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# Modeling bacterial load scenarios in a Texas coastal watershed to support decision-making for improving water quality

Stephanie M. Glenn<sup>1\*</sup>, Ryan M. Bare<sup>2</sup>, Bradley S. Neish<sup>3</sup>

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**Abstract:** The planning for improved health of a stream can be optimized by assessing the watershed system as a whole; state and federal agencies have embraced this watershed approach for managing water quality (USEPA 2008). Using the watershed approach, bacteria loads in the Double Bayou watershed were modeled to identify critical loading areas and develop appropriate voluntary management measures as part of a watershed protection plan. The Spatially Explicit Load Enrichment Calculation Tool (SELECT) model was developed by the Department of Biological and Agricultural Engineering and the Spatial Science Laboratory at Texas A&M University to estimate potential pollutant loadings from fecal indicator bacteria. For this study, SELECT modeling was performed to estimate bacterial loadings from the distribution of livestock, wildlife, a wastewater treatment facility, and on-site sewage facilities. Rankings of each contributing source were assessed for the entire watershed. The objective of this study was to analyze the success of using SELECT to evaluate bacteria loads in a rural coastal watershed; results showed SELECT was successful in the Double Bayou watershed in ranking categories of bacteria sources and revealing spatial load aggregations. This analysis guides discussion on the prioritization of management measures to improve water quality in the Double Bayou watershed.

**Keywords:** bacteria, bacterial load modeling, watersheds, water quality

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## Terms used in paper

Short name or acronym	Descriptive name
AU	Animal unit
BST	Bacterial source tracking
C-CAP	Coastal Change Analysis Program
CFU	Colony forming units
GPD	Gallons per day
MGD	Million gallons per day
OSSFs	On-site sewage facilities
RMU	Resource management unit
SELECT	Spatially Explicit Load Enrichment Calculation Tool
TCEQ	Texas Commission on Environmental Quality
USDA	U.S. Department of Agriculture
USEPA	U.S. Environmental Protection Agency
WPP	Watershed protection plan
WWTF	Wastewater treatment facility

## INTRODUCTION

The planning for improved water quality can be optimized by assessing the watershed system as a whole (Flotemersch et al. 2015). State and federal water resource management and environmental protection agencies have embraced the watershed approach for managing water quality (USEPA 2008). In Texas, the Texas Commission on Environmental Quality (TCEQ) manages programs to prevent and abate urban nonpoint source pollution and the Texas State Soil and Water Conservation Board manages programs to prevent and abate agriculture/silvicultural nonpoint source pollution. The TCEQ is charged with managing the quality of Texas' water bodies and water resources, including establishing the state's surface water quality standards and setting the surface water quality criteria.

Management plans in the form of regulatory total maximum daily loads or nonregulatory watershed protection plans (WPPs) are necessary tools to develop tailored best management practices for specific watersheds. Due to their nonregulatory holistic approach, WPPs are increasingly favored across Texas. The watershed approach is successful because watershed stakeholders bring together their collective knowledge and experience to preserve, protect, and improve water quality. The result is a collection of watershed-specific plans that can serve as a framework for regional water quality improvement and guidance for watershed management.

Pathogens are the most common source of water body impairments in the state. In 2014, Texas had 508 water body segments listed as impaired; of those, 346 (68%) were listed as impaired for contact recreation due to elevated levels of bacteria (TCEQ 2014). To develop a WPP that contains specifications for the technical and financial framework designed to reduce water quality impairments due to pathogens, bacteria source contributions must be characterized and understood at the watershed scale.

Due to the complex and resource-intensive approach of monitoring and identifying individual pathogens in the environment, fecal indicator bacteria are utilized to estimate the level of potential health risk from fecal contamination (Field and Samadpour 2007). According to the U.S. Environmental Protection Agency (USEPA), Enterococci are the preferred indicator bacterium to determine the level of health risk of fecal contamination in estuarine and tidal waters used for recreation, while *E. coli* are most commonly utilized to assess nontidal waterways (USEPA 2012). Indicator bacteria are an effective alternative monitoring strategy because they are enteric in nature, residing in the gastrointestinal tract of warm-blooded animals, and therefore are capable of alerting resource managers that associated harmful pathogens are present in the environment (Katouli 2010; Pandey et al. 2014).

Although monitoring water quality for bacteria can quantify presence, it does not indicate the source or location of potential contributors.

Fecal waste can be introduced through a variety of pathways: directly to surface waters from wastewater treatment facility effluents, sanitary sewer overflows, and boater waste discharge events; indirectly from stormwater runoff containing pet, wildlife, and agricultural waste; and from leaking on-site septic systems (Perkins et al. 2014). Bacterial source tracking (BST) can help identify possible source categories, but the high cost of the practice compared to the limited information the results provide make it impractical to implement for many WPPs. Therefore, models that can characterize and rank source-specific bacterial loads such as the Spatially Explicit Load Enrichment Calculation Tool (SELECT) are utilized to assist with the development of watershed-specific best management practices (Teague et al. 2009).

This discussion focuses on SELECT methodology used to rank and spatially aggregate source-specific bacterial loads for the Double Bayou WPP. SELECT was developed by the Department of Biological and Agricultural Engineering and the Spatial Science Laboratory at Texas A&M University (Riebschleager et al. 2012). SELECT has been successfully used to estimate bacteria loads in other Texas watersheds, including the inland rural watersheds of Buck Creek, Little Brazos River, and Lampasas River; the readily developing mixed land-use Plum Creek watershed, the coastal mixed land-use transitional Cedar Bayou watershed, and the coastal rural Mission River and Aransas River watersheds (Borel et al. 2012a; Borel et al. 2015). The Double Bayou watershed SELECT analysis provides a case study showing that SELECT can successfully be applied in rural coastal watersheds with limited historical water quality and flow data.

## STUDY WATERSHED

The Double Bayou watershed is located in the upper Texas Gulf Coast on the eastern shore of Trinity Bay predominantly in Chambers County, Texas. The primary waterways in the watershed are the East Fork Double Bayou and the West Fork Double Bayou. The watershed drains 62,764 acres of predominantly rural and agricultural land directly into the Trinity Bay system and ultimately into Galveston Bay. The most abundant land-use/land-cover class is pasture/hay (34,853 acres) followed by cultivated crops (12,993 acres). There are several residential centers located in the watershed. The city of Anahuac, Texas is located on the Trinity River and the northeast bank of Trinity Bay and has a total area of 1,277 acres. This rural community is the largest area of developed land in the watershed. Half of the unincorporated community of Oak Island is located in the Double Bayou watershed. Double Bayou, a third smaller

community in the watershed is located in proximity to the East Fork.

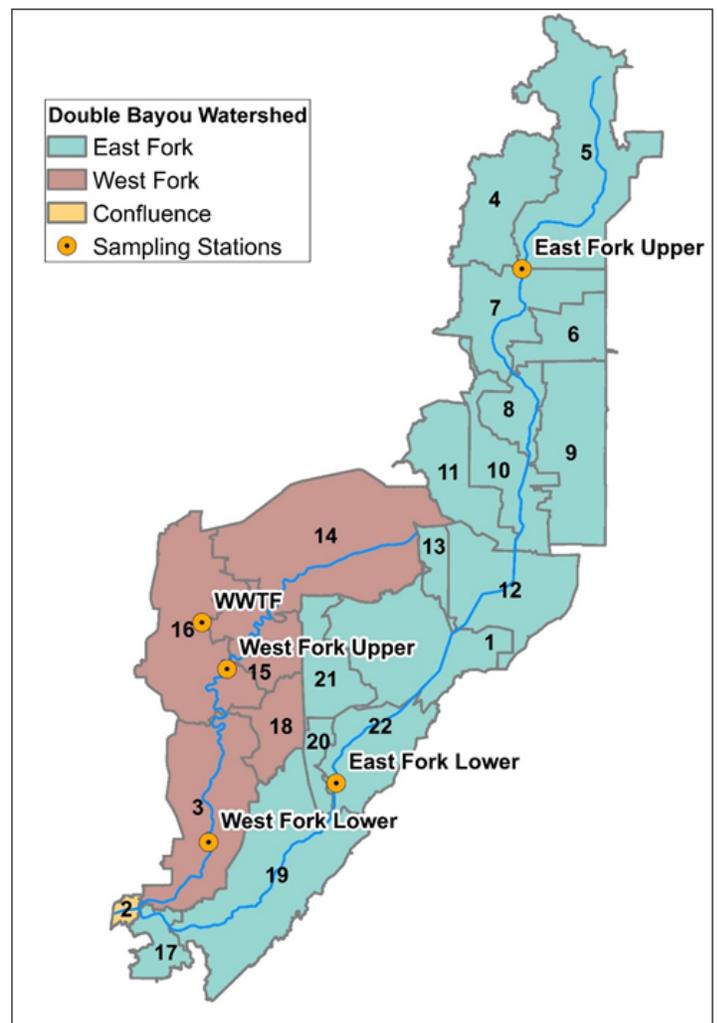
The East Fork of Double Bayou originates in Liberty County (Figure 1) and follows a relatively straight channel southwest toward Trinity Bay for a total of 43 kilometers. The West Fork of Double Bayou is approximately 22 kilometers and is characterized by a meandering channel. The lower portions of the bayous are tidally influenced. The 2 bayous form a 400-meter confluence before joining Trinity Bay at Oak Island, Texas. Trinity Bay is 78,720 acres and is designated as unclassified oyster waters and as a classified estuary.

Both East Fork Double Bayou and West Fork Double Bayou are listed as impaired for contact recreation on the 2014 Texas Integrated Report for elevated levels of bacteria (TCEQ 2014). This study is the first bacteria load monitoring or modeling performed for the watershed, outside of the TCEQ's routine surface water quality monitoring. To effectively plan for mitigation, the bacteria source contribution and fate and transport processes must be characterized and understood at the watershed scale. Possible contributing sources of bacteria in the Double Bayou watershed include leaking septic systems, sanitary sewer overflows, cattle, horses, deer, feral hogs, and goats. The bacteria impairments of Double Bayou could economically dampen one of the last remaining rural watersheds in the Houston-Galveston region. In addition, the bayou system drains into Trinity Bay, just up-current from the largest oyster harvesting operation in Texas.

## METHODOLOGY

SELECT modeling for the Double Bayou watershed was performed to estimate bacterial loadings from point and nonpoint sources to identify critical loading areas within the watershed. SELECT Version 1 was used for the Double Bayou watershed modeling. SELECT data inputs included land-use, location and numbers of bacterial sources, bacterial production rates and population estimates. All model inputs and results were discussed with stakeholders and outputs were assessed for management measure implementations.

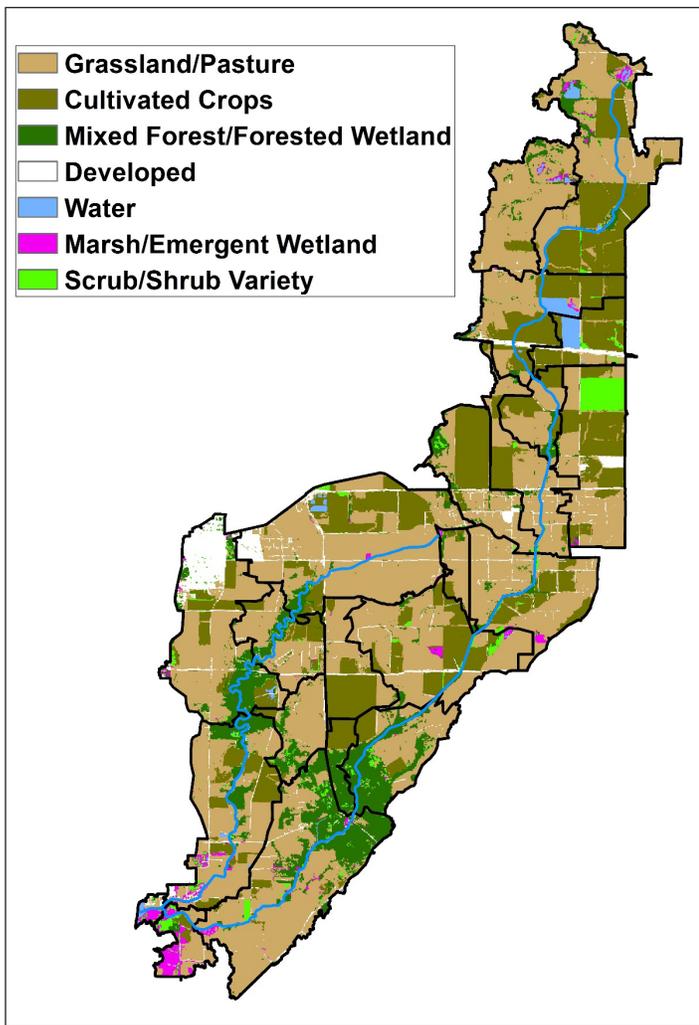
Using the ArcHydro model (a component of ArcGIS), the Double Bayou watershed was delineated into 22 subwatersheds (Figure 1). The ArcHydro model incorporates elevation and hydrological characteristics into a watershed delineation process. The results of the SELECT model are individual 30-meter grid cell raster files for each identified bacterial source. The raster files were added together spatially to create a total load raster for the entire watershed. Units for the SELECT analysis are discussed in *E. coli* concentrations, colony forming units (cfu); note, however, water quality analysis results will use appropriate *E. coli* (nontidal) or Enterococci (tidal) cfu, depending on the location in watershed.



**Figure 1.** Double Bayou watershed in Texas.

Land use is a critical SELECT input and analysis was completed by using 2010 NOAA Coastal Change Analysis Program (C-CAP) land-cover data based upon 30-meter Landsat imagery. To increase model accuracy, stakeholder input was used as local knowledge to better define land-cover inputs because they were aware of recent land-use changes (i.e. changing of farm to ranch land or new developments). Land-cover categories used as inputs for SELECT reflect an aggregation of the 22 types of land-use classes available in the 2010 C-CAP data. These 22 land-cover classes were distilled into 7: Grassland/Pasture, Cultivated Crops, Mixed Forest/Forested Wetland, Developed, Water, Marsh/Emergent Wetland, and Scrub/Shrub Variety (Figure 2). Furthermore, stakeholders recognized that certain Grassland/Pasture areas were strictly hay (unfenced, cannot hold livestock) and some Scrub/Shrub land was left without cattle. These land classes were removed from SELECT modeled land-cover inputs.

The land cover is considered a “snapshot” of land use in



**Figure 2.** Land cover in the Double Bayou watershed.

the watershed. Agriculture practices are dynamic and may vary depending on the growing season, weather, and livestock grazing requirements. These changing practices may shift the distribution of the associated nonpoint source pollutants to different locations within the watershed from year to year. For example, rice crops may be rotated to different fields and then alternated with other agricultural crops, cattle, or left fallow. The alternating fields typically remain in the same subwatershed. However, the overall number of cattle and acres of crop land in the watershed do not change significantly even when they are rotated between subwatersheds, so this would not greatly impact the overall load contribution.

SELECT was used to generate high, mid, and low bacteria loading scenarios according to the range of loading parameters decided upon by the stakeholders. This sensitivity analysis accommodated a range of scenarios and provided insight on the approximate range of potential load from a given source. High and low scenarios were developed for sources that had

variable population inputs; on-site sewage facilities (OSSFs) (malfunction rate of system), cattle (stocking density), and feral hogs (population density). High, medium and low scenarios were generated for the wastewater treatment facility (WWTF). Single scenarios were generated for horse, goat, and deer sources because their population assumptions were based upon fixed values. Stakeholders decided to use high loading scenarios for all possible sources to determine priority and placement of management measures.

Modifications to certain SELECT data inputs were implemented with stakeholder feedback to achieve a more accurate model taking into account data availability and specific characteristics of the watershed (similar types of data input modifications were suggested in Borel et al. 2012b). For example, feral hogs were evaluated as SELECT inputs at 2 different densities since stakeholder input reflected that feral hogs have a high potential to utilize most land classes in the watershed. In addition, the WWTF SELECT input was modified by water quality monitoring results. The effluent quality and flow rate of the WWTF was monitored at the point of release to formulate SELECT input for the WWTF (except for the mid-range scenario, which is based on permitted bacteria and flow rates). Based on these assumptions, SELECT generated an estimated maximum loading for the WWTF under a high rain event scenario.

Water quality monitoring was conducted as part of the Double Bayou Watershed Protection Plan development process under an USEPA-approved Quality Assurance Protection Plan. Routine water quality monitoring dates were scheduled to measure ambient water quality conditions. Targeted water quality monitoring was conducted during rain events to measure water quality conditions during high flow events. Water quality monitoring stations were located on both bayous (Figure 1) (marked as WWTF, West Fork Upper, West Fork Lower, East Fork Upper, and East Fork Lower). Over a 20-month sampling period (October 2013 through June 2015), a total of 194 water quality samples were collected during 39 sampling days (38 at the WWTF station).

## POTENTIAL BACTERIAL SOURCES AND LOAD ESTIMATION IN THE DOUBLE BAYOU WATERSHED

To identify the various sources of bacteria pollution, stakeholders discussed all possible primary point and nonpoint source contributors with known quantifiable bacteria source excretion rates and population inputs for SELECT analysis. The remainder of this section is dedicated to the discussion of source variables and loading rates for each bacterial source.

## Deer

Due to data restraints, the only native wildlife analyzed with SELECT was deer. Although other wildlife, such as migratory birds or raccoons, are likely contributors to bacterial loads in the watershed, their potential bacteria contributions and population dynamics are unknown. A total deer population estimate was based on the Texas Parks and Wildlife Department's deer density for Resource Management Unit 13 (RMU 13), where Double Bayou watershed is located. RMU 13 has an average estimated deer density of 5.15 deer/1,000 acres, with a 95% confidence interval of 2.2-12.3 deer/1,000 acres. Stakeholders agreed that the average estimated deer density provided a reasonable assumption. The mixed forest/forested wetland land class was determined to be the only land class suitable for deer (Figure 2). The population estimate of 5.15 deer/1,000 acres was applied to the 6,321 acres of suitable habitat generating a total watershed deer population of 33 animals.

The average potential cfu per daily *E. coli* load was estimated for each subwatershed as

$$\text{Deer Load} = \# \text{Deer} * 3.5 \times 10^8 \text{ cfu/day} * 0.63,$$

where  $3.5 * \text{cfu/day} * 0.63$  (*E. coli* conversion factor) is the average daily *E. coli* production per deer (USEPA 2001).

## Feral hogs

There are no direct measurements of feral hog density in Texas. However, several studies estimate feral hog densities depending on land use and location. For the Double Bayou watershed project, an estimated maximum feral hog density of 33.3 acres per hog and a minimum density of 50.7 acres per hog was applied (Borel et al. 2012c; Timmons et al. 2012). The SELECT scenario applied 33.3 acres per feral hog to the land-cover categories of Grassland/Pasture, Scrub/Shrub Variety, Mixed Forest/Forested Wetland, and Cultivated Crops, plus a 100-meter buffer zone from any water source, including flooded rice fields. A density of 50.7 acres per hog was applied to the remaining watershed land-cover categories. Based on these rates, the feral hog population was estimated to be 1,519 hogs.

The average potential daily *E. coli* load for each subwatershed was estimated by

$$\text{Feral Hog Load} = \# \text{Hogs} * 1.1 \times 10^{10} \text{ cfu/day} * 0.63,$$

where  $1.1 * 10^{10} \text{ cfu/day} * 0.63$  (*E. coli* conversion factor) is the average daily *E. coli* production per pig (used as a proxy for feral hog) (USEPA 2001).

## Cattle

Most cattle operations within the watershed are cow-calf. There are no confined animal feeding operations. The SELECT land-cover input categories for cattle are grassland/pasture and scrub/shrub. An animal unit (AU) is a standardized unit of measure used for agricultural planning. One AU is equivalent to 1 adult cow and a nursing calf. Using local knowledge of the watershed, stakeholders generated estimated stocking rates of 1 ac/AU, 7-8 ac/AU, 9 ac/AU, and 12-15 ac/AU, and spatially allocated the densities to appropriate sections of the watershed. The total number of cattle was calculated based on these stocking rates. The total estimate of cattle in the watershed was determined to be 4,074 AUs. This stakeholder estimate of cattle population compared favorably with county estimates from the U.S. Department of Agriculture (USDA) Census of Agriculture (USDA 2012).

The average potential daily *E. coli* load for each subwatershed was estimated by

$$\text{Cattle Load} = \# \text{Cattle} * 1 \times 10^{10} \text{ cfu/day} * 0.63,$$

where  $1 * 10^{10} \text{ cfu/day} * 0.63$  (*E. coli* conversion factor) is the SELECT model default average daily *E. coli* production per head of cattle (USEPA 2001).

## Horses

The bacteria nonpoint source contributions from horses were modeled based on an estimated population of 294 horses in the Double Bayou watershed. This estimate came from the 2012 Census of Agriculture, the percent of suitable land in watershed/county and input from the stakeholder workgroup (USDA 2012). The land-cover categories for horses were determined to be the same as cattle (grassland/pasture and scrub/shrub). Stakeholders noted that in Double Bayou, horses are typically used to support cattle ranching operations and are spread out over the watershed (not concentrated for agricultural production).

The average potential daily *E. coli* load for each subwatershed was estimated by

$$\text{Horse Load} = \# \text{Horse} * 4.2 \times 10^8 \text{ cfu/day} * 0.63,$$

where  $4.2 * 10^8 \text{ cfu/day} * 0.63$  (*E. coli* conversion factor) is the average daily *E. coli* production per horse (USEPA 2001).

## Goats

Stakeholders stated that goats are not used for agricultural production but are kept by some landowners for subsistence

use. Based on Texas Agricultural Statistics, 11 goats were identified in the Liberty County portion of the watershed. According to the Texas Agricultural Statistics, there were no goats in Chambers County at the time of this study. However, stakeholders determined that an estimated 200 goats existed in the Chambers County portion of the watershed. A population of 211 goats was determined to be a reasonable watershed estimate. The bacterial loading rate for sheep of  $1.2 \times 10^{10}$  cfu per sheep per day was used as a proxy for goats because no SELECT bacterial loading rate for goats is available (Borel et al. 2012a).

The average potential daily *E. coli* load for each subwatershed was estimated by

$$\text{Goat Load} = \# \text{ Goat} * 1.2 \times 10^{10} \text{ cfu/day} * 0.63,$$

where  $1.2 \times 10^{10}$  cfu/day \* 0.63 (*E. coli* conversion factor) is the average daily *E. coli* production per sheep (known goat SELECT loading rate is not available) (USEPA 2001).

### Wastewater treatment facility

The Anahuac WWTF was identified by the stakeholders as a potential point source of bacteria in the watershed. Because the Anahuac WWTF is a point source, the bacteria contributions are from a fixed location and can be allocated to 1 subwatershed. The maximum potential *E. coli* loading rate of 49,000 cfu/100 mL and the approximate daily maximum flow of 1,000,000 MGD (million gallons per day) were used as SELECT model inputs to generate the high scenario for the facility. The maximum potential *E. coli* loading rate is based on the highest recorded wet weather (rain event) bacteria sample collected at the outfall of the WWTF and the daily maximum flow from the USEPA's Enforcement and Compliance History Online database.

The average potential daily *E. coli* load was estimated by

$$\text{WWTF Maximum Load} = \frac{49,000 \text{ cfu}}{100 \text{ mL}} * \frac{3,785 \text{ mL}}{\text{gallon}} * 1,000,000 \text{ GPD}.$$

### On-site sewage facilities

Locations of 91 of the estimated 465 OSSFs in the watershed were obtained from Houston-Galveston Area Council's OSSF database. Additional OSSF locations were identified by stakeholders who have in-depth local knowledge. The identified systems were then overlaid and filtered to eliminate the possibility of double counting OSSFs. The majority of identified OSSFs were found to be distributed in subwatersheds 19 and 20 to the southeast and subwatersheds 16 and 14 to the northwest. The SELECT model considers the effectiveness of OSSFs based on soil type (different types of soils have differ-

**Table 1.** SELECT results: potential contribution to bacterial load by source.

Source	cfu/day
Cattle	2.7E+13
Feral Hog	1.1E+13
WWTF	1.9E+12
Goat	2.4E+11
Horse	7.8E+10
OSSF	1.2E+10
Deer	7.2E+09
<b>Total</b>	<b>4E+13</b>

ent rates of wastewater absorption), the age of the system, and the estimated failure rate. The clay, clay loam, or sandy clay loam soils of the watershed have a low capacity for absorption, which means effluent from the septic tank cannot be effectively treated by soil microorganisms.

To establish SELECT OSSF inputs, stakeholders discussed and generated system age, based on a neighborhood-by-neighborhood analysis. The age ranges established for OSSFs were: 0-15 years old, 16-30 years old, and greater than 31 years old. The OSSF stakeholder workgroup assigned approximate malfunction rates to systems, based on age and known failure rates. A failure rate of 10% was applied to the 0-15 age group; 30% to the 16-30 age groups; and a 50% failure rate was applied to the 31+ age group. A U.S. Census average of 2.4 people per household was used.

The average potential daily *E. coli* load for each subwatershed was estimated by

$$\text{Septic Load} = \text{OSSFs} * \text{Malfunction Rate} * \frac{10 \times 10^6 \text{ cfu}}{100 \text{ mL}} * \frac{60 \text{ gal}}{\text{person}} * 0.63.$$

## RESULTS AND DISCUSSION

In the Double Bayou watershed, the SELECT analysis indicated that each of the 22 subwatersheds has the potential to contribute total daily bacterial loads ranging from  $5.4 \times 10^{10}$  to  $5.4 \times 10^{12}$  cfu/day (Figure 3). Of the total potential bacteria contributions, cattle was the leading source category followed by feral hogs, the WWTF, goats, horses, OSSFs, and deer. The 2 highest ranked categories of cattle and feral hogs contribute 95% of the total potential daily bacteria load in the Double Bayou watershed (Table 1). The ratio of potential daily contribution to bacterial load for the sources goat, horse, OSSFs,

**Table 2.** Bacteria geometric means for samples collected bi-monthly from October 2013 through June 2015.

Nontidal, <i>E. coli</i> , geometric mean criterion 126 cfu/100 mL		Tidal, Enterococci, geometric mean criterion 35 cfu/100mL		
WWTF	East Fork Upper	East Fork Lower	West Fork Upper	West Fork Lower
5 cfu/100 mL	94 cfu/100 mL	72 cfu/100 mL	123 cfu/100 mL	78 cfu/100 mL

and deer were a smaller magnitude; they are not visible in the subwatershed's ratio of total potential load (Figure 3). SELECT determined subwatersheds 14, 16, 5, 19, and 1, in that order, to be the subwatersheds with the highest potential total daily load contributions although the source ratios within each subwatershed vary. However, cattle and feral hogs are consistently the 2 leading source contribution categories in all subwatersheds except in subwatershed 16 where the WWTF is located (Figure 3).

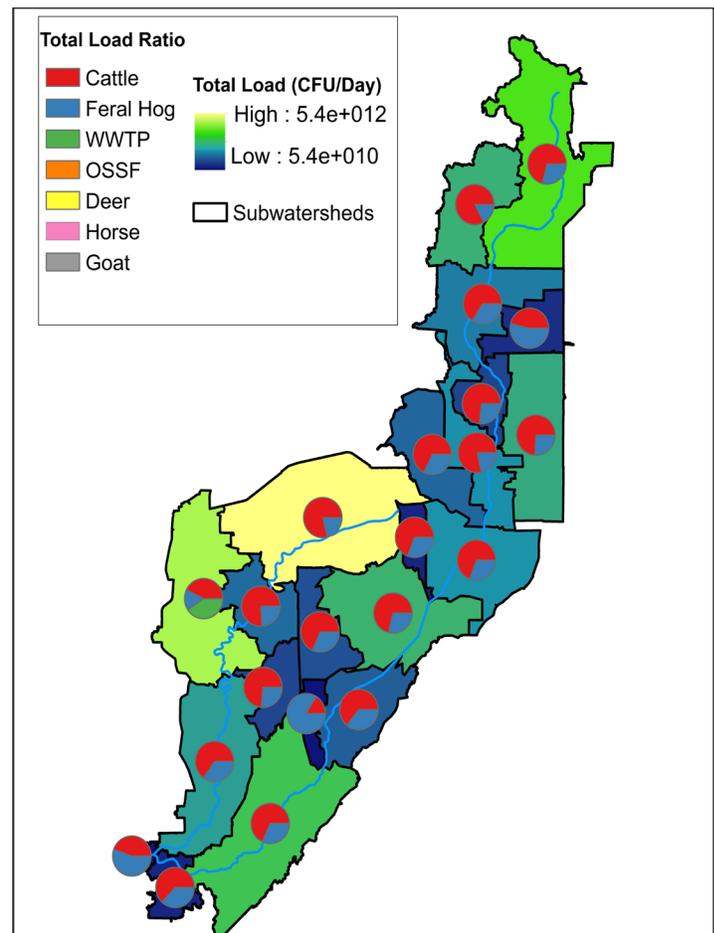
Table 2 contains the bacteria geometric means calculated for water quality samples collected during the project. TCEQ uses criteria based on the geometric mean to indicate impairments for recreational uses of water bodies due to bacteria levels; the geometric mean criterion for *E. coli* is 126 cfu/100 mL while the geometric mean criterion for Enterococci is 35 cfu/100 mL (TCEQ 2014). All 3 Double Bayou tidal monitoring stations exceeded the criteria; of the 3 tidal stations, the West Fork Upper station had the highest geometric mean, while the East Fork Lower station had the lowest. The East Fork Upper station did not exceed the geometric mean criterion and the WWTF station had a geometric mean significantly lower.

Only routine ambient water quality samples are used to calculate bacteria geometric means; targeted samples, collected during rain events, resulted in higher bacteria levels. Rain events can cause greater amounts of bacteria to be transported from the land to the bayou in associated surface runoff. The stations with the highest magnitude of bacteria geometric means spatially correspond to the subwatersheds with the highest potential contribution load as determined by SELECT (Figure 1). Subwatersheds 14 and 16 were determined to have the highest potential contribution load, and West Fork Upper had the highest bacteria geometric mean sampling results. The results of the water quality sampling support the potential contribution load results of SELECT.

As discussed in the Introduction, SELECT has been previously successful in estimating bacterial loads in Texas watersheds. Previous studies that used SELECT analysis in rural and mixed land use Texas watersheds confirms that cattle are the leading contributor to bacteria impairments followed by other livestock (horses, goats, and sheep) (Borel et al. 2012a; Borel et al. 2015). The SELECT results generated for the Double Bayou watershed support the assumption that cattle are the leading contributor to bacteria impairments in rural watersheds. However, the remaining livestock categories (horses,

goats, and sheep), which are found to be high contributors for these previous studies, were shown to have a low degree of contribution in the Double Bayou watershed (sheep were not included for analysis because stakeholders determined that a substantial population was not present). For Double Bayou, feral hogs were ranked as the second leading contributors of bacteria.

Analysis of the feral hog SELECT category across Texas watersheds where SELECT has been applied indicates that feral hogs are typically ranked toward the bottom of bacteria



**Figure 3.** Double Bayou Load Contribution by subwatershed. (Note that all sources were used in the total load calculations, but that the percent contribution of the total load for deer, OSSFs, goat and horse were a minor portion of the overall load and therefore are not visible in the contribution pie charts)

source categories, even in rural watersheds. This distinction between current literature and the use of SELECT in Double Bayou reflects the degree of influence that stakeholders' collective experiences have over the SELECT and watershed protection planning process. In the Double Bayou SELECT analysis, stakeholders familiar with the habits of feral hogs in their watershed determined that feral hogs should be evaluated at a higher density per acre on preferred land-cover classes plus a 100-meter buffer zone from any water source, including flooded rice fields. As a result of the analysis in Double Bayou, feral hog management will be a focus of implementation across the watershed and will likely have lasting effects toward improving instream bacteria concentrations.

The WWTF analysis for Double Bayou used mid- and low-range scenarios to represent permitted and average ambient conditions, respectively. Previous SELECT studies have used only 1 input for the WWTF analysis (Borel et al. 2012a; Borel et al. 2015). By monitoring effluent quality at the point of release, more accurate SELECT scenarios were generated because SELECT assumptions have traditionally been based on the maximum permitted discharge and criterion for the maximum allowable bacteria concentration in the facilities' effluent, which may not represent actual conditions. Stakeholders wanted to plan for the worst case, so the maximum scenario was used for analysis. However, the low scenario, which assumes the WWTF effluent contains a minimal concentration of *E. coli* (3.51 cfu/100 mL) and releases at a flow rate of 300,000 GPD, is likely the best representation of average ambient contributions.

In recent years, BST studies in rural watersheds with similar characteristics to the Double Bayou watershed have concluded average instream bacteria contributions can be attributed to 55% wildlife, 21% domestic livestock, 16% unidentified, and 8% human source categories (averaged BST results from the Buck Creek, Little Brazos River, and Big Cypress Creek watersheds) (Giovanni et al. 2013). These results attribute a larger proportion of instream bacteria to wildlife than earlier studies indicated. The wildlife category from these BST studies includes bacteria contributions from feral hogs. These findings support the Double Bayou SELECT results that determined feral hogs as a major potential bacteria source (Table 1). Had the full contribution of wildlife inputs been available for inclusion to SELECT, the potential wildlife and feral hog load would be much higher. Many of the management measures implemented in the watershed to control bacteria inputs from livestock and overland flow can also reduce bacteria contributions from feral hogs and native wildlife. A BST study specific to the Double Bayou watershed could further validate the SELECT results and guide adaptive governance during the implementation phase.

SELECT could be strengthened by adding the capability to analyze direct or near stream deposition of fecal waste by livestock and wildlife (including *Sus scrofa*). Direct deposition is the most concentrated delivery mechanism of bacteria to instream water quality. For example, the amount of bacteria cattle may contribute to the bayou (Larsen et al. 1988) correlates with the stocking rate of the adjacent land, distance from the bayou, and the amount of time cattle spend near or in the bayou. In Larsen et al. 1988, a manure deposition distance of 0.61 meters and 2.1 meters from a stream showed an 83% and 95% reduction of bacteria compared to fecal waste that is directly deposited into the stream (Larsen et al. 1988). Providing cattle with alternative water sources has been shown (Wagner et al. 2013) to reduce the overall loading rate from  $1.11 \times 10^7$  cfu/day to  $6.34 \times 10^6$  cfu/day (Larsen et al. 1988). The amount of time cattle spent instream was also reduced by 43% with the provision of alternative water sources.

SELECT model analysis could be strengthened with additional analysis on environmental fate and transport mechanisms. Inputs of death and decay rates, differences of absorptive capacity between native and invasive riparian vegetation, and the inclusion of varying meteorological conditions such as precipitation and UV radiation would allow the SELECT model to better predict instream bacteria source contributions. However, the current edition of the SELECT model weighs the input-benefit analysis with the goal of the model outcome and has the added benefit of requiring limited data. The inclusion of the above variables would lead to a data and resource intensive modeling process that could provide insight on important fate and transport mechanisms but would also be more costly and time-consuming, limiting the use in the development of stakeholder driven WPPs.

## CONCLUSIONS

The primary objective of SELECT analysis is to rank categories of bacteria sources and reveal spatial aggregations to provide stakeholders information to improve their local waterways; in this capacity, SELECT was successful in the Double Bayou watershed. A total estimated load scenario was created for analysis by summing SELECT results for potential bacterial loads from 22 Double Bayou subwatersheds. Since data were not available for all potential source contributors, such as a variety of specific wildlife sources, the SELECT model results did not reflect the entire suite of the Double Bayou watershed's potential bacterial load contributors, but it provided comprehensive bacteria spatial patterns from the available data.

The SELECT model results determined that feral hogs and cattle were the largest sources of potential contributors. Results indicated that the majority of cattle source loads can

be attributed to subwatersheds that are predominately grassland/pasture and that feral hog densities were determined to be highest in riparian forested wetlands. The analysis can help guide discussion on the prioritization of management measures that result in the greatest reduction of bacteria. To have the greatest impact, management measures can be prioritized to subwatersheds with the highest potential daily bacterial loads as well as focused specifically on the range of sources identified as the largest potential contributors.

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