891, and KS1774752) are the predominant soil types in this watershed. The model was verified at Upper Wakarusa watershed.

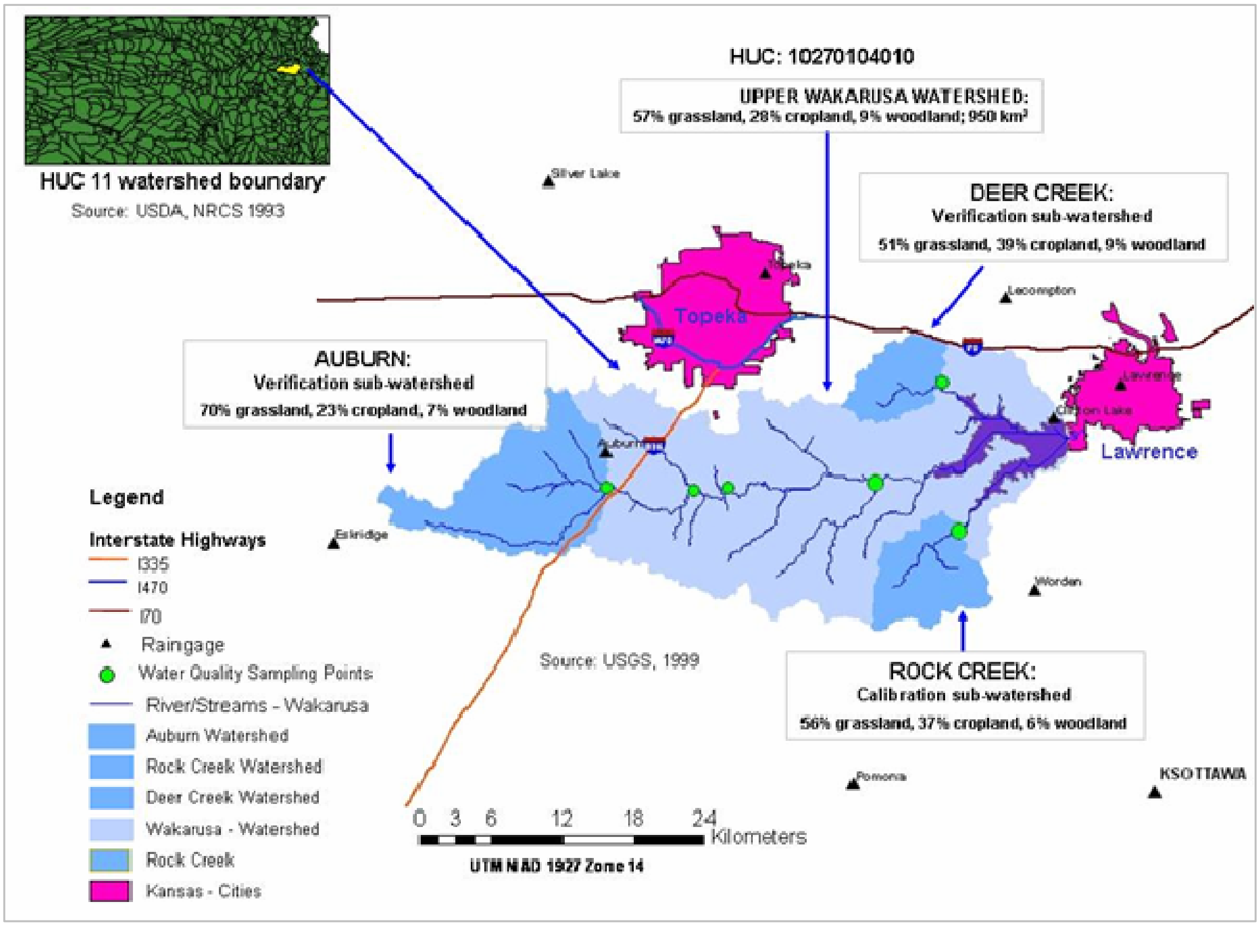

Figure 5.1. Location map of calibration and verification watersheds in NE Kansas

5.3.1.5 Stream Monitoring

Stream flow and bacteria data were collected at the outlet of the each watershed (Fig. 5.1) to validate model results. Grab samples (about 250 ml) were collected from the mid point of the flowing stream at each watershed outlet. Samples were placed immediately into an ice chest, and transferred to laboratory refrigerator within two to four hours of collection. Bacteria enumeration procedures were started within 24 hours. Serial dilution method (Clesceri et al., 1998) was applied to enumerate fecal coliform bacteria colonies. Bacterial samples typically required four serial dilutions to obtain reasonable bacteria colony counts.

Flow was calculated at the time of sample collection using Manning’s equation, as outlined by Ward and Elliot (1995). Flow depth, cross-sectional area, and channel slope were measured, and channel roughness factor was estimated based on the channel roughness characteristics, and degree of meandering (Cowan, 1956). The calculated flow was validated based on ratio of the watershed area using data from the USGS Richland gage station. The calculated flow data showed very good correlation (>90%) with the weighted area flow data. This study used the data collected from January, 2004 to April, 2006.

5.3.2 SWAT Microbial sub-model

The SWAT model utilizes geospatially referenced data to satisfy the necessary input parameters. United State Geological Survey (USGS, 1999) 7.5-minute elevation data was used to delineate the watershed boundaries and topography. Soil Survey Geographic Database (SSURGO) was utilized to create a soil database (USDA, 2005). The GAP (GAP Analysis Program) land-cover data of 2001 that depicts twenty general land-cover classes for the state of Kansas (KARS, 2001) was used. Wardlow and Egbert (2003) evaluated GAP (2001) and National Land Cover Data NLCD (1992) landuse data for the State of Kansas. The Kansas GAP provided better discrimination of most land-cover classes as compared to NLCD. Accuracy assessment found an overall accuracy of 87 percent for GAP and 81 percent for NLCD, and GAP had higher accuracies for most individual land-coverclasses. The Kansas GAP and NLCD land-cover products were found to be comparable in terms of characterizing broad scale land-cover patterns, but the Kansas GAP land-cover map appears to be more appropriate for localized applications that require detailed and accurate land-cover information.

The land-use classes were re-classified into eight classes (grazedland, non-grazedland/hay, cropland, woodland, Conservation Reserve Program, water, urban areas and quarry) based on field-verified landuse conditions (Mankin and Koelliker, 2001; Mankin et al., 2003). Parameters for each Hydrologic Response Unit (HRU) in each watershed were defined on the basis of soil, landuse, and topographic characteristics of the watershed as described in the SWAT documentation version 2005 (Neitsch et al., 2005).

The microbial survival and transport component was added to the SWAT model in 2000 and modified in 2005. The SWAT model microbial component considers the fate and transport of organisms for bacterial concentration. The microbial sub-model uses first-order kinetics, as revised by Moore et al. (1989), to model fecal bacteria die-off and re-growth. The first order decay equation, determines the quantity of bacteria that are removed or added by die-off and re-growth, as described by Sadeghi and Arnold (2002), and is given by the equation (5.1).

$$C_t = C_o \times e^{-K_{20} t \theta^{(T-20)}} \tag{5.1}$$

where,

C_t = bacteria concentration at time t, count/100mL

C_o = initial bacteria concentration, count/100mL

K_{20} = first-order die-off rate at 20°C, day^{-1}

t = exposure time, days

θ = temperature adjustment factor (TBACT in SWAT)

T = temperature, °C

5.3.3 Model Calibration Procedures

5.3.3.1 Calibration Parameters

Three widely used flow calibration parameters (Table 5.1), curve number (CN), and soil evaporation compensation factor (esco), plant uptake compensation factor (epco), were selected (Santhi et al., 2001; Saleh and Du, 2004; White and Chaubey, 2005; Choi et al., 2005). The NRCS CN is a function of the soil's permeability, land use and antecedent soil water conditions. The esco is a soil evaporation compensation factor that allows the model to modify depth distribution used to meet the soil evaporative demand to account for the effect of capillary action. As the value of esco is reduced, the model can extract more water from the lower levels to meet the evaporative demand. The epco is a plant uptake compensation factor that allows the model to meet the potential water uptake by the plant. The epco approaches 1.0, means the model allows more of the water uptake demand to be met by lower layers in the soil. As epco approaches 0.0, the model allows less variation from the original depth distribution to take place.

Two widely used sediment calibration factors, Universal Soil Loss Equation (USLE) crop cover management factor (C), and USLE support practice factor (P), were used (Table 5.1). The USLE cover and management factor, C, is defined as the ratio of soil loss from land cropped under specified conditions to the corresponding loss from clean-tilled, continuous fallow (Wischmeier and Smith, 1978). The support practice factor, P, is defined as the ratio of soil loss with a specific support practice to the corresponding loss with up-and-down slope culture. Support practices include contour tillage, stripcropping on the contour, and terrace systems. Stabilized waterways for the disposal of excess rainfall are a necessary part of each of these practices (Wischmeier and Smith, 1978).

No calibration parameters were used for phosphorus and nitrogen except turning on QUAL2E stream flow process for the model simulation and using organic nitrogen settling rate 0.10 day^{-1} (Bowie et al., 1985). Experience showed that significant amount of phosphorus and nitrogen were decreased when applying the stream flow process within the model. Bacteria Partition Coefficient in Surface Runoff (BACTKDQ) and Temperature Adjustment Factor (TBACT) model parameters were used for bacteria calibration. The less persistent fecal bacteria in manure/fertilizer were partitioned (0.90), 3 days half-life for bacteria die-off rate in solution, and 1/10 of the bacteria in solution die -off rate for bacteria die-off rate in sorbed conditions were used. The bacteria partition coefficient in the fertilizer database separates bacteria concentration in sorbed and solution phases. As the bacteria partition coefficient approaches 0, bacteria is primarily sorbed to soil particles, and as it approaches 1, bacterium is primarily in solution phase (Soupir et al., 2006). Based on 3 days half-life, bacteria die-off rate in solution phase manure was estimated 0.40 day^{-1} and one-tenth of this value, 0.04 day^{-1}, was used for bacteria adsorbed to soil particles (Baffaut and Benson, 2003).

Table 5.1. SWAT model parameters test and adjustment during calibration

Parameters	Default value	Test range value	Final value
Flow:			
Curve Number (CN)	73-83	73-83	77-79
Cropland	83	74-83	78
Pastureland	79	75-82	79
Woodland	73	73-80	77
Soil evaporation compensation factor (ESCO)	0.95	0.01 to 1.00	0.40
Sediment:			
USLE cover and management factor (C)	Crop varied	0 to 0.50	0.15
Bacteria:			
Bacteria Partition Coefficient in Surface Runoff (BACTKDQ)	175	1.75 to 262	175
Temperature Adjustment Factor (TBACT)	1.07	0.96 to 1.18	1.07

5.3.3.2 Calibration Procedure

Daily flow, sediment, total phosphorus, total nitrogen, and total fecal coliform bacteria concentration data collected from the outlet of the each watershed were used to calibrate and validate the model. Data from the Richland gaging station were used to calibrate flow. Data from the Rock Creek sampling location were used to calibrate sediment and fecal bacteria. Model predictions were statistically evaluated with the coefficient of determination (R^2) and the Nash-Sutcliffe Efficiency Index (E) between measured values and model predicted values after each parameter run. The CN parameters were continuously modified within the range of values during the calibration phase to find the local maximum value that has maximum model efficiency. The curve number range of 77-79 (77 for woodland, 78 for cropland, and 79 for grassland) determined the maximum efficiency range to use in the model. The Fig. 5.2 showed the highest model efficiency using CN value of 78.

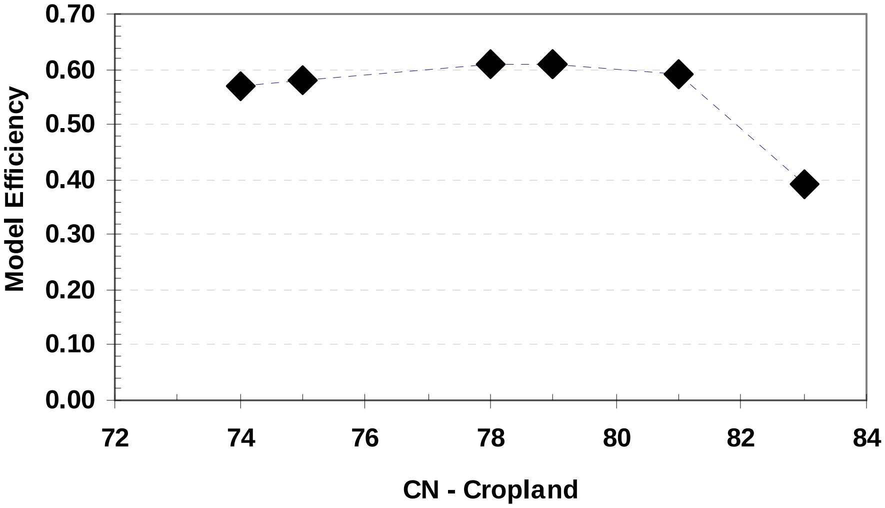

Figure 5.2. Cropland curve number (CN) and model efficiency response for daily flow for Richland gaging station.

The esco and epco parameters were tested, although the epco parameter was found not to be sensitive; therefore, epco was not used for flow calibration. The esco parameter was manually calibrated throughout the range of potential values (0.01 to 1.00). The CN calibrations utilized esco value of 0.10. Although other esco values (0.01, 0.10, and 0.25; Fig. 5.3) showed up to nine percent higher model efficiency, an esco value of 0.40 was chosen to represent what many authors feel is a physically reasonable value. Saleh and Du (2004), Choi et al. (2005), and Wang et al. (2006) all reported esco values within the range of 0.51 to 0.70. Using an esco value of 0.40 was considered to be a reasonable compromise between better model fit of lower values (0.25 and less) and better alignment with physically recommended values (0.51 and greater). The result of this compromise esco value was that it allowed less variability of soil moisture distribution with depth to meet the soil evaporative demand than would have occurred with lower esco values.

The USLE (Universal Soil Loss Equation) cover and management factor was manually calibrated for corn and soybean crop over the range from 0.05 to 0.20. The C factor of 0.15 provided the best model efficiency in this study (Fig. 5.4). The USLE practice factor was fixed to 0.10, which represents the current condition of croplands in the watersheds. After calibration, the model input parameters were not changed during validation process.

The BACTKDQ (Bacteria Partition Coefficient in Surface Runoff) factor was manually calibrated for fecal bacteria prediction over the range of 1.75 to 262. The BACTKDQ of 175, which is given as default in the model provided good model efficiency in this study (Fig. 5.5). The TBACT (Temperature Adjustment Factor) was manually calibrated over the range of 0.96 to 1.18. The TBACT of 1.07, which is given as default in the model provided reasonable model efficiency in this study (Fig. 5.6).

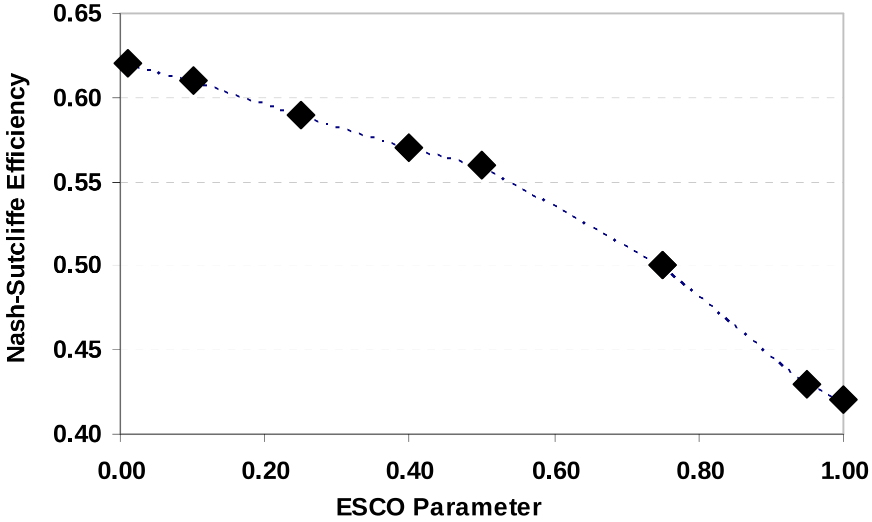

Figure 5.3. Soil evaporation compensation factor (esco) model efficiency response for daily flow for Richland gaging station

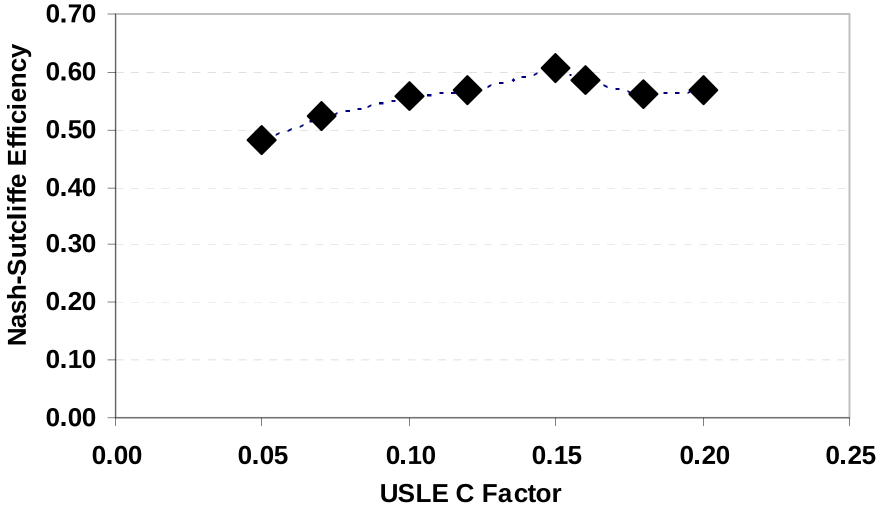

Figure 5.4. Universal soil loss equation (USLE) model efficiency response for daily sediment yield for Rock Creek

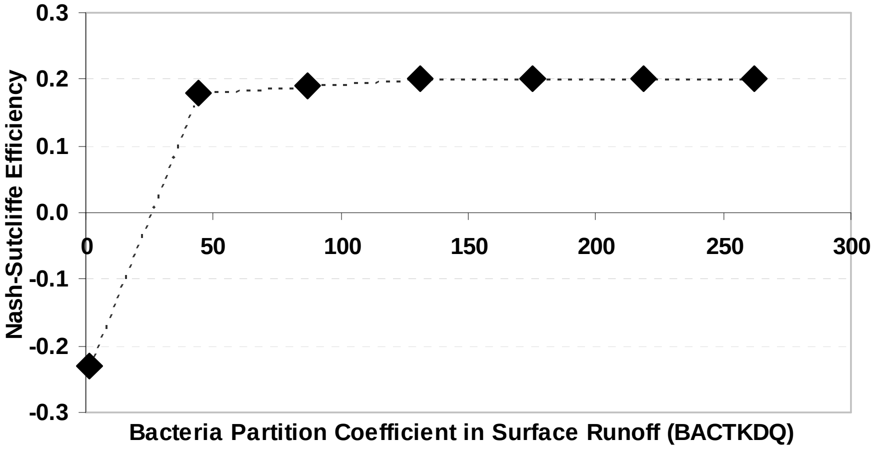

Figure 5.5. Bacteria Partition Coefficient in Surface Runoff (BACTKDQ) model efficiency response for daily fecal bacteria prediction for Rock Creek

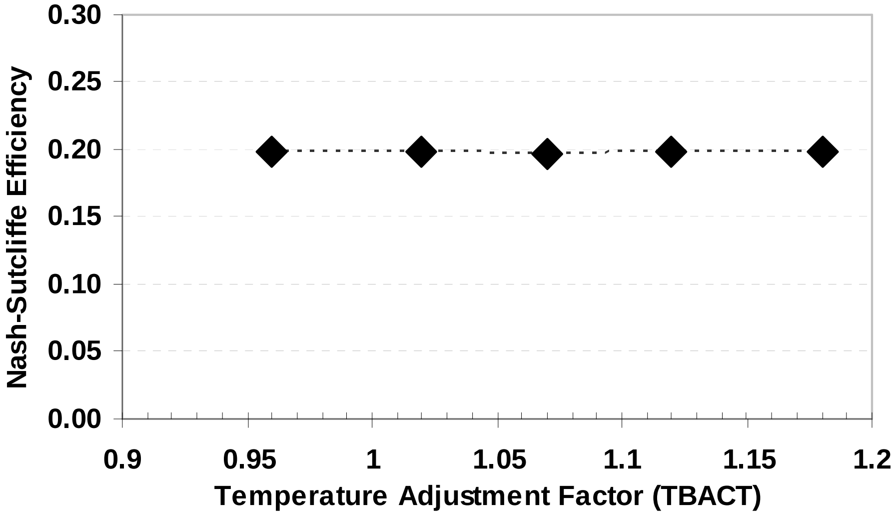

Figure 5.6. Temperature Adjustment Factor (TBACT) model efficiency response for daily fecal bacteria prediction for Rock Creek

5.3.4 Fecal Bacterial Source Characterization

Since the watershed is characterized as an agricultural rural area, there are many bacteria sources, including livestock, failing septic systems, wildlife and other domestic animals. Three bacterial sources were modeled in this study: livestock, failing septic systems, and wildlife. For source-specific bacteria modeling, first the total bacteria, then each separate source of bacteria were modeled to represent source-specific fecal bacteria. Three combinations of three bacteria sources: (a) livestock and human, (b) livestock and wildlife, and (c) human and wildlife were modeled to test the model efficiency. A modified deterministic method, which assumes multiple sources of bacteria to determine source probability of each isolate event based fraction, was used to utilize BST data. Bacteria source characteristics for livestock, human, and wildlife were utilized as described by Parajuli et al. (2007), (chapters 2, 3, and 4 of this dissertation). Data utilized in this study including estimation of each source loads, permitted livestock population, and estimated point loads for source-specific fecal bacteria are provided in the appendix A to C.

5.3.5 Management Scenarios

The pastureland, cropland, and woodland management scenarios for the Upper Wakarusa watershed, as described by Parajuli et al. (2007), were utilized in this study.

5.3.6 Bacteria Source Tracking

Bacterial source tracking (BST) is a technique using indicator organisms to determine the source of fecal bacteria. Antibiotic resistance analysis (ARA), a widely used method of determining the sources of fecal contamination, was applied to water quality samples of the Upper Wakarusa watershed. ARA involves isolation of indicator bacteria (enterococci) from different known fecal samples, as well as from unknown water samples. Isolates samples were obtained from 18 known sources and placed into three categories: human, livestock, and wildlife. Human samples were obtained from Virginia Polytechnic Institute, livestock and most of the wildlife samples except deer (Virginia polytechnic institute) were obtained from the K-State veterinary center, surrounding farms, and research and extension office in Garden City, Kansas.

Antibiotics and their concentrations were chosen following a protocol from Virginia Tech (Booth et al., 2003), which recommended to use nine antibiotics: amoxicillin (AMX) (Sigma); cephalothin (CEPH) (sigma); chlortetracycline hydrochloride (CTC) (Sigma); erythromycin (ERY) (Sigma); neomycin (NEO) (Sigma); oxytetracycline hydrochloride (OXY) (Sigma); streptomycin (STP) (Sigma); tetracycline (TET) (Sigma); and vancomycin (VAN) (Sigma). Bacteria colonies that demonstrated growth on a given antibiotic concentration were considered resistant (Marchin and Henry, 2006).

Source identification was accomplished by using the statistical method of discriminant analysis to classify each isolate extracted from water by comparing its antibiotic resistance patterns with the resistance patterns of isolates taken from known fecal samples. A database of 3,128 fecal enterococci (synonymous to streptococcus) isolates was developed from known human, livestock, and wildlife sources. Three potential sources of fecal contamination (livestock, humans, and wildlife) were tested for the Upper Wakarusa watershed. Samples collected at various stations (Rock Creek, Deer Creek, Auburn, HWY 75, Lewelling Road, Richland) during the three years study period (2004-2006) were processed using ARA. Isolates obtained from the Wakarusa River were compared against the known isolates and classified as 45% wildlife, 36% livestock, and 19% human sources (Marchin and Henry, 2006). The results indicated that wildlife and livestock sources were the major sources of fecal pollution in Upper Wakarusa watershed and the human pollution was also a significant contributor to fecal contamination. Discriminant analysis of the antibiotic resistance analysis patterns of fecal enterococci demonstrated the ability to determine pollution sources and aid in the management of watershed water quality.

The probability of the bacteria sources can be determined using standard or deterministic methods. The standard method (probabilistic method), which is commonly used to determine bacterial source probability, assumes an isolate of an event-based water sample has a single source. Each isolate is assigned to the source with greatest probability. The event-based source probability is the ratio of the number of isolates assigned a given source to the total number of isolates. A modified deterministic method assumes an isolate of an event-based water sample may have multiple sources of bacteria. The event-based probability assigned to a given source is the average of the probabilities for all isolates from that sample. This study used modified deterministic method to determine bacteria sources (Appendix D). The event-based source probability was used to approximate the event-based percentage of each source, which was used to determine the fraction of measured fecal coliform bacteria associated with each source.

5.3.7 Source Specific Bacteria Modeling

Bacteria source tracking using ARA/discriminant analysis identified three sources of fecal bacteria (livestock, human and wildlife) from the Upper Wakarusa watershed. Based on source tracking data, it appeared that certain water quality samples were dominated by certain sources of bacteria during the study, which means that on a certain day there may be a chance of bacteria source tracking of only one bacterial source such as wildlife (100%). However, the probability percentage of varied range (0 to 87) was found in this study. This study modeled first each source of fecal bacteria separately for livestock, human, and wildlife. This study also considered combination of two sources of bacteria (livestock and human, livestock and wildlife, and human and wildlife) in modeling using the combined bacteria source tracking data.

5.3.8 Weather and Hydrologic Data

Weather data, such as daily precipitation and daily ambient temperatures, were extracted from the National Climatic Data Center (NCDC), and the records maintained by Kansas State Climatologist were also utilized. The SWAT model requires daily precipitation (mm), daily maximum and minimum temperatures in (degrees Celsius), daily solar radiation (MJ m^{-2} day^{-1}), daily wind speed in (m sec^{-1}) and daily relative humidity (fraction) to run the model. The daily precipitation data were used from nine weather stations near the watershed: Clinton Lake, Auburn, Silver Lake, Overbrook, Eskridge, Pomona Lake, Lawrence, Lecompton, and Topeka. Silver Lake weather database was utilized for the daily solar radiation, daily wind speed, and daily relative humidity data (Fig 5.1). The missing data were adjusted using SWAT database simulation. The SWAT model uses Ottawa weather station (Franklin County) data for simulation, which is located about 24 km south-east from the nearest point of the watershed.

The daily precipitation data for the Rock Creek watershed was used from the Overbrook weather station (4.8 km south), for Deer Creek watershed from Lecompton (6.5 km north-east) and Topeka (12.2 km north-west) weather stations, and for Auburn watershed from Auburn (located with in watershed) and Eskridge, which is located 5 km west from the nearest point of the watershed (Table 5.2). The 2004 to 2006 average annual rainfall data measured, 939 mm for Overbrook, 955 mm for Lecompton, 1008 mm for Topeka, 935 mm for Auburn and 942 mm for Eskridge.

Table 5.2. Description of weather stations rainfall data used in the study

Station name	Year[1]	Total (mm $year^{-1}$)	Peak rainfall (mm day^{-1})	Growing season (%)[2]	No. of rainfall-events[3]	No. of potential runoff-events[4]
Overbrook	2004	1126	69	69	83	29
	2005	1180	81	77	70	23
	2006	512	53	72	44	12
Lecompton	2004	1206	83	69	102	28
	2005	1029	87	72	81	23
	2006	629	40	68	59	18
Topeka	2004	1013	62	67	91	25
	2005	1239	142	74	82	24
	2006	772	64	81	62	20
Auburn	2004	1146	114	70	93	27
	2005	1013	82	71	76	19
	2006	646	60	73	59	17
Eskridge	2004	960	67	73	85	25
	2005	1185	125	75	87	28
	2006	681	58	75	65	16

[1] Year 2006 rainfall data from Jan to Oct only

[2] % of rainfall between April to September

[3] Rainfall greater than 1 mm

[4] Rainfall events greater than 14 mm (I_a for CN_{avg} 78; SCS, 1972)

5.3.9 Statistical Analysis

The SWAT model responses were evaluated based on measured data. There were fifteen daily rainfall-runoff measured events utilized in this study from each watershed. The slope of the regression line, coefficient of determination (R^2) and Nash-Sutcliffe Efficiency Index (E) were used to evaluate measured and predicted flow, sediment, total phosphorus, total nitrogen, total fecal coliform bacteria, and source-specific fecal enterococci bacteria.

The slope of the regression measures both the direction and the magnitude of the relation between measured/observed data and predicted results. When the two variables are positively correlated, the slope will also be positive, whereas when the two variables are negatively correlated, the slope will be negative. The every unit increase in the dependent variable (x), the independent variable (y) is changed by the slope.

The R^2 estimates the combined dispersion against the single dispersion of the observed and predicted series using equation 5.2. The R^2 value indicates how consistently do measured vs. predicted values follow a best fit line. The R^2 lies between 0.0 (poor model) and 1.0 (perfect model) and describes how much of the observed dispersion is explained by the prediction. Since only the dispersion is quantified, it is one of the major drawbacks of R^2 if it is considered alone (Maidment, 1993).

$$R^2 = \left(\frac{\sum_{i=1}^{n} \left(O_i - \overline{O}\right)\left(P_i - \overline{P}\right)}{\sqrt{\sum_{i=1}^{n} \left(O_i - \overline{O}\right)^2} \sqrt{\sum_{i=1}^{n} \left(P_i - \overline{P}\right)^2}} \right)^2 \qquad (5.2)$$

where

O = observed value

P = predicted value

The over-bar denotes the mean (observed or predicted) for the entire time period of the evaluation.

The Nash-Sutcliffe Efficiency (E) indicates how consistently measured values match predicted values (Nash and Sutcliffe, 1970). The E is defined as one minus the sum of the absolute squared differences between the predicted and observed values normalized by the variance of the observed values during the period under investigation (equation 5.3). The E ranges from minus infinity (poor model) to 1.0 (perfect model). For example, if the sum of squared differences between the model predictions and the observations is as large as the variability in the observed data, then E = 0.0, and if the sum of squared differences exceeds observed variability, then E < 0.0 (i.e., the observed mean is a better predictor than P_i). Thus, a value of zero for the E indicates that the observed mean is an equally good predictor as the model, whereas negative values indicate that the observed mean is a better predictor than the model. The Nash-Sutcliffe Efficiency has been widely used to evaluate the performance of hydrologic models (Wilcox et al., 1990).

The E value may vary depending on duration of model simulations, such as yearly, monthly, or daily. Generally, model simulation for longer duration time period (such as yearly) will provide better results than short duration (such as daily).

$$E = 1 - \frac{\sum_{i=1}^{n} \left(O_i - P_i\right)^2}{\sum_{i=1}^{n} \left(O_i - \overline{O}\right)^2} \qquad (5.3)$$

where

O = observed value

P = predicted value

The over-bar denotes the mean (observed or predicted) for the entire time period of the evaluation.

As similar to Moriasi et al. (2007) the model efficiencies were classified as excellent ($E \geq 0.90$), very good ($E = 0.75$ to 0.89), good ($E = 0.50$ to 0.74), fair ($E = 0.25$ to 0.49), poor (0 to 0.24), and unsatisfactory (< 0).

5.4 Results and Discussion

SWAT simulations of daily flow, total suspended solids, total phosphorus, total nitrogen, total fecal bacteria and source-specific fecal bacteria reasonably matched measured values during the model calibration and verification (Table 5.2).

5.4.1 Flow

The calibrated SWAT model for Rock Creek watershed predicted mean daily flow of the watershed with a very good agreement ($R^2 = 0.84$ and $E = 0.83$) when compared with mean daily measured flow values (Fig. 5.7a). The calibrated model, when verified at Deer Creek and Auburn watersheds showed very good agreement with $R^2 = 0.83$ and $E = 0.82$ for Deer Creek (Fig. 5.7b) and $R^2 = 0.69$ and $E = 0.76$ for Auburn (Fig. 5.7c) between mean daily measured and mean daily predicted flow values. Rock Creek and Deer Creek simulations resulted in equally good agreement, probably because both sub-watersheds were similar in size, climate and landuse characteristics. The model prediction accuracy slightly decreased when verified at Auburn watershed. The watershed size of Auburn is about twice that of Deer Creek and three times greater than Rock Creek. The watershed had more grassland areas than in Rock Creek and Deer Creek. Therefore, small decrease in the model accuracy was anticipated. The flow prediction was consistently reasonable the model was applied to the whole Upper Wakarusa watershed (Fig. 5.8a to 5.8e). However, slight decrease in the coefficient of determination, model efficiency and slope were noticed because of the greater spatial variability from using a greater number of weather stations and spatial averaging from lumping landuse and soil characteristics. For example, when the SWAT model was applied to the Deer Creek watershed only, the model determined R^2 of 0.83, E of 0.82, and slope of 0.98. However, when the model was applied at the whole Upper Wakarusa watershed, model determined R^2 of 0.52, E of 0.58, and slope of 0.65 for the outlet of the Deer Creek sub-watershed.

Watershed models are used to represent watershed landscape processes that exhibit spatial and temporal heterogeneity. Watershed models describe a relatively large watershed area by spatially designating land areas into hydrologically connected units with each having its own characteristics that affect flow and water quality. Watershed models generally provide some ability for the user to specify spatial representation within the watershed in the form of cells, sub-basins, or some other form of spatial unit (Grayson and Blöschl, 2000). Therefore, it is often to the user's discretion how the watershed is divided spatially. The manner in which a watershed is designated into unique units is important in modeling because this generally is the smallest spatial unit for which characteristics can be entered and for which predicted outputs can be simulated. Hence, how the user chooses to delineate a watershed into smaller units will influence the ability of the model to mimic the natural system and predict representative output (Grayson and Blöschl, 2000; Lopes and Canfield, 2004).

Very small differences due to sub-basin delineation on flow (up to 10%) were reported by previous studies (Bingner et al., 1997; FitzHugh and Mackay, 2000; Jha et al., 2004; White and Chaubey, 2004). They evaluated a given model in a single watershed by changing numbers of sub-basins with in the watershed. They did not discuss the hydrologic inputs especially rainfall data. The SWAT model assigns the nearest weather station data to each sub-basin. The change in the size of watershed basins may change in assigning weather stations by SWAT model when a watershed is surrounded by numbers of weather stations, which is common in the field conditions of the most of the agricultural watersheds in the country. The daily rainfall amount is spatially highly variable.

This study determined more difference (up to 32% on average) on flow when comparing results of Deer Creek watershed with whole Upper Wakarusa watershed. This study used separate SWAT models for Deer Creek watershed and Upper Wakarusa watershed. The Deer Creek watershed used Lecompton and Topeka weather station rainfall data, which are about 22 km apart. The Deer Creek watershed had 28 sub-basins in which 84% of the sub-basins used Lecompton weather station rainfall data, whereas 16% used Topeka weather station rainfall data.

The whole Upper Wakarusa watershed had 53 sub-basins in which only four represented Deer Creek watershed. The whole Upper Wakarusa watershed assigned three sub-basins to use weather data from the Lecompton weather station whereas only one sub-basin for the Topeka weather station. Some rainfall events that impacted flow included 6/18/04, 8/24/04, and 6/3/04 that each averaged about 38% daily rainfall amount difference between two weather station's rainfall data.

Table 5.3. Statistics of the daily parameters as determined for the model calibrated and verified watersheds

Parameters	Calibration watershed	Verification sub-watersheds		Verification at multiple points of Upper Wakarusa watershed				
	Rock Creek	Deer Creek	Auburn	*Auburn*	*HWY 75*	*Lewelling Rd*	*Richland*	*Deer Creek*
Runoff								
Slope	0.76	0.98	0.58	0.84	1.24	1.04	1.00	0.65
R^2	0.84	0.83	0.69	0.75	0.90	0.73	0.81	0.52
E	0.83	0.82	0.76	0.76	0.76	0.67	0.79	0.58
Sediment Yield								
Slope	0.43	0.97	0.75	0.36	0.95	1.00	1.05	0.56
R^2	0.63	0.76	0.76	0.50	0.65	0.76	0.75	0.60
E	0.61	0.74	0.87	0.55	0.54	0.64	0.71	0.68
Total Phosphorus								
Slope	0.73	0.51	0.70	0.77	1.05	0.97	0.21	1.33
R^2	0.85	0.26	0.33	0.55	0.62	0.61	0.45	0.72
E	0.80	0.14	0.23	0.59	0.47	0.46	0.34	0.18
Total Nitrogen								
Slope	0.40	1.77	1.18	1.09	1.16	1.00	0.35	1.14
R^2	0.68	0.75	0.35	0.21	0.31	0.52	0.20	0.56
E	0.58	0.79	-1.92	-3.55	-1.42	0.18	0.12	0.19
Total FCB conc.[1]								
Slope	0.39	0.63	0.80	0.68	0.55	0.55	0.43	0.47
R^2	0.42	0.41	0.36	0.40	0.37	0.42	0.41	0.52
E	0.20	0.31	-2.20	0.38	0.27	0.28	0.24	0.29

[1] Total fecal coliform bacteria concentration

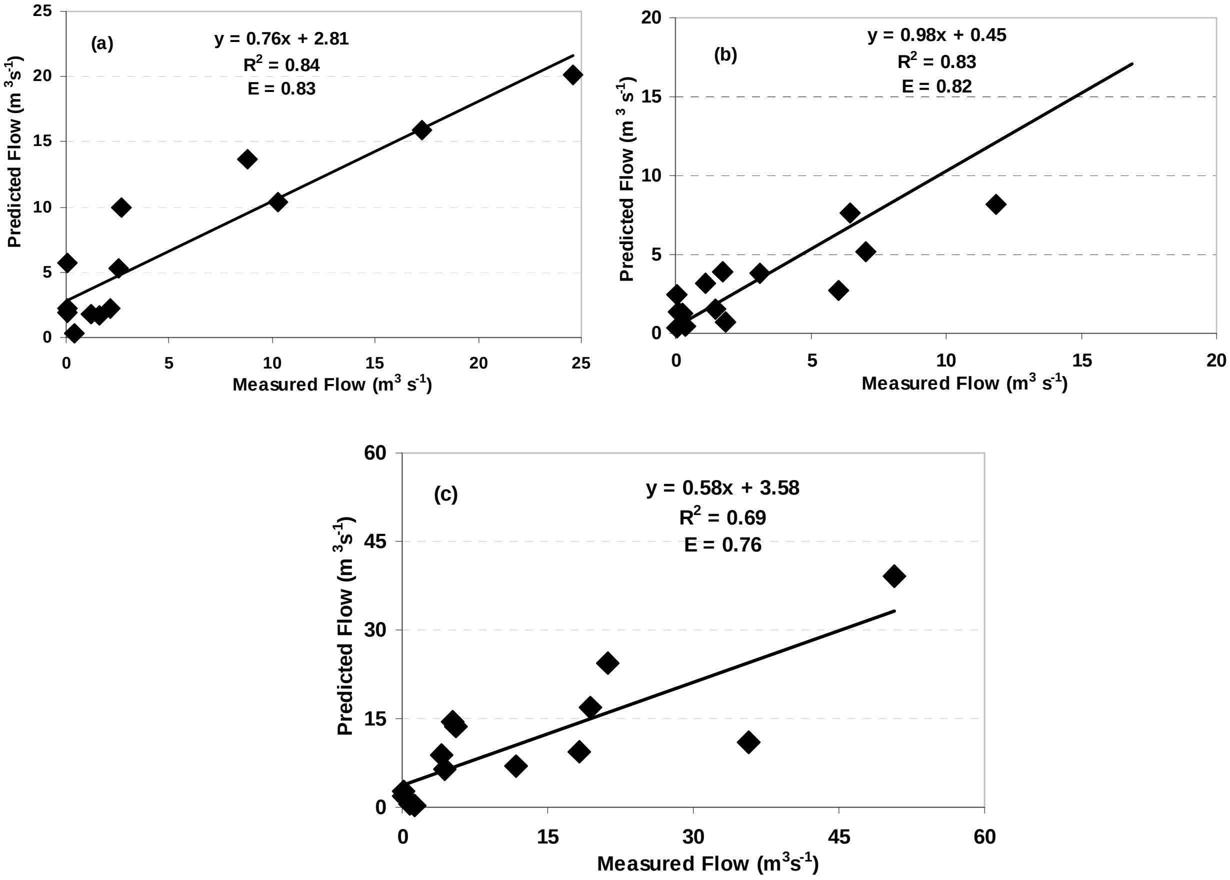

Figure 5.7. Measured daily flow model response for (a) Rock Creek, (b) Deer Creek, and (c) Auburn watersheds

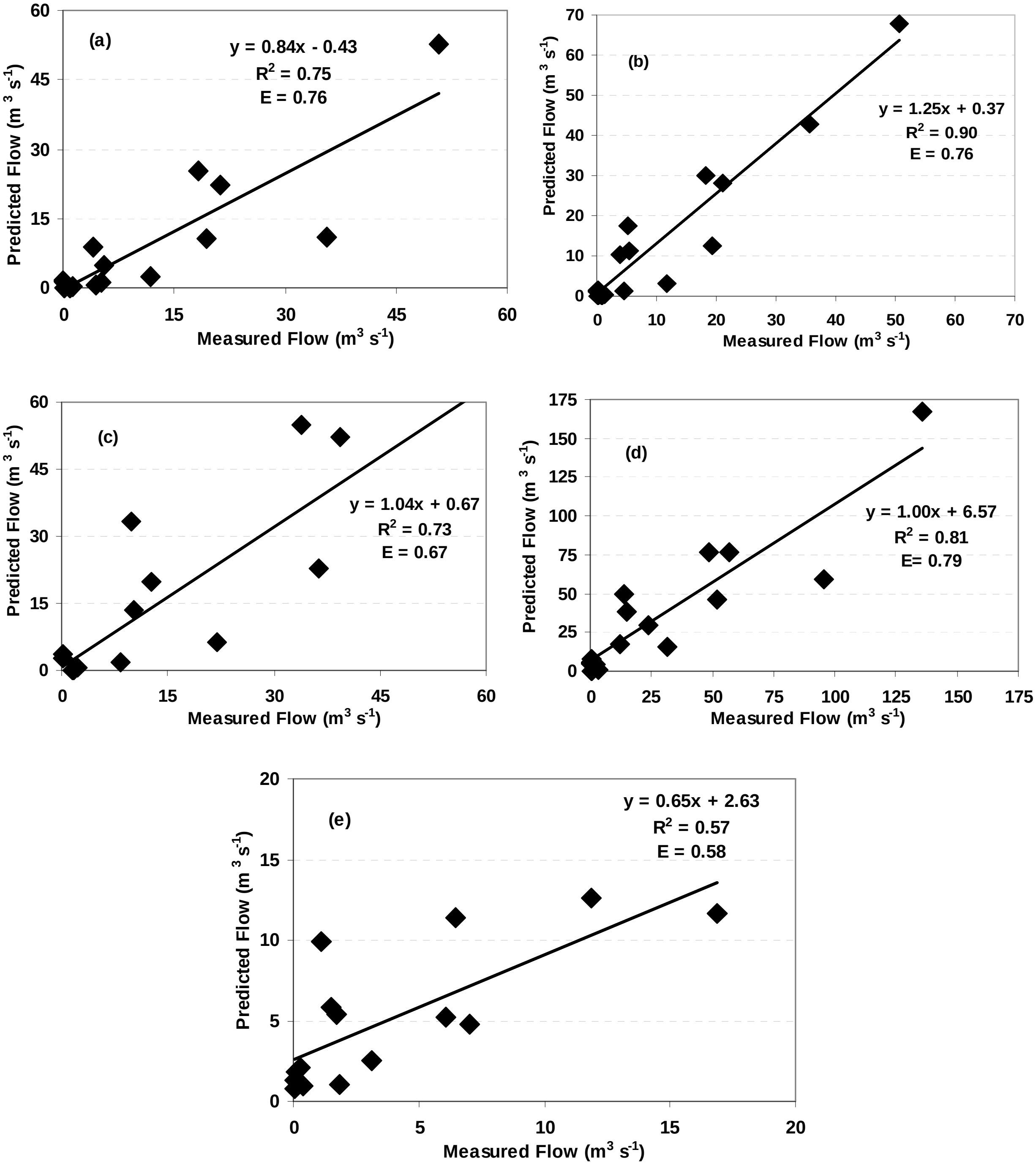

Figure 5.8. Measured daily flow model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

5.4.2 Sediment

The calibrated SWAT model for Rock Creek watershed determined good agreement for sediment (R^2 = 0.63 and E = 0.61) between daily measured and daily mean predicted sediment. When the model was verified at Deer Creek and Auburn watersheds, the model showed good to very good agreement (R^2 = 0.76, E = 0.74 for Deer Creek and R^2 = 0.76, E = 0. 87 for Auburn) between mean daily measured and mean daily predicted flow values (Table 5.2). Model showed better coefficient of determination and model efficiencies at both verified watersheds than at model calibrated watershed for sediment prediction.

Although, sediment component of the model is more sensitive with the spatial variations of the watershed, the SWAT model predicted sediment reasonably at different outlets of the Upper Wakarusa watershed. However, slight decreases in the coefficient of determination, model efficiency and slope were noticed because of the greater spatial variability from using a greater number of weather stations and spatial averaging from lumping landuse and soil characteristics. For example, when applied model at the Deer Creek sub-watershed only, the model determined R^2 of 0.76, E of 0.74 and slope 0.97. However, when the model applied at the whole Upper Wakarusa watershed, model determined R^2 of 0.60, E of 0.68, and slope of 0.56 for the outlet of the Deer Creek sub-watershed. These results are similar to previous studies that indicated minimal influence of sub-basin delineation on flow and significant influence of sub-basin delineation on sediment yield (Bingner et al., 1997; FitzHugh and Mackay, 2000; Jha et al., 2004).

Bingner et al. (1997) evaluated SWAT model to predict annual sediment yield from Goodwin Creek watershed in northern Mississippi. A varied range (23% to 56%) of the annual sediment yield prediction was determined from different level of watershed sub-divisions. The topographic parameters selected to describe sub-watersheds play an important part in the determination of sediment yield. As sub-watershed size varies the sub-watershed slope and slope length can change. Slope and slope length parameters are used in the calculation of the USLE topographic factor (LS-factor) and, thus, can affect sediment yield through the use of MUSLE in SWAT. This study determined difference in both sediment and flow due to variation in rainfall input to the model (Fig. 5.9a to 5.9c and 5.10a to 5.10e).

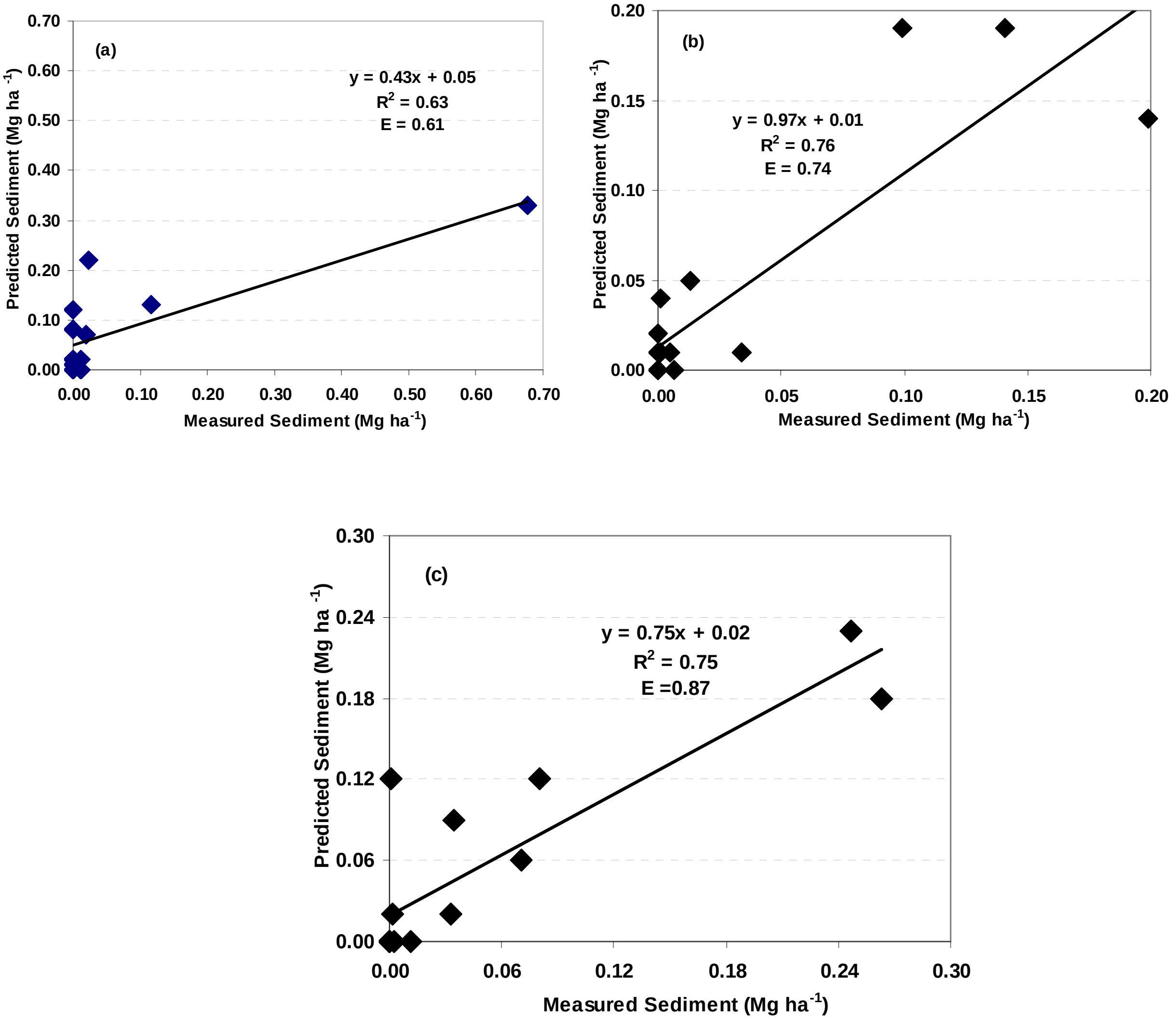

Figure 5.9. Measured daily sediment model response for (a) Rock Creek, (b) Deer Creek, and (c) Auburn watersheds

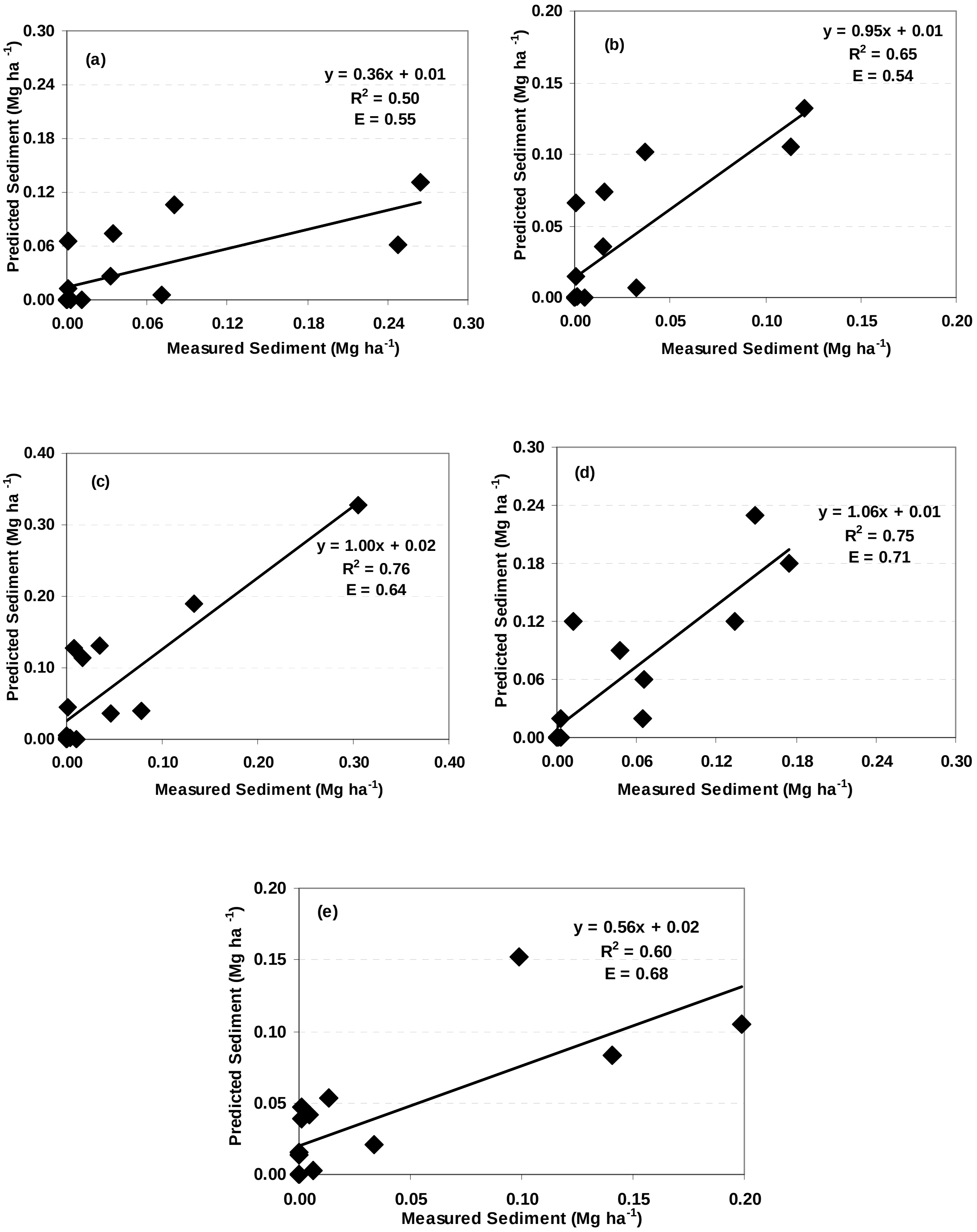

Figure 5.10. Measured daily sediment model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

5.4.3 Total Phosphorus

The un-calibrated SWAT model predicted mean daily total phosphorus prediction from the Rock Creek watershed (Fig. 5.11a) with very good agreement ($R^2 = 0.85$ and $E = 0.80$) when compared with the daily measured phosphorus loss values (Table 5.3). The un-calibrated model, when applied to the Deer Creek and Auburn watersheds for verification, predicted total phosphorus (Fig. 5.11b to 5.11c) with poor agreement but reasonable correlation ($R^2 = 0.26$ and $E = 0.14$ for Deer Creek and $R^2 = 0.33$ and $E = 0.23$ for Auburn). The model over-predicted total phosphorus from the verified watersheds. Although, phosphorus component of the model is more sensitive with the spatial variations of the watershed as similar to sediment, model predicted total phosphorus loss had poor to good agreement but reasonable correlation (Fig. 5.12a to 5.12e) at different outlets of the Upper Wakarusa watershed (R^2 and E values range from 0.18 to 0.72).

Previous studies also determined similar results. Santhi et al. (2001) calibrated and validated SWAT model in the Bosque River watershed, TX. The calibrated SWAT model showed E values of 0.53 to 0.70 for monthly phosphorus when compared with the measured data. The validated model had E values of 0.39 to 0.72 for phosphorus when compared with the measured data. White et al. (2004) evaluated SWAT model in the War Eagle Creek watershed in Northwest Arkansas. The SWAT model predicted monthly total phosphorus yields with a coefficient of determination (R^2) of 0.34 in their study. Saleh and Du (2004) calibrated and validated SWAT model to the Upper North Bosque watershed, TX. The watershed was 98% rural with the primary land uses being rangeland (43%) and forage fields (23%). The SWAT model results showed E values of 0.01 for daily total phosphorus calibration and 0.59 for daily total phosphorus verification when compared with the measured data among sampling sites within the studied watershed.

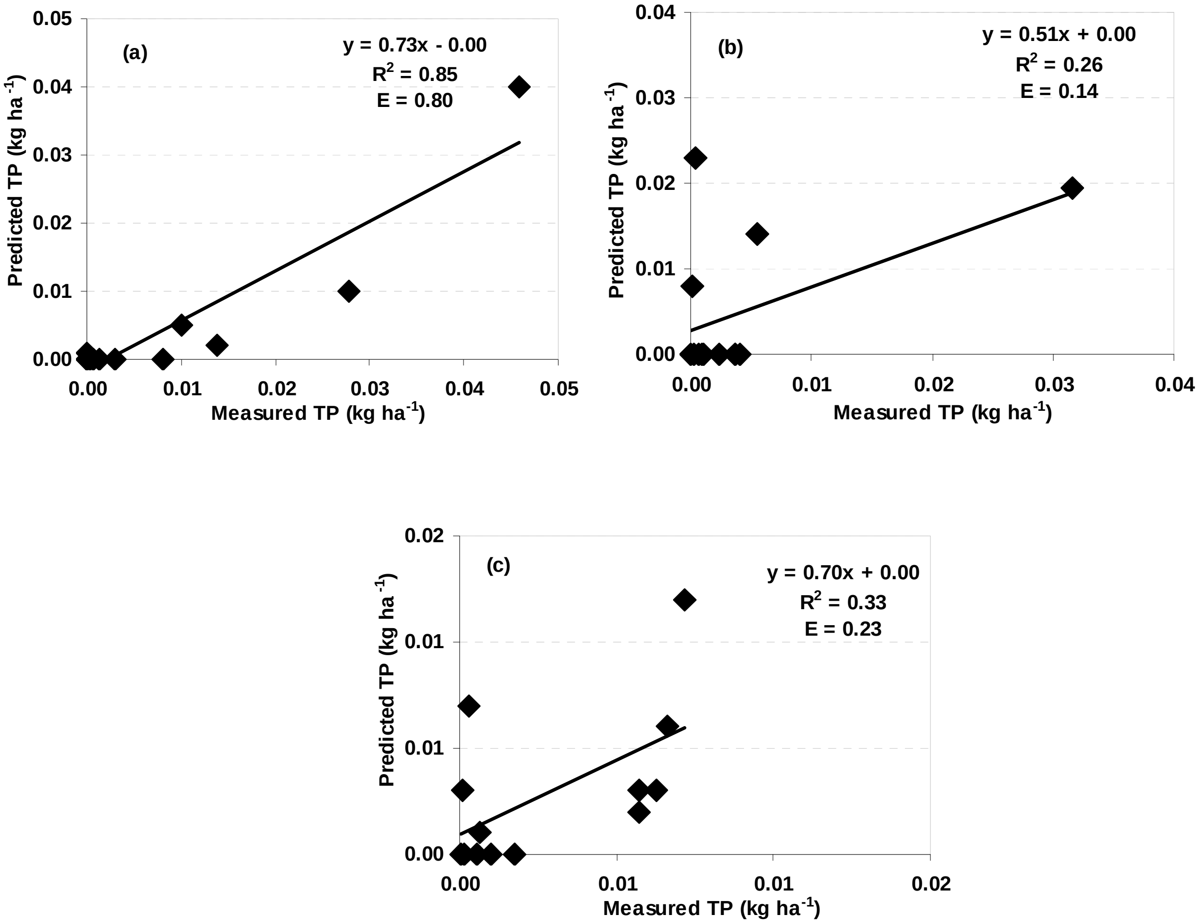

Figure 5.11. Measured daily total phosphorus model response for (a) Rock Creek, (b) Deer Creek, and (c) Auburn watersheds

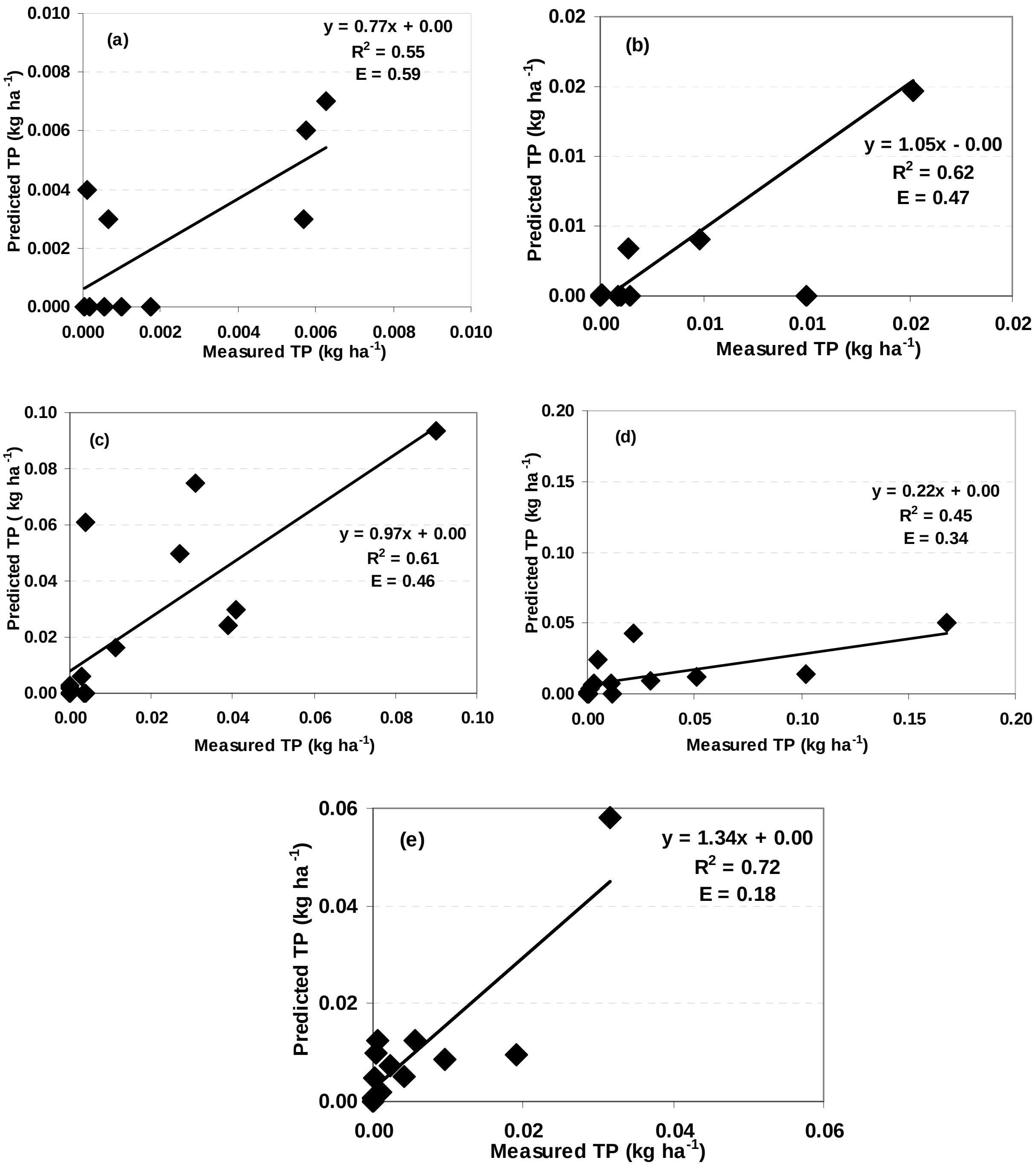

Figure 5.12. Measured daily phosphorus model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

5.4.4 Total Nitrogen

The un-calibrated SWAT model predicted mean daily total nitrogen from the Rock Creek watershed (Fig. 5.13a) with good agreement (R^2 = 0.68 and E = 0.58) when compared with the daily measured nitrogen loss values (Table 5.3). The un-calibrated model, when applied to the Deer Creek and Auburn watershed for verification, predicted total nitrogen (Fig. 5.13b to 5.13c) with unsatisfactory to very good agreement but reasonable correlation (R^2 = 0.75 and E = 0.79 for Deer Creek, R^2 = 0.35 and E = -1.02 for Auburn) when compared with the daily measured nitrogen loss values. Although model efficiency at Auburn was determined negative, the slope of the model predicted values was reasonable (1.18). Although, the nitrogen component of the model is more sensitive to spatial variations of the watershed as similar to sediment, model predicted (Fig. 5.14a to 5.14e) most of the total nitrogen loss with unsatisfactory to good agreement at different outlets of the Upper Wakarusa watershed (R^2 and E values range from -3.55 to 0.56). The model over-predicted total nitrogen at Auburn and Hwy 75 sampling points but the slope of the model-predicted values were reasonable (1.09 for auburn and 1.16 for Hwy 75).

Previous studies determined similar results. Santhi et al. (2001) calibrated and validated SWAT model in the Bosque River watershed, TX. The calibrated SWAT model showed E values of -0.08 to 0.58 for monthly nitrogen when compared with the measured data. The validated model had E values of 0.43 to 0.73 for monthly nitrogen when compared with the measured data. Saleh and Du (2004) calibrated and validated SWAT model to the Upper North Bosque watershed, TX. The SWAT model predicted results showed E values of 0.09 for daily total nitrogen calibration and 0.65 for daily total nitrogen verification when compared with the measured data among sampling sites within the studied watershed.

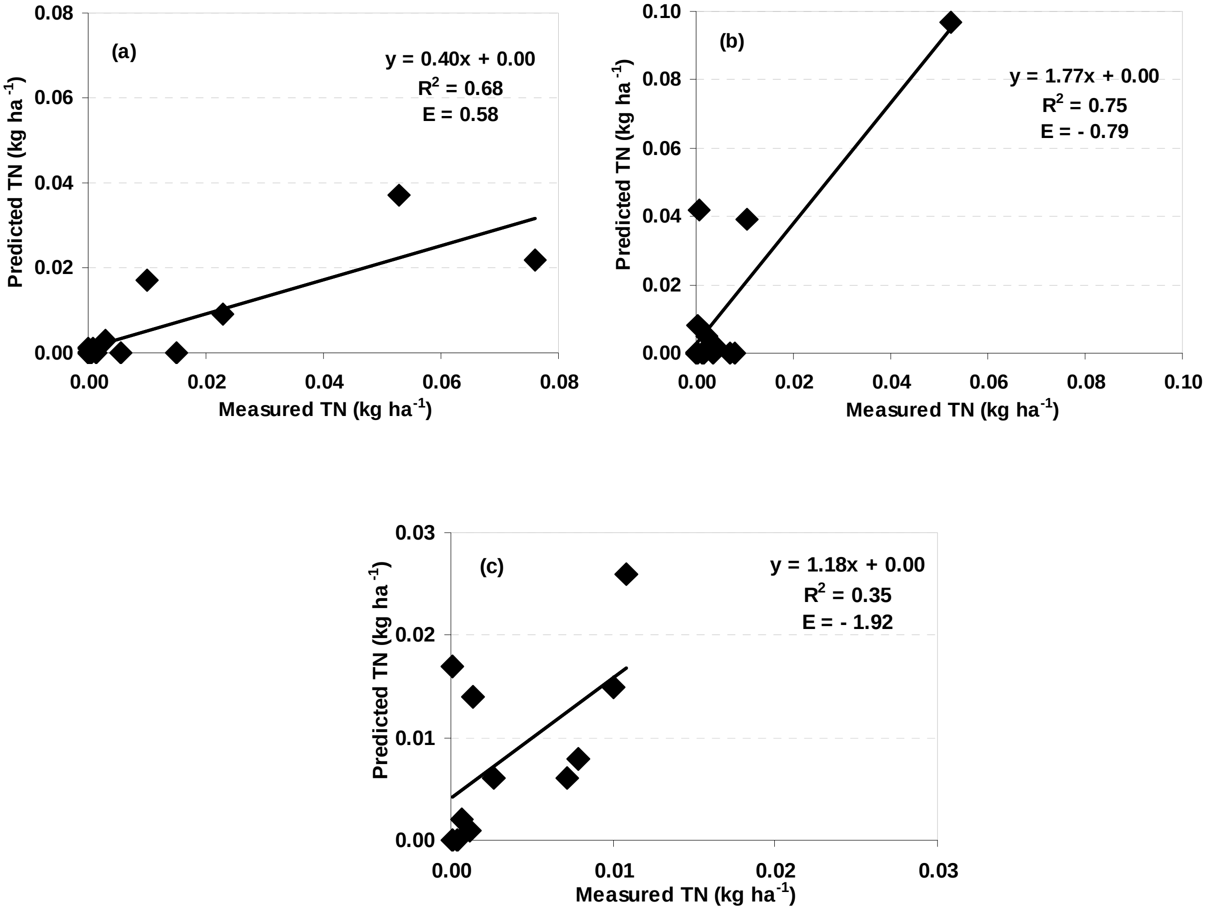

Figure 5.13. Measured daily total nitrogen model response for (a) Rock Creek, (b) Deer Creek, and (c) Auburn watersheds

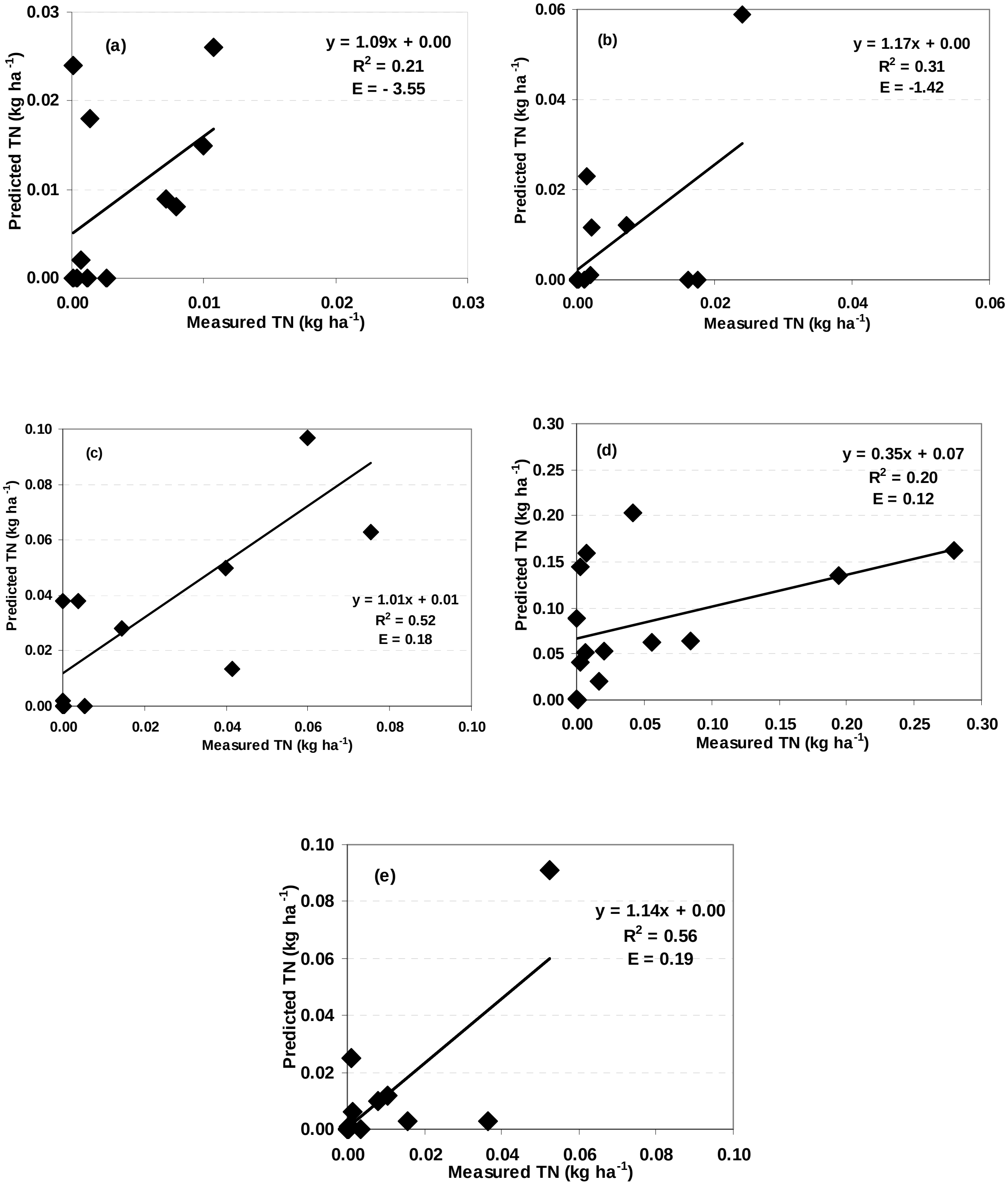

Figure 5.14. Measured daily total nitrogen model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

5.4.5 Fecal Coliform Bacteria

The calibrated SWAT model for Rock Creek watershed predicted fecal coliform bacteria concentration (Fig. 5.15a) with a poor agreement but reasonable correlation (R^2 = 0.42 and E = 0.20) when compared with the daily measured fecal coliform bacteria concentration. The SWAT model showed unsatisfactory to fair agreement but reasonable correlation between daily measured and mean daily predicted fecal coliform bacteria concentration (Fig. 5.15b to 5.15c) when verified at Deer Creek and Auburn watersheds (R^2 = 0.41 and E = 0.31 for Deer Creek; R^2 = 0.36 and E = -2.2 for Auburn). Although model results showed negative model efficiency for the Auburn watershed, the slope of the model-predicted values was reasonable (0.80). Although bacteria prediction of the model is the least-tested of the parameters studied, the SWAT model predicted fecal coliform bacteria concentration (Fig. 5.16a to 5.16e) from the various outlets of the Upper Wakarusa watershed with poor to good agreement (R^2 and E values range from 0.24 to 0.52).

Applying model at the Upper Wakarusa watershed may have given more residence time to bacteria die-off and less initial bacteria concentration due to stream processes. The point load input in the model had more contribution than non-point load inputs of total bacteria transported from the each outlets of the watershed. In a similar type of study, Baffaut and Benson (2003) used frequency analysis method to test the model simulated results using average plus or minus one standard deviation. The model simulated results were verified for up to 70% of the frequency curve.

Uncertainty is defined as the estimated amount by which an observed or calculated value may depart from the true value (Lepedes, 1978). Modeling fecal bacteria may have one of the highest possible errors and less confidence in the current modeling as compared to surface hydrology, sediment and nutrients (Novotny, 2003). This study has utilized the best available DEM, landuse, soils, and climatic data as described in the chapter 3 and 4 of this dissertation. In addition, sensitivity analyses were accomplished (chapter 2 and 3), and the SWAT model was calibrated and validated (chapter 4). However, potential uncertainty in the model results may be existed due to GIS data inputs. The GIS-integrated modeling frameworks have been widely used in water quality assessment, which greatly benefit in pre-processing of input data, model run, post-processing of model outputs and visualization. However, with the excitement of the technology and its convenience, users may overlook factors contributing to the uncertainty of model predictions that are introduced by these techniques (Shirmohammadi et al., 2006).

The potential sources of errors may come from the spatial data used in generating model inputs, including digital elevation models (DEMs), land use data, soils data, and weather data.

Climatic data are required inputs for almost all hydrologic and water quality models. Precipitation is one of the most critical input characteristics to any hydrologic simulation, potential errors due to climatic data can have significant impact on the accuracy of the model results. The climatic data may include precipitation, and air temperatures, which can all exhibit considerable variability based on measurement methods. Precipitation data are frequently collected by point measurements such as using raingages, which typically have an associated error of up to 5%, (Shirmohamadi et al., 2006).

The discussion about uncertainty is especially important in water quality modeling because models are increasingly used to guide decisions regarding water resource policy, management, and regulation (Beck, 1987; Sharpley et al., 2002). It is important that decision makers appreciate the uncertainty in measured water quality data and its effect on model output. The adequate understanding on uncertainty of measured runoff water quality data is required within the scientific community for water quality management.

Harmel et al. (2006) examined the cumulative probable uncertainty in measured streamflow, sediment, and nutrient data using error propagation method. They examined best case, typical, and worst case “data quality” scenarios. The averaged across all constituents, the calculated cumulative probable uncertainty (±%) contributed under typical scenarios ranged from 6% to 19% for streamflow measurement, from 4% to 48% for water quality sample collection, from 2% to 16% for sample preservation/storage, and from 5% to 21% for laboratory analysis. Under typical conditions, errors in storm loads ranged from 8% to 104% for dissolved nutrients, from 8% to 110% for TN and TP, and from 7% to 53% for sediment. Results indicated that uncertainty can increase substantially under poor measurement conditions and limited quality control effort. Although they did not do potential error measurement in bacteria concentration, the potential uncertainty particularly in the measurement of streamflow and sediment could largely effect in the model prediction of bacteria concentration.

Benham et al. (2006) recommended that a substantial additional research needed to improve the methods and models used to develop bacteria-impairment water quality assessment. Regardless of the tool or method used to develop to assess the water quality, accurate characterization of bacteria sources and load quantification was needed. Despite large uncertainty for bacteria modeling, this study demonstrated improved source characterization needed to better estimate animal populations, fecal production, and application methods to come up with reasonable results.

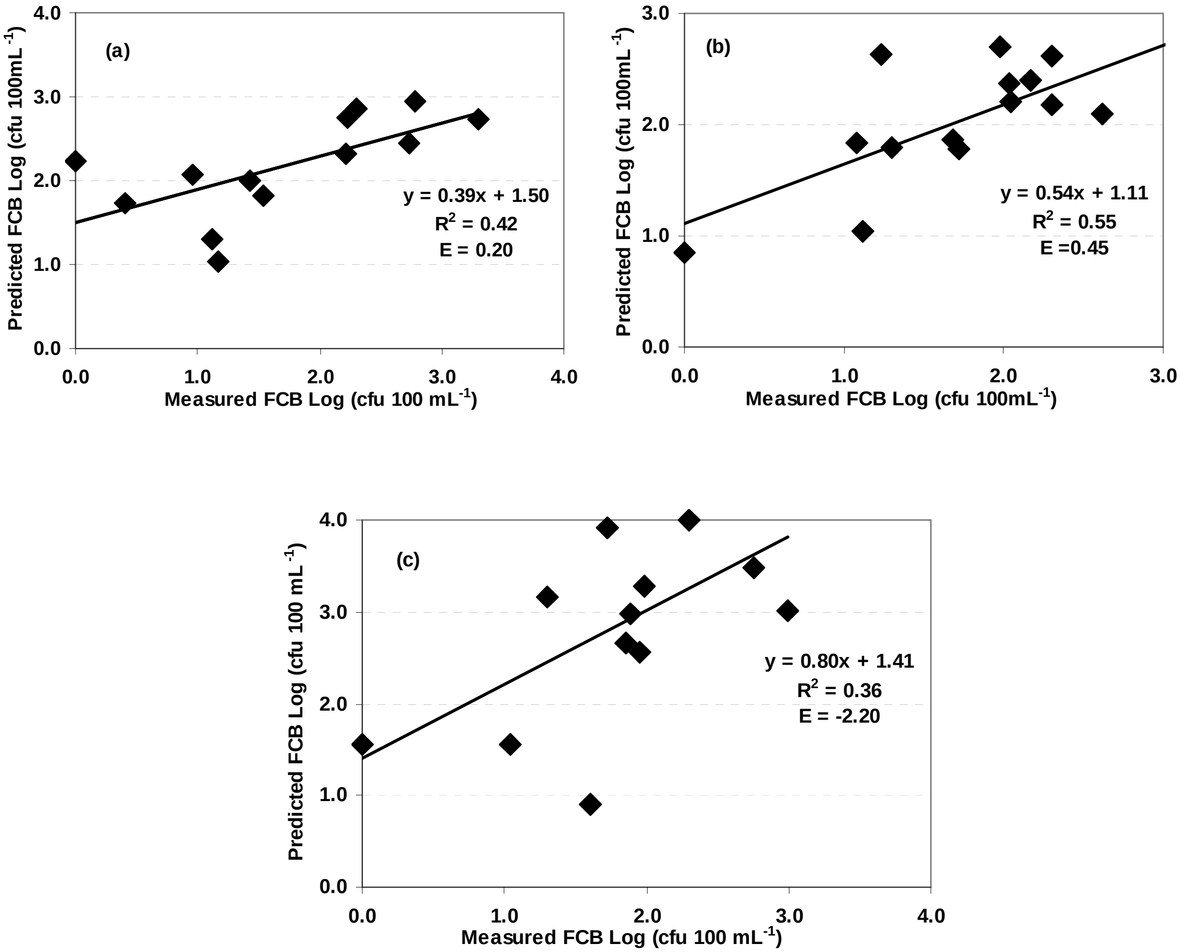

Figure 5.15. Measured daily total fecal coliform bacteria concentration model response for (a) Rock Creek, (b) Deer Creek, and (c) Auburn watersheds

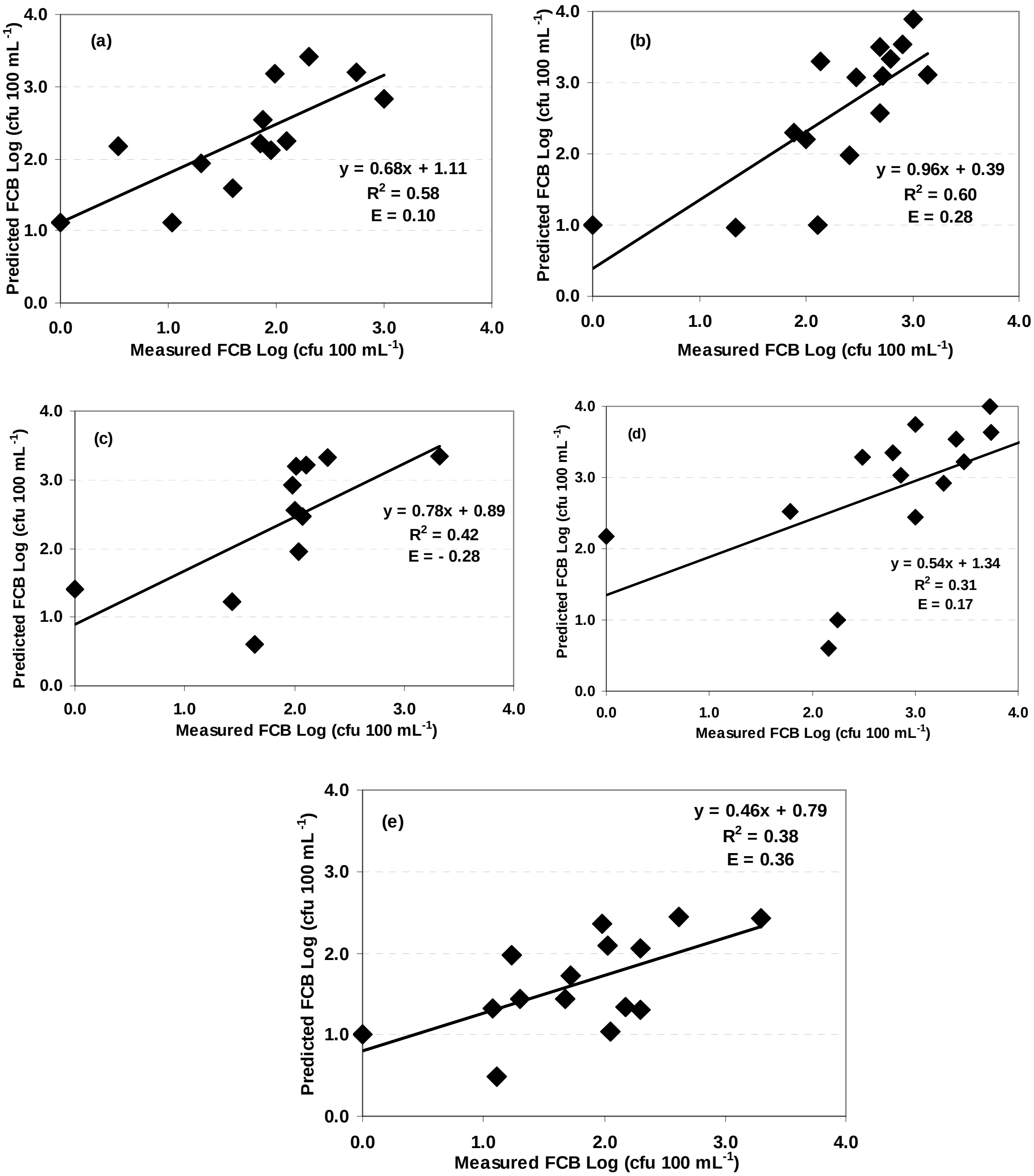

Figure 5.16. Measured daily total fecal coliform bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

5.4.6 Source Specific Fecal Coliform Bacteria

This study modeled source-specific bacteria using a model previously calibrated for flow and sediment. The first attempt was to model single source of bacteria (livestock, human, wildlife) at the Upper Wakarusa watershed using five water quality sampling points (Auburn, Hwy 75, Lewelling Rd, Richland, Deer Creek). The SWAT model results were compared with the event-based observed modified deterministic probability of the BST data for each source. The SWAT results when compared with the observed BST data determined unsatisfactory to fair agreement with R^2 and E values range of -5.03 to 0.39 for each separate source of fecal bacteria (Fig. 5.17a to 5.17e for livestock, Fig. 5.18a to 5.18e for human, and Fig. 5.19a to 5.19e for wildlife). It appeared that a single source of bacteria modeling had decreased agreement and coefficient of determination as compared to total fecal bacteria concentration. However, the slopes (up to 0.73) of the model results were found reasonable (Table 5.4).

The second attempt was to model combination of two sources of fecal bacteria (livestock and human, livestock and wildlife, and human and wildlife) at the Upper Wakarusa watershed using five water quality sampling points (Auburn, Hwy 75, Lewelling Rd, Richland, Deer Creek). The SWAT results when compared with the observed BST data predicted unsatisfactory to good agreement (R^2 and E values range from -2.92 to 0.71) for the combinations of source-specific fecal coliform bacteria concentration (Fig. 5.20a to 5.20e for livestock and human, Fig. 5.21a to 5.21e for livestock and wildlife, and Fig. 5.22a to 5.22e for human and wildlife) from the various outlets of the Upper Wakarusa watershed. Although some model predicted results showed negative model efficiency when compared with the observed BST data, the slopes of the model-predicted values were reasonable (up to 0.80).

The combination of human and wildlife source of bacteria showed better correlation and model efficiency (R^2 and E values range from -0.23 to 0.69) than the combination of livestock and wildlife (R^2 and E values range from -0.97 to 0.71) or the combination of livestock and human (R^2 and E values range from -2.92 to 0.46) sources in this study. The SWAT model over-predicted (overall about 17% in log scale) fecal bacteria when using any combination with livestock source because livestock source loads, both land-application and point source, had relatively greater contribution of bacteria loads as compare to human and wildlife loads. The livestock source bacteria had greater bacteria concentration (cfu 100 mL^{-1}) than human and wildlife sources (Appendix C). The initial and continuous bacteria source loads input in the model in conjunction with other environmental factors such as rainfall-runoff events determines the concentration of bacteria prediction. The contribution of point loads in total fecal bacteria prediction had relatively higher than land-application source loads for all sources. About 10% of the each source load (livestock, human, wildlife) was considered direct point load. Livestock source dominated the fecal bacteria prediction when combined with either human or wildlife sources.

Parajuli et al. (2006) and chapter 2 of this dissertation, determined human source of land-applied bacteria had no sensitivity in the SWAT model. The human source point load application method was reported to have moderate sensitivity. In a separate study, increasing wildlife point source loads to 50% did not much help to improve modeling performance for the single source bacteria (slope ranged from 0.21 to 1.23, R^2 ranged from 0.08 to 0.38, and E ranged from -2.13 to 0.20) when the SWAT model was applied at the Upper Wakarusa watershed.

In overall, the SWAT model demonstrated reasonable results while modeling the combined sources of fecal bacteria due to reduction in various sources of uncertainty, spatial variability, better representation of bacteria source characterization, and bacteria source tracking as compared to the single source of bacteria. The single source of source-specific bacteria modeling had the largest possible uncertainty than combined bacteria sources or total bacteria sources in this study. The average rate of correct classification (ARCC) of known fecal enterococci database was averaged 77%. The ARCC values for livestock were 80%, human 82%, and wildlife 70% (Marchin and Henry, 2006). The previous studies accomplished in different part of the country using ARA have employed discriminant analysis to obtain ARCC, had reported in the range of 34% to 90% (Wiggins et al., 1999; Bowman et al., 2000; Bower, 2000; Graves 2000; Harwood et al., 2000).

ARA necessitates the construction of a library of phenotypic fingerprints obtained from bacteria isolated from the feces of known human and animal sources. The database should be designed to include sufficient representatives from the most likely sources of contamination in a given watershed to reduce the uncertainty due to potential misclassification of bacteria sources (Choi et al., 2003). The appropriate size of a representative library to reduce uncertainty is still not well known. It is said that a library should be large enough to represent a large geographical area. Wiggins et al., (2003) reported that libraries from six watersheds in Virginia could be merged to produce a representative library, although the ARCC of the library was found only 57%. It is still unknown that antibiotic resistance patterns in a given geographic area can predict the source of fecal contamination in a different area (Harwood et al., 2000). Changes in antibiotic use may change the antibiotic resistance pattern of fecal bacteria. Some studies suggested that ARA might not be suitable for wildlife isolates because wildlife might consume feed destined for livestock as the results of their close proximity (Meays et al., 2004), which means that a livestock fecal bacteria source may be potentially misclassified as wildlife fecal bacteria source. All of these previous studies described potential uncertainties that may remain in BST determination. The uncertainties contained in BST analysis directly affects in the source-specific bacteria modeling performance.

Table 5.4. Source-specific bacteria modeling performance at Upper Wakarusa watershed

Parameters	**Verification at multiple points of Upper Wakarusa watershed**				
	Auburn	***HWY 75***	***Lewelling Rd***	***Richland***	***Deer Creek***
Total FCB conc.[1]					
Slope	0.68	0.55	0.55	0.43	0.47
R^2	0.40	0.37	0.42	0.41	0.52
E	0.38	0.27	0.28	0.24	0.29
Source-specific FCB conc.[2]					
Single source					
Livestock					
Slope	0.49	0.73	0.50	0.36	0.27
R^2	0.15	0.24	0.12	0.25	0.20
E	-1.16	-0.79	-4.16	-0.20	0.17
Human					
Slope	0.26	0.36	0.23	0.33	0.10
R^2	0.15	0.39	0.15	0.34	0.02
E	-0.62	-0.20	0.04	-1.31	-0.64
Wildlife					
Slope	0.40	0.32	0.28	0.07	0.05
R^2	0.18	0.34	0.14	0.13	0.02
E	-1.07	-3.69	-2.38	-5.03	0.13
Combined source					
Livestock and Human					
Slope	0.74	0.89	0.80	0.46	0.42
R^2	0.42	0.46	0.28	0.36	0.38
E	0.05	0.02	-2.92	0.14	0.34
Livestock and Wildlife					
Slope	0.63	0.88	0.52	0.59	0.68
R^2	0.36	0.71	0.16	0.63	0.49
E	0.04	0.46	-0.97	0.58	0.41
Human and Wildlife					
Slope	0.72	0.68	0.27	0.43	0.87
R^2	0.44	0.55	0.27	0.66	0.69
E	0.23	-0.23	0.25	0.04	0.63

[1] Total fecal coliform bacteria concentration

[2] Source-specific fecal coliform bacteria concentration

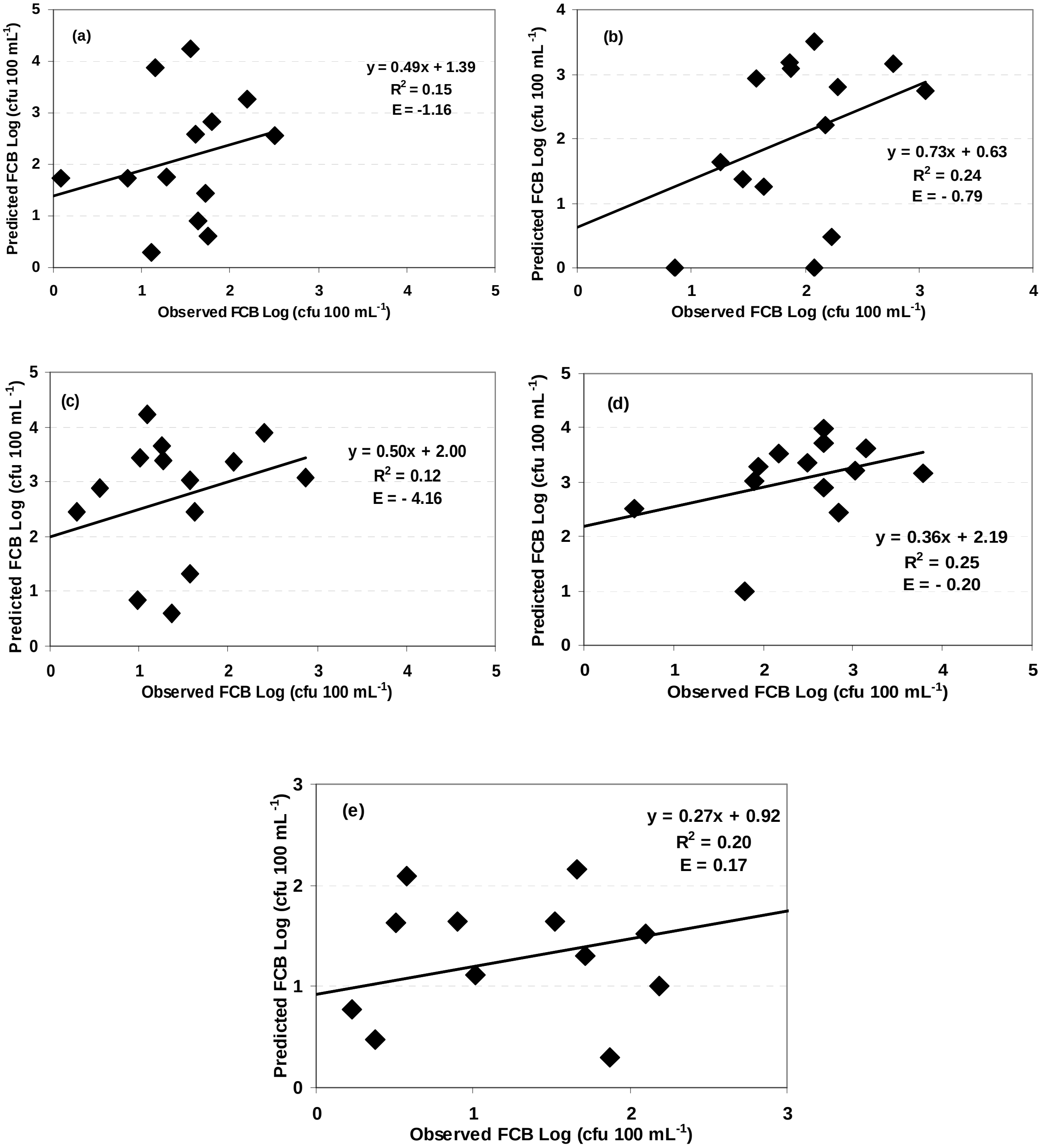

Figure 5.17. Measured daily livestock source of fecal bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

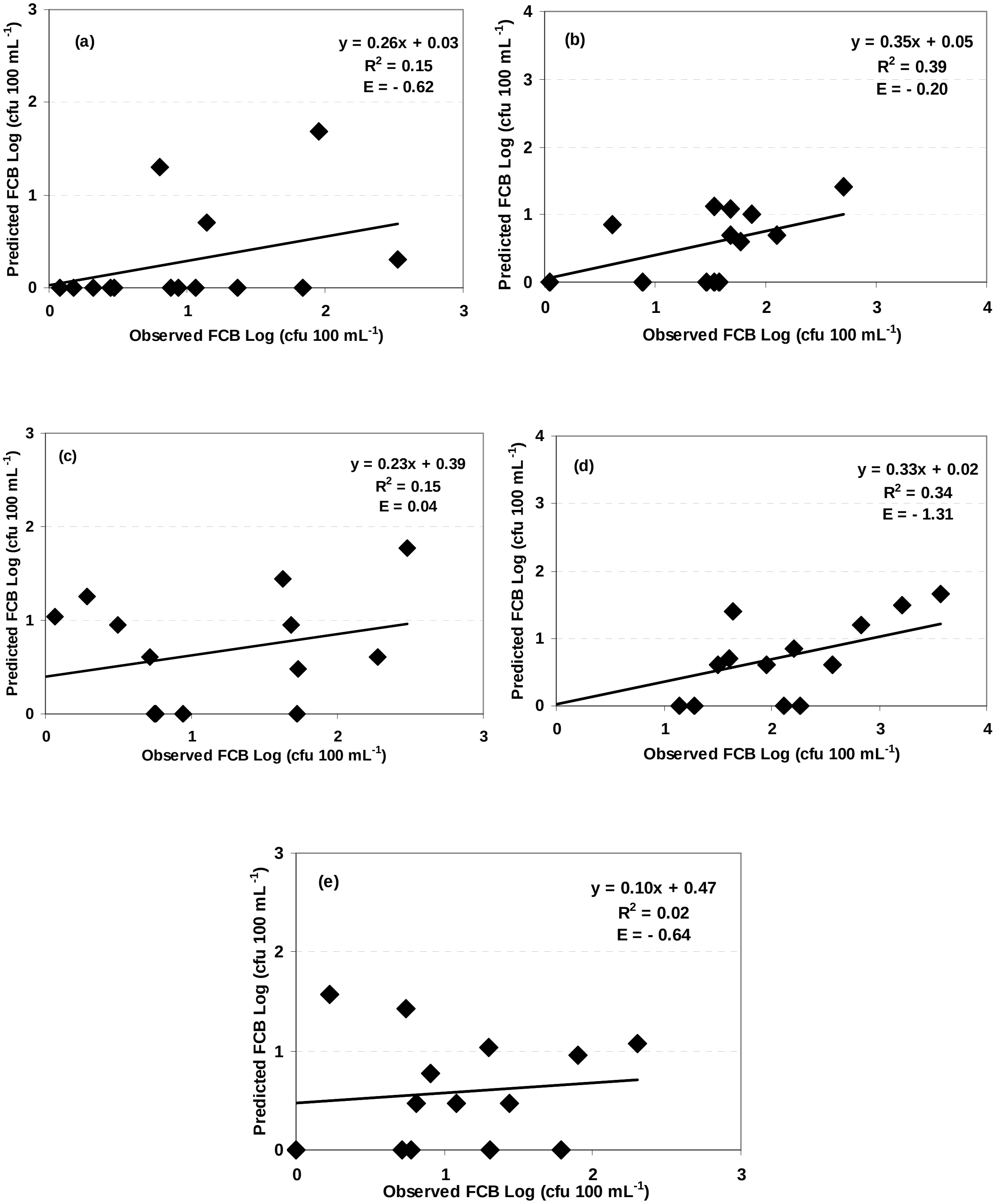

Figure 5.18. Measured daily human source of fecal bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

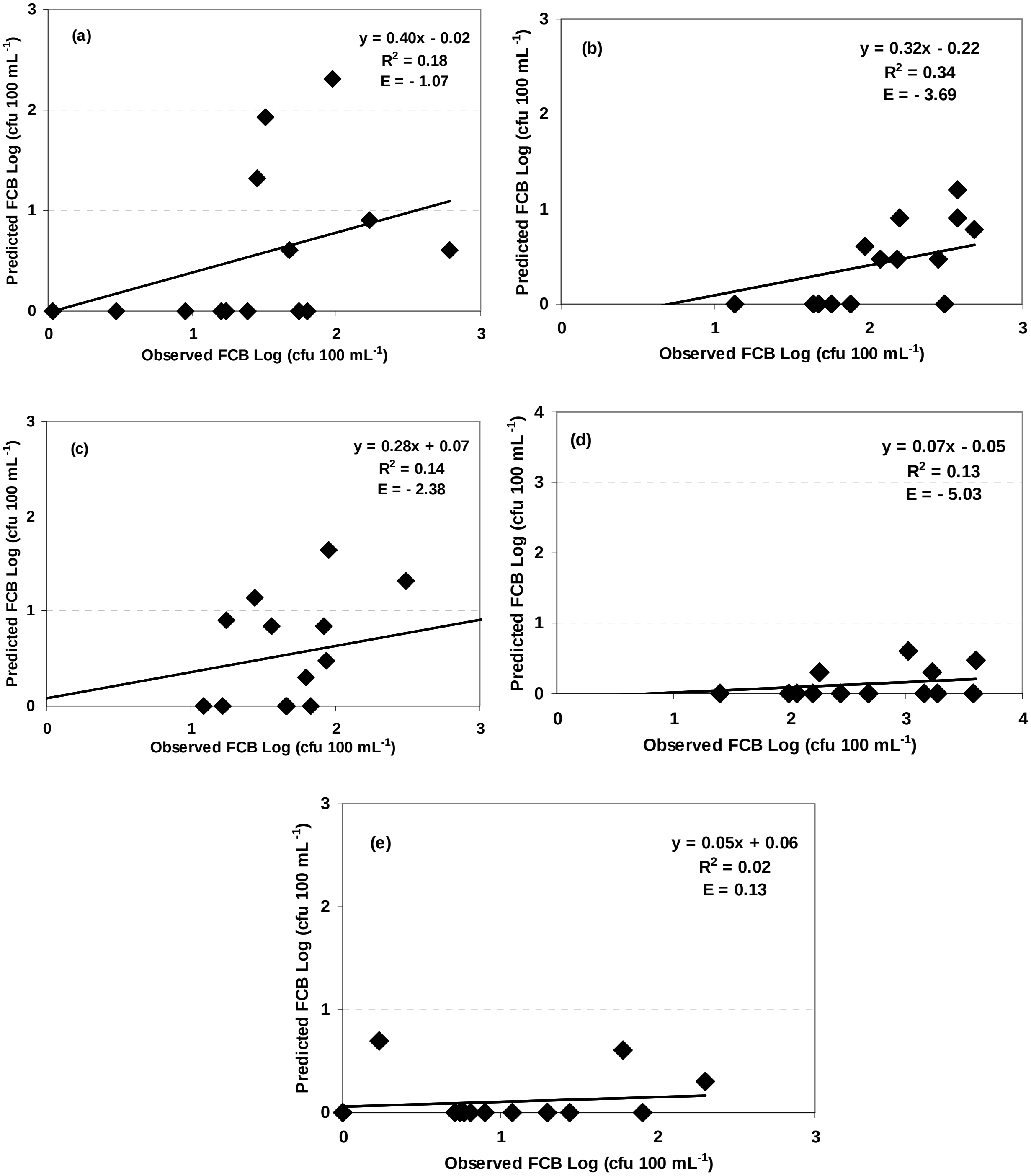

Figure 5.19. Measured daily wildlife source of fecal bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

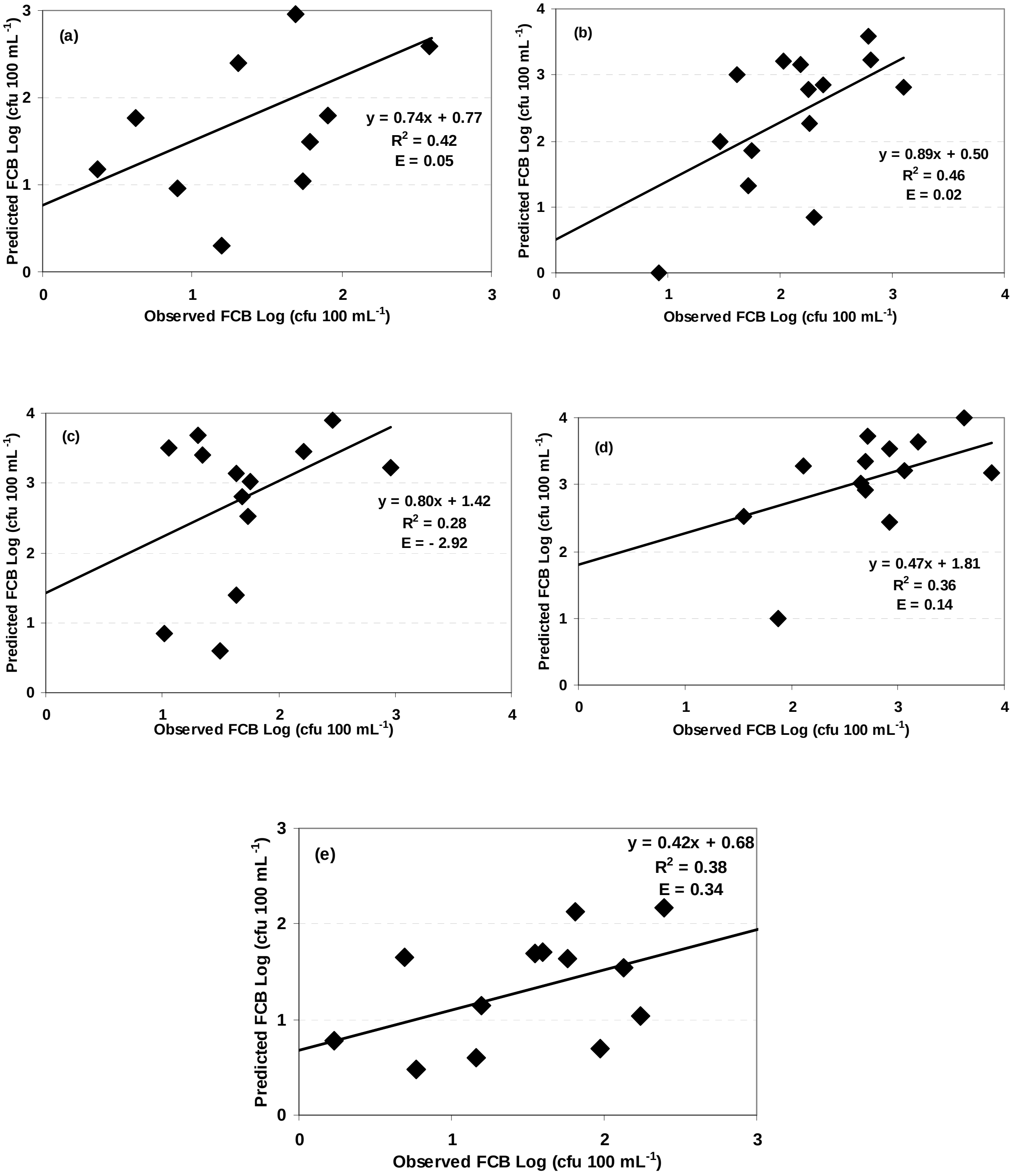

Figure 5.20. Measured daily livestock and human source of fecal bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

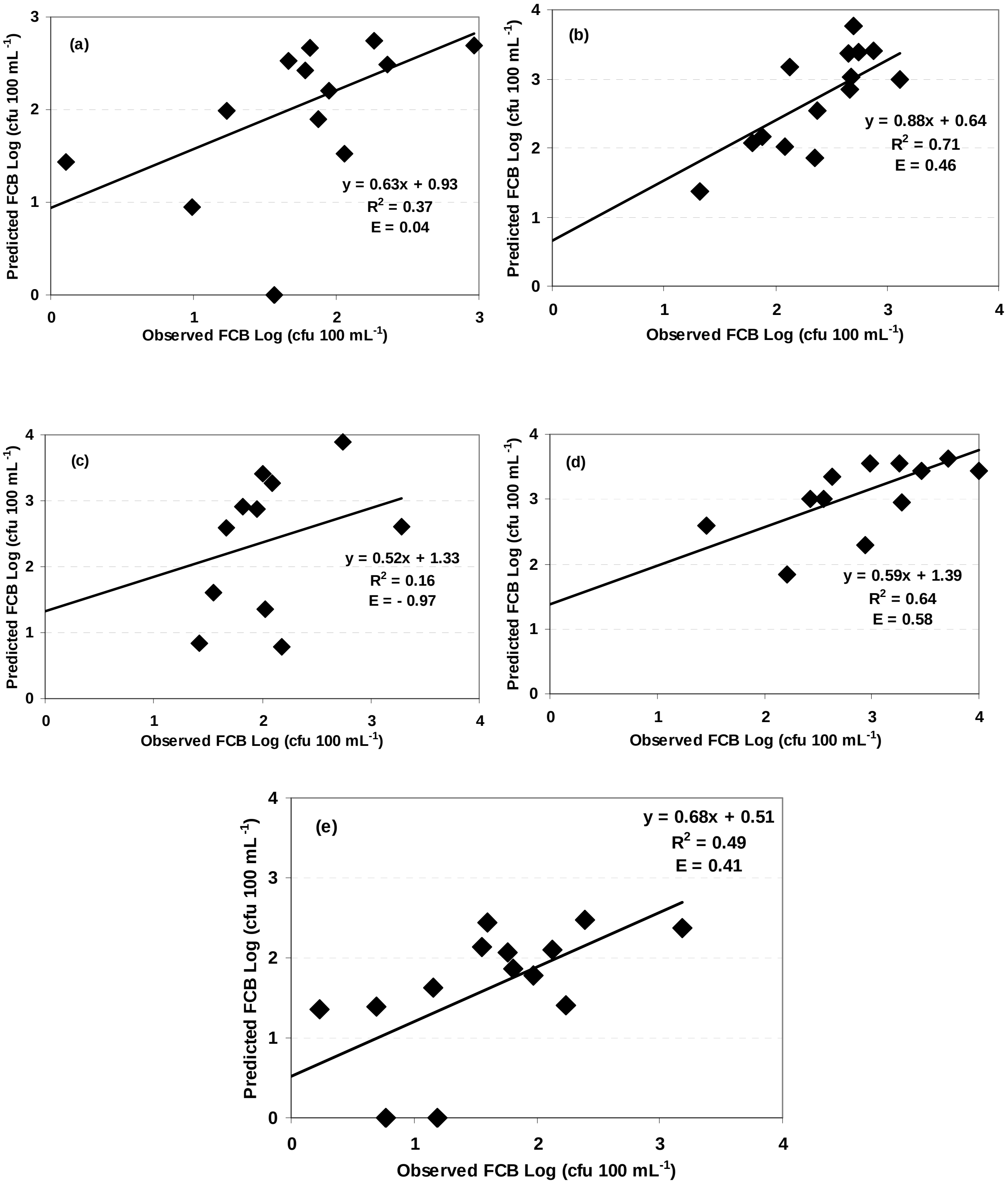

Figure 5.21. Measured daily livestock and wildlife source of fecal bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

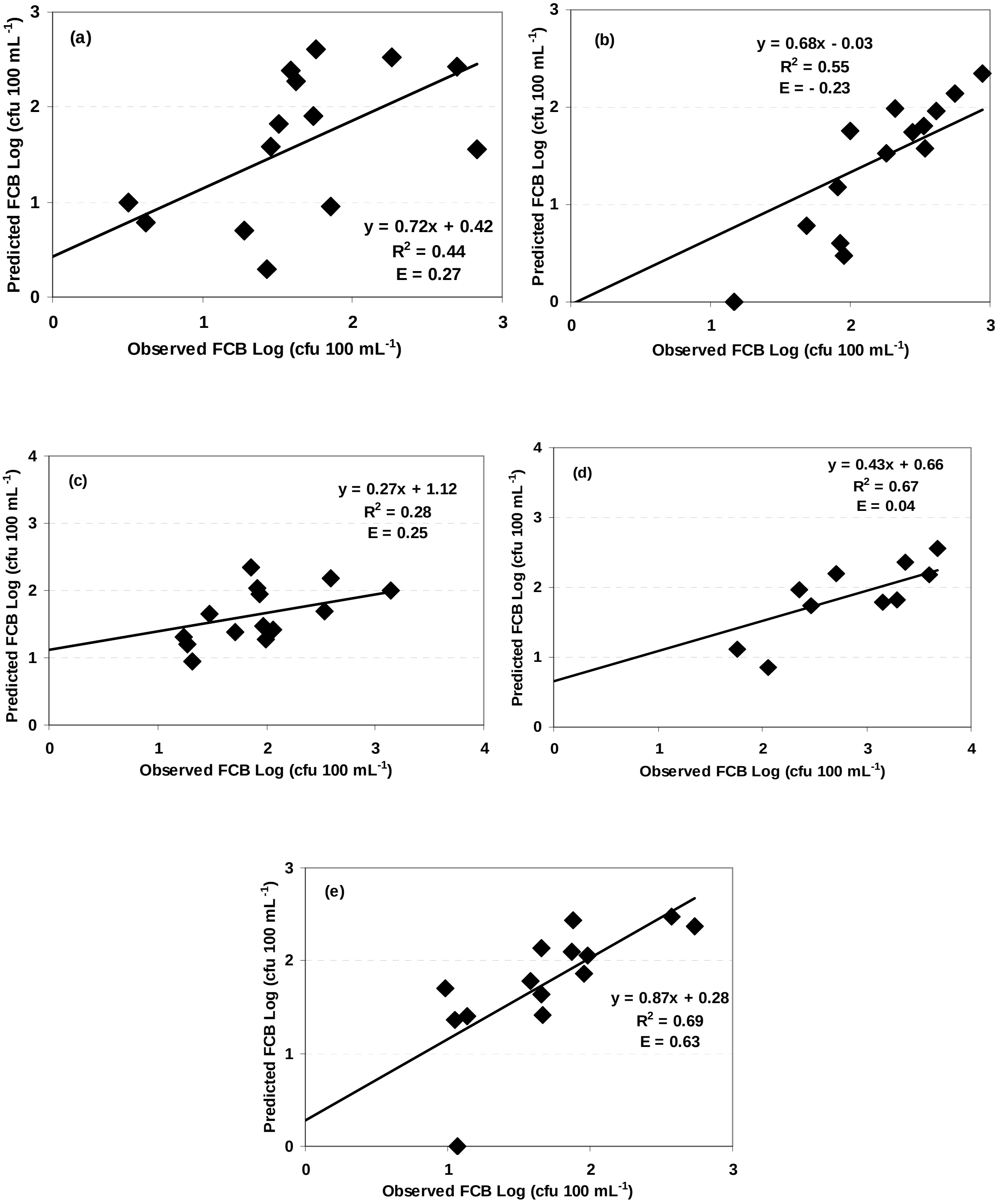

Figure 5.22. Measured daily human and wildlife source of fecal bacteria concentration model response for Upper Wakarusa watershed (a) Auburn, (b) Hwy 75, (c) Lewelling Rd, (d) Richland, and (e) Deer Creek

5.5 Conclusions

This study evaluated SWAT model for source-specific fecal bacteria modeling using three years of observed modified deterministic probability of BST data, and measured hydrologic and water quality data. Limited numbers of rainfall runoff events were observed during 3 years period. The year 2006 was relatively drier than other two.

This study determined more difference (average up to 32%) in daily flow prediction when comparing results of Deer Creek watershed with whole Upper Wakarusa watershed, as compared to other studies. Flow difference was mainly influenced by different rainfall input in the SWAT model due to spatial variation. However as similar to other studies sediment was determined spatially variable due to slope and slope length change through the use of MUSLE in the SWAT model.

This study calibrated (Rock Creek) and verified (Deer Creek, Auburn, Upper Wakarusa watersheds) SWAT model using measured flow, sediment, nutrients, and total fecal coliform bacteria concentrations. Even though R^2 and E values for each source-specific bacteria found were not overwhelming; it is first effort of its kind to model daily source-specific fecal bacteria concentrations from agricultural watersheds using the SWAT model. Although model determined decreased agreement for each separate source of bacteria, the SWAT model reasonably predicted combinations of the source-specific fecal bacteria.

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CHAPTER 6 - BMP TARGETING TO ABATE FECAL BACTERIA POLLUTION USING SWAT

Abstract

A goal in the design of pollution reduction programs is to achieve the greatest possible reduction for the money spent. A strategy to identify critical areas in a watershed may be pollutants specific. The objectives of this study were to rank sub-watersheds, test the effectiveness of various vegetative filter strip (VFS) lengths, and demonstrate the Soil and Water Assessment Tool (SWAT) model's ability to evaluate effectiveness of the VFS application to abate fecal bacteria and sediment yield using target and random approach. The study area "Upper Wakarusa watershed" is a high priority TMDL designation for fecal bacteria.

The fifteen meter VFS was determined reasonable to reduce fecal bacteria from the watershed. The highest difference between target and random approach fecal bacteria reduction was determined at 50% VFS adoption where target approach removed about 60% of the fecal bacteria whereas random approach removed about 42%. For sediment yield the highest reduction was estimated at 25% BMP adoption between target and random approach where target approach removed about 63% of the sediment yield whereas random approach removed about 33%. A targeted watershed modeling approach using SWAT was found to be effective in reducing both fecal bacteria concentration and sediment yield.

6.1 Introduction

Non-point source (NPS) pollution from agricultural lands is one of the contributors to water quality degradation. In the last several decades there has been increasing concern over water, sediment and fecal pathogens that influence human health or that restrict human activities. Federal and state government regulations, such as the Clean Water Act and Total Maximum Daily Load (TMDL) planning, are placing growing emphasis on NPS pollution control. The TMDL program as mandated by the Clean Water Act 1972, is a watershed management process that integrates watershed planning and remediation with water quality assessment and protection (Benham et al., 2006). Developing a TMDL involves a study that quantifies the pollutant contribution from each source and determines the pollutant reduction from each source required to meet applicable state water-quality standards. One method of control is through implementation of best management practices (BMPs), i. e., vegetative or management methods by which NPS pollution is eliminated or reduced sufficiently to meet water quality criteria without disturbing environmental quality (Novotny and Olem, 1994). One of the popularly applied BMP methods for removing sediment and fecal bacteria is vegetative filter strip (VFS).

The installation of VFS has increased dramatically since 1997 when the USDA National Resource Conservation Service’s Buffer Initiative Program was established (Vennix and Northcott, 2002). The program has encouraged the use of VFS in agricultural watersheds by compensating landowners based on how many acres they invest in the program (SWCS, 2001). However, like most watershed programs the Buffer Initiative Program does not have an evaluation process to determine buffer effectiveness along every stream segment of any given watershed. Large-scale field evaluation procedures can be expensive and time consuming therefore better approaches to express buffer efficacy would be to incorporate a spatially distributed hydrologic/water quality model (Corwin et al., 1997; Benham et al., 2006). A model is needed that would not only evaluate buffer effectiveness at the watershed outlet, but also evaluate buffer efficacy on every stream segment throughout the watershed.

For the past decade, research has determined that best management practices such as implementing VFS within agricultural watersheds will aid in the reduction of pollutants into rivers or streams (Park et al., 1994; Inamdar et al., 2001). Various studies have been conducted in past decades to determine the effectiveness of VFS. It has been found that the effectiveness of VFS is influenced by factors like length of the VFS, type of vegetation, slope of strip, sediment size distribution in the runoff and concentration of flow. Length of the strip is considered in many studies as the most important parameter that affects its sediment removal efficiency. Studies have concluded that increasing the flow length beyond 10 m does not help increase the VFS efficiency by large margins (Gharabhaghi et al., 2001; Lee et al., 2003; Zreig et al., 2004).

Ree et al. (1949) studied the sediment trapping efficiency of VFS of length 1, 4-5 and 10 m and recorded efficiencies as 50-60 percent for 1 m, 60-90 percent for 4-5 m, and 90-99 percent for 10 m VFS lengths. Studies like Meyer et al. (1995) and Gharabhaghi et al. (2001) indicated that smaller sized sediments take longer to separate out, therefore, requiring a longer filter. Gharabhaghi et al. (2001) concluded that the first five meters of VFS play a significant role in removal of the suspended solids and aggregates greater than 40 microns. Fecal bacteria are less than 0.45 micron (Wang et al., 2003).

In the study by Zreig (2001), trapping efficiencies of 0% for 1 meter filter strip length and 47% for 15 filter strip length were observed for clay particles. Lee et al. (2003) installed three plots where each of cropland source area was matched with no buffer strip, switchgrass buffer (7 m), and a switchgrass/woody plant buffer strip (16.3m) to determine the effectiveness riparian buffer strips in removing pollutants carried by cropland runoff. Efficiencies higher than 92% and 97% were seen for the switchgrass and switchgrass/ woody buffer respectively. It was concluded that the switchgrass was an effective measure for removing coarse particles, unlike the switchgrass/woody buffer, which is more suitable for finer particles. Zreig et al. (2004) conducted twenty field experiments with filter lengths of 2, 5, 10, 15 m. and slopes of 2.3 and 5%. An exponentially decreasing trend between sediment trapping efficiency and length beyond 10 m was seen. Another important factor that affects the performance of the filters is the sediment size distribution of the incoming runoff.

BMPs effectiveness, optimization analysis, and cost effectiveness have been researched using many available modeling tools (Moore et al., 1992; Niu et al., 2001; Zreig, 2001; Veith, 2002; Vennix and Northcott, 2002; Bracmort et al., 2004). One question always remained quite un-answered that where in the watershed first the BMPs to be implemented that ensures the most effectiveness of the dollars money spent to reduce pollution. The location of the BMP targeting can be varied due to pollutant variation. For example, targeting for the sediment and fecal bacteria reduction may or may not be in the same HRUs or sub-watersheds. The recent watershed water quality physically based and spatially distributed models can take into account physical and spatial processes in detail.

A goal in the design of pollution reduction programs is to achieve the greatest possible reduction for the money spent (Heatwole et al., 1987). Braden et al. (1989) discussed the economic advantage of selectively applying BMPs to reduce NPS pollution. They stressed that selective applications are likely to be cheaper and less disruptive overall. Implementing stricter pollution control in areas where it will be most cost-effective is known as targeting (Veith et al., 2001). Targeting focuses on critical areas within the watershed. As a result, targeting often reduces costs as compared to first-come, first-served approaches such as cost-share. A number of studies have developed targeting procedures to enable watershed-specific evaluation of NPS pollution control. Targeting methods incorporating pollution prediction models have been demonstrated. Additionally, spatial variability at the watershed level or hydrologic response units (HRUs) level has been shown to be an important aspect of effective targeting. In addition, the application of different filter strip lengths may have different level of pollutant removal efficiency. It is not always possible to apply selected BMPs in overall watershed due to resources limit and management. It is therefore important to know the critical locations of the watershed where BMP implementation could make the most effective impact.

The VFS are commonly used to decrease the pollutant loads from manured fields and pastures (Guber et al., 2007). The SWAT model placed VFS along the edges of HRUs. The Riparian Ecosystem Management Model (REMM), the Kinematic Runoff Erosion Model (KINEROS), and the Vegetative Filter Strip Model (VFSMOD) models have recently been utilized the SWAT output to evaluate the VFS pollutants removal capacity for sediments (Allison et al., 2006; USEPA, 2005, Goodrich et al., 2006).

Recent interest to the fate and transport of manure-borne pathogens has generated a substantial increase in data on fate and transport of pathogens and indicator organisms in VFS. Several excellent reviews have been published (Jamieson et al., 2002, Ferguson et al., 2003, Tyrrel and Quinton, 2003, Unc and Goss, 2004, Oliver et al., 2005) in regard to VFS. The existing knowledge shows that the efficiency of VFSs as barriers for pollutants depends to large extent on slope lengths and other hydrologic factors such as soil moisture content before the rainfall event, rainfall intensity and duration (Munoz-Carpena et al., 1999; Helmers et al., 2006).

By the frequency of being the cause of water quality impairment, pathogens rank first and sediment ranked second after mercury among five leading pollutants in US water bodies (USEPA, 2006). In Kansas the cause of water quality impairment due to pathogen is reported about 15.44% which third ranked. A wide range of opinions exists on the VFS efficiency with respect to pathogens and/or indicator organisms (Pachepsky et al., 2006). Tools to evaluate the efficiency of VFS and select its parameters with respect to manure-borne pathogens have been developed during 80s. They include the Agricultural Runoff Management II: Animal Waste Version (ARM II) model (Overcash et al., 1983), the Utah State (UTAH) model (Springer et al., 1983), the MWASTE model (Moore et al., 1988), and the COLI model (Walker et al., 1990).

6.1.1 Targeting and Cost Effectiveness

In the United States, programs have focused primarily on helping pay for the cost of conservation practices and paying for farmers to remove from cultivation land that bears a high risk of erosion. Programs are voluntary, although some farmers are required to participate in some ostensibly voluntary programs in order to be eligible for certain other attractive farm supports (Kerr et al., 2007). While there is widespread acceptance that farmers will need financial assistance to adopt soil conservation practices whose benefits will accrue only partially to them, there remain questions about how to design programs such that financial assistance will be as cost-effective as possible.

Cost effectiveness entails achieving the greatest reduction in pollutants such as sediment, pathogen at a given level of cost or, equivalently, achieving a given level of reduction in pollutants at the least cost. The best that can be achieved is to intervene in a way that maximizes the likely reduction in pollutants for the lowest cost. Horan and Ribaudo (1999) recommend incentive-based approaches as the most efficient way to encourage soil conservation. Current programs select certain blunt eligibility targets for recruiting farmers to participate and for sharing investment costs with them. A common approach is to pay farmers 75% of the cost of approved conservation practices like VFS. All land within one quarter mile of waterways is eligible for such cost sharing (Kerr et al., 2007). Targeting and prioritizing the areas for implementation of BMPs rather than random or general areal application is the key to the cost-effective water quality improvement. Identifying fields/areas with high pollution potential and then treating these fields first would be a more efficient way to control expenditures and non-point source pollution.

Watershed modeling approach for identifying and prioritizing critical areas and impacts of best management practices were demonstrated by a number of studies. Dickinson et al. (1990) identified areas with estimated sediment yield rates exceeding a selected tolerable sediment yield rate and areas with estimated soil loss rates exceeding a selected soil loss tolerance value as “target 1 zones”. They then applied four different remedial strategies and concluded that targeting is more effective in reducing sediment loads compared to random approach. Tim et al. (1992) integrated simulation modeling with GIS and used soil erosion rate, sediment yield, and phosphorus loading to identify watershed areas that are potentially high, medium, and low sources of non-point source pollution. Tripathi et al. (2003) identified and prioritized critical areas on the basis of average annual sediment yield and nutrient losses using SWAT. Mankin et al. (2005) and Tuppad et al. (2006) found that the targeted watershed modeling approach using the SWAT model was effective in reducing the sediment loads from the Kanopolis watershed in Kansas. However, all of these studies did not consider targeting pathogen from the agricultural watersheds.

6.2 Objectives

This study used a watershed model (SWAT) to explore effectiveness of different VFS lengths alternative possibilities for targeting conservation programs in order to reduce non-point source pollution. The overall objectives of this research were to characterize fecal bacteria sources, calibration and validation of the SWAT model for targeting BMPs to abate fecal bacteria pollution from the Upper Wakarusa watershed. This study utilized the model input and output information from previous studies done in chapter three and four of this dissertation. The three specific objectives of this study include: (a) test the effectiveness of various filter strip lengths (0 m, 10 m, 15 m, 20 m) for removing overland flow fecal bacteria concentration, (b) rank sub-watersheds after determining the fecal bacteria contribution (base condition) of each sub-watershed by overland flow process, (c) evaluate the effectiveness of BMP application using target approach and random approach.

6.3 Materials and Methods

6.3.1 Watershed Stream Monitoring

6.3.1.1. Upper Wakarusa Watershed

The Upper Wakarusa watershed (Fig. 6.1) is located in Douglas, Shawnee, Osage and Wabaunsee Counties, which consists of 950 km^2 with average elevation of 304 m. The watershed has three major landuses including grassland (57%), cropland (28%), and woodland (9%). The silty-clay textured soils (SSSURGO stmuid: KS 1777302, KS1977302, KS 0457302, KS 0457325, KS 1773891, and KS 1774752) is a major predominant soil type in this watershed. The model was verified at Upper Wakarusa watershed.

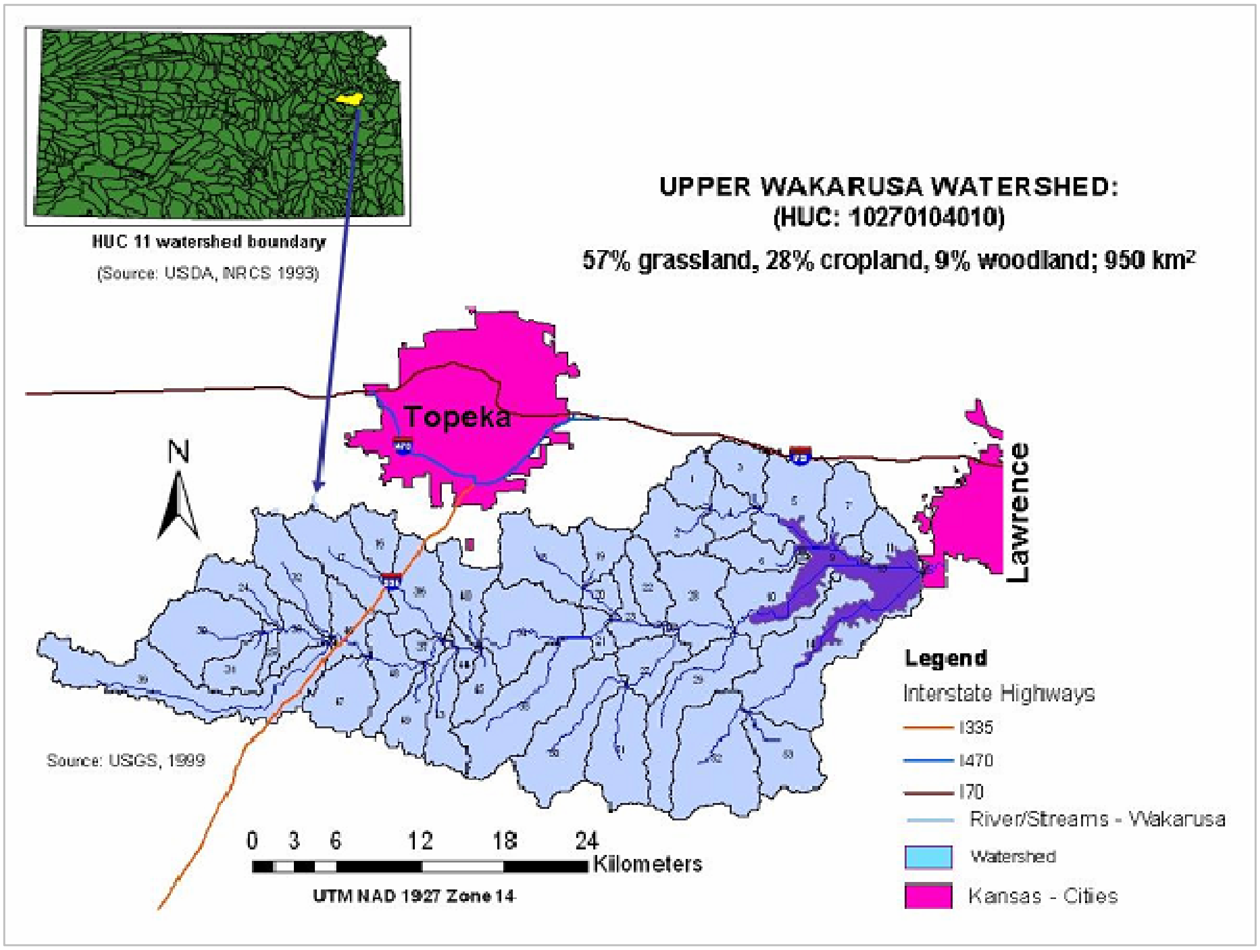

Figure 6.1. Location map of the Upper Wakarusa watershed in NE Kansas

6.3.1.2 Stream Monitoring

Stream flow and bacteria data were collected at the outlet of the each watershed to validate model results. Grab samples (about 250 ml) were collected from the mid point of the flowing stream at each watershed outlet. Samples were placed immediately into an ice chest, and transferred to laboratory refrigerator within two to four hours of collection. Bacteria enumeration procedures were started with in 24 hours. Serial dilution method (Clesceri et al., 1998) was applied to enumerate fecal coliform bacteria colonies. Bacterial samples typically required four serial dilutions to obtain reasonable bacteria colony counts.

Flow was calculated at the time of sample collection using Manning's equation, as outlined by Ward and Elliot (1995). Flow depth, cross-sectional area, and channel slope were measured, and channel roughness factor was estimated based on the channel roughness characteristics, and degree of meandering (Cowan, 1956). The calculated flow was validated based on ratio of the watershed area using data from the USGS Richland gage station data. The calculated flow data showed very good correlation (>90%) with the weighted area flow data. This study used the data collected from January 2004 to April 2006.

6.3.2 Management Scenarios

The pastureland, cropland, and woodland management scenarios and fecal bacteria source characterization methods for the Upper Wakarusa watershed as described by Parajuli et al. (2007) were utilized in this study.

6.3.3 Vegetative Filter Strips

This study utilized the previously calibrated and validated SWAT model at Upper Wakarusa watershed. The VFS was considered one of the BMPs in this study. Various lengths of VFS (Table 6.1) were evaluated to reduce fecal bacteria transport through overland flow process. A longer VFS can generally reduce more sediment and fecal bacteria concentration than the shorter one.

Table 6.1. Vegetative Filter Strip (VFS) Lengths

Scenarios	FS length (m)
Vegetative Filter Strip	0
Vegetative Filter Strip	10
Vegetative Filter Strip	15
Vegetative Filter Strip	20

After the SWAT model was tested for various VFS lengths for the whole watershed, the recommended VFS length was applied in to the selected (0%, 10%, 25%, 50%, and 100%) sub-watersheds based on target and random methods.

6.3.4 SWAT model

The SWAT model utilizes geospatially referenced data to satisfy the necessary input parameters. United State Geological Survey (USGS, 1999) 7.5-minute elevation data was used to delineate the watershed boundaries and topography. Soil Survey Geographic Database (SSURGO) was utilized to create a soil database (USDA, 2005). The GAP (GAP Analysis Program) land cover data of 2001 that depicts twenty general land cover classes for the state of Kansas (KARS, 2001) was used. Wardlow and Egbert (2003) evaluated GAP (2001) and National Land Cover Data NLCD (1992) landuse data for the State of Kansas. The Kansas GAP provided better discrimination of most land-cover classes as compared to NLCD. Accuracy assessment found an overall accuracy of 87 percent for GAP and 81 percent for NLCD, and GAP had higher accuracies for most individual land-coverclasses. The Kansas GAP and NLCD land-cover products were found to be comparable in terms of characterizing broad scale land-cover patterns, but the Kansas GAP land-cover map appears to be more appropriate for localized applications that require detailed and accurate land-cover information.

The land use classes were re-classified into eight classes (grazedland, non-grazedland/hay, cropland, woodland, Conservation Reserve Program, water, urban areas and quarry) based on field-verified landuse conditions (Mankin and Koelliker, 2001; Mankin et al., 2003). The stream threshold area was defined as 950 ha, which is about 10% of the total watershed area (95, 252 ha). The SWAT model delineated 53 sub-basins ranging from 0.003 km^2 to 66.709 km^2. The watershed parameters for each Hydrologic Response Unit (HRU) in each watershed were defined on the basis of soil, landuse, and topographic characteristics of the watershed as described in the SWAT documentation version 2005 (Neitsch et al., 2005).

The microbial survival and transport sub-model was added to the SWAT model in 2000 and modified in 2005. The SWAT model microbial component considers the fate and transport of organisms for bacterial concentration. The microbial sub-model uses Chick's Law, as revised by Moore et al. (1989), to model fecal bacteria die-off and re-growth. Chick's law, a first order decay equation, determines the quantity of bacteria that are removed or added by die-off and re-growth as described by Sadeghi and Arnold, 2002 which is given by the equation (6.1),

$$C_t = C_o \times e^{-K_{20}\, t\, \theta^{(T-20)}} \tag{6.1}$$

where

C_t = bacteria concentration at time t, count/100mL

C_o = initial bacteria concentration, count/100mL

K_{20} = first-order die-off rate at 20^0C, day^{-1}

t = exposure time, days

θ = temperature adjustment factor

T = temperature, ^{0}C

As described in the SWAT model (Neitsch et al., 2005), in the stream bacteria die-off is the only process modeled. SWAT calculates loading of pathogens and indicator bacteria for pathogens from land areas in the watershed. The VFS are generally provided at the edge-of the field. It can be defined in an HRU. The sediment, and bacteria loads in surface runoff from overland flow process are reduced as the surface runoff passes through the filter strip.The filter strip trapping efficiency for fecal bacteria (Moore et al., 1988) is calculated using equation 6.2:

$$trap_{ef,bact} = \frac{\left(11.8 + 4.3 \cdot width_{filtstrip}\right)}{100} \tag{6.2}$$

where $trap_{ef,bact}$ is the fraction of the bacteria loading trapped by the filter strip, and $width_{filtstrip}$ is the width of the filter strip (m).

Looking at equation 6.2, the 20.5 m is the maximum VFS length that can be used in the model to remove 100% of the fecal bacteria. The equation 6.2 is recommended not to exceed more than 75% of the bacteria removal and the equation is still under research.

The VFS trapping efficiency for sediment is calculated using equation 6.3:

$$trap_{ef} = 0.367 \cdot \left(width_{filtstrip}\right)^{0.2967} \tag{6.3}$$

where $trap_{ef}$ is the fraction of the constituent loading trapped by the filter strip, and $width_{filtstrip}$ is the width of the filter strip (m).

The SWAT water quality model has been applied, calibrated and validated for one or more pollutant parameters such as runoff, sediment yield, and nutrient losses from watersheds at different geographic locations, conditions, and management practices (Saleh et al., 1999; Spruill et al., 2000; Santhi et al., 2001; Kirsch et al., 2002; Van Liew et al., 2003; White et al., 2004; Qi and Grunwald, 2005; White and Chaubey, 2005; Wang et al., 2006; Jha et al., 2007; Gassman et al., 2007). Limited research has been performed using the SWAT (2005) model for targeting BMPs to abate pathogen transport from the agricultural watersheds. Parajuli et al (2007) reasonably calibrated (Rock Creek) and verified (Upper Wakarusa) the SWAT model using three years (2004-2006) of measured daily flow, and sediment data. The verified model at the Upper Wakarusa watershed reasonably predicted total fecal bacteria concentration (R^2 from 0.37 to 0.52 and E from 0.24 to 0.38). The SWAT model has not been used for targeting to reduce fecal bacteria concentration from agricultural watersheds.

6.3.5 Weather and Hydrologic Data

Weather data such as daily precipitation and daily ambient temperatures were extracted from the National Climatic Data Center (NCDC) and the records maintained by Kansas State Climatologist were also utilized. The SWAT model requires daily precipitation in mm, daily maximum and minimum temperatures in degrees Celsius, daily solar radiation in MJ m^{-2} day^{-1}, daily wind speed in m sec^{-1} and daily relative humidity in fraction to run the model. The daily precipitation data were used from nine weather stations near the watershed that includes; Clinton Lake, Auburn, Silver Lake, Overbrook, Eskridge, Pomona Lake, Lawrence, Lecompton, and Topeka. Silver Lake weather database was utilized for the daily solar radiation, daily wind speed, and daily relative humidity data. The missing data were adjusted using SWAT database simulation. The SWAT model uses Ottawa weather station (Franklin County) data for simulation which is, located about 24 kilometers south-east from the nearest point of the watershed.

The daily precipitation data for the Rock Creek watershed was used from the Overbrook weather station (4.8 km south), for Deer Creek watershed from Lecompton (6.5 km north-east) and Topeka (12.2 km north-west) weather stations, and for Auburn watershed from Auburn (located with in watershed) and Eskridge which is located 5 km west from the nearest point of the watershed (Fig 5.3). The 2004 to 2006 average annual rainfall data measured for Overbrook 939 mm, for Lecompton 955 mm, for Topeka 1008 mm, Auburn 935 mm and for Eskridge 942 mm (Table 6.2).

Table 6.2. Description of weather stations rainfall data used in the study

Station name	Year[1]	Total (mm year^{-1})	Peak rainfall (mm day^{-1})	Growing season (%)[2]	No. of rainfall-events[3]	No. of potential runoff-events[4]
Overbrook	2004	1126	69	69	83	29
	2005	1180	81	77	70	23
	2006	512	53	72	44	12
Lecompton	2004	1206	83	69	102	28
	2005	1029	87	72	81	23
	2006	629	40	68	59	18
Topeka	2004	1013	62	67	91	25
	2005	1239	142	74	82	24
	2006	772	64	81	62	20
Auburn	2004	1146	114	70	93	27
	2005	1013	82	71	76	19
	2006	646	60	73	59	17
Eskridge	2004	960	67	73	85	25
	2005	1185	125	75	87	28
	2006	681	58	75	65	16

[1] Year 2006 rainfall data from Jan to Oct only

[2] % of rainfall between April to September

[3] Rainfall greater than 1 mm

[4] Rainfall events greater than 14 mm (I_a for CN_{avg} 78; SCS, 1972)

6.4 Results and Discussion

The SWAT model predicted daily flow and sediment reasonably matched measured values during previous calibration and verification studies for the Upper Wakarusa watershed (Parajuli et al., 2007; Chapter 5 of this dissertation).

6.4.1 Vegetative Filter Strip Length

Figure 6.2 shows that increasing the length of a VFS was simulated to reduce average overland annual fecal bacteria concentration from watershed. The first 10 m of VFS reduced about 57% of the fecal bacteria. The additional 5 m of VFS or total of 15 m VFS reduced up to 80% of the fecal bacteria, which was reasonable. The 20 m of VFS removed about 100% of the fecal bacteria which was anticipated based on equation 6.3 used in the model. Similarly, the figure 6.3 shows a similar trend as figure 6.2. About 73% of the sediment yield was reduced when using 10 m length of VFS. The 15 m length of VFS removed sediment yield up to 82% and 89% by 20 m VFS length, which was anticipated using equation 6.4 in the model. A more noticeable result in figures 6.2 and 6.3 was that using equation 6.2 in the model, a 20 m of VFS can remove all 100% of the fecal bacteria whereas for sediment using equation 6.3 in the model requires 30 m of VFS to remove 100% of the sediments.

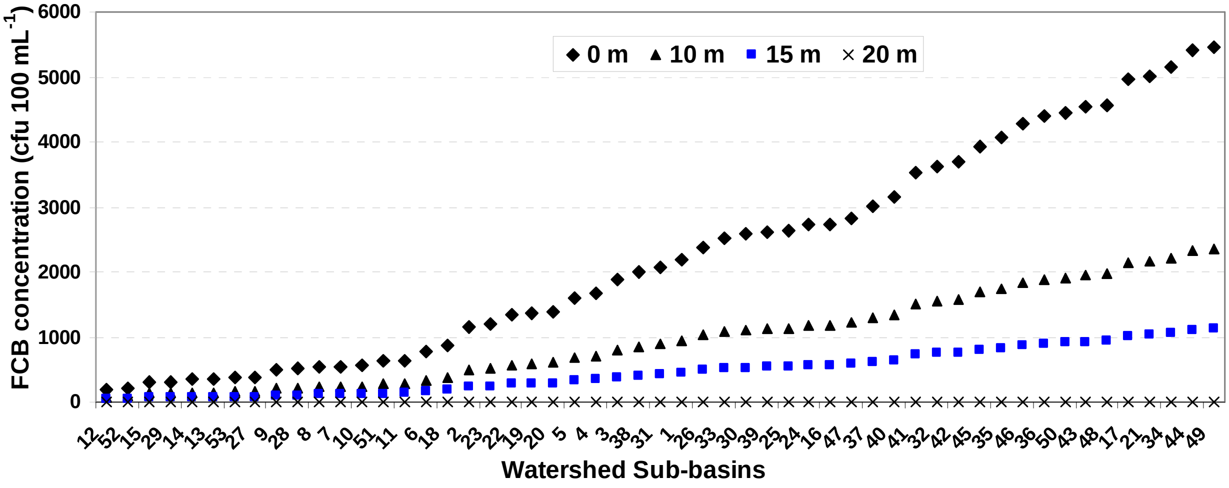

Figure 6.2. Watershed sub-basins and annual average overland flow fecal bacteria response

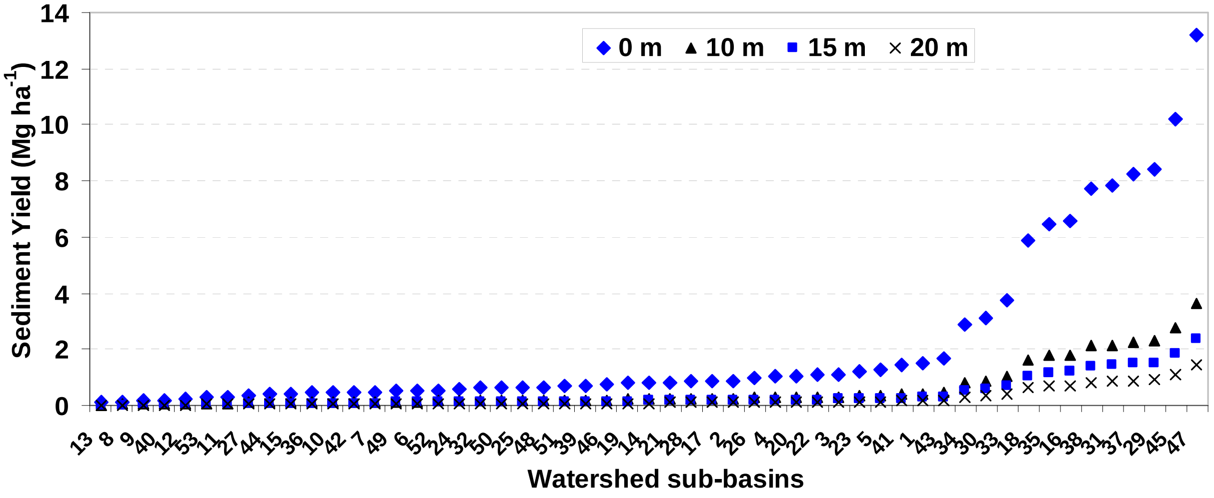

Figure 6.3. Watershed sub-basins and annual average overland sediment yield response

Parajuli et al. (2005), tested different lengths of VFS (0 to 25 m) using SWAT 2000 and recommended 20 m of VFS as the best to reduce fecal bacteria concentration from the agricultural watershed. They did not find any reduction in fecal bacteria concentration using 25 m of VFS. However, the SWAT, VFS equation 6.2, which is slightly changed in SWAT 2005 was recommended to use for up to 75% bacteria removal efficiency. It is therefore recommended 15 m of VFS length in this study. The impact of applying vegetative filter strips (15 m length) into 0%, 10%, 25%, 50%, and 100% sub-basins of the watershed was estimated using two selection methods: targeted and random (Table 6.3).

Table 6.3. Vegetative Filter Strip (VFS) Lengths Scenario for Target and Random Methods

% of sub-basins VFS	FS length (m)
0	15
10	15
25	15
50	15
100	15

Table 6.4. Fecal bacteria ranking for targeting

Sub-basin	Bacteria (cfu 100 mL^{-1})	Rank
49	5460	1
44	5407	2
34	5163	3
21	5011	4
17	4954	5
48	4573	6
43	4532	7
50	4456	8
36	4397	9
46	4293	10
35	4074	11
45	3936	12
42	3693	13
32	3626	14
41	3523	15
40	3144	16
37	3008	17
47	2834	18
16	2724	19
24	2723	20
25	2629	21
39	2610	22
30	2580	23
33	2519	24
26	2387	25
1	2185	26
31	2059	27
38	1989	28
3	1872	29
4	1667	30
5	1599	31
20	1397	32
19	1361	33
22	1334	34
23	1202	35
2	1153	36
18	864	37
6	770	38
11	636	39
51	630	40
10	561	41
7	539	42
8	535	43
28	514	44
9	483	45
27	375	46
53	366	47
13	346	48
14	345	49
29	313	50
15	313	51
52	219	52
12	189	53

Table 6.5. Sediment yield ranking for targeting

Sub-basin	Sediment yield (Mg ha^{-1})	Rank
48	13.22	1
46	10.18	2
30	8.42	3
38	8.25	4
32	7.83	5
39	7.73	6
35	7.44	7
16	6.58	8
36	6.47	9
18	5.86	10
31	3.11	11
44	1.65	12
34	1.53	13
1	1.48	14
42	1.42	15
5	1.25	16
23	1.19	17
3	1.12	18
22	1.07	19
20	1.04	20
4	1.03	21
27	0.96	22
2	0.88	23
17	0.85	24
29	0.84	25
21	0.82	26
19	0.79	27
14	0.73	28
47	0.72	29
40	0.69	30
52	0.66	31
49	0.64	32
26	0.64	33
51	0.61	34
33	0.61	35
25	0.57	36
24	0.56	37
53	0.54	38
6	0.51	39
50	0.50	40
7	0.48	41
43	0.46	42
10	0.45	43
37	0.45	44
15	0.43	45
45	0.43	46
28	0.37	47
11	0.31	48
12	0.25	49
41	0.18	50
9	0.17	51
8	0.13	52
13	0.10	53

The resulting distribution is shown in the figures 6.4 and 6.5. For the target method sub-basins were selected separately for fecal bacteria and sediment contribution by overland flow based on ranking. Sub-watersheds were ranked separately for sediment and fecal bacteria prediction because model identified top ranking sub-watersheds for sediment and fecal bacteria were different (Table 6.4 and 6.5), which was anticipated. The SWAT model uses the modified universal soil loss equation (William, 1995) to estimate sediment yield. The slope and slope length parameters in this equation can directly impact in estimating sediment yield. Therefore,   average slope of each HRU/sub-watershed generally influenced in sediment prediction whereas total water yield from each HRU/sub-basins influenced fecal bacteria prediction.

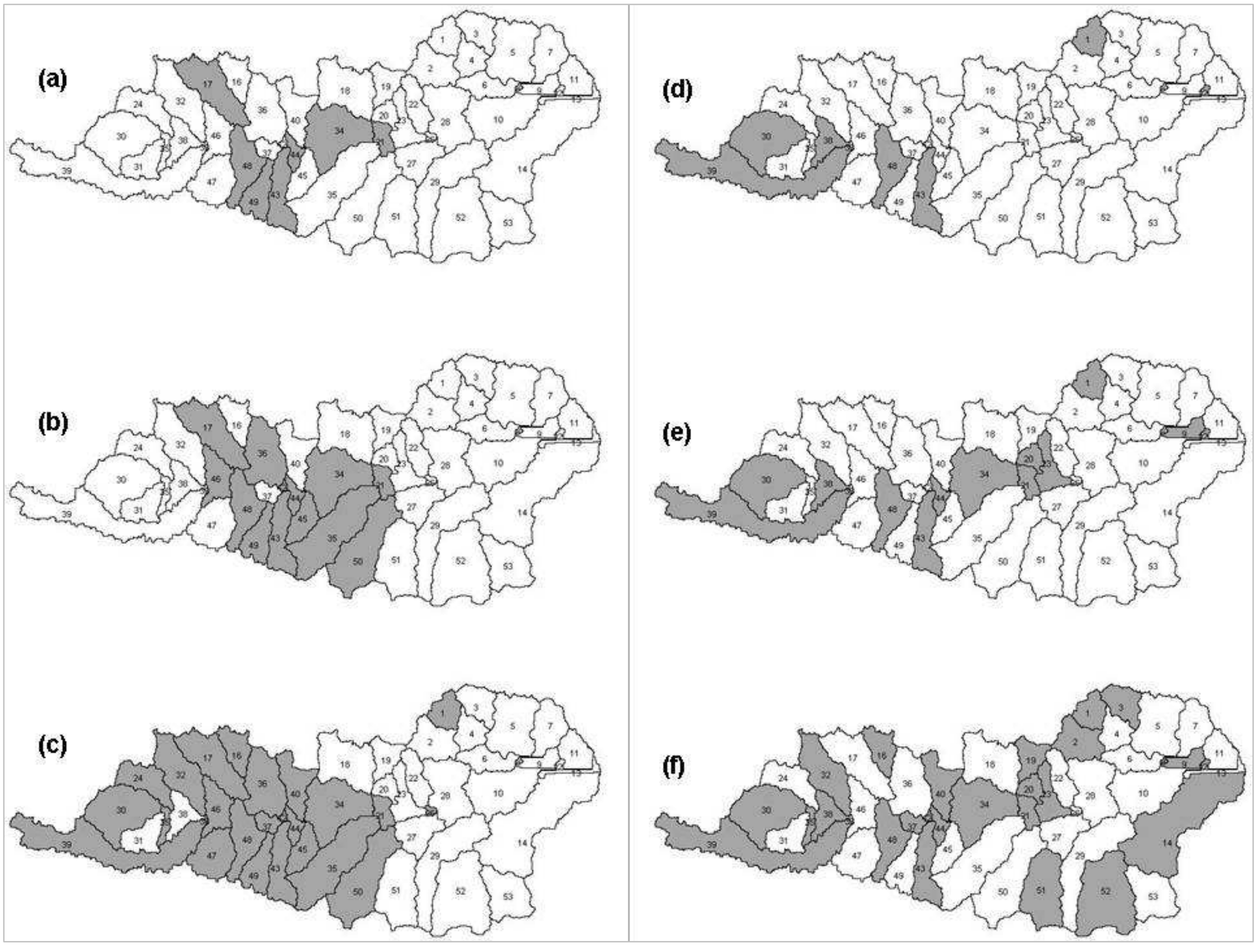

Figure 6.4. Distribution of watershed sub-basins for fecal bacteria BMP selection: target method (a) 10%, (b) 25%, (c) 50% and random method (d) 10%, (e) 25%, and (f) 50%

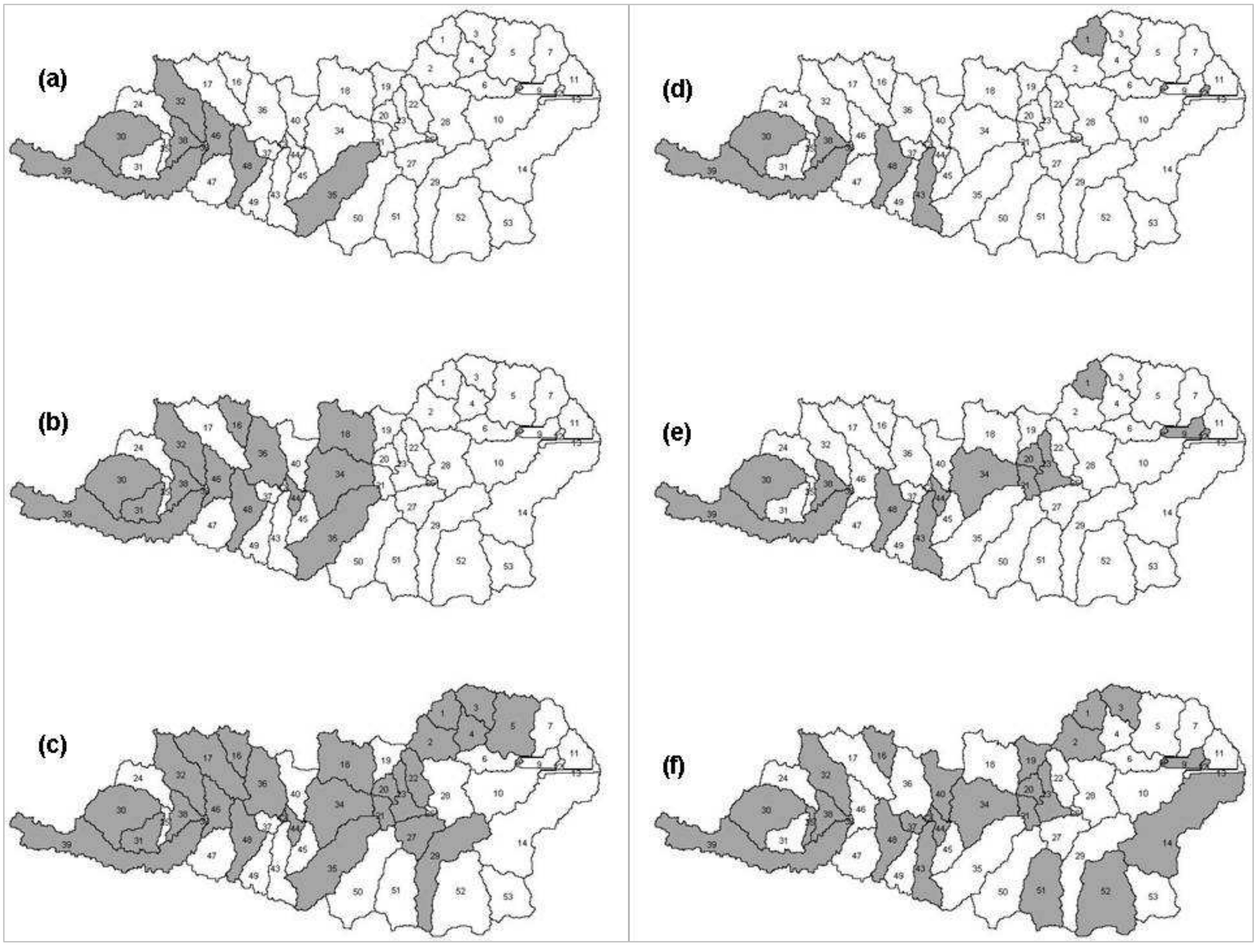

Figure 6.5. Distribution of watershed sub-basins for sediment BMP selection: target method (a) 10%, (b) 25%, (c) 50% and random method (d) 10%, (e) 25%, and (f) 50%

6.4.2 Fecal Bacteria and Sediment Yields

6.4.2.1 Overland Flow Output

The removal in annual average fecal bacteria concentration and sediment yields by overland flow process were impacted due to BMP adoption. When the VFS were applied in 100% sub-basins of the watershed, the reduction in annual average fecal bacteria concentration was about 79%, from 2134 cfu 100 mL^{-1} to 438 cfu 100 mL^{-1}. The reduction in fecal bacteria concentration due to 10% BMP adoption was 20% for target approach whereas it was about 12% for random approach. The highest difference between target and random approach fecal bacteria reduction was determined at 50% BMP adoption where target approach removed about 60% of the fecal bacteria whereas random approach removed about 42% (Fig. 6.6). The larger numbers of fecal bacteria were coming out from the grazed-lands as compared to non-grazed or cropland in this watershed. Grazed-lands were about equally distributed in the watershed. Since many of the sub-watersheds were ranked (Table 6.4) with about close concentration of fecal bacteria, the highest reduction only occurred when 50% of the sub-watersheds adopted BMP.

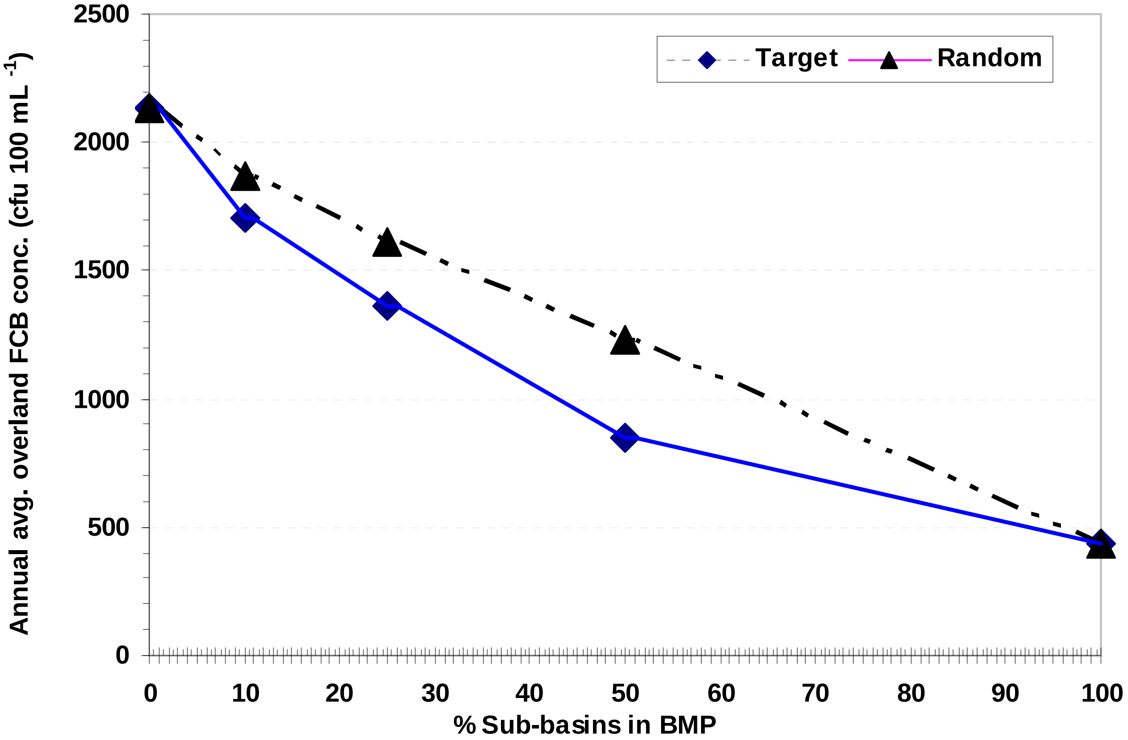

Figure 6.6. Watershed sub-basins and annual average overland flow fecal bacteria response

The annual average sediment yield removal by overland flow process was also impacted due to BMP adoption. When the VFS were applied in to the 100% of the sub-basins of the watershed, the reduction in annual average sediment yield was about 82%, from 2.17 ton ha^{-1} to 0.39 ton ha^{-1}. The reduction in sediment yield due to 10% BMP adoption was 46% for target approach whereas it was about 28% for random approach. The highest difference between target and random approach sediment yield reduction was seen at 25% BMP adoption where target approach removed about 63% of the sediment yield whereas random approach removed about 33% (Fig. 6.7). The sediment yield was mostly dependent on the slope of the HRU/sub-basin, and % cropland area in the sub-basins.

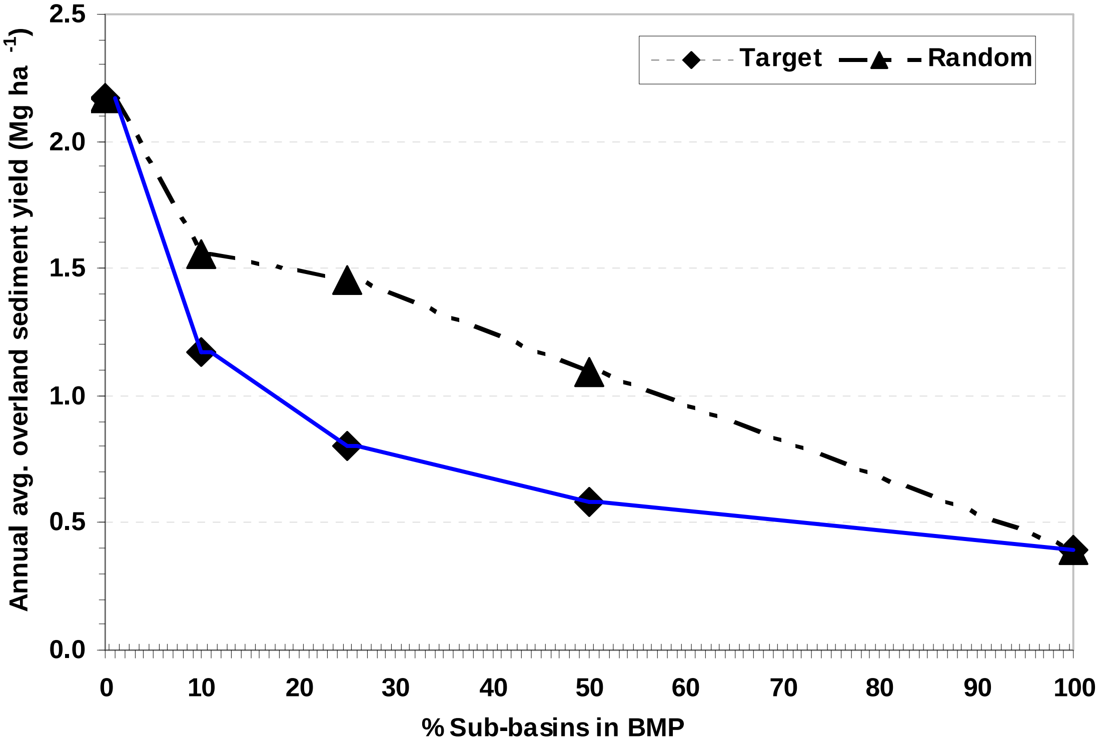

Figure 6.7. Watershed sub-basins and annual average overland flow sediment yield response

6.4.2.2 Watershed Outlet Flow Output

The application of VFS to the edge of the HRUs did not yield measurable differences in annual average fecal bacteria concentration at the outlet of the watershed (Richland outlet). Applying VFS showed good impact only in the overland flow process. Since the estimated direct point loads from livestock (8.5%), human (10%), and wildlife (10%) sources were input in the model, direct point loads dominated the total fecal bacteria prediction at the outlet of the watershed. The fecal bacteria source loads applied on the land was determined to have no or less sensitivity in previous study (chapter 2). The direct point loads were found more sensitive due to only channel flow process in the model. The contribution of overland flow process fecal bacteria at 0% BMP adoption (Log 3.3) was less than 1% of the total fecal bacteria (Log 5.79) predicted at the outlet of the watershed (Richland) where direct point source loads were inputted (Fig. 6.8). It is one of the interesting results determined in this study, which is possible when direct point load conditions are simulated. The non-point source loads of bacteria had chances of reduction through die-off and sorption during overland flow process whereas point loads had only channel flow process.

The annual average sediment yield removal at the outlet of the watershed (compared with Richland outlet) was about 36%, from 5009 tons to 3175 tons when applying BMP to 100% of the sub-basins. The reduction in sediment yield due to 10% BMP adoption was 12% for target approach and about 2% for random approach. The highest difference between target and random approach sediment yield reduction was seen at 50% BMP adoption where target approach removed about 22% of the sediment yield whereas random approach removed about 7% (Fig. 6.9).

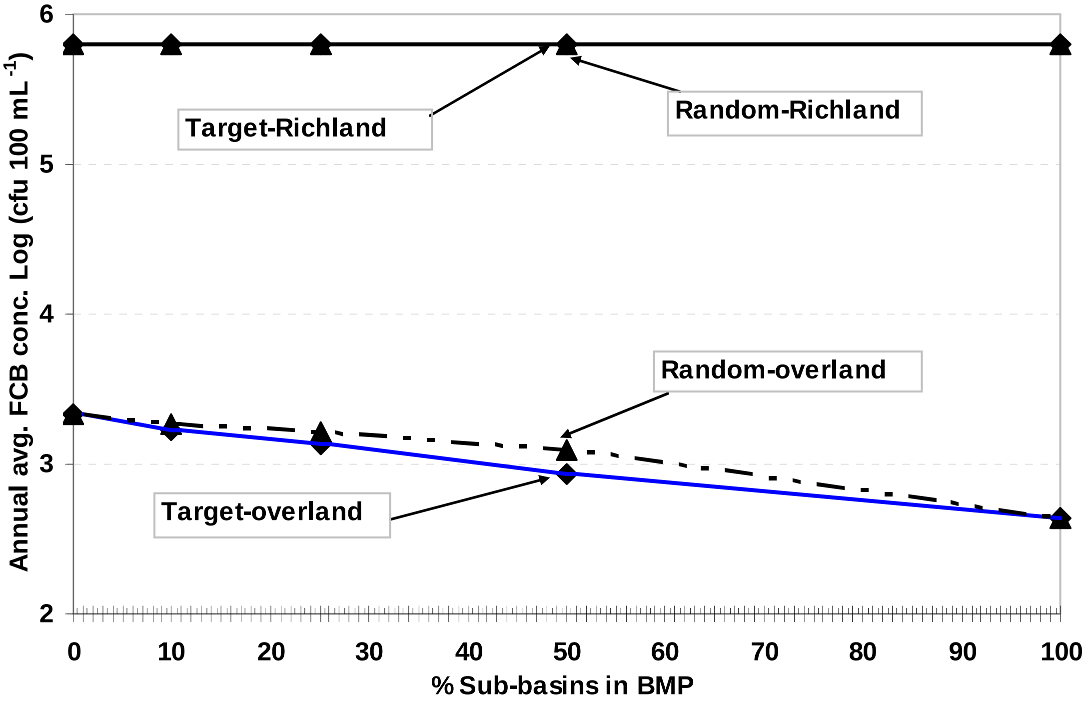

Figure 6.8. Watershed sub-basins and annual average overland and watershed outlet fecal bacteria response

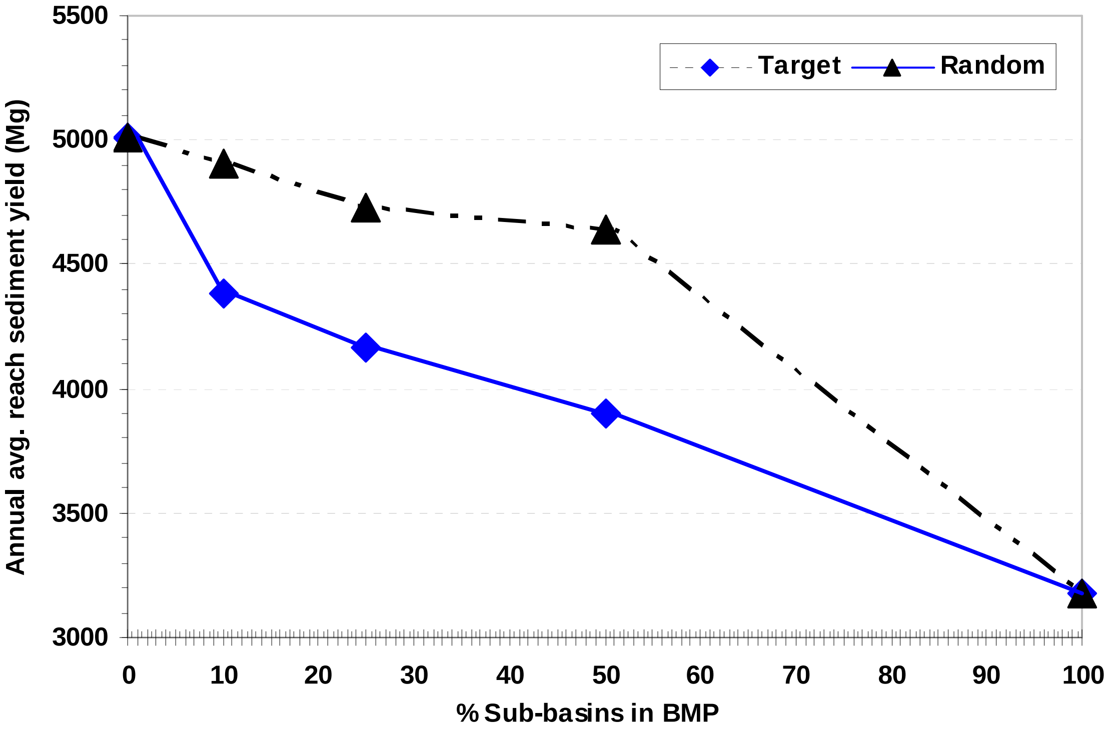

Figure 6.9. Watershed sub-basins and annual average overland flow and watershed outlet sediment yield response

6.5 Conclusions

The concept of identifying, selecting, and targeting critical areas of point and non-point source pollution has been widely recognized and studied for pollutant remediation. A watershed modeling approach was used to quantify the impacts of implementing a single BMP on incremental increases in watershed sub-basins scale to evaluate the effectiveness of the targeted approach vs. the random approach in reducing the estimated pollutant loadings, both overland and at the watershed outlet (Richland). Priority areas for the targeted approach were selected based on the model predicted sediment yield and fecal bacteria concentration. A targeted watershed modeling approach using SWAT was found to be more effective in reducing the sediment yield load for both overland and at watershed outlet whereas it was effective only for reducing overland flow bacteria. This study evaluated effectiveness of various VFS lengths in removing fecal bacteria and sediment yield from the agricultural watershed using SWAT model. This study determined that applying BMPs using target approach can be more cost-effective than random approach. However, other BMPs such as stream fencing to reduce cattle access to the stream, rotational grazing, and variable percentage of direct point loads could be tested for future studies.

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CHAPTER 7 - CONCLUSIONS AND RECOMMENDATIONS

7.1 Conclusions

Pathogen transport processes can be modeled at the watershed scale from the location of fecal matter deposition to the receiving waters. These models can help in evaluating methods to abate pathogen pollution to surface waters. This study developed and demonstrated methods to characterize fecal bacteria source loads and to assess the local and global sensitivity of model parameters, input parameters and bacteria source application methods. The potential fecal bacteria source loads were characterized using readily available data for livestock, human, and wildlife to use in modeling at the watershed scale that can be used for any other agricultural watersheds in the nation. It is essential to know the influence of the model parameter and input parameters to improve model accuracy. Therefore, the results of this study can help in watershed management and modeling decisions choosing more realistic model parameters to the natural life perspectives.

Calibration and validation of the SWAT model (2005) in two sub-watersheds of the Upper Wakarusa watershed using about one year (January to December, 2004) of measured data for daily flow (R^2 and E values up to 0.89) and sediment (R^2 and E values up to 0.77) allowed model to reasonably predict nutrients (R^2 and E values up to 0.78) and total fecal bacteria concentration (R^2 and E values up to 0.46). The model- predicted results varied spatially with size of the watersheds, landuse, topography, etc; however, the overall results were reasonable.

The calibrated and validated model in three sub-watersheds and whole Upper Wakarusa watershed using about three years (2004 to 2006) for measured data for daily flow (R^2 and E values up to 0.84), and sediment (R^2 and E values up to 0.87) allowed model to reasonably predict nutrients (R^2 and E values up to 0.85), and total fecal bacteria (R^2 and E values up to 0.52). The SWAT model worked reasonably with three years of climatic variations and spatially varied watershed characteristics. However, it appeared that modeling fecal bacteria had some potential uncertainties, as similar to other pollutants. The uncertainty in model performance potentially came through the spatial data used in generating model inputs, climatic data, monitoring data, and BST data. Although source-specific fecal bacteria modeling had more uncertainty than total bacteria modeling, the SWAT model evaluation for the source-specific bacteria modeling was successful to the combination of two sources of fecal bacteria concentration (R^2 and E values up to 0.71) at the watershed scale.

The SWAT model evaluation for each single source-specific fecal bacterium had low fit of model performance (R^2 and E values up to 0.39). However, the slopes (up to 0.73) of the model results were found reasonable. The single source of source-specific bacteria modeling had the largest possible uncertainty than combined bacteria sources or total bacteria sources in this study. Although

R^2 and E values found were not overwhelming for bacteria concentration it is the first effort of its kind to predict total and source-specific fecal bacteria concentrations at daily time scale.

The year 2006 was relatively drier than other two. There was only one water quality sample collected for year 2006. This study utilized only fifteen water quality samples over the three years period, which is still low. More data points might have allowed more conclusive results. The SWAT model prediction was sensitive to the daily rainfall-runoff events and fecal bacteria loadings from different sources, especially direct point loads.

7.2 Recommendations for Future Research

Water quality models are beneficial in helping develop TMDLs and as educational tools for the watershed and source characterization process for both stakeholders and modelers. Variability in model output caused by inaccurate input estimates can be reduced by decreasing the uncertainty in the inputs through increasing the number of measurements of the parameter and improving the methods used to measure the parameter (Haan and Skaggs, 2003). Benham et al. (2006) emphasize that fecal bacteria simulation using water quality models needs more research in improving source characterization of both animal (behavior patterns, habitat and population density, and accurate estimations of bacteria production types and variability) and human sources (reliable surveys of septic/sewage locations and bacteria productions for different populations).

This dissertation considered three sources of fecal bacteria (livestock, human, and wildlife) in modeling. Uncertainty in both model and measurements resulted in fair simulation of all sources, but poor agreement was found for individual sources, due to the added uncertainty in bacteria source tracking methods. However, future study may focus on the following recommended studies (especially for MS students).

The SWAT bacteria sub-model user should have, in addition to hydrologic and pollutant transport expertise, holistic knowledge of bacteria type and sources, die-off and re-growth, transport process, and current knowledge on pathogen modeling to develop reasonable assumptions and results. In addition, model use to predict fecal bacteria concentration at the watershed scale may require some knowledge in selection of input parameter values and bacteria source application methods.

7.2.1 Small Watershed Source-Specific Fecal Bacteria Modeling

The current research in fecal bacteria transport modeling are focused on either laboratory, plot scale, large watershed scale and is typically oriented to develop or support TMDLs. The results from the laboratory or plot scale studies can not be replicated into large watershed studies because they are done in either controlled or micro-environmental conditions such as temperature, soil characteristics, climate, etc. It is therefore important to conduct small watershed scale studies that can help reduce uncertainties in source-specific fecal bacteria modeling. In addition, bacteria source characterization for more specific sources of fecal bacteria (three sources or more) may be needed for site-specific bacteria modeling to reduce the uncertainty. Chapter 5 of this dissertation described the uncertainty inherent in the fecal bacteria modeling. The degree of uncertainty even increased when modeling a single source of fecal bacteria. However, more site specific bacteria source characterization, and accurate microbial source tracking may help in modeling a single source of bacteria separately.

The objectives of this study would be to calibrate and validate the SWAT model in a small-watershed scale using field-measured hydrological and water quality data for (a) single source-specific fecal bacteria (fecal coliform and *E. coli*) and (b) *Bacteroidales* 16S rDNA based source-specific microbial source tracking (MST) data. These results will be compared to determine strengths and limitations of each method.

At least three small scale watersheds (about 1 km^2) in Kansas will be selected for both calibration and validation of this study. The SWAT model will be calibrated first in a watershed then validated in two additional watersheds. The watershed specific management condition data will be collected for the period of the study, which is typically 3 years. Other required data will be collected to input in the model. In addition to the fecal bacteria source characterization described in Chapter 4 of this dissertation, more sources of bacteria may be identified. The stream flow will be measured using the method described in Chapter 2 of this dissertation and water quality samples will be taken and analyzed (flow, sediment, pathogen concentration, and MST data) for the period of the study. The *Bacteroidales* 16S rDNA method will be utilized for MST.

Vogel et al. (2007) successfully utilized the *Bacteroidales* 16S rDNA based MST method to fraction fecal bacteria sources from livestock, wildlife and human in Plum Creek watershed (580 km^2) in south-central Nebraska. Although the *Bacteroidales* 16S rDNA method uses expensive equipment, it does not require culturing and data library, which reduce the uncertainty of source tracking. The field measured and lab analysis results will be used to calibrate and validate the SWAT results. The model-predicted results will be compared with measured data using mean, median, standard deviation, coefficient of determination, and Nash-Sutcliffe efficiency index (Nash and Sutcliffe, 1970).

7.2.2 Evaluate BMP Targeting methods using SWAT and AnnAGNPS models

A goal in the design of pollution reduction programs is to achieve the greatest possible reduction for the money spent (Heatwole et al., 1987). Braden et al. (1989) discussed the economic advantage of selectively applying BMPs to reduce NPS pollution. They stressed that selective applications are likely to be cheaper and less disruptive overall. Implementing stricter pollution control in areas where it will be most cost-effective is known as targeting (Veith et al., 2001). Targeting focuses on critical areas within the watershed. As a result, targeting often reduces costs as compared to first-come, first-served approaches such as cost-share. A number of studies have developed targeting procedures to enable watershed-specific evaluation of NPS pollution control. Targeting methods incorporating pollution prediction models have been demonstrated. Additionally, spatial variability at the watershed level or hydrologic response units (HRUs) level has been shown to be an important aspect of effective targeting.

The objectives of this study would be to (a) calibrate and validate the SWAT and Annualized Agricultural Non-Point Source (AnnAGNPS) models for flow, sediment, and nutrients, (b) use the SWAT model to model pathogen transport, (c) identify the critical locations of the watershed from the perspective of each pollutant where BMP implementation could make the most effective impact, and (d) test and recommend the BMPs suitable to reduce each pollutant to meet the Kansas water quality standards.

At least three large scale watersheds (about 1000 km^2) in Kansas will be selected for this study. The flow data will be measured following the methods used in Chapter 2 of this dissertation and the water quality grab samples will be collected from the outlet of each watershed and the data will be analyzed for the sediment, nutrients, and pathogens. The SWAT and AnnAGNPS model will be calibrated in the first watershed then verified in the additional two watersheds for the study period, which is typically 3 years. The SWAT model will be utilized to model pathogens in the watersheds using fecal bacteria source characterization methods developed in Chapter 4 of this dissertation. Both SWAT and AnnAGNPS will be utilized to compare target vs. random BMP implementation methods as described in Chapter 6 of this dissertation. In order to test the BMP effects on sediment and nutrients, the reduced tillage managements (conservation till, no-till) and VFS will be used. In addition, other BMPs for pathogen reduction (reduced cattle access to the stream, rotational grazing) will be considered. The models predicted results will be compared with measured data using mean, median, standard deviation, coefficient of determination, and Nash-Sutcliffe efficiency index (Nash and Sutcliffe, 1970) to know, which model is performing better. The pollutants based BMP targeting will be recommended for the field level application.

7.2.3 Fecal Bacteria Transport from Manure-applied Clay Textured watersheds

Manure application to crop-land is a common agricultural practice. This common practice however, poses a potential threat of fecal contamination of surface water. Several scientists have found that temperature and soil water content affect fecal bacteria survival, and that soil texture and structure affect their transport (Howell, 1996; Jiang et al., 2002; Collins, 2003; Stevik et al., 2004; Unc and Goss, 2004; Wang et al., 2004). The objective of this research will be to conduct a field experiment monitoring the movement of fecal bacteria through three clay dominated watersheds after an un-incorporated manure application using the SWAT model.

Three small homogeneous watersheds (about 1 km^2) having clay dominated textured soils, similar land uses (similar cropping system and rotation) will be selected. The model input data will be developed for each watershed as described in Chapter 4 of this dissertation. The three watersheds will be characterized for: soil texture (physical characterization), bulk density, organic matter content, surface roughness, soil fecal bacteria concentration, flow discharge from each watershed outlet, and concentration of fecal bacteria at the outlet of each watershed. Once all of the preliminary characterization measurements are made to describe each watershed, the beef manure application can be made before planting. Different manure application rates and dates (April and October) can be tested. The manure application method will be broadcast as a solid without any incorporation. In addition, the manure at time of application will be tested for the concentration of fecal bacteria present.

The watershed outlet will be monitored continuously by establishing a “gage station” (equipped with H-flume, a stilling well with a potentiometer, ISCO 3700 sampler, CR10X data logger, raingages) as described by Parajuli (2003) to measure the fecal bacteria concentration due to transport. The ISCO sampler will collect water quality samples when any runoff events occur. Water samples should be started several weeks prior to manure application to establish a baseline for fecal bacteria transport. In addition to the runoff measurements, measurements from the treated soil will be made to monitor the survival and filtration of the bacteria by the soil. Continuous measurements of soil temperature, soil water content, air temperature, and rainfall will be made to monitor the watershed over time. The soil temperature and soil water content can be measured using CS615 water content reflectometer in the selected points to represent each watershed. The water quality sample collected from each watershed outlet will be analyzed (sediment, fecal bacteria concentration). The SWAT model input data will be modified when necessary based on the watershed conditions. The model predicted results will be compared with measured data using mean, median, standard deviation, coefficient of determination, and Nash-Sutcliffe efficiency index (Nash and Sutcliffe, 1970).

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Appendix A - Detail methods for modeling three sources of fecal bacteria

Appendix A. Detail methods for modeling three sources of fecal bacteria

- **Wildlife categories in Wakarusa**
    - Large mammals: *deers*
    - Small mammals: *raccoon* (37.8%), *opossum* (20.8%), *skunk* (21.8%) which is 80.4% of total road-kill data for Kansas.
    - Birds, indigenous: *wild turkey*.
    - Birds, migratory: ducks, geese and sandhill cranes

- **Data we need for wildlife model inputs:**
    - Density (animals/mi^2) to get total wildlife population in watershed,
    - Bacteria excreted (cfu/animal) to get total bacteria load
    - Manure produced (lb/day/animal) to get land application amount (NOTE: If data are in lb/day/lb live weight, then also need average live weight)
    - Habitat Land-use type where defecation occurs to know where to land-apply the manure

- **Large mammals: Deer**
    - Density: 19 deer management units (DMU) – 3.16 deer/mi^2 for whole state. But based on deer harvest data, 28% of deer in DMU 9, 10, 19, and 14 (NE Kansas) were harvested in 2004-05 – this led to 9.13 deer/mi^2 in NE Kansas. Deer in Wakarusa: 3356 based on land area.
    - Bacteria: FCB 7.72 E9 cfu/head/day (Yagow, 2001)
      FCB 3.5 E8 cfu/day/animal (Va Tech Bacteria Load Calculator)
    - Manure: current assumption is 50 lb/1000 lb deer (AU)
    - Live weight: average live weight of a deer was assumed 200 lbs (http://www.gpnc.org/deerwt.htm)
    - Habitat: forest, cropland and rangeland. However, they mostly defecate into the forest and croplands.

- **Small mammals: Raccoons, Opossum, Skunk**
    - Density: Roadside Indices (animals per 1000 mi driven) from road-kill data collected by 76 KDWP employees to and from work (we used Summer 2002, though there were other years). We will assume driven miles were well distributed among land-use types. *Raccoon* (2511, 37.8%), *opossum* (1383, 20.8%), *skunk* (1449, 21.8%) (6647, 80.4% of total road-kill data for Kansas; if the 597 [9.0%] armadillos are removed, since they would not be found in NE KS, the three species represent 41.5%, 22.9%, 24.0%, and 88.3% of road kill, respectively). The indices are summarized by 5 KDWP Regions
    - Bacteria: FCB 8.14 E9 cfu/day/head (raccoon) and 5.45 E7 cfu/day/animal (muskrat) – (source for both: Yagow, 2001)
    - Manure: Assuming 10% live weight per day. Live weight varied from 8-30 lb, depending on species (Raccoon: 30 lb; Opossum: 10 lb; Skunk: 8 lb)
    - Habitat: forest

- **Birds indigenous: Turkey**
    - Density: Don't have total population data, but we have some indices for each region of Kansas, quantified as turkeys/100 mi^2 driven from mail carriers. East KS: more forests, can see only a few meters; West KS: can see 100s of meters. So indices vary from E to W Kansas. We assumed 50 m sight distance in Wakarusa to convert 18.85 turkey/100 mi (2004) to 303 turkey/mi^2; 36.96 turkey/100 mi (2005) to 595 turkey/mi^2. Total turkey population in Wakarusa of 111,568 (2004) and 218,755 (2005). Assumed driven miles were well distributed among land-use types.
    - Bacteria: FCB 0.62 E10 cfu/day/AU (AU=1000 lb live weight) – ASABE Standard Manure: 47 lb/day/AU (AU=1000 lb live weight) – ASABE Standard. Assumed average turkey weight is 15

    lb. Jim Pitman, (KDWP) found juvenile female (8 lb), juvenile male (15 lb), adult female (15 lb), and adult male (20 lb).
  - <u>Habitat:</u> forest, cropland and rangeland. However, they mostly defecate into the forest and croplands. (Jim Pitman, KDWP) said that we can't say specific proportion that occurs in woodland or cropland. But they defecate in cropland while feeding. Also prefer to defecate in roost trees (where they spend nights).

- **Birds migratory: ducks, geese and sandhill cranes**
  - Based on Kansas Waterfowl Migration Report 2003 and 2004, migratory birds in Kansas will be available during 7 months of the year (September to March).
  - Migratory birds including duck, geese, and sandhill crane's population will be taken 2 times a month during 7 months of the year.
  - Data for migratory birds will be taken from Kansas water reservoirs and wetlands.
  - Based on water surface areas in the Wakarusa watershed, a monthly population of about 1883 ducks, 3905 geese, and 487 sandhill cranes are estimated for the watershed.
  - Although water bodies and wetlands are the primary habitat for these migratory birds they also defecate into the cropland when feeding.
  - FCB concentration: duck-8.1x10^{11} colonies^{-1}day^{-1}AU^{-1} (ARURI, 2002), geese-2.03x10^{14} colonies/day/AU (vTech, 2006), sandhill crane 1.71x10^{9} cfu/day/AU (USDA, animal and plant health inspection service, 1998).

- **Livestock categories in Wakarusa**
  - <u>Beef cattle, feedlots/barnyards</u>: October through April: cattle held largely in confined areas.
  - <u>Beef cattle, grazing</u>: Mostly summer grazing (April to September) in pastures (native grass, fescue). Fescue starts one month earlier than native.
    - Cattle behavior - may need to model different behaviors and resulting "manure application methods" to simulate these behaviors (ranging from well-distributed on grazing lands to point source load into stream.
  - <u>Beef cattle, winter feeding</u>: about 40% of the total pasturelands are used for winter feeding areas (Will Boyer, 2006).

<u>Beef cattle, grazing</u>

<u>Density</u>:

- USDA report (2002 Ag Census, www.nationalatlas.gov/atlasftp.html) with total cattle (animals, including feedlots, grazing, etc.) per 100 ac of farm-land in each county.
- Used Farm-to-total area ratio [(crop/land) / (crop/farm) = (farm/land)] to express Census data as cattle per total-land area rather than cattle per farm-land area.
- Then, used total county area land-area to determine total animals/county.
- Assuming cattle were well distributed across all land area in each county, multiplied animals/county by % of each county in Wakarusa watershed to get total animals (by county) in Wakarusa watershed.
- Subtracted permitted (KDHE permits and certifications) cattle from total animals/county to estimate number in grazing situation in each county. (working with animals, not AUs). Same thing done for total animals (by county) in Wakarusa watershed.
- Thus, we had two estimates of # of cattle/calf per ha grazed: by total county data (0.2048/ha average) and by portion of each county data in watershed (0.2086/ha average). This also yielded two estimates of the ratio of grazed animals to total animals (0.81 and 0.77, respectively).
- Using total grazing land in watershed (=54,967.52 ha, assuming 57% of watershed in grassland from 1997 windshield survey) was compared to grazing land needed to support these (15,527) cattle at 3.04 ha/pair (= 47,202.71 ha). Thus, needed 85.87% of grazing land to support estimated

  cattle in watershed. This number reasonably represents field conditions but grassland is being converted to residential grassland in the watershed (Will Boyer, 2006).

- Bacteria excreted (cfu/AU) [ASAE Standards]
- Manure produced (lb/day/AU) [ASAE Standards] to get land application amount
- Location The estimated numbers of animals is good for the summer grazing period. The fate of summer grazing livestock – 40% of these return to confined feedlots in winter (these would not be included in KDHE data), 40% return to winter feeding areas in pasture, and 20% sold/slaughtered (Will Boyer, 2006).

Onsite Wastewater System

- Number of failing systems. Used GIS to designate rural households and failing septic systems
    - Rural household: House or group of houses with an approach road/driveway
    - Assuming every rural household has 1 septic system, Wakarusa watershed has 2136 septic systems.
    - Based on KDHE's estimation for Kansas, assume 40% septic systems are failing (not meeting design objectives)
    - Thus, 854 would be considered failing.
    - WRAPS 2003 document suggests 1057 systems are failing.
- Bacteria Load.
    - One failing septic system contributes 0.79 m^3 effluent/day (based on 3 people, 70 $gal^{-1}person^{-1}day$).
    - Bacteria concentration $6.3x10^6$ cfu/100 mL (Overcash & Davidson)
    - No Failing = no pollutant load to watershed
    - Failing systems:
        - Estimate number of failing systems per sub-watershed
        - Estimate land areas to land apply daily septic tank effluent (number of failing systems x assumed land area of soil absorption field)
        - Land apply septic effluent into non-grazed land HRUs that are located near by residential area
        - Use similar calculation as above to estimate daily application volume, bacteria concentration, etc.

Appendix B - Permitted/certified active feedlots at Upper Wakarusa watershed

Appendix B. Permitted/certified active feedlots at Upper Wakarusa watershed

Permit animal	County	Location	Total animal	Longitude	Latitude
Beef	Douglas	Lawrence	24	-95.40005	38.97860
Beef	Douglas	Lawrence	34	-95.40005	38.97860
Dairy	Douglas	Overbrook	34	-95.45473	38.87703
Beef	Douglas	Lawrence	200	-95.45503	38.97847
Beef	Shawnee	Wakarusa	280	-95.69635	38.90616
Beef	Shawnee	Wakarusa	110	-95.67787	38.90625
Beef	Shawnee	Wakarusa	299	-95.67805	38.92078
Beef	Shawnee	Berryton	250	-95.69646	38.92072
Beef	Shawnee	Wakarusa	150	-95.65929	38.89175
Beef	Shawnee	Auburn	350	-95.90015	38.90630
Beef	Osage	Carbondale	300	-95.63963	38.83330
Beef	Osage	Overbrook	60	-95.50956	38.86229
Swine	Osage	Carbondale	390	-95.62102	38.80418
Swine	Wabaunsee	Harveyville	3000	-95.95565	38.86266
Beef	Osage	Carbondale	100	-95.58423	38.84762
Swine	Osage	Carbondale	610	-95.63957	38.78977
Swine	Osage	Berryton	120	-95.60303	38.86231
Beef	Osage	Overbrook	360	-95.52802	38.83314
Swine	Shawnee	Wakarusa	525	-95.77062	38.90560
Beef	Douglas	Berryton	800	-95.47278	38.92054
Beef	Osage	Carbondale	360	-95.62102	38.80418

Appendix C - Estimated point loadings of fecal bacteria sources for Upper Wakarusa watershed sub-basins

Appendix C. Estimated point loadings of fecal bacteria sources for Upper Wakarusa watershed sub-basins

	Estimated loadings day^{-1}			Estimated fecal bacteria concentration in sources			
	Live + wild[1]	Human + wild[2]	Live + human[3]	Live + human	Livestock + wild	Human + wild	All sources
Sub-basin	effluent (m^3)	effluent (m^3)	effluent (m^3)	cfu 100 mL^{-1}	cfu 100 mL^{-1}	cfu 100 mL^{-1}	cfu 100 mL^{-1}
1	0.252	0.741	0.877	37113	126904	1173	34973
2	0.423	2.256	2.485	37780	212935	2088	36519
3	0.309	0.595	0.762	63456	155914	955	58309
4	0.254	0.519	0.656	49820	127984	916	45959
5	0.714	2.021	2.407	106903	359596	1518	100545
6	0.300	0.132	0.294	153016	150966	1617	124579
7	0.402	2.093	2.310	36716	202396	2033	35461
8	0.012	0.003	0.010	8034	6217	125	6217
9	0.146	0.034	0.113	95196	73661	1480	73661
10	0.742	0.504	0.905	305297	373941	2658	258081
11	0.288	0.066	0.221	187263	144901	2911	144901
12	0.025	0.006	0.019	16079	12442	250	12442
13	0.080	0.018	0.061	51898	40158	807	40158
14	1.582	1.729	2.584	486201	797355	3634	428200
15	0.283	0.065	0.218	184077	142436	2862	142436
16	0.652	2.118	2.471	87178	328415	1560	82573
17	0.698	1.145	1.522	160725	351450	1461	146080
18	0.251	0.994	1.130	29201	126555	1516	27905
19	0.137	0.127	0.201	47206	69222	549	40989
20	0.146	0.240	0.319	33912	73598	680	30824
21	0.283	0.954	1.107	37216	142481	1336	35311
22	0.268	0.236	0.381	94774	135157	896	81961
23	0.387	0.454	0.663	113561	195107	1063	100594
24	0.079	0.034	0.077	40774	39774	463	33127
25	0.024	0.005	0.018	15329	11861	238	11861
26	0.369	0.879	1.078	63870	185765	1118	59488
27	0.658	0.628	0.983	221153	331675	1820	192556
28	0.867	1.104	1.573	240062	436982	1918	214054
29	0.787	0.784	1.210	257084	396636	2068	224677
30	0.296	0.465	0.625	70475	148912	884	63857
31	0.602	0.758	1.083	168262	303531	1441	149886
32	0.006	0.001	0.005	3878	3001	60	3001
33	0.798	1.104	1.536	208373	402201	1717	187002
34	0.997	2.515	3.054	163886	502318	1731	153155
35	0.609	0.727	1.057	176317	306898	1490	156414
36	0.110	0.089	0.148	40959	55351	477	35157
37	0.239	0.420	0.549	52413	120223	834	47872
38	1.330	1.528	2.247	394958	670040	2978	349283
39	0.391	0.376	0.587	130857	197090	1164	114007
40	0.001	0.000	0.001	935	723	15	723
41	0.017	0.052	0.061	3246	8575	1021	3060
42	0.415	0.778	1.003	86726	209264	1077	79553
43	0.110	0.136	0.196	31051	55243	527	27634
44	0.264	0.886	1.029	34984	133093	1317	33184
45	0.321	0.487	0.660	78576	161693	918	71005
46	0.478	1.047	1.305	88392	240883	1191	81904
47	0.455	0.946	1.192	87656	229307	1150	80957
48	0.322	0.471	0.645	80867	162167	917	72882
49	0.902	1.271	1.759	232497	454684	1875	208939
50	0.712	0.942	1.327	192095	358926	1605	171788
51	1.058	1.370	1.942	289390	533178	2242	258383
52	0.534	0.583	0.871	164011	268813	1401	144447
53	0.000	0.000	0.000	35	27	1	27

[1] Livestock and wildlife

[2] Human and wildlife

[3] Livestock and human

Appendix D – Measured flow, sediment, nutrients and fecal bacteria

Appendix D. Measured flow, sediment, nutrients and fecal bacteria

Auburn

Day	Flow	Fecal bact. conc.[1]	TSS[2]	TN[3]	TP[4]
2004	**cfs[5]**	**cfu 100/mL**	**mg/L**	**mg/L**	**mg/L**
166	9.7	40	68	ND[6]	ND
170	686.3	96	2336	0.284	0.178
179	414.0	76	1104	0.206	0.149
180	746.0	53	296	0.334	0.201
187	30.2	11	12	0.044	0.020
191	158.2	20	472	0.111	0.089
206	1257.0	560	1360	0.201	0.144
222	5.2	3	24	ND	ND
237	1790.4	220	292	0.129	0.078
2005					
98	44.0	124	4.2	0.003	0.001
156	193.6	990	88.0	0.123	0.099
162	641.6	200	332.9	0.328	0.201
232	184.6	72	46.1	0.143	0.067
258	3.0	1	0.2	ND	ND
2006					
119	141.5	89	42.5	0.154	0.103

Lewelling Road

Day	Flow	Fecal bact. conc.	TSS	TN	TP
2004	**cfs**	**cfu 100/mL**	**mg/L**	**mg/L**	**mg/L**
166	63.4	27	40	0.004	0.001
170	1280.6	130	2884	0.334	0.206
179	772.6	95	1216	0.249	0.166
180	1392.0	48	148.9	0.458	0.223
187	56.4	44	8	0.062	0.026
191	295.1	120	400	0.124	0.092
206	2345.0	29	236	0.226	0.171
222	9.7	100	12	0.001	ND
237	3341.0	410	484	0.156	0.091
2005					
98	82.1	111	13.1	0.003	0.002
156	361.2	2100	140.0	0.145	0.105
162	1197.1	600	355.0	0.386	0.231
232	344.5	105	59.0	0.155	0.103
258	5.6	1	0.5	ND	ND
2006					
119	446.0	200	214.3	0.101	0.089

[1] Fecal coliform bacteria concentration

[2] Total suspended solid

[3] Total nitrogen

[4] Total phosphorus

[5] Cubic feet per second

[6] No data

Hwy 75

Day	Flow	Fecal bact. conc.	TSS	TN	TP
2004	**cfs**	**cfu 100/mL**	**mg/L**	**mg/L**	**mg/L**
166	21.2	22	24	0.001	0.001
170	1501.4	530	3720	0.377	0.254
179	905.8	490	1760	0.226	0.177
180	1632.0	490	460	0.521	0.354
187	66.1	260	16	0.068	0.034
191	346.0	100	368	0.154	0.113
206	2749.9	630	1444	0.389	0.201
222	11.4	77	4	0.002	0.001
237	3916.8	1000	377	0.412	0.326
2005					
98	96.3	129	12.9	0.006	0.003
156	423.5	1400	128	0.178	0.129
162	1403.5	800	410	0.392	0.312
232	403.9	137	95	0.201	0.131
258	6.6	1	0.81	ND	ND
2006					
119	514.6	300	245	0.121	0.100

Richland

Day	Flow	Fecal bact. conc.	TSS	TN	TP
2004	**cfs**	**cfu 100/mL**	**mg/L**	**mg/L**	**mg/L**
170	1840	3000	2080.0	0.772	0.411
179	1110	1900	1504.0	0.479	0.254
180	2000	5400	612.0	1.077	0.653
187	81	1000	32.0	0.753	0.328
191	424	730	43.2	0.172	0.151
206	3370	2500	1328.0	1.475	0.777
222	14	61	2.0	0.003	0.001
237	4800	5300	716.0	1.490	0.898
2005					
98	118.0	175	12.2	0.130	0.072
156	519.0	11600	152.0	0.386	0.249
162	1720.0	1000	956.0	0.622	0.320
232	495.0	311	142.0	0.322	0.172
258	8.1	1	1.5	ND	ND
2006					
119	835.0	610	365.6	0.522	0.358

Deer Creek

Day	Flow	Fecal bact. conc.	TSS	TN	TP
2004	**cfs**	**cfu 100/mL**	**mg/L**	**mg/L**	**mg/L**
170	228.2	108	912.00	0.096	0.051
173	13.4	13	40.00	0.015	0.009
180	248.0	148	112.00	0.134	0.081
187	10.0	20	0.28	0.093	0.041
191	52.6	53	35.00	0.021	0.019
206	417.9	418	1000.00	0.183	0.096
215	4.0	48	28.00	0.003	0.001
222	1.7	12	0.36	ND	ND
237	595.2	95	496.00	0.185	0.111
2005					
154	39.1	2000	256	0.023	0.015
156	64.4	200	212	0.048	0.031
162	213.3	200	332.9	0.078	0.040
232	61.4	17	6.1	0.040	0.021
258	1.0	1	0.2	ND	ND
2006					
119	110.1	112	23.4	0.065	0.045

Rock Creek

Day	Flow	Fecal bact. conc.	TSS	TN	TP
2004	**cfs**	**cfu 100/mL**	**mg/L**	**mg/L**	**mg/L**
170	333.0	103	996.00	0.14	0.07
173	19.5	20	3.40	0.02	0.01
179	200.9	81	532.00	0.09	0.05
180	362.0	162	136.00	0.19	0.12
187	14.7	15	1.20	0.14	0.06
191	76.7	27	344.00	0.03	0.03
206	610.0	610	2328.00	0.27	0.14
222	2.5	3	2.40	0.00	0.00
237	868.8	169	280.00	0.27	0.16
2005					
154	57.0	540	95	0	0
156	93.9	2000	240	0	0
162	311.3	200	125.6	0.1	0.1
232	89.6	9	21.3	0.1	0.0
258	1.5	1	0.2	ND	ND
2006					
119	42.6	35	6.4	0.1	0.1

Appendix E - Percentage probability of fecal bacteria sources

Appendix E. Percentage probability of fecal bacteria sources

Standard probabilistic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-14-04	0.049	0.275	0.675
Auburn 6-14-04	0.107	0.549	0.344
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.577	0.156	0.267
Auburn 6-14-04	0.107	0.549	0.344
Auburn 6-14-04	0.240	0.129	0.630
Auburn 6-14-04	0.240	0.129	0.630
Auburn 6-14-04	0.073	0.323	0.604
Auburn 6-14-04	0.003	0.139	0.858
Auburn 6-14-04	0.013	0.311	0.676
Auburn 6-14-04	0.045	0.505	0.450
Auburn 6-14-04	0.034	0.348	0.619
Auburn 6-14-04	0.034	0.348	0.619
Auburn 6-14-04	0.011	0.509	0.480
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.006	0.686	0.308
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.008	0.117	0.875
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Isolates (total 24) =	1	5	18
Probability (%) =	4	21	75

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-14-04	0.049	0.275	0.675
Auburn 6-14-04	0.107	0.549	0.344
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.577	0.156	0.267
Auburn 6-14-04	0.107	0.549	0.344
Auburn 6-14-04	0.240	0.129	0.630
Auburn 6-14-04	0.240	0.129	0.630
Auburn 6-14-04	0.073	0.323	0.604
Auburn 6-14-04	0.003	0.139	0.858
Auburn 6-14-04	0.013	0.311	0.676
Auburn 6-14-04	0.045	0.505	0.450
Auburn 6-14-04	0.034	0.348	0.619
Auburn 6-14-04	0.034	0.348	0.619
Auburn 6-14-04	0.011	0.509	0.480
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.006	0.686	0.308
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.008	0.117	0.875
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Auburn 6-14-04	0.024	0.295	0.681
Avergare fraction =	0.073	0.322	0.605
Average (%) =	7	32	60

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-18-04	0.162	0.450	0.388
Auburn 6-18-04	0.011	0.509	0.480
Auburn 6-18-04	0.024	0.295	0.681
Auburn 6-18-04	0.032	0.727	0.241
Auburn 6-18-04	0.020	0.531	0.449
Auburn 6-18-04	0.009	0.493	0.499
Auburn 6-18-04	0.012	0.280	0.708
Auburn 6-18-04	0.020	0.531	0.449
Auburn 6-18-04	0.032	0.727	0.241
Auburn 6-18-04	0.006	0.686	0.308
Auburn 6-18-04	0.006	0.686	0.308
Auburn 6-18-04	0.786	0.036	0.178
Auburn 6-18-04	0.006	0.292	0.702
Auburn 6-18-04	0.074	0.043	0.883
Auburn 6-18-04	0.351	0.040	0.608
Auburn 6-18-04	0.006	0.686	0.308
Auburn 6-18-04	0.162	0.450	0.388
Auburn 6-18-04	0.034	0.348	0.619
Auburn 6-18-04	0.024	0.295	0.681
Auburn 6-18-04	0.038	0.265	0.697
Auburn 6-18-04	0.032	0.727	0.241
Auburn 6-18-04	0.038	0.265	0.697
Auburn 6-18-04	0.049	0.275	0.675
Auburn 6-18-04	0.032	0.727	0.241
Avergare fraction =	0.082	0.432	0.486
Average (%) =	8	43	49

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-27-04	0.001	0.052	0.948
Auburn 6-27-04	0.006	0.292	0.702
Auburn 6-27-04	0.001	0.052	0.948
Auburn 6-27-04	0.001	0.123	0.876
Auburn 6-27-04	0.223	0.764	0.013
Auburn 6-27-04	0.008	0.117	0.875
Auburn 6-27-04	0.001	0.142	0.857
Auburn 6-27-04	0.034	0.348	0.619
Auburn 6-27-04	0.112	0.699	0.189
Auburn 6-27-04	0.001	0.130	0.870
Auburn 6-27-04	0.000	0.055	0.945
Auburn 6-27-04	0.006	0.283	0.711
Auburn 6-27-04	0.011	0.509	0.480
Auburn 6-27-04	0.001	0.123	0.876
Auburn 6-27-04	0.001	0.123	0.876
Auburn 6-27-04	0.006	0.292	0.702
Auburn 6-27-04	0.006	0.292	0.702
Auburn 6-27-04	0.049	0.275	0.675
Auburn 6-27-04	0.001	0.033	0.967
Auburn 6-27-04	0.000	0.055	0.945
Auburn 6-27-04	0.006	0.292	0.702
Auburn 6-27-04	0.011	0.509	0.480
Auburn 6-27-04	0.006	0.292	0.702
Auburn 6-27-04	0.001	0.052	0.948
Avergare fraction =	0.020	0.246	0.734
Average (%) =	2	25	73

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-28-04	0.024	0.295	0.681
Auburn 6-28-04	0.024	0.295	0.681
Auburn 6-28-04	0.004	0.110	0.887
Auburn 6-28-04	0.078	0.354	0.569
Auburn 6-28-04	0.032	0.115	0.853
Auburn 6-28-04	0.026	0.451	0.523
Auburn 6-28-04	0.024	0.295	0.681
Auburn 6-28-04	0.009	0.181	0.810
Auburn 6-28-04	0.575	0.392	0.033
Auburn 6-28-04	0.019	0.176	0.805
Auburn 6-28-04	0.162	0.450	0.388
Auburn 6-28-04	0.016	0.336	0.647
Auburn 6-28-04	0.024	0.295	0.681
Auburn 6-28-04	0.240	0.129	0.630
Auburn 6-28-04	0.104	0.510	0.386
Auburn 6-28-04	0.019	0.176	0.805
Auburn 6-28-04	0.240	0.129	0.630
Auburn 6-28-04	0.377	0.237	0.386
Auburn 6-28-04	0.577	0.156	0.267
Auburn 6-28-04	0.020	0.531	0.449
Auburn 6-28-04	0.240	0.129	0.630
Auburn 6-28-04	0.024	0.295	0.681
Auburn 6-28-04	0.049	0.275	0.675
Auburn 6-28-04	0.008	0.117	0.875
Avergare fraction =	0.121	0.268	0.611
Average (%) =	12	27	61

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 7-05-04	0.064	0.867	0.069
Auburn 7-05-04	0.107	0.643	0.250
Auburn 7-05-04	0.024	0.841	0.134
Auburn 7-05-04	0.065	0.756	0.179
Auburn 7-05-04	0.035	0.344	0.620
Auburn 7-05-04	0.714	0.197	0.090
Auburn 7-05-04	0.138	0.796	0.066
Auburn 7-05-04	0.153	0.835	0.012
Auburn 7-05-04	0.024	0.423	0.553
Auburn 7-05-04	0.275	0.617	0.108
Auburn 7-05-04	0.052	0.898	0.050
Auburn 7-05-04	0.010	0.037	0.953
Auburn 7-05-04	0.024	0.841	0.134
Auburn 7-05-04	0.008	0.365	0.627
Auburn 7-05-04	0.745	0.231	0.024
Auburn 7-05-04	0.000	0.992	0.008
Auburn 7-05-04	0.012	0.475	0.514
Auburn 7-05-04	0.076	0.543	0.380
Auburn 7-05-04	0.021	0.734	0.245
Auburn 7-05-04	0.002	0.972	0.026
Auburn 7-05-04	0.004	0.360	0.636
Auburn 7-05-04	0.065	0.756	0.179
Auburn 7-05-04	0.012	0.475	0.514
Auburn 7-05-04	0.007	0.887	0.106
Avergare fraction =	0.110	0.620	0.270
Average (%) =	11	62	27

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 7-09-04	0.541	0.039	0.420
Auburn 7-09-04	0.162	0.062	0.776
Auburn 7-09-04	0.283	0.123	0.594
Auburn 7-09-04	0.283	0.123	0.594
Auburn 7-09-04	0.034	0.027	0.939
Auburn 7-09-04	0.349	0.056	0.595
Auburn 7-09-04	0.035	0.025	0.940
Auburn 7-09-04	0.014	0.024	0.962
Auburn 7-09-04	0.006	0.009	0.984
Auburn 7-09-04	0.073	0.060	0.866
Auburn 7-09-04	0.035	0.025	0.940
Auburn 7-09-04	0.407	0.091	0.502
Auburn 7-09-04	0.006	0.009	0.984
Auburn 7-09-04	0.016	0.028	0.956
Auburn 7-09-04	0.006	0.009	0.984
Auburn 7-09-04	0.173	0.129	0.698
Auburn 7-09-04	0.072	0.063	0.865
Auburn 7-09-04	0.283	0.123	0.594
Auburn 7-09-04	0.072	0.063	0.865
Auburn 7-09-04	0.081	0.073	0.846
Auburn 7-09-04	0.034	0.027	0.939
Auburn 7-09-04	0.283	0.123	0.594
Auburn 7-09-04	0.072	0.063	0.865
Auburn 7-09-04	0.162	0.062	0.776
Avergare fraction =	0.145	0.060	0.795
Average (%) =	15	6	80

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 7-24-04	0.676	0.059	0.265
Auburn 7-24-04	0.795	0.090	0.114
Auburn 7-24-04	0.797	0.040	0.162
Auburn 7-24-04	0.843	0.017	0.141
Auburn 7-24-04	0.472	0.049	0.478
Auburn 7-24-04	0.899	0.039	0.062
Auburn 7-24-04	0.443	0.045	0.512
Auburn 7-24-04	0.872	0.106	0.022
Auburn 7-24-04	0.145	0.029	0.826
Auburn 7-24-04	0.240	0.107	0.653
Auburn 7-24-04	0.157	0.803	0.040
Auburn 7-24-04	0.884	0.002	0.114
Auburn 7-24-04	0.797	0.040	0.162
Auburn 7-24-04	0.400	0.045	0.556
Auburn 7-24-04	0.676	0.059	0.265
Auburn 7-24-04	0.899	0.039	0.062
Auburn 7-24-04	0.174	0.013	0.812
Auburn 7-24-04	0.177	0.717	0.106
Auburn 7-24-04	0.899	0.039	0.062
Auburn 7-24-04	0.843	0.017	0.141
Auburn 7-24-04	0.962	0.009	0.028
Auburn 7-24-04	0.240	0.107	0.653
Auburn 7-24-04	0.871	0.026	0.103
Auburn 7-24-04	0.130	0.025	0.845
Avergare fraction =	0.595	0.105	0.299
Average (%) =	60	11	30

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 8-09-04	0.898	0.019	0.083
Auburn 8-09-04	0.898	0.019	0.083
Auburn 8-09-04	0.898	0.019	0.083
Auburn 8-09-04	0.268	0.024	0.708
Auburn 8-09-04	0.443	0.045	0.512
Auburn 8-09-04	0.639	0.028	0.334
Auburn 8-09-04	0.443	0.045	0.512
Auburn 8-09-04	0.797	0.040	0.162
Auburn 8-09-04	0.986	0.004	0.010
Auburn 8-09-04	0.446	0.043	0.511
Auburn 8-09-04	0.797	0.040	0.162
Auburn 8-09-04	0.466	0.523	0.011
Auburn 8-09-04	0.240	0.107	0.653
Auburn 8-09-04	0.899	0.039	0.062
Auburn 8-09-04	0.797	0.040	0.162
Auburn 8-09-04	0.662	0.030	0.308
Auburn 8-09-04	0.443	0.045	0.512
Auburn 8-09-04	0.797	0.040	0.162
Auburn 8-09-04	0.587	0.132	0.281
Auburn 8-09-04	0.270	0.023	0.707
Auburn 8-09-04	0.881	0.009	0.110
Auburn 8-09-04	0.249	0.020	0.731
Auburn 8-09-04	0.249	0.020	0.731
Auburn 8-09-04	0.813	0.016	0.171
Avergare fraction =	0.619	0.057	0.323
Average (%) =	62	6	32

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 8-24-04	0.505	0.013	0.482
Auburn 8-24-04	0.818	0.040	0.142
Auburn 8-24-04	0.240	0.107	0.653
Auburn 8-24-04	0.676	0.059	0.265
Auburn 8-24-04	0.081	0.741	0.178
Auburn 8-24-04	0.505	0.013	0.482
Auburn 8-24-04	0.120	0.198	0.682
Auburn 8-24-04	0.026	0.007	0.967
Auburn 8-24-04	0.117	0.531	0.352
Auburn 8-24-04	0.735	0.123	0.142
Auburn 8-24-04	0.004	0.741	0.255
Auburn 8-24-04	0.481	0.047	0.472
Auburn 8-24-04	0.000	0.048	0.952
Auburn 8-24-04	0.026	0.015	0.959
Auburn 8-24-04	0.481	0.047	0.472
Auburn 8-24-04	0.043	0.890	0.067
Auburn 8-24-04	0.639	0.028	0.334
Auburn 8-24-04	0.240	0.107	0.653
Auburn 8-24-04	0.013	0.029	0.958
Auburn 8-24-04	0.881	0.009	0.110
Auburn 8-24-04	0.639	0.028	0.334
Auburn 8-24-04	0.881	0.009	0.110
Auburn 8-24-04	0.881	0.009	0.110
Auburn 8-24-04	0.881	0.009	0.110
Avergare fraction =	0.413	0.160	0.427
Average (%) =	41	16	43

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 4-06-05	0.028	0.066	0.906
Auburn 4-06-05	0.115	0.572	0.313
Auburn 4-06-05	0.012	0.962	0.026
Auburn 4-06-05	0.115	0.572	0.313
Auburn 4-06-05	0.115	0.572	0.313
Auburn 4-06-05	0.038	0.376	0.586
Auburn 4-06-05	0.094	0.480	0.427
Auburn 4-06-05	0.005	0.650	0.345
Auburn 4-06-05	0.022	0.588	0.389
Auburn 4-06-05	0.158	0.587	0.255
Auburn 4-06-05	0.061	0.870	0.069
Auburn 4-06-05	0.038	0.376	0.586
Auburn 4-06-05	0.019	0.176	0.805
Auburn 4-06-05	0.021	0.427	0.552
Auburn 4-06-05	0.078	0.354	0.569
Auburn 4-06-05	0.404	0.246	0.351
Auburn 4-06-05	0.083	0.210	0.707
Auburn 4-06-05	0.115	0.572	0.313
Auburn 4-06-05	0.004	0.068	0.928
Auburn 4-06-05	0.034	0.348	0.619
Auburn 4-06-05	0.078	0.354	0.569
Auburn 4-06-05	0.115	0.572	0.313
Auburn 4-06-05	0.001	0.024	0.976
Auburn 4-06-05	0.004	0.068	0.928
Avergare fraction =	0.073	0.420	0.507
Average (%) =	7	42	51

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-05-05	0.002	0.379	0.620
Auburn 6-05-05	0.021	0.427	0.552
Auburn 6-05-05	0.013	0.142	0.845
Auburn 6-05-05	0.781	0.161	0.058
Auburn 6-05-05	0.005	0.593	0.402
Auburn 6-05-05	0.009	0.408	0.583
Auburn 6-05-05	0.012	0.280	0.708
Auburn 6-05-05	0.135	0.176	0.689
Auburn 6-05-05	0.006	0.327	0.667
Auburn 6-05-05	0.036	0.384	0.579
Auburn 6-05-05	0.013	0.311	0.676
Auburn 6-05-05	0.024	0.295	0.681
Auburn 6-05-05	0.078	0.354	0.569
Auburn 6-05-05	0.013	0.311	0.676
Auburn 6-05-05	0.024	0.295	0.681
Auburn 6-05-05	0.002	0.070	0.928
Auburn 6-05-05	0.114	0.633	0.253
Auburn 6-05-05	0.009	0.448	0.543
Auburn 6-05-05	0.106	0.223	0.671
Auburn 6-05-05	0.149	0.574	0.277
Auburn 6-05-05	0.013	0.314	0.673
Auburn 6-05-05	0.006	0.026	0.968
Auburn 6-05-05	0.008	0.346	0.645
Auburn 6-05-05	0.024	0.295	0.681
Avergare fraction =	0.067	0.324	0.609
Average (%) =	7	32	61

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 6-11-05	0.114	0.871	0.014
Auburn 6-11-05	0.000	0.468	0.532
Auburn 6-11-05	0.445	0.496	0.060
Auburn 6-11-05	0.066	0.070	0.865
Auburn 6-11-05	0.135	0.533	0.332
Auburn 6-11-05	0.004	0.928	0.068
Auburn 6-11-05	0.001	0.909	0.090
Auburn 6-11-05	0.059	0.936	0.005
Auburn 6-11-05	0.032	0.927	0.041
Auburn 6-11-05	0.007	0.884	0.109
Auburn 6-11-05	0.059	0.936	0.005
Auburn 6-11-05	0.003	0.965	0.032
Auburn 6-11-05	0.099	0.855	0.046
Auburn 6-11-05	0.016	0.960	0.024
Auburn 6-11-05	0.006	0.983	0.011
Auburn 6-11-05	0.004	0.928	0.068
Auburn 6-11-05	0.016	0.960	0.024
Auburn 6-11-05	0.139	0.852	0.009
Auburn 6-11-05	0.028	0.321	0.650
Auburn 6-11-05	0.001	0.909	0.090
Auburn 6-11-05	0.389	0.610	0.001
Auburn 6-11-05	0.058	0.906	0.036
Auburn 6-11-05	0.007	0.884	0.109
Auburn 6-11-05	0.081	0.884	0.035
Avergare fraction =	0.074	0.791	0.136
Average (%) =	7	79	14

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 8-20-05	0.172	0.758	0.070
Auburn 8-20-05	0.217	0.513	0.270
Auburn 8-20-05	0.280	0.254	0.466
Auburn 8-20-05	0.008	0.658	0.334
Auburn 8-20-05	0.178	0.761	0.062
Auburn 8-20-05	0.404	0.246	0.351
Auburn 8-20-05	0.178	0.761	0.062
Auburn 8-20-05	0.118	0.602	0.280
Auburn 8-20-05	0.020	0.831	0.149
Auburn 8-20-05	0.087	0.742	0.171
Auburn 8-20-05	0.374	0.392	0.234
Auburn 8-20-05	0.178	0.761	0.062
Auburn 8-20-05	0.001	0.592	0.407
Auburn 8-20-05	0.020	0.831	0.149
Auburn 8-20-05	0.178	0.761	0.062
Auburn 8-20-05	0.093	0.629	0.278
Auburn 8-20-05	0.178	0.761	0.062
Auburn 8-20-05	0.404	0.486	0.110
Auburn 8-20-05	0.017	0.750	0.233
Auburn 8-20-05	0.374	0.392	0.234
Auburn 8-20-05	0.052	0.388	0.560
Auburn 8-20-05	0.039	0.866	0.095
Auburn 8-20-05	0.220	0.388	0.392
Auburn 8-20-05	0.007	0.224	0.770
Avergare fraction =	0.158	0.598	0.244
Average (%) =	16	60	24

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 9-15-05	0.130	0.588	0.282
Auburn 9-15-05	0.130	0.588	0.282
Auburn 9-15-05	0.130	0.588	0.282
Auburn 9-15-05	0.066	0.188	0.746
Auburn 9-15-05	0.492	0.133	0.375
Auburn 9-15-05	0.061	0.526	0.412
Auburn 9-15-05	0.178	0.761	0.062
Auburn 9-15-05	0.061	0.526	0.412
Auburn 9-15-05	0.821	0.087	0.091
Auburn 9-15-05	0.366	0.187	0.447
Auburn 9-15-05	0.990	0.004	0.006
Auburn 9-15-05	0.130	0.588	0.282
Auburn 9-15-05	0.130	0.588	0.282
Auburn 9-15-05	0.066	0.247	0.687
Auburn 9-15-05	0.212	0.092	0.696
Auburn 9-15-05	0.130	0.588	0.282
Auburn 9-15-05	0.862	0.002	0.136
Auburn 9-15-05	0.212	0.092	0.696
Auburn 9-15-05	0.061	0.526	0.412
Auburn 9-15-05	0.455	0.402	0.143
Auburn 9-15-05	0.562	0.124	0.315
Auburn 9-15-05	0.125	0.444	0.432
Auburn 9-15-05	0.178	0.395	0.427
Auburn 9-15-05	0.990	0.004	0.006
Avergare fraction =	0.314	0.345	0.341
Average (%) =	31	34	34

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Auburn 4-29-06	0.231	0.751	0.017
Auburn 4-29-06	0.239	0.712	0.048
Auburn 4-29-06	0.239	0.712	0.048
Auburn 4-29-06	0.231	0.751	0.017
Auburn 4-29-06	0.126	0.820	0.054
Auburn 4-29-06	0.214	0.784	0.002
Auburn 4-29-06	0.927	0.064	0.010
Auburn 4-29-06	0.927	0.064	0.010
Auburn 4-29-06	0.021	0.870	0.109
Auburn 4-29-06	0.126	0.820	0.054
Auburn 4-29-06	0.021	0.870	0.109
Auburn 4-29-06	0.081	0.741	0.178
Auburn 4-29-06	0.124	0.734	0.142
Auburn 4-29-06	0.014	0.636	0.350
Auburn 4-29-06	0.039	0.801	0.160
Auburn 4-29-06	0.239	0.712	0.048
Auburn 4-29-06	0.042	0.900	0.058
Auburn 4-29-06	0.432	0.524	0.044
Auburn 4-29-06	0.129	0.725	0.146
Auburn 4-29-06	0.927	0.064	0.010
Auburn 4-29-06	0.239	0.712	0.048
Auburn 4-29-06	0.612	0.356	0.033
Auburn 4-29-06	0.007	0.474	0.519
Auburn 4-29-06	0.124	0.734	0.142
Avergare fraction =	0.263	0.639	0.098
Average (%) =	26	64	10

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 6-14-04	0.073	0.323	0.604
Hw 75 6-14-04	0.107	0.549	0.344
Hw 75 6-14-04	0.032	0.727	0.241
Hw 75 6-14-04	0.024	0.295	0.681
Hw 75 6-14-04	0.032	0.727	0.241
Hw 75 6-14-04	0.049	0.275	0.675
Hw 75 6-14-04	0.024	0.295	0.681
Hw 75 6-14-04	0.049	0.275	0.675
Hw 75 6-14-04	0.046	0.126	0.829
Hw 75 6-14-04	0.025	0.907	0.068
Hw 75 6-14-04	0.001	0.090	0.909
Hw 75 6-14-04	0.096	0.152	0.752
Hw 75 6-14-04	0.006	0.292	0.702
Hw 75 6-14-04	0.006	0.292	0.702
Hw 75 6-14-04	0.013	0.311	0.676
Hw 75 6-14-04	0.034	0.348	0.619
Hw 75 6-14-04	0.032	0.079	0.889
Hw 75 6-14-04	0.019	0.176	0.805
Hw 75 6-14-04	0.006	0.408	0.586
Hw 75 6-14-04	0.006	0.327	0.667
Hw 75 6-14-04	0.240	0.129	0.630
Hw 75 6-14-04	0.192	0.130	0.678
Hw 75 6-14-04	0.130	0.156	0.714
Hw 75 6-14-04	0.020	0.531	0.449
Average fraction =	0.053	0.330	0.617
Average (%) =	5	33	62

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 6-18-04	0.011	0.509	0.480
Hw 75 6-18-04	0.082	0.507	0.411
Hw 75 6-18-04	0.034	0.348	0.619
Hw 75 6-18-04	0.024	0.295	0.681
Hw 75 6-18-04	0.024	0.295	0.681
Hw 75 6-18-04	0.034	0.348	0.619
Hw 75 6-18-04	0.024	0.295	0.681
Hw 75 6-18-04	0.082	0.507	0.411
Hw 75 6-18-04	0.215	0.473	0.312
Hw 75 6-18-04	0.242	0.598	0.159
Hw 75 6-18-04	0.006	0.292	0.702
Hw 75 6-18-04	0.024	0.295	0.681
Hw 75 6-18-04	0.082	0.507	0.411
Hw 75 6-18-04	0.011	0.509	0.480
Hw 75 6-18-04	0.049	0.275	0.675
Hw 75 6-18-04	0.815	0.043	0.142
Hw 75 6-18-04	0.082	0.507	0.411
Hw 75 6-18-04	0.006	0.292	0.702
Hw 75 6-18-04	0.082	0.507	0.411
Hw 75 6-18-04	0.024	0.295	0.681
Hw 75 6-18-04	0.006	0.292	0.702
Hw 75 6-18-04	0.082	0.507	0.411
Hw 75 6-18-04	0.024	0.295	0.681
Hw 75 6-18-04	0.008	0.117	0.875
Average fraction =	0.086	0.371	0.543
Average (%) =	9	37	54

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 6-27-04	0.045	0.505	0.450
Hw 75 6-27-04	0.002	0.439	0.560
Hw 75 6-27-04	0.011	0.631	0.358
Hw 75 6-27-04	0.003	0.134	0.863
Hw 75 6-27-04	0.008	0.117	0.875
Hw 75 6-27-04	0.018	0.150	0.832
Hw 75 6-27-04	0.008	0.117	0.875
Hw 75 6-27-04	0.024	0.295	0.681
Hw 75 6-27-04	0.001	0.123	0.876
Hw 75 6-27-04	0.215	0.473	0.312
Hw 75 6-27-04	0.008	0.117	0.875
Hw 75 6-27-04	0.001	0.123	0.876
Hw 75 6-27-04	0.645	0.118	0.237
Hw 75 6-27-04	0.082	0.507	0.411
Hw 75 6-27-04	0.010	0.176	0.814
Hw 75 6-27-04	0.003	0.134	0.863
Hw 75 6-27-04	0.008	0.117	0.875
Hw 75 6-27-04	0.033	0.544	0.424
Hw 75 6-27-04	0.001	0.052	0.948
Hw 75 6-27-04	0.129	0.346	0.524
Hw 75 6-27-04	0.000	0.702	0.297
Hw 75 6-27-04	0.082	0.507	0.411
Hw 75 6-27-04	0.000	0.123	0.877
Hw 75 6-27-04	0.012	0.793	0.195
Average fraction =	0.056	0.306	0.638
Average (%) =	6	31	64

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 6-28-04	0.032	0.727	0.241
Hw 75 6-28-04	0.005	0.213	0.782
Hw 75 6-28-04	0.130	0.156	0.714
Hw 75 6-28-04	0.024	0.295	0.681
Hw 75 6-28-04	0.029	0.066	0.904
Hw 75 6-28-04	0.020	0.170	0.811
Hw 75 6-28-04	0.013	0.027	0.960
Hw 75 6-28-04	0.001	0.022	0.977
Hw 75 6-28-04	0.024	0.295	0.681
Hw 75 6-28-04	0.010	0.025	0.965
Hw 75 6-28-04	0.001	0.052	0.948
Hw 75 6-28-04	0.001	0.052	0.948
Hw 75 6-28-04	0.004	0.068	0.928
Hw 75 6-28-04	0.001	0.052	0.948
Hw 75 6-28-04	0.001	0.052	0.948
Hw 75 6-28-04	0.019	0.176	0.805
Hw 75 6-28-04	0.024	0.295	0.681
Hw 75 6-28-04	0.010	0.027	0.964
Hw 75 6-28-04	0.010	0.025	0.965
Hw 75 6-28-04	0.571	0.188	0.241
Hw 75 6-28-04	0.262	0.179	0.560
Hw 75 6-28-04	0.001	0.052	0.948
Hw 75 6-28-04	0.001	0.177	0.822
Hw 75 6-28-04	0.473	0.197	0.331
Average fraction =	0.069	0.149	0.781
Average (%) =	7	15	78

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 7-05-04	0.115	0.727	0.157
Hw 75 7-05-04	0.270	0.647	0.082
Hw 75 7-05-04	0.014	0.662	0.324
Hw 75 7-05-04	0.053	0.933	0.015
Hw 75 7-05-04	0.049	0.713	0.238
Hw 75 7-05-04	0.642	0.251	0.107
Hw 75 7-05-04	0.013	0.943	0.044
Hw 75 7-05-04	0.024	0.841	0.134
Hw 75 7-05-04	0.002	0.271	0.726
Hw 75 7-05-04	0.377	0.300	0.323
Hw 75 7-05-04	0.017	0.504	0.478
Hw 75 7-05-04	0.044	0.735	0.222
Hw 75 7-05-04	0.002	0.682	0.316
Hw 75 7-05-04	0.045	0.909	0.046
Hw 75 7-05-04	0.171	0.649	0.179
Hw 75 7-05-04	0.455	0.513	0.032
Hw 75 7-05-04	0.099	0.855	0.046
Hw 75 7-05-04	0.374	0.566	0.059
Hw 75 7-05-04	0.144	0.832	0.025
Hw 75 7-05-04	0.019	0.433	0.549
Hw 75 7-05-04	0.014	0.469	0.517
Hw 75 7-05-04	0.020	0.935	0.044
Hw 75 7-05-04	0.019	0.433	0.549
Hw 75 7-05-04	0.155	0.788	0.058
Average fraction =	0.131	0.650	0.220
Average (%) =	13	65	22

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 7-09-04	0.967	0.001	0.031
Hw 75 7-09-04	0.639	0.028	0.334
Hw 75 7-09-04	0.662	0.030	0.308
Hw 75 7-09-04	0.270	0.023	0.707
Hw 75 7-09-04	0.446	0.043	0.511
Hw 75 7-09-04	0.639	0.028	0.334
Hw 75 7-09-04	0.797	0.040	0.162
Hw 75 7-09-04	0.898	0.019	0.083
Hw 75 7-09-04	0.446	0.043	0.511
Hw 75 7-09-04	0.287	0.705	0.008
Hw 75 7-09-04	0.002	0.977	0.021
Hw 75 7-09-04	0.000	0.029	0.971
Hw 75 7-09-04	0.117	0.005	0.878
Hw 75 7-09-04	0.382	0.054	0.564
Hw 75 7-09-04	0.117	0.076	0.807
Hw 75 7-09-04	0.270	0.023	0.707
Hw 75 7-09-04	0.047	0.337	0.616
Hw 75 7-09-04	0.004	0.741	0.255
Hw 75 7-09-04	0.098	0.381	0.522
Hw 75 7-09-04	0.056	0.085	0.859
Hw 75 7-09-04	0.014	0.598	0.388
Hw 75 7-09-04	0.270	0.023	0.707
Hw 75 7-09-04	0.797	0.040	0.162
Hw 75 7-09-04	0.797	0.040	0.162
Average fraction =	0.376	0.182	0.442
Average (%) =	38	18	44

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 7-24-04	0.073	0.060	0.866
Hw 75 7-24-04	0.023	0.094	0.883
Hw 75 7-24-04	0.630	0.337	0.033
Hw 75 7-24-04	0.030	0.117	0.853
Hw 75 7-24-04	0.072	0.063	0.865
Hw 75 7-24-04	0.072	0.063	0.865
Hw 75 7-24-04	0.001	0.006	0.994
Hw 75 7-24-04	0.283	0.123	0.594
Hw 75 7-24-04	0.173	0.376	0.451
Hw 75 7-24-04	0.031	0.022	0.947
Hw 75 7-24-04	0.072	0.063	0.865
Hw 75 7-24-04	0.035	0.025	0.940
Hw 75 7-24-04	0.072	0.063	0.865
Hw 75 7-24-04	0.148	0.055	0.797
Hw 75 7-24-04	0.016	0.028	0.956
Hw 75 7-24-04	0.000	0.161	0.839
Hw 75 7-24-04	0.148	0.055	0.797
Hw 75 7-24-04	0.003	0.010	0.987
Hw 75 7-24-04	0.312	0.131	0.557
Hw 75 7-24-04	0.073	0.060	0.866
Hw 75 7-24-04	0.034	0.027	0.939
Hw 75 7-24-04	0.021	0.780	0.199
Hw 75 7-24-04	0.090	0.021	0.889
Hw 75 7-24-04	0.420	0.039	0.541
Average fraction =	0.118	0.116	0.766
Average (%) =	12	12	77

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.020	0.531	0.449
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.003	0.139	0.858
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.003	0.363	0.634
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.020	0.614	0.366
Hw 75 8-09-04	0.020	0.531	0.449
Hw 75 8-09-04	0.013	0.804	0.184
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.013	0.609	0.378
Hw 75 8-09-04	0.020	0.531	0.449
Hw 75 8-09-04	0.001	0.123	0.876
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.013	0.311	0.676
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.006	0.292	0.702
Hw 75 8-09-04	0.020	0.531	0.449
Hw 75 8-09-04	0.012	0.280	0.708
Average fraction =	0.009	0.370	0.621
Average (%) =	1	37	62

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 8-24-04	0.881	0.009	0.110
Hw 75 8-24-04	0.268	0.024	0.708
Hw 75 8-24-04	0.505	0.013	0.482
Hw 75 8-24-04	0.035	0.344	0.620
Hw 75 8-24-04	0.505	0.013	0.482
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.803	0.038	0.159
Hw 75 8-24-04	0.144	0.030	0.826
Hw 75 8-24-04	0.165	0.808	0.027
Hw 75 8-24-04	0.082	0.573	0.345
Hw 75 8-24-04	0.505	0.013	0.482
Hw 75 8-24-04	0.050	0.202	0.748
Hw 75 8-24-04	0.881	0.009	0.110
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.639	0.028	0.334
Hw 75 8-24-04	0.064	0.483	0.453
Hw 75 8-24-04	0.505	0.013	0.482
Hw 75 8-24-04	0.676	0.059	0.265
Hw 75 8-24-04	0.881	0.009	0.110
Hw 75 8-24-04	0.639	0.028	0.334
Average fraction =	0.502	0.119	0.378
Average (%) =	50	12	38

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 4-06-05	0.215	0.473	0.312
Hw 75 4-06-05	0.215	0.473	0.312
Hw 75 4-06-05	0.043	0.159	0.798
Hw 75 4-06-05	0.107	0.549	0.344
Hw 75 4-06-05	0.024	0.423	0.553
Hw 75 4-06-05	0.013	0.311	0.676
Hw 75 4-06-05	0.047	0.227	0.726
Hw 75 4-06-05	0.107	0.549	0.344
Hw 75 4-06-05	0.006	0.292	0.702
Hw 75 4-06-05	0.009	0.448	0.543
Hw 75 4-06-05	0.024	0.423	0.553
Hw 75 4-06-05	0.034	0.348	0.619
Hw 75 4-06-05	0.019	0.176	0.805
Hw 75 4-06-05	0.018	0.152	0.830
Hw 75 4-06-05	0.107	0.549	0.344
Hw 75 4-06-05	0.107	0.549	0.344
Hw 75 4-06-05	0.096	0.152	0.752
Hw 75 4-06-05	0.034	0.348	0.619
Hw 75 4-06-05	0.036	0.384	0.579
Hw 75 4-06-05	0.003	0.139	0.858
Hw 75 4-06-05	0.006	0.292	0.702
Hw 75 4-06-05	0.024	0.295	0.681
Hw 75 4-06-05	0.078	0.354	0.569
Hw 75 4-06-05	0.020	0.170	0.811
Average fraction =	0.058	0.343	0.599
Average (%) =	6	34	60

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw75 6-05-05	0.153	0.835	0.012
Hw75 6-05-05	0.036	0.934	0.030
Hw75 6-05-05	0.008	0.877	0.116
Hw75 6-05-05	0.072	0.916	0.012
Hw75 6-05-05	0.112	0.718	0.171
Hw75 6-05-05	0.072	0.916	0.012
Hw75 6-05-05	0.072	0.916	0.012
Hw75 6-05-05	0.007	0.944	0.048
Hw75 6-05-05	0.029	0.931	0.039
Hw75 6-05-05	0.014	0.880	0.106
Hw75 6-05-05	0.030	0.924	0.046
Hw75 6-05-05	0.975	0.021	0.003
Hw75 6-05-05	0.074	0.915	0.011
Hw75 6-05-05	0.036	0.730	0.234
Hw75 6-05-05	0.030	0.924	0.046
Hw75 6-05-05	0.008	0.967	0.025
Hw75 6-05-05	0.032	0.860	0.109
Hw75 6-05-05	0.014	0.636	0.350
Hw75 6-05-05	0.034	0.948	0.018
Hw75 6-05-05	0.030	0.924	0.046
Hw75 6-05-05	0.007	0.952	0.041
Hw75 6-05-05	0.032	0.610	0.358
Hw75 6-05-05	0.004	0.388	0.608
Hw75 6-05-05	0.235	0.697	0.068
Average fraction =	0.088	0.807	0.105
Average (%) =	9	81	11

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 6-11-05	0.030	0.924	0.046
Hw 75 6-11-05	0.015	0.969	0.015
Hw 75 6-11-05	0.114	0.871	0.014
Hw 75 6-11-05	0.002	0.545	0.453
Hw 75 6-11-05	0.015	0.627	0.357
Hw 75 6-11-05	0.185	0.619	0.196
Hw 75 6-11-05	0.041	0.871	0.089
Hw 75 6-11-05	0.015	0.627	0.357
Hw 75 6-11-05	0.001	0.730	0.268
Hw 75 6-11-05	0.080	0.647	0.273
Hw 75 6-11-05	0.008	0.950	0.043
Hw 75 6-11-05	0.008	0.950	0.043
Hw 75 6-11-05	0.016	0.940	0.044
Hw 75 6-11-05	0.008	0.877	0.116
Hw 75 6-11-05	0.007	0.515	0.479
Hw 75 6-11-05	0.030	0.955	0.014
Hw 75 6-11-05	0.038	0.931	0.031
Hw 75 6-11-05	0.001	0.442	0.556
Hw 75 6-11-05	0.007	0.884	0.109
Hw 75 6-11-05	0.590	0.372	0.038
Hw 75 6-11-05	0.024	0.841	0.134
Hw 75 6-11-05	0.011	0.752	0.236
Hw 75 6-11-05	0.080	0.647	0.273
Hw 75 6-11-05	0.078	0.354	0.569
Average fraction =	0.059	0.743	0.198
Average (%) =	6	74	20

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 9-15-05	0.001	0.050	0.949
Hw 75 9-15-05	0.061	0.870	0.069
Hw 75 9-15-05	0.039	0.801	0.160
Hw 75 9-15-05	0.070	0.289	0.641
Hw 75 9-15-05	0.214	0.442	0.344
Hw 75 9-15-05	0.492	0.477	0.031
Hw 75 9-15-05	0.512	0.211	0.278
Hw 75 9-15-05	0.373	0.585	0.042
Hw 75 9-15-05	0.282	0.470	0.247
Hw 75 9-15-05	0.282	0.470	0.247
Hw 75 9-15-05	0.455	0.100	0.445
Hw 75 9-15-05	0.282	0.470	0.247
Hw 75 9-15-05	0.059	0.520	0.421
Hw 75 9-15-05	0.689	0.220	0.090
Hw 75 9-15-05	0.064	0.547	0.389
Hw 75 9-15-05	0.316	0.127	0.557
Hw 75 9-15-05	0.026	0.119	0.855
Hw 75 9-15-05	0.026	0.119	0.855
Hw 75 9-15-05	0.064	0.547	0.389
Hw 75 9-15-05	0.006	0.447	0.547
Hw 75 9-15-05	0.368	0.544	0.088
Hw 75 9-15-05	0.070	0.289	0.641
Hw 75 9-15-05	0.072	0.280	0.648
Hw 75 9-15-05	0.282	0.470	0.247
Average fraction =	0.213	0.394	0.393
Average (%) =	21	39	39

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Hw 75 4-29-06	0.110	0.713	0.177
Hw 75 4-29-06	0.568	0.401	0.031
Hw 75 4-29-06	0.244	0.701	0.056
Hw 75 4-29-06	0.031	0.575	0.393
Hw 75 4-29-06	0.002	0.316	0.683
Hw 75 4-29-06	0.047	0.355	0.598
Hw 75 4-29-06	0.000	0.028	0.972
Hw 75 4-29-06	0.076	0.543	0.380
Hw 75 4-29-06	0.841	0.109	0.049
Hw 75 4-29-06	0.010	0.361	0.629
Hw 75 4-29-06	0.010	0.361	0.629
Hw 75 4-29-06	0.110	0.713	0.177
Hw 75 4-29-06	0.002	0.426	0.572
Hw 75 4-29-06	0.007	0.288	0.705
Hw 75 4-29-06	0.314	0.556	0.130
Hw 75 4-29-06	0.000	0.365	0.634
Hw 75 4-29-06	0.568	0.401	0.031
Hw 75 4-29-06	0.569	0.202	0.229
Hw 75 4-29-06	0.634	0.254	0.112
Hw 75 4-29-06	0.011	0.086	0.903
Hw 75 4-29-06	0.361	0.595	0.043
Hw 75 4-29-06	0.183	0.706	0.111
Hw 75 4-29-06	0.015	0.627	0.357
Hw 75 4-29-06	0.001	0.009	0.990
Average fraction =	0.196	0.404	0.400
Average (%) =	20	40	40

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 6-18-04	0.049	0.275	0.675
Richland 6-18-04	0.002	0.439	0.560
Richland 6-18-04	0.045	0.505	0.450
Richland 6-18-04	0.003	0.139	0.858
Richland 6-18-04	0.049	0.275	0.675
Richland 6-18-04	0.012	0.280	0.708
Richland 6-18-04	0.012	0.280	0.708
Richland 6-18-04	0.073	0.323	0.604
Richland 6-18-04	0.049	0.275	0.675
Richland 6-18-04	0.047	0.355	0.598
Richland 6-18-04	0.049	0.275	0.675
Richland 6-18-04	0.011	0.509	0.480
Richland 6-18-04	0.045	0.505	0.450
Richland 6-18-04	0.002	0.439	0.560
Richland 6-18-04	0.012	0.280	0.708
Richland 6-18-04	0.006	0.292	0.702
Richland 6-18-04	0.082	0.507	0.411
Richland 6-18-04	0.002	0.439	0.560
Richland 6-18-04	0.012	0.280	0.708
Richland 6-18-04	0.104	0.510	0.386
Richland 6-18-04	0.012	0.280	0.708
Richland 6-18-04	0.006	0.292	0.702
Richland 6-18-04	0.012	0.280	0.708
Richland 6-18-04	0.012	0.280	0.708
Avergare fraction =	0.030	0.346	0.624
Average (%) =	3	35	62

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 6-27-04	0.024	0.295	0.681
Richland 6-27-04	0.002	0.439	0.560
Richland 6-27-04	0.011	0.509	0.480
Richland 6-27-04	0.002	0.150	0.848
Richland 6-27-04	0.002	0.439	0.560
Richland 6-27-04	0.000	0.055	0.945
Richland 6-27-04	0.011	0.509	0.480
Richland 6-27-04	0.002	0.073	0.926
Richland 6-27-04	0.000	0.055	0.945
Richland 6-27-04	0.045	0.505	0.450
Richland 6-27-04	0.034	0.348	0.619
Richland 6-27-04	0.003	0.139	0.858
Richland 6-27-04	0.001	0.052	0.948
Richland 6-27-04	0.012	0.201	0.787
Richland 6-27-04	0.000	0.055	0.945
Richland 6-27-04	0.000	0.248	0.752
Richland 6-27-04	0.002	0.439	0.560
Richland 6-27-04	0.003	0.050	0.947
Richland 6-27-04	0.008	0.158	0.834
Richland 6-27-04	0.002	0.073	0.926
Richland 6-27-04	0.002	0.439	0.560
Richland 6-27-04	0.000	0.012	0.988
Richland 6-27-04	0.010	0.144	0.846
Richland 6-27-04	0.011	0.509	0.480
Avergare fraction =	0.008	0.245	0.747
Average (%) =	1	25	75

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 6-28-04	0.035	0.338	0.628
Richland 6-28-04	0.011	0.509	0.480
Richland 6-28-04	0.107	0.549	0.344
Richland 6-28-04	0.006	0.292	0.702
Richland 6-28-04	0.006	0.686	0.308
Richland 6-28-04	0.019	0.176	0.805
Richland 6-28-04	0.003	0.139	0.858
Richland 6-28-04	0.034	0.348	0.619
Richland 6-28-04	0.073	0.323	0.604
Richland 6-28-04	0.037	0.784	0.179
Richland 6-28-04	0.000	0.038	0.962
Richland 6-28-04	0.003	0.139	0.858
Richland 6-28-04	0.004	0.021	0.975
Richland 6-28-04	0.004	0.021	0.975
Richland 6-28-04	0.001	0.052	0.948
Richland 6-28-04	0.240	0.129	0.630
Richland 6-28-04	0.021	0.065	0.915
Richland 6-28-04	0.020	0.170	0.811
Richland 6-28-04	0.013	0.311	0.676
Richland 6-28-04	0.003	0.134	0.863
Richland 6-28-04	0.003	0.134	0.863
Richland 6-28-04	0.003	0.139	0.858
Richland 6-28-04	0.073	0.323	0.604
Richland 6-28-04	0.011	0.509	0.480
Avergare fraction =	0.030	0.264	0.706
Average (%) =	3	26	71

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 7-05-04	0.099	0.855	0.046
Richland 7-05-04	0.099	0.855	0.046
Richland 7-05-04	0.729	0.261	0.010
Richland 7-05-04	0.568	0.401	0.031
Richland 7-05-04	0.568	0.401	0.031
Richland 7-05-04	0.042	0.691	0.268
Richland 7-05-04	0.001	0.491	0.507
Richland 7-05-04	0.568	0.401	0.031
Richland 7-05-04	0.122	0.817	0.061
Richland 7-05-04	0.002	0.838	0.160
Richland 7-05-04	0.027	0.607	0.366
Richland 7-05-04	0.024	0.841	0.134
Richland 7-05-04	0.024	0.841	0.134
Richland 7-05-04	0.024	0.841	0.134
Richland 7-05-04	0.008	0.872	0.120
Richland 7-05-04	0.008	0.872	0.120
Richland 7-05-04	0.019	0.433	0.549
Richland 7-05-04	0.024	0.841	0.134
Richland 7-05-04	0.024	0.841	0.134
Richland 7-05-04	0.065	0.889	0.047
Richland 7-05-04	0.008	0.365	0.627
Richland 7-05-04	0.024	0.841	0.134
Richland 7-05-04	0.030	0.924	0.046
Richland 7-05-04	0.064	0.867	0.069
Avergare fraction =	0.132	0.704	0.164
Average (%) =	13	70	16

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 7-09-04	0.797	0.040	0.162
Richland 7-09-04	0.797	0.040	0.162
Richland 7-09-04	0.240	0.107	0.653
Richland 7-09-04	0.797	0.040	0.162
Richland 7-09-04	0.797	0.040	0.162
Richland 7-09-04	0.443	0.045	0.512
Richland 7-09-04	0.973	0.005	0.021
Richland 7-09-04	0.797	0.040	0.162
Richland 7-09-04	0.899	0.039	0.062
Richland 7-09-04	0.676	0.059	0.265
Richland 7-09-04	0.027	0.054	0.919
Richland 7-09-04	0.443	0.045	0.512
Richland 7-09-04	0.881	0.009	0.110
Richland 7-09-04	0.881	0.009	0.110
Richland 7-09-04	0.505	0.013	0.482
Richland 7-09-04	0.112	0.792	0.095
Richland 7-09-04	0.268	0.024	0.708
Richland 7-09-04	0.505	0.013	0.482
Richland 7-09-04	0.000	0.007	0.993
Richland 7-09-04	0.662	0.030	0.308
Richland 7-09-04	0.030	0.012	0.959
Richland 7-09-04	0.037	0.926	0.037
Richland 7-09-04	0.443	0.045	0.512
Richland 7-09-04	0.240	0.107	0.653
Avergare fraction =	0.510	0.106	0.384
Average (%) =	51	11	38

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 7-24-04	0.472	0.049	0.478
Richland 7-24-04	0.797	0.040	0.162
Richland 7-24-04	0.030	0.012	0.959
Richland 7-24-04	0.446	0.043	0.511
Richland 7-24-04	0.797	0.040	0.162
Richland 7-24-04	0.030	0.012	0.959
Richland 7-24-04	0.269	0.060	0.671
Richland 7-24-04	0.708	0.004	0.287
Richland 7-24-04	0.030	0.012	0.959
Richland 7-24-04	0.064	0.028	0.908
Richland 7-24-04	0.797	0.040	0.162
Richland 7-24-04	0.000	0.071	0.928
Richland 7-24-04	0.145	0.029	0.826
Richland 7-24-04	0.001	0.165	0.835
Richland 7-24-04	0.001	0.177	0.822
Richland 7-24-04	0.145	0.029	0.826
Richland 7-24-04	0.003	0.309	0.687
Richland 7-24-04	0.000	0.132	0.868
Richland 7-24-04	0.030	0.012	0.959
Richland 7-24-04	0.145	0.029	0.826
Richland 7-24-04	0.240	0.107	0.653
Richland 7-24-04	0.145	0.029	0.826
Richland 7-24-04	0.662	0.030	0.308
Richland 7-24-04	0.443	0.045	0.512
Avergare fraction =	0.267	0.063	0.671
Average (%) =	27	6	67

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 8-09-04	0.797	0.040	0.162
Richland 8-09-04	0.899	0.039	0.062
Richland 8-09-04	0.662	0.030	0.308
Richland 8-09-04	0.898	0.019	0.083
Richland 8-09-04	0.587	0.132	0.281
Richland 8-09-04	0.587	0.132	0.281
Richland 8-09-04	0.881	0.009	0.110
Richland 8-09-04	0.587	0.132	0.281
Richland 8-09-04	0.062	0.011	0.927
Richland 8-09-04	0.443	0.045	0.512
Richland 8-09-04	0.595	0.346	0.060
Richland 8-09-04	0.062	0.011	0.927
Richland 8-09-04	0.446	0.043	0.511
Richland 8-09-04	0.130	0.025	0.845
Richland 8-09-04	0.899	0.039	0.062
Richland 8-09-04	0.062	0.011	0.927
Richland 8-09-04	0.130	0.025	0.845
Richland 8-09-04	0.443	0.045	0.512
Richland 8-09-04	0.973	0.005	0.021
Richland 8-09-04	0.443	0.045	0.512
Richland 8-09-04	0.268	0.024	0.708
Richland 8-09-04	0.240	0.107	0.653
Richland 8-09-04	0.898	0.019	0.083
Richland 8-09-04	0.587	0.132	0.281
Avergare fraction =	0.524	0.061	0.415
Average (%) =	52	6	41

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 8-24-04	0.881	0.009	0.110
Richland 8-24-04	0.505	0.013	0.482
Richland 8-24-04	0.096	0.082	0.822
Richland 8-24-04	0.881	0.009	0.110
Richland 8-24-04	0.788	0.109	0.103
Richland 8-24-04	0.196	0.767	0.038
Richland 8-24-04	0.898	0.019	0.083
Richland 8-24-04	0.898	0.019	0.083
Richland 8-24-04	0.977	0.007	0.015
Richland 8-24-04	0.130	0.025	0.845
Richland 8-24-04	0.976	0.001	0.023
Richland 8-24-04	0.881	0.009	0.110
Richland 8-24-04	0.909	0.019	0.072
Richland 8-24-04	0.639	0.028	0.334
Richland 8-24-04	0.973	0.012	0.015
Richland 8-24-04	0.670	0.028	0.302
Richland 8-24-04	0.791	0.041	0.168
Richland 8-24-04	0.196	0.767	0.038
Richland 8-24-04	0.909	0.019	0.072
Richland 8-24-04	0.909	0.019	0.072
Richland 8-24-04	0.479	0.201	0.320
Richland 8-24-04	0.881	0.009	0.110
Richland 8-24-04	0.639	0.028	0.334
Richland 8-24-04	0.881	0.009	0.110
Avergare fraction =	0.707	0.094	0.199
Average (%) =	71	9	20

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 4-06-05	0.009	0.181	0.810
Richland 4-06-05	0.035	0.338	0.628
Richland 4-06-05	0.257	0.143	0.600
Richland 4-06-05	0.004	0.534	0.462
Richland 4-06-05	0.115	0.572	0.313
Richland 4-06-05	0.024	0.295	0.681
Richland 4-06-05	0.005	0.154	0.841
Richland 4-06-05	0.006	0.029	0.965
Richland 4-06-05	0.009	0.448	0.543
Richland 4-06-05	0.003	0.134	0.863
Richland 4-06-05	0.390	0.234	0.377
Richland 4-06-05	0.078	0.354	0.569
Richland 4-06-05	0.215	0.473	0.312
Richland 4-06-05	0.002	0.131	0.867
Richland 4-06-05	0.013	0.311	0.676
Richland 4-06-05	0.006	0.686	0.308
Richland 4-06-05	0.013	0.311	0.676
Richland 4-06-05	0.057	0.422	0.521
Richland 4-06-05	0.009	0.799	0.193
Richland 4-06-05	0.215	0.473	0.312
Richland 4-06-05	0.034	0.348	0.619
Richland 4-06-05	0.215	0.473	0.312
Richland 4-06-05	0.215	0.473	0.312
Richland 4-06-05	0.004	0.068	0.928
Avergare fraction =	0.080	0.349	0.570
Average (%) =	8	35	57

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 6-05-05	0.019	0.828	0.152
Richland 6-05-05	0.006	0.327	0.667
Richland 6-05-05	0.226	0.704	0.069
Richland 6-05-05	0.093	0.530	0.377
Richland 6-05-05	0.215	0.473	0.312
Richland 6-05-05	0.111	0.583	0.306
Richland 6-05-05	0.073	0.380	0.546
Richland 6-05-05	0.107	0.549	0.344
Richland 6-05-05	0.303	0.310	0.387
Richland 6-05-05	0.006	0.320	0.674
Richland 6-05-05	0.008	0.950	0.043
Richland 6-05-05	0.116	0.684	0.200
Richland 6-05-05	0.034	0.348	0.619
Richland 6-05-05	0.038	0.856	0.107
Richland 6-05-05	0.024	0.841	0.134
Richland 6-05-05	0.131	0.859	0.009
Richland 6-05-05	0.544	0.303	0.152
Richland 6-05-05	0.355	0.383	0.262
Richland 6-05-05	0.377	0.237	0.386
Richland 6-05-05	0.008	0.117	0.875
Richland 6-05-05	0.140	0.705	0.155
Richland 6-05-05	0.066	0.697	0.237
Richland 6-05-05	0.303	0.310	0.387
Richland 6-05-05	0.005	0.127	0.868
Avergare fraction =	0.138	0.518	0.345
Average (%) =	14	52	34

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 6-11-05	0.115	0.572	0.313
Richland 6-11-05	0.000	0.055	0.944
Richland 6-11-05	0.224	0.619	0.157
Richland 6-11-05	0.081	0.884	0.035
Richland 6-11-05	0.002	0.543	0.455
Richland 6-11-05	0.000	0.072	0.928
Richland 6-11-05	0.071	0.555	0.374
Richland 6-11-05	0.049	0.364	0.587
Richland 6-11-05	0.022	0.562	0.416
Richland 6-11-05	0.051	0.214	0.734
Richland 6-11-05	0.165	0.084	0.751
Richland 6-11-05	0.002	0.039	0.959
Richland 6-11-05	0.004	0.317	0.679
Richland 6-11-05	0.006	0.846	0.148
Richland 6-11-05	0.038	0.762	0.200
Richland 6-11-05	0.002	0.666	0.332
Richland 6-11-05	0.001	0.808	0.191
Richland 6-11-05	0.017	0.417	0.566
Richland 6-11-05	0.026	0.775	0.199
Richland 6-11-05	0.026	0.800	0.174
Richland 6-11-05	0.026	0.800	0.174
Richland 6-11-05	0.107	0.549	0.344
Richland 6-11-05	0.024	0.229	0.747
Richland 6-11-05	0.000	0.007	0.993
Avergare fraction =	0.044	0.481	0.475
Average (%) =	4	48	48

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.005	0.124	0.871
Richland 8-20-05	0.015	0.627	0.357
Richland 8-20-05	0.390	0.234	0.377
Richland 8-20-05	0.034	0.348	0.619
Richland 8-20-05	0.115	0.572	0.313
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.000	0.055	0.945
Richland 8-20-05	0.537	0.279	0.183
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.008	0.158	0.834
Richland 8-20-05	0.001	0.019	0.980
Richland 8-20-05	0.005	0.213	0.782
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.038	0.376	0.586
Richland 8-20-05	0.590	0.335	0.075
Richland 8-20-05	0.032	0.115	0.853
Richland 8-20-05	0.404	0.246	0.351
Richland 8-20-05	0.002	0.065	0.933
Richland 8-20-05	0.042	0.165	0.793
Richland 8-20-05	0.901	0.063	0.036
Avergare fraction =	0.141	0.276	0.583
Average (%) =	14	28	58

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 9-15-05	0.603	0.040	0.357
Richland 9-15-05	0.130	0.588	0.282
Richland 9-15-05	0.155	0.339	0.507
Richland 9-15-05	0.455	0.402	0.143
Richland 9-15-05	0.073	0.544	0.383
Richland 9-15-05	0.213	0.622	0.164
Richland 9-15-05	0.541	0.199	0.261
Richland 9-15-05	0.155	0.339	0.507
Richland 9-15-05	0.058	0.580	0.362
Richland 9-15-05	0.090	0.475	0.435
Richland 9-15-05	0.011	0.201	0.788
Richland 9-15-05	0.003	0.665	0.333
Richland 9-15-05	0.017	0.879	0.103
Richland 9-15-05	0.130	0.588	0.282
Richland 9-15-05	0.374	0.410	0.216
Richland 9-15-05	0.272	0.335	0.393
Richland 9-15-05	0.058	0.580	0.362
Richland 9-15-05	0.066	0.697	0.237
Richland 9-15-05	0.155	0.339	0.507
Richland 9-15-05	0.908	0.043	0.048
Richland 9-15-05	0.720	0.065	0.215
Richland 9-15-05	0.067	0.131	0.803
Richland 9-15-05	0.455	0.402	0.143
Richland 9-15-05	0.155	0.339	0.507
Avergare fraction =	0.244	0.408	0.347
Average (%) =	24	41	35

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Richland 4-29-06	0.014	0.587	0.398
Richland 4-29-06	0.014	0.861	0.125
Richland 4-29-06	0.037	0.784	0.179
Richland 4-29-06	0.054	0.641	0.306
Richland 4-29-06	0.370	0.305	0.325
Richland 4-29-06	0.122	0.177	0.701
Richland 4-29-06	0.126	0.820	0.054
Richland 4-29-06	0.799	0.137	0.064
Richland 4-29-06	0.314	0.556	0.130
Richland 4-29-06	0.014	0.638	0.347
Richland 4-29-06	0.225	0.755	0.020
Richland 4-29-06	0.314	0.556	0.130
Richland 4-29-06	0.022	0.021	0.957
Richland 4-29-06	0.122	0.817	0.061
Richland 4-29-06	0.060	0.790	0.150
Richland 4-29-06	0.837	0.119	0.044
Richland 4-29-06	0.927	0.064	0.010
Richland 4-29-06	0.927	0.064	0.010
Richland 4-29-06	0.927	0.064	0.010
Richland 4-29-06	0.122	0.817	0.061
Richland 4-29-06	0.568	0.401	0.031
Richland 4-29-06	0.126	0.820	0.054
Richland 4-29-06	0.129	0.725	0.146
Richland 4-29-06	0.129	0.725	0.146
Avergare fraction =	0.304	0.510	0.186
Average (%) =	30	51	19

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 6-18-04	0.001	0.052	0.948
Deer Creek 6-18-04	0.019	0.176	0.805
Deer Creek 6-18-04	0.073	0.323	0.604
Deer Creek 6-18-04	0.012	0.280	0.708
Deer Creek 6-18-04	0.130	0.156	0.714
Deer Creek 6-18-04	0.240	0.129	0.630
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.021	0.734	0.245
Deer Creek 6-18-04	0.001	0.142	0.857
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.073	0.323	0.604
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.215	0.473	0.312
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.215	0.473	0.312
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.073	0.323	0.604
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.024	0.295	0.681
Deer Creek 6-18-04	0.045	0.505	0.450
Avergare fraction =	0.058	0.305	0.637
Average (%) =	6	31	64

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.011	0.509	0.480
Deer Creek 6-28-04	0.008	0.117	0.875
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.107	0.549	0.344
Deer Creek 6-28-04	0.011	0.310	0.680
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.107	0.549	0.344
Deer Creek 6-28-04	0.049	0.275	0.675
Deer Creek 6-28-04	0.049	0.275	0.675
Deer Creek 6-28-04	0.008	0.158	0.834
Deer Creek 6-28-04	0.008	0.117	0.875
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.035	0.338	0.628
Deer Creek 6-28-04	0.107	0.549	0.344
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.001	0.123	0.876
Deer Creek 6-28-04	0.013	0.780	0.207
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.024	0.295	0.681
Deer Creek 6-28-04	0.107	0.549	0.344
Deer Creek 6-28-04	0.011	0.509	0.480
Deer Creek 6-28-04	0.035	0.338	0.628
Avergare fraction =	0.036	0.350	0.614
Average (%) =	4	35	61

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 7-05-04	0.223	0.632	0.145
Deer Creek 7-05-04	0.008	0.522	0.470
Deer Creek 7-05-04	0.367	0.510	0.123
Deer Creek 7-05-04	0.879	0.111	0.010
Deer Creek 7-05-04	0.004	0.949	0.047
Deer Creek 7-05-04	0.166	0.442	0.392
Deer Creek 7-05-04	0.131	0.609	0.260
Deer Creek 7-05-04	0.131	0.609	0.260
Deer Creek 7-05-04	0.833	0.153	0.015
Deer Creek 7-05-04	0.279	0.352	0.369
Deer Creek 7-05-04	0.394	0.265	0.341
Deer Creek 7-05-04	0.141	0.737	0.123
Deer Creek 7-05-04	0.026	0.617	0.357
Deer Creek 7-05-04	0.031	0.843	0.125
Deer Creek 7-05-04	0.003	0.695	0.303
Deer Creek 7-05-04	0.521	0.334	0.145
Deer Creek 7-05-04	0.131	0.609	0.260
Deer Creek 7-05-04	0.046	0.557	0.397
Deer Creek 7-05-04	0.029	0.792	0.178
Deer Creek 7-05-04	0.454	0.258	0.288
Deer Creek 7-05-04	0.139	0.754	0.106
Deer Creek 7-05-04	0.394	0.265	0.341
Deer Creek 7-05-04	0.275	0.617	0.108
Deer Creek 7-05-04	0.521	0.334	0.145
Avergare fraction =	0.255	0.524	0.221
Average (%) =	26	52	22

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 7-09-04	0.240	0.107	0.653
Deer Creek 7-09-04	0.995	0.001	0.004
Deer Creek 7-09-04	0.587	0.132	0.281
Deer Creek 7-09-04	0.587	0.132	0.281
Deer Creek 7-09-04	0.948	0.002	0.050
Deer Creek 7-09-04	0.443	0.045	0.512
Deer Creek 7-09-04	0.797	0.040	0.162
Deer Creek 7-09-04	0.446	0.043	0.511
Deer Creek 7-09-04	0.587	0.132	0.281
Deer Creek 7-09-04	0.255	0.703	0.042
Deer Creek 7-09-04	0.443	0.045	0.512
Deer Creek 7-09-04	0.587	0.132	0.281
Deer Creek 7-09-04	0.037	0.784	0.179
Deer Creek 7-09-04	0.000	0.605	0.395
Deer Creek 7-09-04	0.767	0.003	0.229
Deer Creek 7-09-04	0.500	0.295	0.205
Deer Creek 7-09-04	0.249	0.020	0.731
Deer Creek 7-09-04	0.130	0.025	0.845
Deer Creek 7-09-04	0.639	0.028	0.334
Deer Creek 7-09-04	0.797	0.040	0.162
Deer Creek 7-09-04	0.881	0.009	0.110
Deer Creek 7-09-04	0.446	0.043	0.511
Deer Creek 7-09-04	0.240	0.107	0.653
Deer Creek 7-09-04	0.797	0.040	0.162
Avergare fraction =	0.517	0.146	0.337
Average (%) =	52	15	34

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 7-24-04	0.984	0.006	0.009
Deer Creek 7-24-04	0.213	0.721	0.066
Deer Creek 7-24-04	0.707	0.227	0.067
Deer Creek 7-24-04	0.973	0.005	0.021
Deer Creek 7-24-04	0.240	0.107	0.653
Deer Creek 7-24-04	0.666	0.245	0.089
Deer Creek 7-24-04	0.795	0.090	0.114
Deer Creek 7-24-04	0.240	0.107	0.653
Deer Creek 7-24-04	0.993	0.007	0.001
Deer Creek 7-24-04	0.176	0.081	0.743
Deer Creek 7-24-04	0.044	0.041	0.915
Deer Creek 7-24-04	0.044	0.041	0.915
Deer Creek 7-24-04	0.494	0.107	0.399
Deer Creek 7-24-04	0.490	0.254	0.257
Deer Creek 7-24-04	0.446	0.043	0.511
Deer Creek 7-24-04	0.124	0.129	0.747
Deer Creek 7-24-04	0.176	0.081	0.743
Deer Creek 7-24-04	0.443	0.045	0.512
Deer Creek 7-24-04	0.130	0.025	0.845
Deer Creek 7-24-04	0.873	0.023	0.104
Deer Creek 7-24-04	0.881	0.009	0.110
Deer Creek 7-24-04	0.797	0.040	0.162
Deer Creek 7-24-04	0.443	0.045	0.512
Deer Creek 7-24-04	0.240	0.107	0.653
Avergare fraction =	0.484	0.108	0.408
Average (%) =	48	11	41

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 8-02-04	0.090	0.021	0.889
Deer Creek 8-02-04	0.351	0.040	0.608
Deer Creek 8-02-04	0.090	0.021	0.889
Deer Creek 8-02-04	0.090	0.021	0.889
Deer Creek 8-02-04	0.090	0.021	0.889
Deer Creek 8-02-04	0.468	0.087	0.445
Deer Creek 8-02-04	0.257	0.052	0.691
Deer Creek 8-02-04	0.420	0.039	0.541
Deer Creek 8-02-04	0.257	0.052	0.691
Deer Creek 8-02-04	0.786	0.036	0.178
Deer Creek 8-02-04	0.014	0.024	0.962
Deer Creek 8-02-04	0.468	0.087	0.445
Deer Creek 8-02-04	0.090	0.021	0.889
Deer Creek 8-02-04	0.090	0.021	0.889
Deer Creek 8-02-04	0.420	0.039	0.541
Deer Creek 8-02-04	0.148	0.055	0.797
Deer Creek 8-02-04	0.541	0.039	0.420
Deer Creek 8-02-04	0.325	0.311	0.363
Deer Creek 8-02-04	0.420	0.039	0.541
Deer Creek 8-02-04	0.073	0.060	0.866
Deer Creek 8-02-04	0.420	0.039	0.541
Deer Creek 8-02-04	0.073	0.060	0.866
Deer Creek 8-02-04	0.014	0.024	0.962
Deer Creek 8-02-04	0.090	0.021	0.889
Avergare fraction =	0.254	0.051	0.695
Average (%) =	25	5	70

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 8-09-04	0.240	0.107	0.653
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.587	0.132	0.281
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.129	0.018	0.853
Deer Creek 8-09-04	0.438	0.006	0.556
Deer Creek 8-09-04	0.240	0.107	0.653
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.044	0.047	0.909
Deer Creek 8-09-04	0.124	0.129	0.747
Deer Creek 8-09-04	0.639	0.028	0.334
Deer Creek 8-09-04	0.062	0.011	0.927
Deer Creek 8-09-04	0.062	0.011	0.927
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.505	0.013	0.482
Deer Creek 8-09-04	0.967	0.001	0.031
Deer Creek 8-09-04	0.898	0.019	0.083
Deer Creek 8-09-04	0.161	0.002	0.838
Deer Creek 8-09-04	0.923	0.008	0.070
Deer Creek 8-09-04	0.899	0.039	0.062
Avergare fraction =	0.457	0.033	0.511
Average (%) =	46	3	51

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 8-24-04	0.898	0.019	0.083
Deer Creek 8-24-04	0.973	0.005	0.021
Deer Creek 8-24-04	0.028	0.166	0.807
Deer Creek 8-24-04	0.639	0.028	0.334
Deer Creek 8-24-04	0.803	0.038	0.159
Deer Creek 8-24-04	0.976	0.001	0.023
Deer Creek 8-24-04	0.587	0.132	0.281
Deer Creek 8-24-04	0.881	0.009	0.110
Deer Creek 8-24-04	0.639	0.028	0.334
Deer Creek 8-24-04	0.881	0.009	0.110
Deer Creek 8-24-04	0.505	0.013	0.482
Deer Creek 8-24-04	0.064	0.028	0.908
Deer Creek 8-24-04	0.923	0.008	0.070
Deer Creek 8-24-04	0.779	0.018	0.203
Deer Creek 8-24-04	0.947	0.002	0.050
Deer Creek 8-24-04	0.639	0.028	0.334
Deer Creek 8-24-04	0.409	0.050	0.541
Deer Creek 8-24-04	0.976	0.001	0.023
Deer Creek 8-24-04	0.686	0.063	0.250
Deer Creek 8-24-04	0.898	0.044	0.058
Deer Creek 8-24-04	0.639	0.028	0.334
Deer Creek 8-24-04	0.004	0.265	0.731
Deer Creek 8-24-04	0.130	0.025	0.845
Deer Creek 8-24-04	0.481	0.047	0.472
Avergare fraction =	0.641	0.044	0.315
Average (%) =	64	4	32

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 6-03-05	0.039	0.866	0.095
Deer Creek 6-03-05	0.000	0.069	0.931
Deer Creek 6-03-05	0.014	0.955	0.031
Deer Creek 6-03-05	0.001	0.730	0.268
Deer Creek 6-03-05	0.039	0.876	0.085
Deer Creek 6-03-05	0.003	0.887	0.110
Deer Creek 6-03-05	0.008	0.877	0.116
Deer Creek 6-03-05	0.010	0.371	0.619
Deer Creek 6-03-05	0.004	0.991	0.005
Deer Creek 6-03-05	0.039	0.866	0.095
Deer Creek 6-03-05	0.015	0.627	0.357
Deer Creek 6-03-05	0.008	0.863	0.129
Deer Creek 6-03-05	0.224	0.604	0.172
Deer Creek 6-03-05	0.178	0.761	0.062
Deer Creek 6-03-05	0.008	0.917	0.075
Deer Creek 6-03-05	0.017	0.750	0.233
Deer Creek 6-03-05	0.008	0.796	0.196
Deer Creek 6-03-05	0.171	0.670	0.159
Deer Creek 6-03-05	0.008	0.950	0.043
Deer Creek 6-03-05	0.037	0.539	0.424
Deer Creek 6-03-05	0.035	0.772	0.193
Deer Creek 6-03-05	0.001	0.730	0.268
Deer Creek 6-03-05	0.008	0.506	0.485
Deer Creek 6-03-05	0.015	0.627	0.357
Avergare fraction =	0.037	0.733	0.229
Average (%) =	4	73	23

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 6-05-05	0.036	0.730	0.234
Deer Creek 6-05-05	0.008	0.950	0.043
Deer Creek 6-05-05	0.394	0.586	0.020
Deer Creek 6-05-05	0.019	0.955	0.026
Deer Creek 6-05-05	0.006	0.536	0.458
Deer Creek 6-05-05	0.083	0.810	0.106
Deer Creek 6-05-05	0.016	0.844	0.140
Deer Creek 6-05-05	0.071	0.555	0.374
Deer Creek 6-05-05	0.757	0.166	0.077
Deer Creek 6-05-05	0.016	0.756	0.227
Deer Creek 6-05-05	0.082	0.727	0.191
Deer Creek 6-05-05	0.243	0.479	0.278
Deer Creek 6-05-05	0.002	0.965	0.034
Deer Creek 6-05-05	0.226	0.704	0.069
Deer Creek 6-05-05	0.038	0.856	0.107
Deer Creek 6-05-05	0.008	0.863	0.129
Deer Creek 6-05-05	0.002	0.965	0.034
Deer Creek 6-05-05	0.017	0.933	0.050
Deer Creek 6-05-05	0.007	0.952	0.041
Deer Creek 6-05-05	0.015	0.969	0.015
Deer Creek 6-05-05	0.018	0.930	0.052
Deer Creek 6-05-05	0.009	0.901	0.090
Deer Creek 6-05-05	0.001	0.730	0.268
Deer Creek 6-05-05	0.226	0.704	0.069
Avergare fraction =	0.096	0.774	0.131
Average (%) =	10	77	13

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 6-11-05	0.030	0.924	0.046
Deer Creek 6-11-05	0.030	0.924	0.046
Deer Creek 6-11-05	0.030	0.924	0.046
Deer Creek 6-11-05	0.002	0.965	0.034
Deer Creek 6-11-05	0.030	0.924	0.046
Deer Creek 6-11-05	0.002	0.224	0.773
Deer Creek 6-11-05	0.013	0.757	0.230
Deer Creek 6-11-05	0.021	0.092	0.887
Deer Creek 6-11-05	0.038	0.376	0.586
Deer Creek 6-11-05	0.030	0.924	0.046
Deer Creek 6-11-05	0.015	0.859	0.126
Deer Creek 6-11-05	0.030	0.924	0.046
Deer Creek 6-11-05	0.010	0.671	0.318
Deer Creek 6-11-05	0.133	0.636	0.230
Deer Creek 6-11-05	0.008	0.117	0.875
Deer Creek 6-11-05	0.006	0.458	0.536
Deer Creek 6-11-05	0.066	0.697	0.237
Deer Creek 6-11-05	0.024	0.485	0.491
Deer Creek 6-11-05	0.014	0.598	0.388
Deer Creek 6-11-05	0.012	0.472	0.515
Deer Creek 6-11-05	0.144	0.765	0.092
Deer Creek 6-11-05	0.202	0.486	0.312
Deer Creek 6-11-05	0.006	0.102	0.892
Deer Creek 6-11-05	0.030	0.924	0.046
Avergare fraction =	0.039	0.635	0.327
Average (%) =	4	63	33

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 8-20-05	0.140	0.170	0.690
Deer Creek 8-20-05	0.001	0.043	0.956
Deer Creek 8-20-05	0.140	0.170	0.690
Deer Creek 8-20-05	0.002	0.020	0.978
Deer Creek 8-20-05	0.002	0.020	0.978
Deer Creek 8-20-05	0.087	0.742	0.171
Deer Creek 8-20-05	0.015	0.211	0.774
Deer Creek 8-20-05	0.073	0.130	0.798
Deer Creek 8-20-05	0.255	0.390	0.354
Deer Creek 8-20-05	0.000	0.013	0.987
Deer Creek 8-20-05	0.069	0.007	0.924
Deer Creek 8-20-05	0.038	0.376	0.586
Deer Creek 8-20-05	0.024	0.634	0.342
Deer Creek 8-20-05	0.002	0.073	0.926
Deer Creek 8-20-05	0.779	0.018	0.203
Deer Creek 8-20-05	0.002	0.073	0.926
Deer Creek 8-20-05	0.000	0.177	0.823
Deer Creek 8-20-05	0.068	0.106	0.826
Deer Creek 8-20-05	0.002	0.224	0.773
Deer Creek 8-20-05	0.420	0.039	0.541
Deer Creek 8-20-05	0.220	0.388	0.392
Deer Creek 8-20-05	0.002	0.224	0.773
Deer Creek 8-20-05	0.002	0.073	0.926
Deer Creek 8-20-05	0.024	0.295	0.681
Avergare fraction =	0.099	0.192	0.709
Average (%) =	10	19	71

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 9-15-05	0.455	0.402	0.143
Deer Creek 9-15-05	0.001	0.138	0.861
Deer Creek 9-15-05	0.642	0.251	0.107
Deer Creek 9-15-05	0.061	0.526	0.412
Deer Creek 9-15-05	0.043	0.413	0.544
Deer Creek 9-15-05	0.455	0.402	0.143
Deer Creek 9-15-05	0.250	0.422	0.328
Deer Creek 9-15-05	0.016	0.756	0.227
Deer Creek 9-15-05	0.455	0.402	0.143
Deer Creek 9-15-05	0.112	0.114	0.774
Deer Creek 9-15-05	0.061	0.526	0.412
Deer Creek 9-15-05	0.455	0.402	0.143
Deer Creek 9-15-05	0.455	0.402	0.143
Deer Creek 9-15-05	0.351	0.165	0.485
Deer Creek 9-15-05	0.130	0.588	0.282
Deer Creek 9-15-05	0.723	0.095	0.182
Deer Creek 9-15-05	0.220	0.388	0.392
Deer Creek 9-15-05	0.814	0.091	0.096
Deer Creek 9-15-05	0.671	0.173	0.156
Deer Creek 9-15-05	0.045	0.404	0.551
Deer Creek 9-15-05	0.115	0.727	0.157
Deer Creek 9-15-05	0.031	0.143	0.825
Deer Creek 9-15-05	0.009	0.552	0.439
Deer Creek 9-15-05	0.155	0.339	0.507
Avergare fraction =	0.280	0.368	0.352
Average (%) =	28	37	35

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Deer Creek 4-29-06	0.499	0.376	0.125
Deer Creek 4-29-06	0.110	0.713	0.177
Deer Creek 4-29-06	0.885	0.013	0.103
Deer Creek 4-29-06	0.209	0.789	0.002
Deer Creek 4-29-06	0.001	0.325	0.674
Deer Creek 4-29-06	0.264	0.352	0.384
Deer Creek 4-29-06	0.122	0.871	0.008
Deer Creek 4-29-06	0.239	0.712	0.048
Deer Creek 4-29-06	0.001	0.516	0.483
Deer Creek 4-29-06	0.013	0.987	0.001
Deer Creek 4-29-06	0.059	0.839	0.102
Deer Creek 4-29-06	0.239	0.712	0.048
Deer Creek 4-29-06	0.065	0.886	0.048
Deer Creek 4-29-06	0.411	0.575	0.014
Deer Creek 4-29-06	0.239	0.712	0.048
Deer Creek 4-29-06	0.568	0.401	0.031
Deer Creek 4-29-06	0.056	0.928	0.016
Deer Creek 4-29-06	0.001	0.529	0.471
Deer Creek 4-29-06	0.035	0.344	0.620
Deer Creek 4-29-06	0.175	0.815	0.010
Deer Creek 4-29-06	0.049	0.918	0.033
Deer Creek 4-29-06	0.062	0.925	0.013
Deer Creek 4-29-06	0.009	0.884	0.107
Deer Creek 4-29-06	0.110	0.713	0.177
Avergare fraction =	0.184	0.660	0.156
Average (%) =	18	66	16

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 6-14-04	0.020	0.531	0.449
Lewelling 6-14-04	0.020	0.531	0.449
Lewelling 6-14-04	0.011	0.509	0.480
Lewelling 6-14-04	0.003	0.139	0.858
Lewelling 6-14-04	0.003	0.139	0.858
Lewelling 6-14-04	0.003	0.139	0.858
Lewelling 6-14-04	0.006	0.292	0.702
Lewelling 6-14-04	0.215	0.473	0.312
Lewelling 6-14-04	0.049	0.275	0.675
Lewelling 6-14-04	0.003	0.139	0.858
Lewelling 6-14-04	0.122	0.701	0.177
Lewelling 6-14-04	0.024	0.295	0.681
Lewelling 6-14-04	0.034	0.348	0.619
Lewelling 6-14-04	0.001	0.454	0.545
Lewelling 6-14-04	0.031	0.447	0.522
Lewelling 6-14-04	0.032	0.727	0.241
Lewelling 6-14-04	0.024	0.295	0.681
Lewelling 6-14-04	0.006	0.686	0.308
Lewelling 6-14-04	0.049	0.275	0.675
Lewelling 6-14-04	0.024	0.295	0.681
Lewelling 6-14-04	0.024	0.295	0.681
Lewelling 6-14-04	0.024	0.295	0.681
Lewelling 6-14-04	0.008	0.117	0.875
Lewelling 6-14-04	0.024	0.295	0.681
Avergare fraction =	0.032	0.362	0.606
Average (%) =	3	36	61

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 6-18-04	0.049	0.275	0.675
Lewelling 6-18-04	0.049	0.275	0.675
Lewelling 6-18-04	0.008	0.117	0.875
Lewelling 6-18-04	0.073	0.323	0.604
Lewelling 6-18-04	0.034	0.348	0.619
Lewelling 6-18-04	0.049	0.275	0.675
Lewelling 6-18-04	0.008	0.117	0.875
Lewelling 6-18-04	0.006	0.327	0.667
Lewelling 6-18-04	0.049	0.275	0.675
Lewelling 6-18-04	0.240	0.129	0.630
Lewelling 6-18-04	0.006	0.292	0.702
Lewelling 6-18-04	0.049	0.275	0.675
Lewelling 6-18-04	0.082	0.507	0.411
Lewelling 6-18-04	0.024	0.295	0.681
Lewelling 6-18-04	0.008	0.117	0.875
Lewelling 6-18-04	0.008	0.117	0.875
Lewelling 6-18-04	0.049	0.275	0.675
Lewelling 6-18-04	0.024	0.295	0.681
Lewelling 6-18-04	0.011	0.509	0.480
Lewelling 6-18-04	0.020	0.531	0.449
Lewelling 6-18-04	0.012	0.280	0.708
Lewelling 6-18-04	0.012	0.280	0.708
Lewelling 6-18-04	0.006	0.292	0.702
Lewelling 6-18-04	0.002	0.439	0.560
Avergare fraction =	0.037	0.290	0.673
Average (%) =	4	29	67

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 6-27-04	0.552	0.305	0.143
Lewelling 6-27-04	0.189	0.705	0.106
Lewelling 6-27-04	0.034	0.348	0.619
Lewelling 6-27-04	0.000	0.266	0.734
Lewelling 6-27-04	0.049	0.275	0.675
Lewelling 6-27-04	0.001	0.123	0.876
Lewelling 6-27-04	0.001	0.123	0.876
Lewelling 6-27-04	0.221	0.750	0.028
Lewelling 6-27-04	0.006	0.292	0.702
Lewelling 6-27-04	0.001	0.052	0.948
Lewelling 6-27-04	0.006	0.986	0.008
Lewelling 6-27-04	0.043	0.085	0.871
Lewelling 6-27-04	0.036	0.489	0.474
Lewelling 6-27-04	0.004	0.688	0.308
Lewelling 6-27-04	0.017	0.890	0.092
Lewelling 6-27-04	0.001	0.345	0.654
Lewelling 6-27-04	0.018	0.958	0.023
Lewelling 6-27-04	0.001	0.345	0.654
Lewelling 6-27-04	0.034	0.530	0.436
Lewelling 6-27-04	0.189	0.705	0.106
Lewelling 6-27-04	0.001	0.052	0.948
Lewelling 6-27-04	0.024	0.423	0.553
Lewelling 6-27-04	0.017	0.297	0.686
Lewelling 6-27-04	0.003	0.874	0.123
Avergare fraction =	0.060	0.454	0.485
Average (%) =	6	45	49

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 6-28-04	0.003	0.715	0.281
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.034	0.348	0.619
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.107	0.549	0.344
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.005	0.525	0.471
Lewelling 6-28-04	0.162	0.450	0.388
Lewelling 6-28-04	0.008	0.158	0.834
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.082	0.507	0.411
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.008	0.117	0.875
Lewelling 6-28-04	0.036	0.930	0.034
Lewelling 6-28-04	0.000	0.467	0.533
Lewelling 6-28-04	0.008	0.117	0.875
Lewelling 6-28-04	0.034	0.348	0.619
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.107	0.549	0.344
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.024	0.295	0.681
Lewelling 6-28-04	0.011	0.509	0.480
Avergare fraction =	0.035	0.385	0.580
Average (%) =	4	38	58

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 7-05-04	0.050	0.237	0.714
Lewelling 7-05-04	0.115	0.727	0.157
Lewelling 7-05-04	0.203	0.370	0.426
Lewelling 7-05-04	0.004	0.697	0.299
Lewelling 7-05-04	0.223	0.632	0.145
Lewelling 7-05-04	0.095	0.687	0.218
Lewelling 7-05-04	0.076	0.543	0.380
Lewelling 7-05-04	0.005	0.300	0.695
Lewelling 7-05-04	0.026	0.617	0.357
Lewelling 7-05-04	0.003	0.492	0.505
Lewelling 7-05-04	0.214	0.441	0.346
Lewelling 7-05-04	0.421	0.549	0.031
Lewelling 7-05-04	0.001	0.559	0.441
Lewelling 7-05-04	0.028	0.321	0.650
Lewelling 7-05-04	0.845	0.135	0.020
Lewelling 7-05-04	0.136	0.833	0.032
Lewelling 7-05-04	0.430	0.498	0.071
Lewelling 7-05-04	0.421	0.549	0.031
Lewelling 7-05-04	0.031	0.843	0.125
Lewelling 7-05-04	0.373	0.585	0.042
Lewelling 7-05-04	0.000	0.226	0.773
Lewelling 7-05-04	0.203	0.649	0.148
Lewelling 7-05-04	0.421	0.549	0.031
Lewelling 7-05-04	0.568	0.401	0.031
Avergare fraction =	0.204	0.518	0.278
Average (%) =	20	52	28

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 7-09-04	0.240	0.107	0.653
Lewelling 7-09-04	0.130	0.025	0.845
Lewelling 7-09-04	0.446	0.043	0.511
Lewelling 7-09-04	0.446	0.043	0.511
Lewelling 7-09-04	0.145	0.029	0.826
Lewelling 7-09-04	0.130	0.025	0.845
Lewelling 7-09-04	0.446	0.043	0.511
Lewelling 7-09-04	0.145	0.029	0.826
Lewelling 7-09-04	0.443	0.045	0.512
Lewelling 7-09-04	0.145	0.029	0.826
Lewelling 7-09-04	0.144	0.030	0.826
Lewelling 7-09-04	0.797	0.040	0.162
Lewelling 7-09-04	0.145	0.029	0.826
Lewelling 7-09-04	0.918	0.061	0.022
Lewelling 7-09-04	0.797	0.040	0.162
Lewelling 7-09-04	0.145	0.029	0.826
Lewelling 7-09-04	0.881	0.009	0.110
Lewelling 7-09-04	0.130	0.025	0.845
Lewelling 7-09-04	0.881	0.009	0.110
Lewelling 7-09-04	0.898	0.019	0.083
Lewelling 7-09-04	0.130	0.025	0.845
Lewelling 7-09-04	0.446	0.043	0.511
Lewelling 7-09-04	0.797	0.040	0.162
Lewelling 7-09-04	0.898	0.019	0.083
Avergare fraction =	0.447	0.035	0.518
Average (%) =	45	3	52

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 7-24-04	0.020	0.531	0.449
Lewelling 7-24-04	0.011	0.359	0.630
Lewelling 7-24-04	0.011	0.509	0.480
Lewelling 7-24-04	0.031	0.447	0.522
Lewelling 7-24-04	0.073	0.323	0.604
Lewelling 7-24-04	0.006	0.327	0.667
Lewelling 7-24-04	0.049	0.275	0.675
Lewelling 7-24-04	0.003	0.139	0.858
Lewelling 7-24-04	0.006	0.292	0.702
Lewelling 7-24-04	0.006	0.292	0.702
Lewelling 7-24-04	0.003	0.139	0.858
Lewelling 7-24-04	0.011	0.119	0.869
Lewelling 7-24-04	0.002	0.180	0.818
Lewelling 7-24-04	0.043	0.575	0.382
Lewelling 7-24-04	0.215	0.473	0.312
Lewelling 7-24-04	0.001	0.516	0.483
Lewelling 7-24-04	0.049	0.275	0.675
Lewelling 7-24-04	0.005	0.593	0.402
Lewelling 7-24-04	0.011	0.359	0.630
Lewelling 7-24-04	0.240	0.129	0.630
Lewelling 7-24-04	0.006	0.292	0.702
Lewelling 7-24-04	0.032	0.727	0.241
Lewelling 7-24-04	0.006	0.292	0.702
Lewelling 7-24-04	0.124	0.156	0.720
Avergare fraction =	0.040	0.347	0.613
Average (%) =	4	35	61

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 8-09-04	0.505	0.013	0.482
Lewelling 8-09-04	0.062	0.011	0.927
Lewelling 8-09-04	0.708	0.004	0.287
Lewelling 8-09-04	0.898	0.019	0.083
Lewelling 8-09-04	0.639	0.028	0.334
Lewelling 8-09-04	0.505	0.013	0.482
Lewelling 8-09-04	0.708	0.004	0.287
Lewelling 8-09-04	0.062	0.011	0.927
Lewelling 8-09-04	0.639	0.028	0.334
Lewelling 8-09-04	0.268	0.024	0.708
Lewelling 8-09-04	0.898	0.019	0.083
Lewelling 8-09-04	0.240	0.107	0.653
Lewelling 8-09-04	0.898	0.019	0.083
Lewelling 8-09-04	0.026	0.007	0.967
Lewelling 8-09-04	0.440	0.006	0.554
Lewelling 8-09-04	0.505	0.013	0.482
Lewelling 8-09-04	0.270	0.023	0.707
Lewelling 8-09-04	0.845	0.016	0.140
Lewelling 8-09-04	0.797	0.040	0.162
Lewelling 8-09-04	0.443	0.045	0.512
Lewelling 8-09-04	0.520	0.003	0.477
Lewelling 8-09-04	0.443	0.045	0.512
Lewelling 8-09-04	0.443	0.045	0.512
Lewelling 8-09-04	0.846	0.011	0.142
Avergare fraction =	0.525	0.023	0.452
Average (%) =	53	2	45

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 8-24-04	0.682	0.002	0.316
Lewelling 8-24-04	0.881	0.009	0.110
Lewelling 8-24-04	0.240	0.107	0.653
Lewelling 8-24-04	0.923	0.008	0.070
Lewelling 8-24-04	0.818	0.040	0.142
Lewelling 8-24-04	0.676	0.059	0.265
Lewelling 8-24-04	0.965	0.024	0.011
Lewelling 8-24-04	0.505	0.013	0.482
Lewelling 8-24-04	0.670	0.028	0.302
Lewelling 8-24-04	0.909	0.019	0.072
Lewelling 8-24-04	0.443	0.045	0.512
Lewelling 8-24-04	0.670	0.028	0.302
Lewelling 8-24-04	0.849	0.105	0.045
Lewelling 8-24-04	0.639	0.028	0.334
Lewelling 8-24-04	0.670	0.028	0.302
Lewelling 8-24-04	0.649	0.072	0.279
Lewelling 8-24-04	0.649	0.072	0.279
Lewelling 8-24-04	0.639	0.028	0.334
Lewelling 8-24-04	0.924	0.053	0.023
Lewelling 8-24-04	0.797	0.040	0.162
Lewelling 8-24-04	0.881	0.009	0.110
Lewelling 8-24-04	0.997	0.003	0.000
Lewelling 8-24-04	0.881	0.009	0.110
Lewelling 8-24-04	0.881	0.009	0.110
Avergare fraction =	0.743	0.035	0.222
Average (%) =	74	3	22

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 4-06-05	0.005	0.127	0.868
Lewelling 4-06-05	0.078	0.354	0.569
Lewelling 4-06-05	0.107	0.549	0.344
Lewelling 4-06-05	0.013	0.311	0.676
Lewelling 4-06-05	0.013	0.311	0.676
Lewelling 4-06-05	0.107	0.549	0.344
Lewelling 4-06-05	0.045	0.505	0.450
Lewelling 4-06-05	0.013	0.311	0.676
Lewelling 4-06-05	0.013	0.311	0.676
Lewelling 4-06-05	0.063	0.175	0.762
Lewelling 4-06-05	0.107	0.549	0.344
Lewelling 4-06-05	0.003	0.139	0.858
Lewelling 4-06-05	0.006	0.292	0.702
Lewelling 4-06-05	0.107	0.549	0.344
Lewelling 4-06-05	0.019	0.176	0.805
Lewelling 4-06-05	0.003	0.139	0.858
Lewelling 4-06-05	0.107	0.549	0.344
Lewelling 4-06-05	0.078	0.354	0.569
Lewelling 4-06-05	0.078	0.354	0.569
Lewelling 4-06-05	0.107	0.549	0.344
Lewelling 4-06-05	0.006	0.029	0.965
Lewelling 4-06-05	0.019	0.176	0.805
Lewelling 4-06-05	0.024	0.295	0.681
Lewelling 4-06-05	0.115	0.572	0.313
Avergare fraction =	0.051	0.343	0.606
Average (%) =	5	34	61

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 6-05-05	0.065	0.800	0.135
Lewelling 6-05-05	0.390	0.234	0.377
Lewelling 6-05-05	0.073	0.323	0.604
Lewelling 6-05-05	0.005	0.387	0.608
Lewelling 6-05-05	0.240	0.129	0.630
Lewelling 6-05-05	0.000	0.050	0.949
Lewelling 6-05-05	0.082	0.751	0.167
Lewelling 6-05-05	0.073	0.323	0.604
Lewelling 6-05-05	0.073	0.323	0.604
Lewelling 6-05-05	0.324	0.616	0.060
Lewelling 6-05-05	0.008	0.117	0.875
Lewelling 6-05-05	0.004	0.269	0.728
Lewelling 6-05-05	0.015	0.627	0.357
Lewelling 6-05-05	0.012	0.280	0.708
Lewelling 6-05-05	0.132	0.090	0.778
Lewelling 6-05-05	0.010	0.371	0.619
Lewelling 6-05-05	0.009	0.025	0.965
Lewelling 6-05-05	0.009	0.553	0.438
Lewelling 6-05-05	0.034	0.348	0.619
Lewelling 6-05-05	0.019	0.176	0.805
Lewelling 6-05-05	0.377	0.237	0.386
Lewelling 6-05-05	0.001	0.592	0.407
Lewelling 6-05-05	0.002	0.379	0.620
Avergare fraction =	0.085	0.348	0.567
Average (%) =	9	35	57

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 6-11-05	0.078	0.354	0.569
Lewelling 6-11-05	0.073	0.323	0.604
Lewelling 6-11-05	0.215	0.473	0.312
Lewelling 6-11-05	0.006	0.292	0.702
Lewelling 6-11-05	0.075	0.625	0.300
Lewelling 6-11-05	0.115	0.572	0.313
Lewelling 6-11-05	0.417	0.471	0.113
Lewelling 6-11-05	0.024	0.295	0.681
Lewelling 6-11-05	0.034	0.348	0.619
Lewelling 6-11-05	0.002	0.167	0.830
Lewelling 6-11-05	0.005	0.113	0.882
Lewelling 6-11-05	0.103	0.837	0.060
Lewelling 6-11-05	0.012	0.280	0.708
Lewelling 6-11-05	0.006	0.320	0.674
Lewelling 6-11-05	0.313	0.523	0.164
Lewelling 6-11-05	0.006	0.292	0.702
Lewelling 6-11-05	0.001	0.762	0.237
Lewelling 6-11-05	0.024	0.295	0.681
Lewelling 6-11-05	0.002	0.962	0.036
Lewelling 6-11-05	0.006	0.292	0.702
Lewelling 6-11-05	0.024	0.295	0.681
Lewelling 6-11-05	0.006	0.292	0.702
Lewelling 6-11-05	0.000	0.255	0.744
Avergare fraction =	0.067	0.410	0.523
Average (%) =	7	41	52

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 8-20-05	0.001	0.010	0.989
Lewelling 8-20-05	0.014	0.219	0.767
Lewelling 8-20-05	0.013	0.027	0.960
Lewelling 8-20-05	0.179	0.592	0.229
Lewelling 8-20-05	0.013	0.027	0.960
Lewelling 8-20-05	0.024	0.295	0.681
Lewelling 8-20-05	0.002	0.073	0.926
Lewelling 8-20-05	0.011	0.372	0.617
Lewelling 8-20-05	0.004	0.068	0.928
Lewelling 8-20-05	0.002	0.224	0.773
Lewelling 8-20-05	0.012	0.296	0.692
Lewelling 8-20-05	0.000	0.055	0.945
Lewelling 8-20-05	0.004	0.068	0.928
Lewelling 8-20-05	0.002	0.224	0.773
Lewelling 8-20-05	0.124	0.156	0.720
Lewelling 8-20-05	0.002	0.224	0.773
Lewelling 8-20-05	0.026	0.046	0.927
Lewelling 8-20-05	0.000	0.177	0.823
Lewelling 8-20-05	0.002	0.224	0.773
Lewelling 8-20-05	0.000	0.004	0.996
Lewelling 8-20-05	0.001	0.205	0.794
Lewelling 8-20-05	0.006	0.320	0.674
Lewelling 8-20-05	0.038	0.376	0.586
Lewelling 8-20-05	0.124	0.156	0.720
Avergare fraction =	0.025	0.185	0.790
Average (%) =	3	18	79

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 9-15-05	0.003	0.936	0.062
Lewelling 9-15-05	0.147	0.176	0.677
Lewelling 9-15-05	0.003	0.936	0.062
Lewelling 9-15-05	0.005	0.683	0.312
Lewelling 9-15-05	0.002	0.886	0.112
Lewelling 9-15-05	0.001	0.835	0.165
Lewelling 9-15-05	0.003	0.936	0.062
Lewelling 9-15-05	0.034	0.081	0.885
Lewelling 9-15-05	0.003	0.026	0.972
Lewelling 9-15-05	0.001	0.835	0.164
Lewelling 9-15-05	0.003	0.038	0.958
Lewelling 9-15-05	0.001	0.835	0.164
Lewelling 9-15-05	0.001	0.835	0.164
Lewelling 9-15-05	0.051	0.052	0.897
Lewelling 9-15-05	0.001	0.835	0.164
Lewelling 9-15-05	0.001	0.791	0.208
Lewelling 9-15-05	0.006	0.048	0.946
Lewelling 9-15-05	0.001	0.835	0.164
Lewelling 9-15-05	0.034	0.954	0.012
Lewelling 9-15-05	0.265	0.158	0.577
Lewelling 9-15-05	0.001	0.262	0.737
Lewelling 9-15-05	0.054	0.134	0.813
Lewelling 9-15-05	0.006	0.048	0.946
Lewelling 9-15-05	0.001	0.156	0.843
Avergare fraction =	0.026	0.513	0.461
Average (%) =	3	51	46

Modified deterministic source probability (%) of fecal bacteria

Sample/date	Human	Livestock	Wildlife
Lewelling 4-29-06	0.009	0.730	0.261
Lewelling 4-29-06	0.009	0.730	0.261
Lewelling 4-29-06	0.799	0.137	0.064
Lewelling 4-29-06	0.003	0.503	0.494
Lewelling 4-29-06	0.239	0.712	0.048
Lewelling 4-29-06	0.239	0.712	0.048
Lewelling 4-29-06	0.225	0.755	0.020
Lewelling 4-29-06	0.129	0.725	0.146
Lewelling 4-29-06	0.967	0.028	0.005
Lewelling 4-29-06	0.060	0.790	0.150
Lewelling 4-29-06	0.010	0.128	0.862
Lewelling 4-29-06	0.126	0.820	0.054
Lewelling 4-29-06	0.153	0.281	0.566
Lewelling 4-29-06	0.568	0.401	0.031
Lewelling 4-29-06	0.120	0.874	0.006
Lewelling 4-29-06	0.479	0.478	0.043
Lewelling 4-29-06	0.568	0.401	0.031
Lewelling 4-29-06	0.239	0.712	0.048
Lewelling 4-29-06	0.340	0.616	0.044
Lewelling 4-29-06	0.129	0.725	0.146
Lewelling 4-29-06	0.124	0.734	0.142
Lewelling 4-29-06	0.110	0.713	0.177
Lewelling 4-29-06	0.072	0.656	0.273
Lewelling 4-29-06	0.082	0.614	0.304
Avergare fraction =	0.242	0.582	0.176
Average (%) =	24	58	18