

# **Source-specific Estimation of Fecal Bacteria Using SWAT: Calibration and Application**

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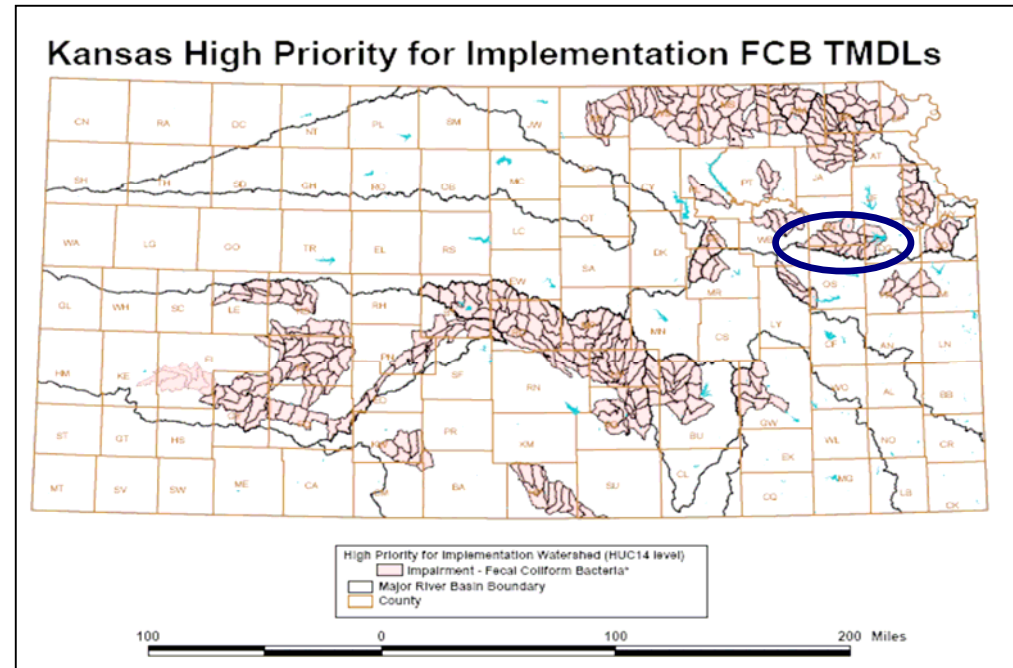
**USDA-CSREES National Water Conference**  
**Research, Extension and Education for Water Quality and Quantity**  
**28 Jan-1 Feb 2007**  
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# Project Overview

## *“Sources and Abatement of Fecal Bacteria in a High Priority TMDL Watershed in NE Kansas”*

### Situation:

- Fecal bacteria contamination of surface waters threatens human health and safety.
- The Upper Wakarusa watershed has bacteria impairment (TMDL) and is a high priority watershed in the State for restoration.
- Focus on livestock operations, particularly cattle winter-feeding sites



(Source: <http://www.kdheks.gov/tmdl/HiPriorityMaps.pdf>)

# Project Overview

## *“Sources and Abatement of Fecal Bacteria in a High Priority TMDL Watershed in NE Kansas”*

### Actions:

- Implement BMPs  
Will Boyer, Joe Harner
- Monitor stream water quality  
Phil Barnes
- Track bacteria sources  
George Marchin, Adam Henry
- Model bacteria fate & transport  
Kyle Mankin, Prem Parajuli
- Evaluate BMPs  
Phil Barnes, Kyle Mankin, Joel DeRouchey
- Educate farmers  
Will Boyer, Dan Devlin, Joel DeRouchey, Phil Barnes, Joe Harner
- Update KSU courses & educational materials  
Kyle Mankin, George Marchin

Cattle moved, grass buffer added



Feed/water moved away from stream

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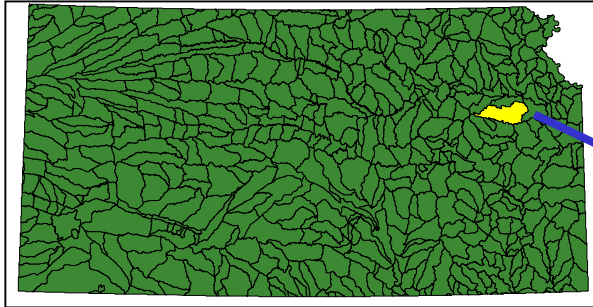
Feed/water moved away from stream

# Specific Objectives of this Study

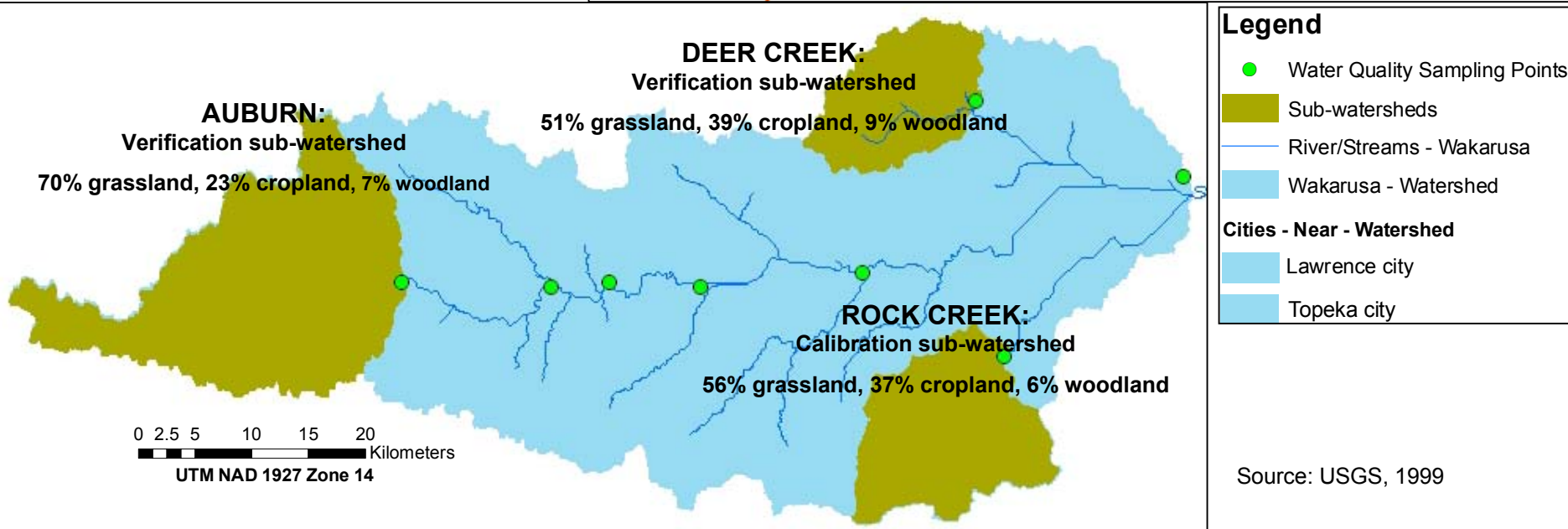
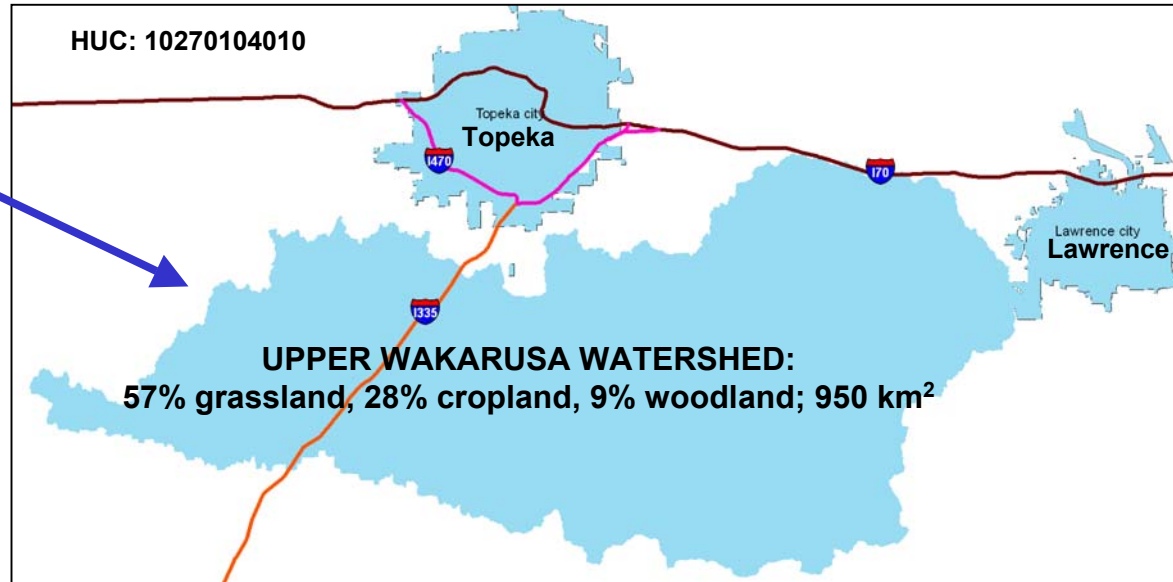
- 1) Develop methods to quantify bacterial input source loads and spatial distributions using readily available data
  - **Livestock** (AFO permitted, grazing lands)
  - **Human** (Onsite)
  - **Wildlife** (Large/Small mammal, Indigenous/Migratory fowl)
  
- 2) Calibrate, Verify SWAT 2005
  - Use BOTH total bacteria AND source-specific bacteria data
  - Use modified % fraction of ARA/Discriminant analysis data
  - Calibrate (Rock Creek) using 3 years data
  - Verify (Deer Creek, Auburn, Upper Wakarusa) using 3 years data

# Materials and Methods

## Study area



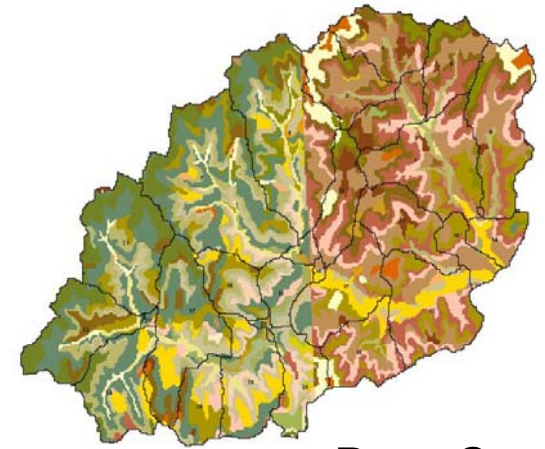
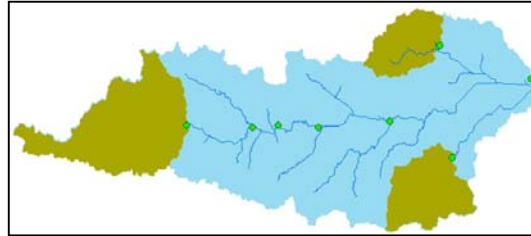
HUC 11 watershed boundary  
Source: USDA, NRCS 1993



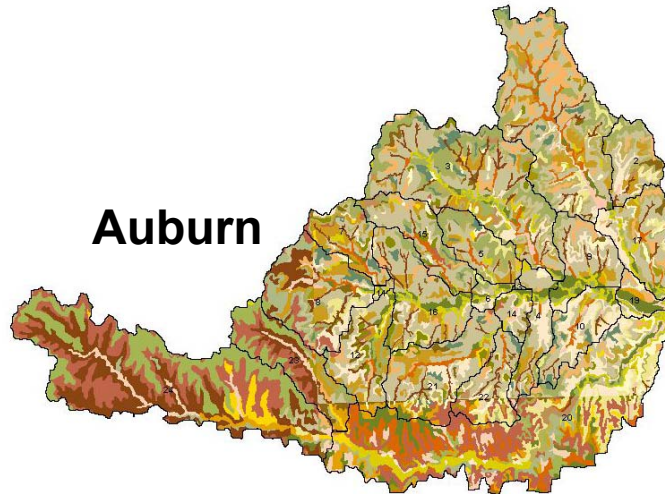
# Materials and Methods

## *SWAT input layers*

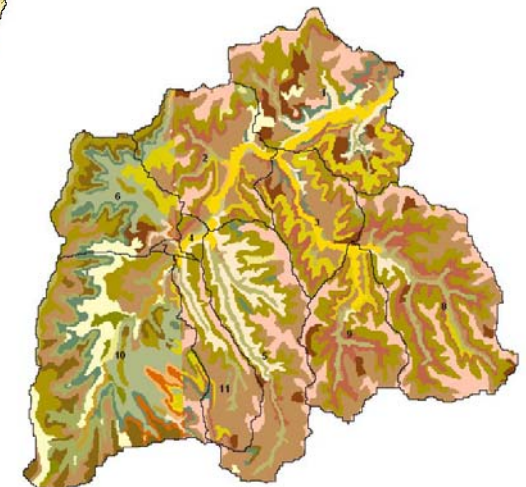
- DEM (30 m x 30 m grid)  
(USGS, 1999)
- SSURGO (USDA, 2005)
- GAP Landuse (KARS, 2001)
  - Reclassified based on field-verified landuse conditions  
(Mankin and Koelliker, 2001; Mankin et al., 2003)
- Weather (NCDC, 2006;  
Kansas State Climatologist)



**Deer Creek**



**Auburn**



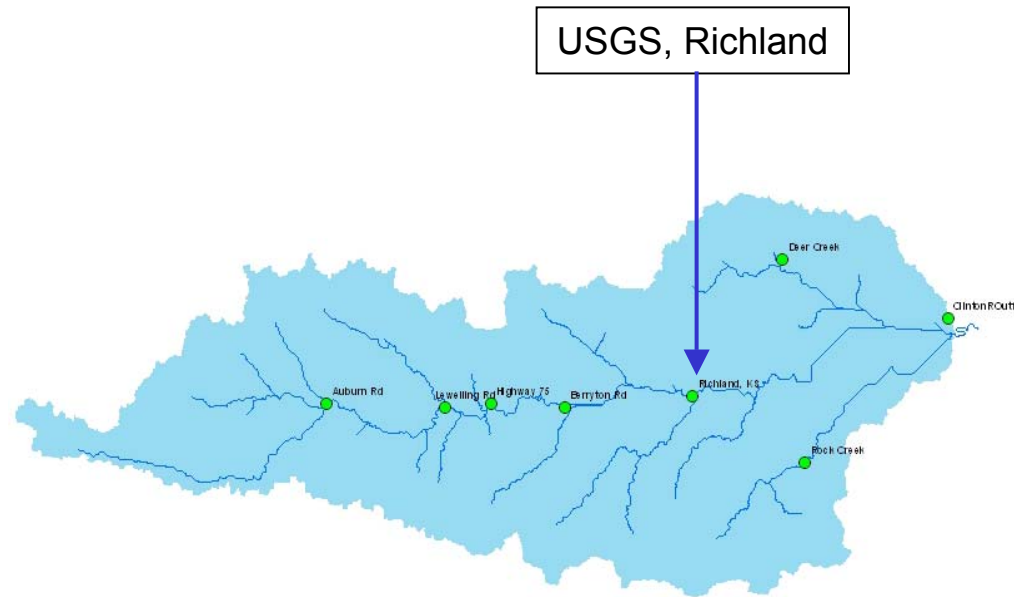
**Rock Creek**

# Materials and Methods

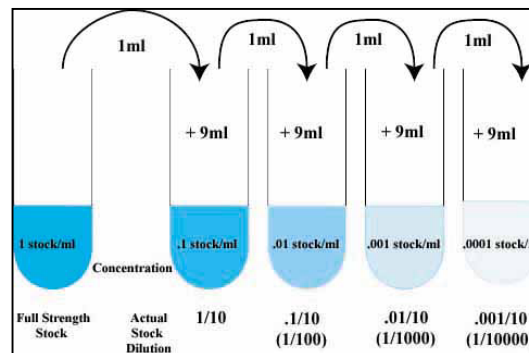
## *Flow, bacteria data collection*

### Flow and Bacteria

- Event flow calculated using flow depth, Manning's eqn.  
(Ward and Elliot, 1995)
- Event flow validated using USGS, Richland data weighted by watershed area
- Grab samples data collected from 2004-2006
- Serial dilution method used to enumerate Fecal coliform bacteria concentration  
(Clesceri et al., 1998)
- Bacteria source tracking using ARA/Discriminant analysis: % of human, livestock, wildlife



### Serial dilution



### Agar Plate

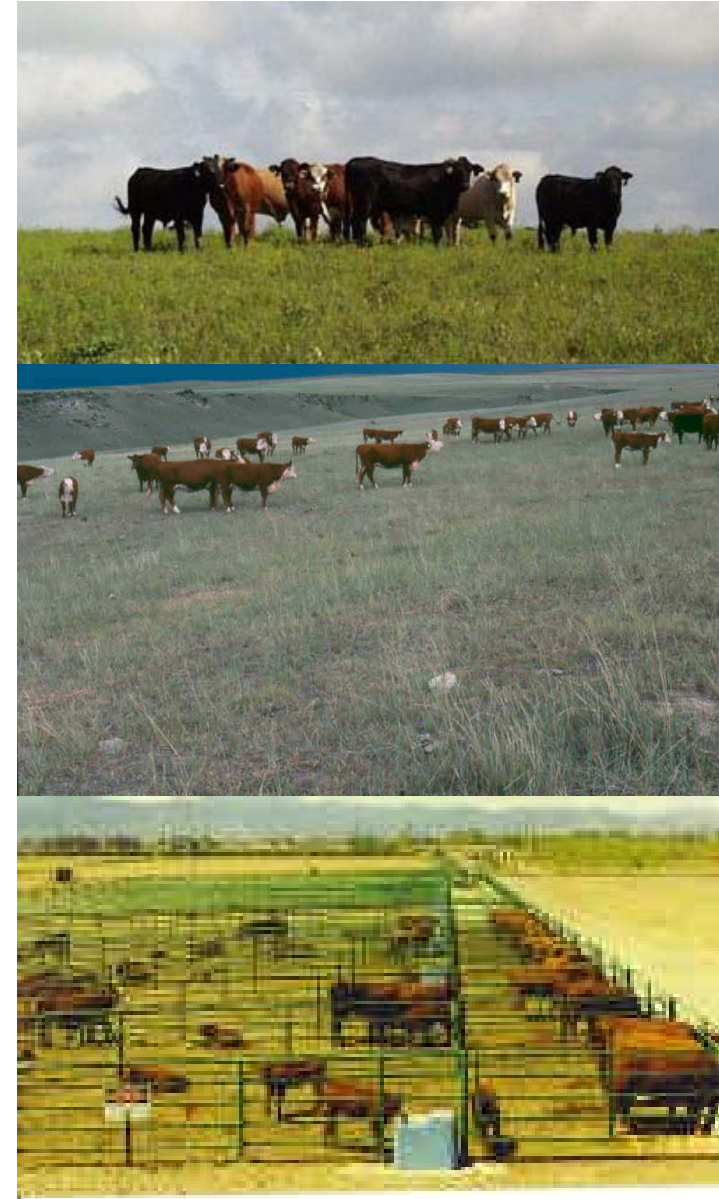




# Materials and Methods

## Quantify Bacteria Source Loads - Livestock

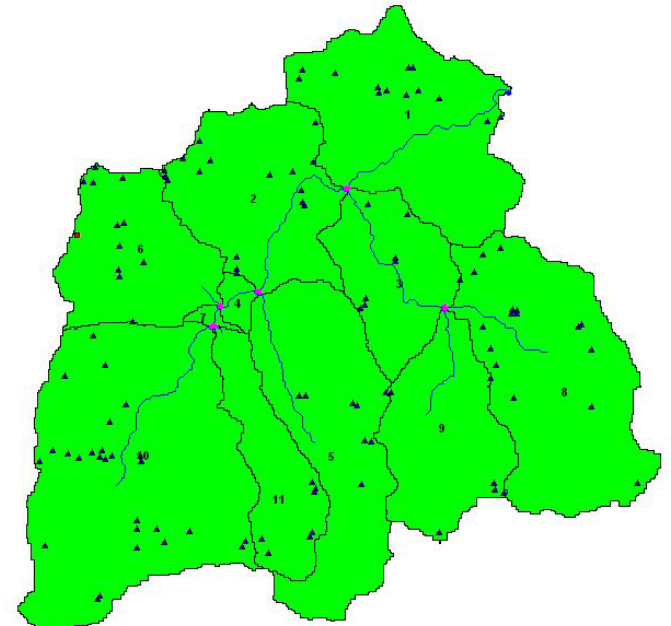
- Utilized County-level GIS-layer livestock population (USDA, 2006) and compared with Kansas Farm Facts (KDA, 2004)
- Utilized permitted livestock data (KDHE, 2005)
- Estimated AUs in the watersheds 3.04 ha per cow/calf pair stocking rate (KDA, 2004)
- Estimated fecal coliform bacteria:  $13 \times 10^{10}$  cfu day<sup>-1</sup> AU<sup>-1</sup> (ASAE, 2000)
- Modeled 4 livestock source loads:
  - Livestock in pastureland
  - Livestock in winter feeding areas
  - Livestock stream or near stream access
  - Livestock in confined areas
- Applied about 8.5% livestock source loads as a direct input to represent cattle access to the stream
- Applied about 15% livestock source loads from confined area as a direct input in the feedlot located sub-watershed



# Materials and Methods

## *Quantify Bacteria Source Loads - Septic*

- **Overlaid** watershed into 1 m resolution Orthophoto, 2002  
(State of Kansas/Sanborn, 2002)
- **Digitized** Orthophoto, 2002 based on physical context to represent each rural household septic systems
- **Determined** failing rate of septic systems
  - 20% for Rock Creek and Deer Creek
  - 40% for Auburn
- **Land application method:** less sensitive  
(Parajuli et al., 2006)
- **Assumed** 10% failing septic source loads as direct input
- **Estimated** Fecal coliform bacteria =  $6.3 \times 10^6$  cfu/100mL  
(Overcash and Davidson, 1980)



# Materials and Methods

## Quantify Bacteria Source Loads - *Wildlife*

- **Large mammals:** Deer harvested information (KDWP) used to populate deers in the watershed (9.12/mile<sup>2</sup>)
- **Small mammals:** Road kill/windshield survey indices (KDWP) used (3.25/mile<sup>2</sup>)
- **Indigenous birds (Turkey):** Road kill/windshield survey regional indices (KDWP) used (303/mile<sup>2</sup>)
- **Migratory birds:** Kansas population data (KDWP) equally distributed over the water surface and wetland area
- **Applied** wildlife source loads into woodlands and croplands
- **Assumed** 10% of wildlife source loads as direct input
- **Estimated** Fecal coliform bacteria using published data:
  - Turkey =  $0.62 \times 10^{10}$  cfu AU<sup>-1</sup> day<sup>-1</sup> (ASAE, 2000)
  - Duck =  $8.1 \times 10^{11}$  cfu AU<sup>-1</sup> day<sup>-1</sup> (ASAE, 2000)



# Materials and Methods

## *Calibration and Verification using 3 years of data*

- **Calibration:** Rock Creek watershed (75.4 km<sup>2</sup>)
- **Verification:** Deer Creek watershed (51.4 km<sup>2</sup>), Auburn watershed (152.4 km<sup>2</sup>), Upper Wakarusa watershed (950 km<sup>2</sup>)
- **Calibration Procedure:**

**Table 1. SWAT model parameters test and adjustment during calibration**

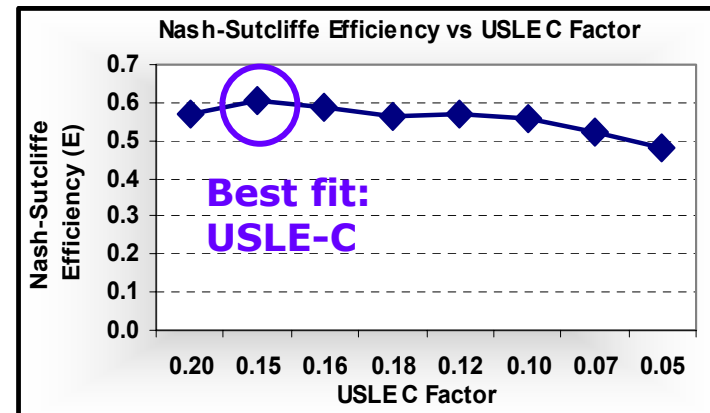
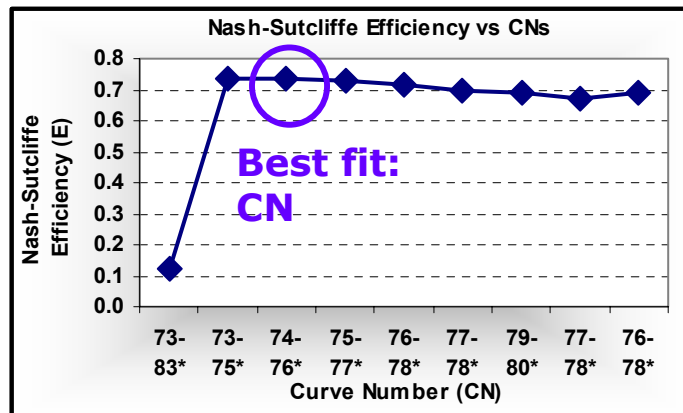
Parameters	Default value	Test range value	Final value
<b>Flow:</b>			
Curve Number (CN)	73-83	73-80	74-76
Soil evaporation compensation factor (ESCO)	0.95	0.01 to 1.00	1
Plant uptake compensation factor (EPCO)	1	0.01 to 1.00	0.01
Threshold depth of water in the shallow aquifer (REVAPMIN)	1	1 to 500	500
<b>Sediment:</b>			
USLE cover and management factor (C)	Crop varied	0 to 0.50	0.15
USLE practice factor (P)	1	0 to 1.00	0.1
Channel Erodibility Factor	0	-0.05 to 0.60	0.05
Channel Cover Factor	0	-0.001 to 1.00	0.3
<b>Bacteria:</b>			
Bacteria partition coefficient in surface runoff (BACTKDQ)	175	0 to 500	175
Temperature Adjustment Factor (TBACT)	1.07	0.80 to 1.2	1.07
Persistent bacteria die-off in solution (WDPQ)	0	0.40 to 0.693	0.4
Persistent bacteria die-off in soil particles (WDPS)	0	0.04 to 0.069	0.04

# Materials and Methods

## *Calibration and Verification using 3 years of data*

### Calibration process & statistics:

- Adjusted selected input parameters
- Compare **measured** vs. **SWAT- simulated**
  - **Daily mean flow** vs. **daily mean flow**
  - **Daily mean sediment yield** vs. **daily mean sediment yield**
  - **Daily discrete bacteria conc.** vs. **daily mean bacteria conc.**
- Nash-Sutcliffe Efficiency Index (E) (Nash and Sutcliffe, 1970)
  - How consistently do **measured** values match **predicted** values (follow 1:1 line)
- Coefficient of Determination ( $R^2$ )
  - How consistently do **measured** vs. **predicted** values follow a best-fit line



# Materials and Methods

## *Bacteria Source Tracking – ARA Method*

- ARA Reference:  
Hagedorn et al. (1999)

### ***Common BST Methods***

- Molecular BST  
(genotypic):
  - Amplified fragment length polymorphism (AFLP)
  - Ribotyping
  - PCR, qPCR
- Biochemical BST  
(phenotypic):
  - ARA (antibiotic resistance patterns)
  - BIOLOG (C sources)

### Antibiotic Resistance Analysis (ARA)

- Collect water sample
- Plate for fecal enterococci
- Randomly select 24 (or 48) bacterial isolates
- Expose each isolate to **four** concentrations of **nine** antibiotics; response is + or – to each
- Combination of responses to all antibiotics is compared statistically (discriminant analysis) to known fecal enterococcus source isolates from human, livestock, and wildlife
- Determine probability of each bacterial source for each isolate

# Materials and Methods

## Bacteria Source Tracking Data

### Standard method: Assume single source

#### – Probabilistic Method

- Determine source probability of each isolate
- Assign isolate to source with greatest probability
- Sum all isolates to assign event-based probability

Sample	Isolates	Human	Livestock	Wildlife
Auburn 1-14-04	48			
Probability				

### Modified method: Assume multiple sources

#### – Deterministic Method

- Determine source probability of each isolate
- Assume source probability = source fraction
- Average all isolates to assign event-based fraction

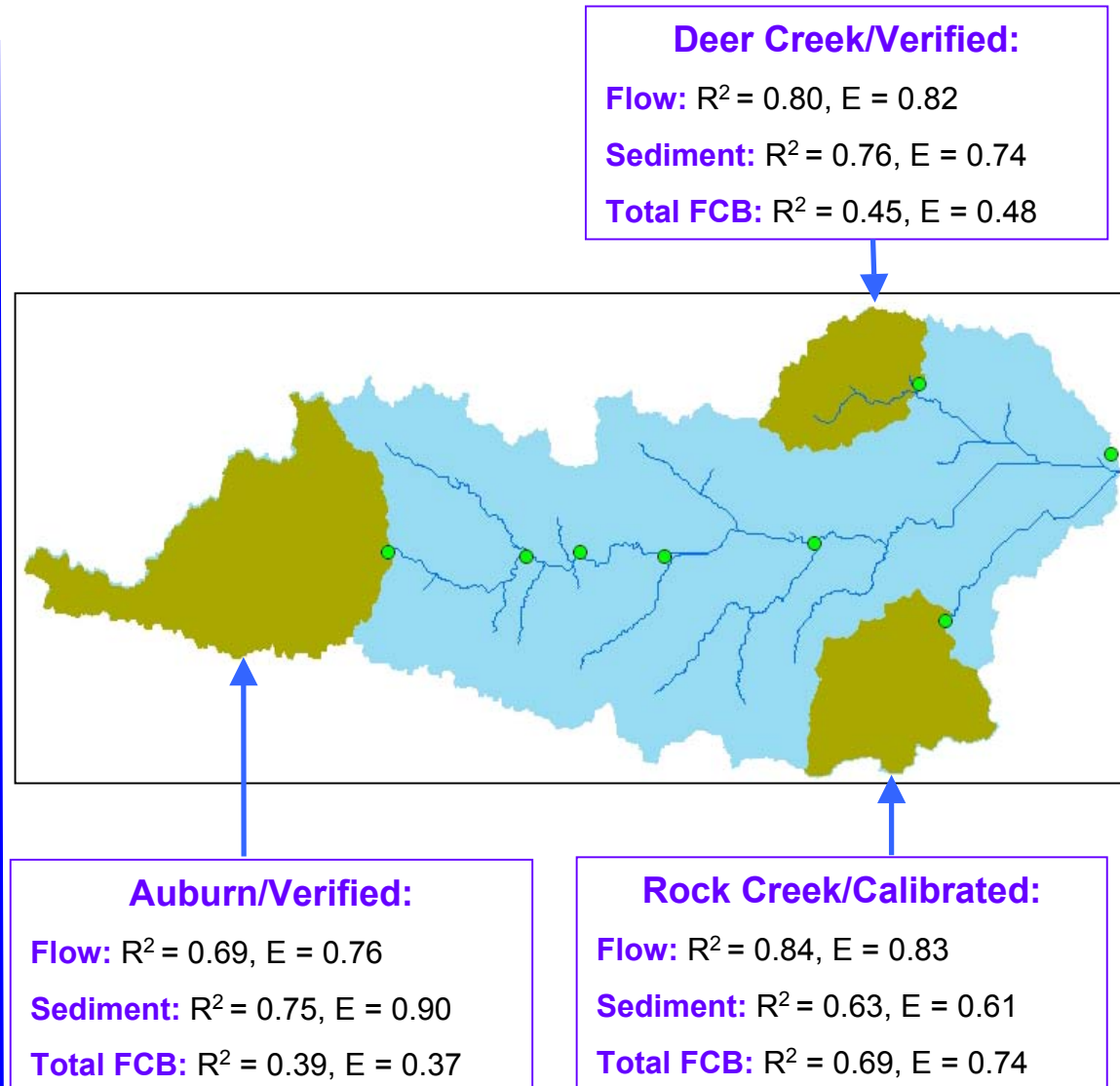
Sample (Auburn 1-14-04)	Human	Livestock	Wildlife
Average fraction =			
Percentage =			

Sample	Probability %		
	Human	Livestock	Wildlife
Auburn 1-14-04		0.004	0.013
Auburn 1-14-04	0.006		0.308
Auburn 1-14-04	0.032		0.241
Auburn 1-14-04	0.162		0.388
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.156	0.267
Auburn 1-14-04	0.162		0.388
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Auburn 1-14-04	0.032		0.241
Auburn 1-14-04		0.013	0.103
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Auburn 1-14-04	0.215		0.312
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Auburn 1-14-04	0.006		0.308
Auburn 1-14-04	0.162		0.388
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04	0.047		0.078
Auburn 1-14-04	0.006		0.308
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Auburn 1-14-04	0.038	0.265	
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04	0.047		0.078
Auburn 1-14-04	0.020		0.449
Auburn 1-14-04		0.011	0.294
Auburn 1-14-04	0.002	0.439	
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04	0.217		0.023
Auburn 1-14-04	0.049	0.275	
Auburn 1-14-04	0.006		0.308
Auburn 1-14-04	0.038	0.265	
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04	0.038	0.265	
Auburn 1-14-04	0.018	0.152	
Auburn 1-14-04		0.011	0.294
Auburn 1-14-04		0.005	0.021
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04	0.045		0.450
Auburn 1-14-04	0.032		0.241
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Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
Auburn 1-14-04		0.013	0.103
<b>Average fraction =</b>			
<b>Average (%) =</b>			

# Results and Discussion

## *Daily Flow/Sediment/Total FCB Conc.*

- Compared 11-15 measured daily events (Jan 2004 – April 2006)
- Year 2006 generally dry yr.
- **Flow:** CN was key calibrating parameter
- **Sediment:** USLE C was key calibrating parameter
- **Bacteria:** Only calibrating parameters adjusted were (a) 3-day half-life value for bacteria die-off in solution and (b) 0.1x that value for sorbed phase (Baffaut and Benson, 2003)

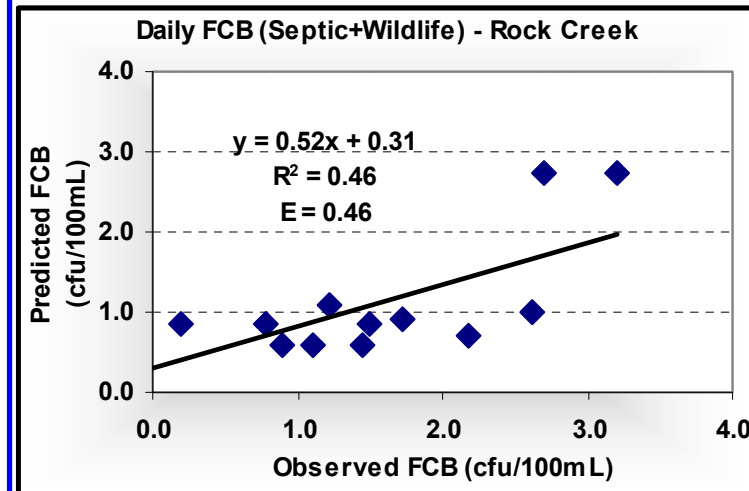
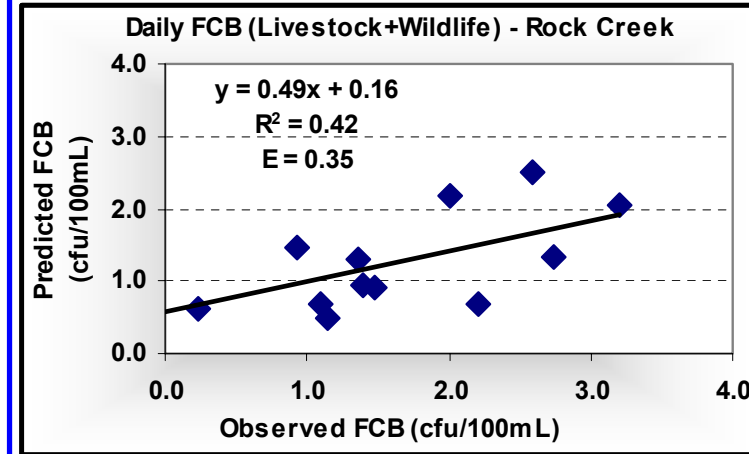
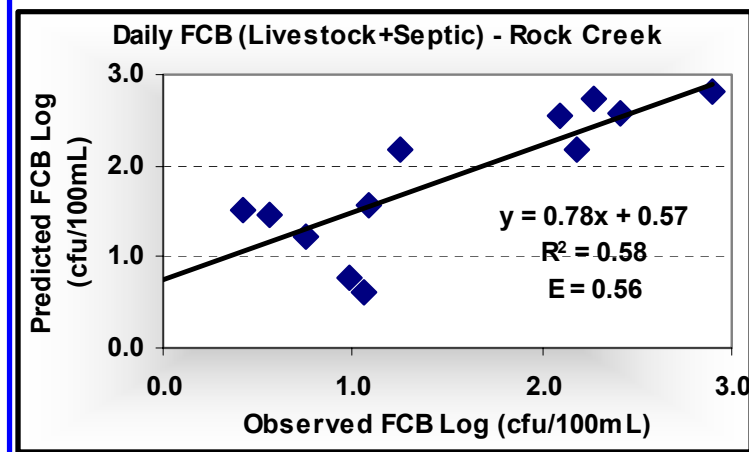




# Results and Discussion

## *Daily Fecal Coliform Bacteria/Rock Creek* *(Source specific/combination of two sources)*

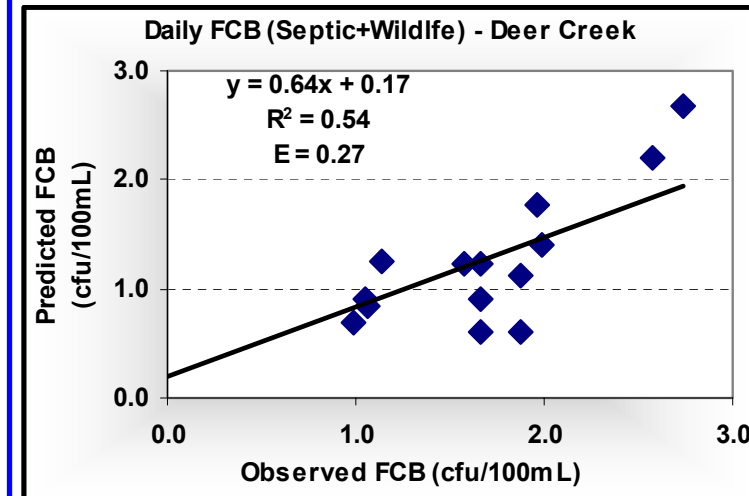
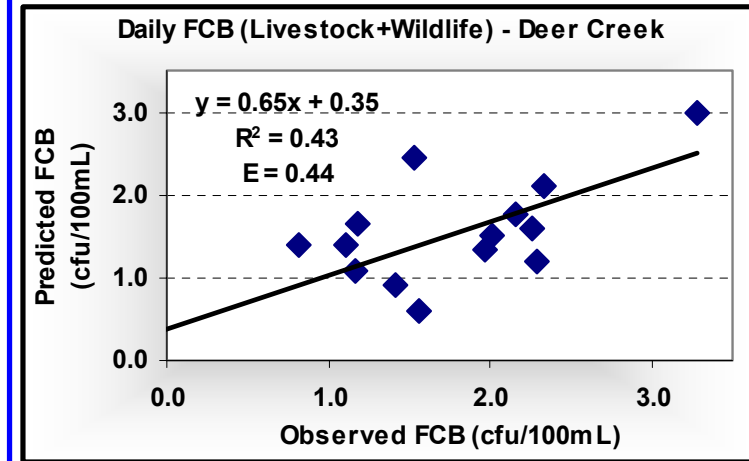
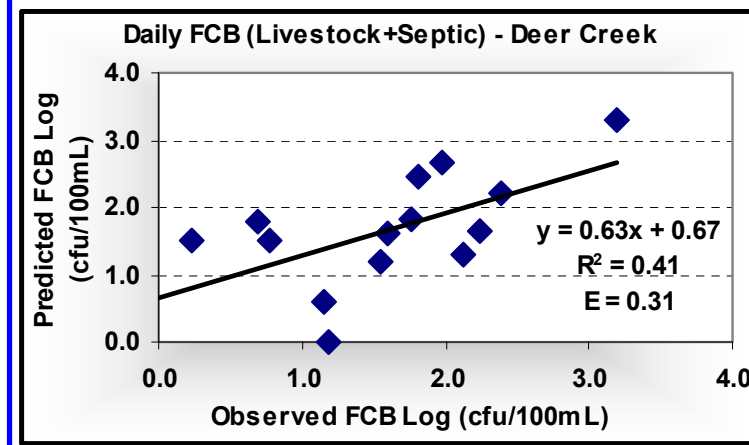
- Compared 11 measured daily total bacteria data (Jan 2004 - April 2006)
- Utilized modified deterministic probability fraction bacteria source tracking data
- Modeled combination of two sources of bacteria each time
- SWAT model predicted combination of two sources of daily fecal coliform bacteria concentration with:
  - $R^2 = 0.42 - 0.58$  and  $E = 0.35 - 0.56$  for **Rock Creek** watershed



# Results and Discussion

## *Daily Fecal Coliform Bacteria/Deer Creek* *(Source specific/combo of two sources)*

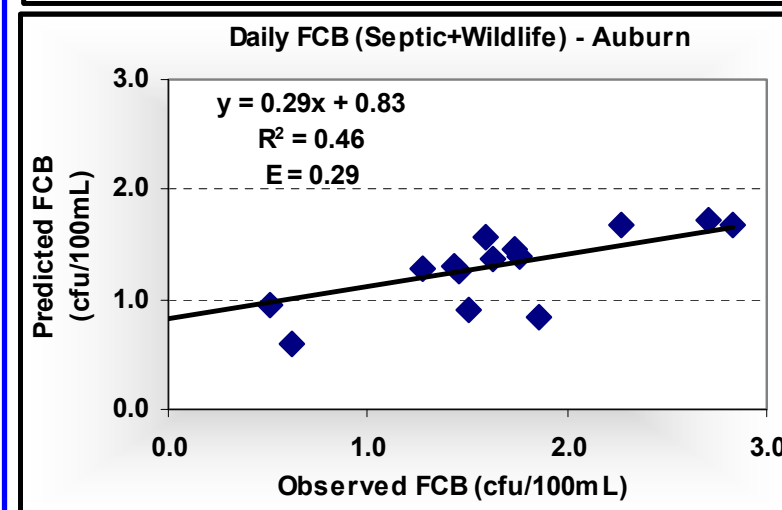
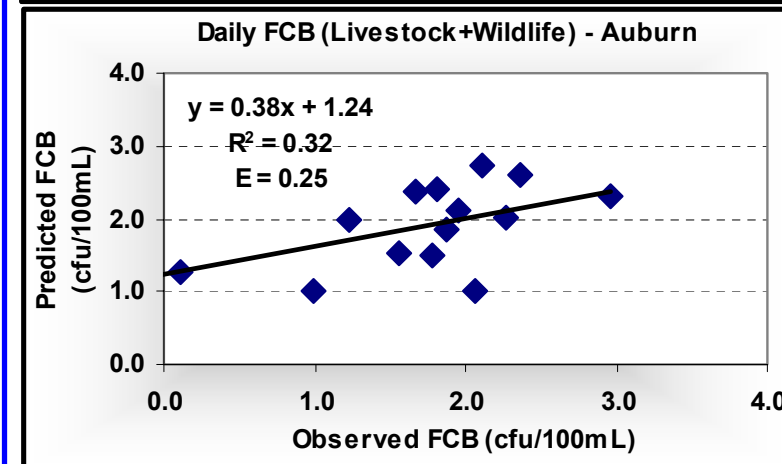
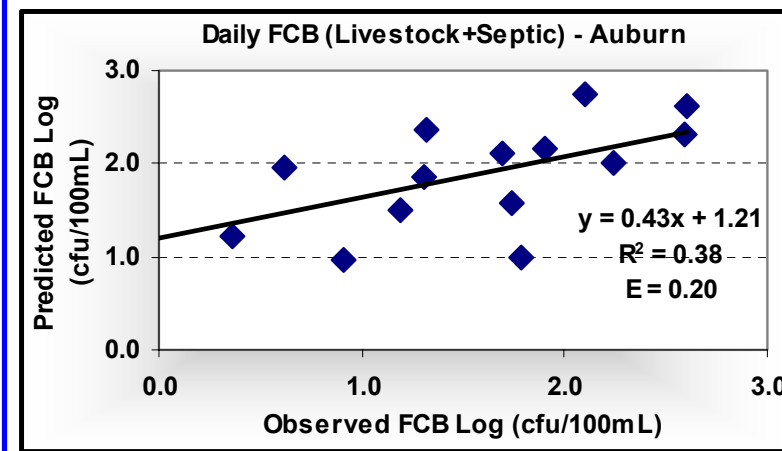
- Compared 15 measured daily total bacteria data (Jan 2004 - April 2006)
- Utilized modified deterministic probability fraction bacteria source tracking data
- Modeled combination of two sources of bacteria each time
- SWAT model predicted combination of two sources of daily fecal coliform bacteria concentration with:
  - $R^2 = 0.41 - 0.54$  and  $E = 0.27 - 0.44$  for **Deer Creek** watershed



# Results and Discussion

## Daily Fecal Coliform Bacteria/Auburn (Source specific/combo of two sources)

- Compared 15 measured daily total bacteria data (Jan 2004 - April 2006)
- Utilized modified deterministic probability fraction bacteria source tracking data
- Modeled combination of two sources of bacteria each time
- SWAT model predicted combination of two sources of daily fecal coliform bacteria concentration with:
  - $R^2 = 0.32 - 0.46$  and  $E = 0.20 - 0.46$  for Auburn watershed



# Results and Discussion

*Overall: Upper Wakarusa watershed*

*Flow/Sediment/Total FCB*

## HWY 75:

**Flow:**  $R^2 = 0.90$ ,  $E = 0.76$

**Sediment:**  $R^2 = 0.65$ ,  $E = 0.54$

**Total FCB:**  $R^2 = 0.37$ ,  $E = 0.27$

## Deer Creek:

**Flow:**  $R^2 = 0.57$ ,  $E = 0.58$

**Sediment:**  $R^2 = 0.60$ ,  $E = 0.68$

**Total FCB:**  $R^2 = 0.52$ ,  $E = 0.29$

## Auburn:

**Flow:**  $R^2 = 0.75$ ,  $E = 0.76$

**Sediment:**  $R^2 = 0.50$ ,  $E = 0.55$

**Total FCB:**  $R^2 = 0.40$ ,  $E = 0.38$

## Lewelling Rd:

**Flow:**  $R^2 = 0.73$ ,  $E = 0.67$

**Sediment:**  $R^2 = 0.75$ ,  $E = 0.64$

**Total FCB:**  $R^2 = 0.37$ ,  $E = 0.26$

## Richland:

**Flow:**  $R^2 = 0.81$ ,  $E = 0.79$

**Sediment:**  $R^2 = 0.75$ ,  $E = 0.71$

**Total FCB:**  $R^2 = 0.41$ ,  $E = 0.24$

# Summary and Conclusions

- **Methods quantifying bacterial source loads:**
  - Used readily available data for livestock, septic systems, and wildlife to characterize fecal bacteria sources in rural watershed
  - Similar approach might work in other watersheds
- **Model results promising:**
  - SWAT microbial submodel provided good calibration ( $E > 0.74$ ) and validation ( $E > 0.48$ ) results with 3 years of data
  - Source-specific bacteria modeling showed good modeling efficiency ( $E$  up to 0.58) when model combination of two sources of bacteria each simulation

# Future Study

- Refine source-specific modeling methods:
  - Refine source-specific model parameterization
  - Calibrate and verify model in the whole Upper Wakarusa watershed using bacteria source-tracking data
- Use SWAT model results to:
  - Target critical sources and source areas
  - Evaluate management practice effectiveness
  - Assess strategies to meet TMDL
- Test other bacteria models:
  - LSPC, WARMF

# ***Acknowledgements***

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**Mr. Matt Peek**, Furbearer Biologist, KDWP

**Dr. Lloyd Fox**, Big Game Coordinator, KDWP

**Mr. Jim Pitman**, Small Game Coordinator, KDWP

**Mr. Marvin Kraft**, Waterfowl Research Biologist, KDWP

**Thanks !**



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